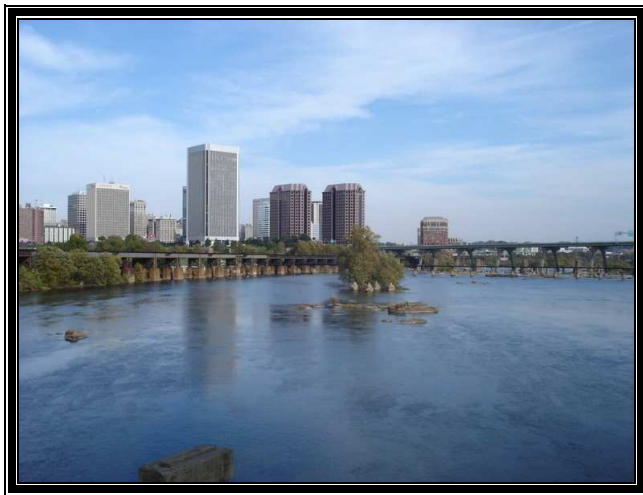
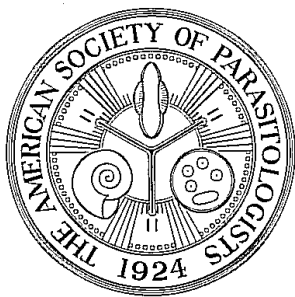


# **The 87<sup>th</sup> Annual Meeting of the American Society of Parasitologists**

Omni Richmond Hotel  
Richmond, Virginia, July 13-16, 2012



**Richmond, VA on the James River**



**Lewis Ginter Botanical Garden**

## **Program & Abstracts**

## *Thanks to Everyone Who Helped Make this Meeting Possible ...*

The American Society of Parasitologists gratefully acknowledges the following for their support, sponsorship, and hard work in putting together this year's annual meeting.

### ASP Local Arrangements Committee

**Dr. Ghislaine Mayer, Virginia Commonwealth University**

### Scientific Program Officers

**Dr. Herman Eure, Wake Forest University**

**Dr. Kelli Sapp, High Point University**

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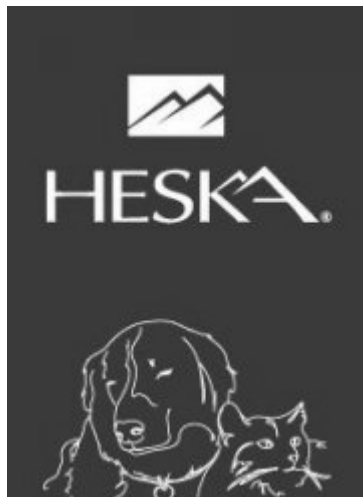
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**Susan (Upton) and David Lovro of Sante Fe, NM (sponsors of the Steve Upton Party for ASP Students; Susan is the sister of the late Dr. Steve J. Upton)**





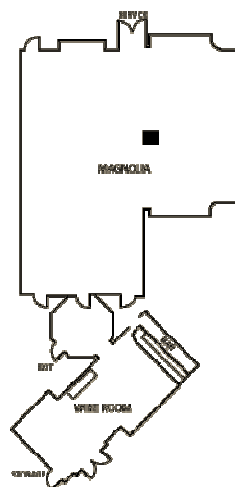
We would like to welcome you to the 87<sup>th</sup> annual meeting of the American Society of Parasitologists (ASP).

**Herman Eure and Kelli Sapp**, Scientific Program Officers

## SECOND FLOOR



## LOBBY LEVEL



<b><u>Day/Times</u></b>	<b><u>Activity/Function</u></b>	<b><u>Room/Space</u></b>
<b><u>July 13 (Friday)</u></b>		
8:00 a.m.-Noon	ASP Council	Magnolia Room
1:00-5:00 p.m.	Host Parasite Interactions I	James River Salon A
1:00-4:45 p.m.	Life Cycles and Epidemiology	James River Salon B
4:30-6:30 p.m.	Student Research Workshop	Potomac Salon E&F
2:45-3:15 p.m.	Coffee Break	James River Foyer
7:00-10:00 p.m.	Welcome Reception	James River Salon C&D
<b><u>July 14 (Saturday)</u></b>		
7:00-8:30 a.m.	Editorial Board Breakfast	Roanoke Room
8:30-10:30 a.m.	ASP President's Symposium	James River Salon C
10:30-11:00 a.m.	Coffee Break	James River Foyer
11:00-Noon	Bueding and von Brand Lecture	James River Salon C
1:00-2:45 p.m.	Taxonomy, Systematics, Phylogeny I	Potomac Salon E&F
1:00-3:00 p.m.	Biochemistry, Cell Biology, Chemotherapy, Vector Biology	James River Salon D
1:00-3:00 p.m.	Ecology I	Potomac Salon G
3:00-3:30 p.m.	Coffee Break	James River Foyer
3:30-5:30 p.m.	ASP Students' Symposium	Potomac Salon E&F
5:30-6:30 p.m.	ASP Student Social	Potomac Salon G
3:00-6:00 p.m.	Auction Set Up	James River Salon A&B
6:00-7:00 p.m.	Auction Preview	James River Salon A&B
7:00-9:00 p.m.	22 <sup>nd</sup> Annual ASP Student Auction	James River Salon A&B
<b><u>July 15 (Sunday)</u></b>		
8:30-10:15 a.m.	Associate Editors Symposium	James River Salon A
9:00 -11:45 a.m.	Genetics and Molecular Biology	Potomac Salon E&F
9:00-11:45 a.m.	44 <sup>th</sup> Coccidiosis Conference	Potomac Salon G
10:15-10:30 a.m.	Coffee Break	James River Foyer
1:00-2:00 p.m.	ASP President's Address	James River Salon C
2:15-5:30 p.m.	Ecology II	Potomac Salon G
2:15-5:30 p.m.	Taxonomy, Systematics, Phylogeny II	Potomac Salon E&F
2:15-5:00 p.m.	Immunology	James River Salon A
3:45-4:00 p.m.	Coffee Break	James River Foyer
4:00-5:30 p.m.	Authors may set up posters	James River Salon C
7:00-10:00 p.m.	Lewis Ginter Botanical Garden	
<b><u>July 16 (Monday)</u></b>		
8:00-11:15 a.m.	Ecology III	James River Salon A
8:00-11:45 a.m.	Host Parasite Interactions II	James River Salon B
8:45-11:00 a.m.	Taxonomy, Systematics, Phylogeny III	Potomac Salon E&F
8:00-11:45 a.m.	Nematomorpha Symposium	James River Salon D
9:45-10:00 a.m.	Coffee Break	James River Foyer
8:30-10:30 a.m.	Authors complete poster set up	James River Salon C
12:00-1:30 p.m.	Poster Session, coffee, snacks	James River Salon C
1:45-2:45 p.m.	H.B. Ward Lecture	James River Salon D
2:45-4:30 p.m.	ASP Awards and Business Meeting	James River Salon D

## Friday Morning, 2012-07-13

**08:00 am – Noon    *ASP Council Meeting, Magnolia Room***

**Presiding:**      A.M. Kuris, University of California Santa Barbara

## Friday Afternoon, 2012-07-13

**1:00-5:00 pm    *Host Parasite Interactions I***

***Location: James River Salon A***

**Presiding:**      K. Jacobson, NOAA Fisheries  
                     F. Reyda, State University of New York

### **Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

- 1:00 (1)†**      **M.B. Sherman**, M.C. Curran. WHAT IS THE EFFECT OF THE PARASITIC ISOPOD *PROBOPYRUS PANDALICOLA* ON THE STARVATION RATE OF DAGGERBLADE GRASS SHRIMP *PALAEMONETES PUGIO* AT TWO DIFFERENT TEMPERATURES?
- 1:15 (2)†**      **L.E. Reid**, M.L. Thies, T.J. Cook. HELMINTHS OF *MICAELAMYS NAMAQUENSIS* AND *AETHOMYS CHRYSOPHILUS* (RODENTIA: MURIDAE) FROM NORTHWESTERN BOTSWANA.
- 1:30 (3)†**      **K. Gustafson**. LANDSCAPE ECOLOGY OF AMPHIBIAN HELMINTHS IN THE SHEYENNE NATIONAL GRASSLANDS, ND.
- 1:45 (4)†**      **M.M. Lloyd**, R. Poulin. FITNESS BENEFITS OF A DIVISION OF LABOR IN PARASITIC TREMATODE COLONIES: DEFENSE AGAINST COMPETITORS?
- 2:00 (5)†**      **B.P. Rolfsen**. COMPATIBILITY OF *FASCIOLOIDES MAGNA* MIRACIDIA AND FOUR SNAIL SPECIES: MIRACIDIAL CHOICE AND SNAIL RESPONSE.
- 2:15 (6)†**      **C.M. Wiles**. PARASITE COMMUNITY STRUCTURE IN 5 SPECIES OF DAMSEFLIES (ODONATA: ZYGOPTERA) FROM TEAL RIDGE, STILLWATER OKLAHOMA.
- 2:30 (7)†**      **M.A. Hudgell**, M.A. Forys, E.S. Loker. REVEALING THE MECHANISTIC DETERMINANTS OF HOST SPECIFICITY: USING THE PARASITE *SCHISTOSOMA MANSONI* AND THE SNAIL *BIOMPHALARIA OBSTRUCTA* AS A MODEL SYSTEM.
- 2:45-3:15 pm**                      **COFFEE BREAK**
- 3:15 (8)†**      **W.D. Helenbrook**. A TALE OF ANTHROPOGENIC DISTURBANCE: HOW FOREST DEGRADATION AND HUMAN PROXIMITY TO NONHUMAN PRIMATE POPULATIONS INFLUENCE PARASITISM.

- 3:30 (9)†** **J. Omololu-Aso**, A.O. Oluduro, O.O. Omololu-Aso, S.O. Ajisebutu, K. Adejuwon, W.R. Duruji. ASSESSMENT OF *PLASMODIUM FALCIPARUM* CASE-BASED SURVEILLANCE AT THE TWO MAJOR UNIVERSITY TEACHINGS HOSPITAL SOUTH WESTERN NIGERIA: A COMPARATIVE STUDY.
- 3:45 (10)†** **K.L. Weinersmith**, R.L. Earley, A.F. Hanninen, R.F. Hechinger, A.M. Kuris, K.D. Lafferty, A. Sih. TWO MANIPULATIVE TREMATODE PARASITES MODIFY THE PHYSIOLOGY AND BEHAVIOR OF CALIFORNIA KILLIFISH (*FUNDULUS PARVIPINNIS*).
- 4:00 (11)†** **A.B. Mora**. ANTI-PARASITE DEFENSE IN THE CALIFORNIA FIDDLER CRAB, *UCA CRENULATA*: BEHAVIOR AND SEX DIFFERENCES.
- 4:15 (12)†** **K.L. Sheehan**. PARASITES OF RESIDENT AND MIGRATORY DOUBLE-CRESTED CORMORANTS (*PHALACROCORAX AURITUS*).
- 4:30 (13)†** **S.K. Buddenborg**, L.E. Agola, I.N. Mwangi, G.M. Mkoji, E.S. Loker. A NEW APPROACH FOR MONITORING AND MEASURING SCHISTOSOMIASIS TRANSMISSION IN AFRICA: EXPOSURE OF SENTINEL MICE COUPLED WITH GENOTYPING OF RECOVERED ADULT WORMS.
- 4:45 (14)†** **J.P. Bernot**, J.N. Caira, M. Pickering. DAVID AND GOLIATH: EXAMINATION OF ADDITIONAL COMPLEXITY IN THE GENUS *CALLIOBOTHRIUM* (CESTODA: TETRAPHYLLIDEA) IN SMOOTHFOUND SHARKS OF THE GENUS *MUSTELUS* (CARACHARHINIFORMES: TRIAKIDAE).

## **1:00-4:45 pm Life Cycles and Epidemiology**

### **Location: James River Salon B**

**Presiding:** B. Dixon, Bureau of Microbial Hazards, Food Directorate, HPFB, Health Canada  
R. Fayer, USDA, ARS, Beltsville Agricultural Research Center

#### **Time (Abstract No.)**

† denotes student presentation in the Best Student Presentation Competition

- 1:00 (15)** **R. Fayer**, M. Santin-Duran, D. Macarisin. COMPARISON OF PCR AND IFA FOR DETECTION OF BLASTOCYSTIS IN FOOD ANIMALS.
- 1:15 (16) †** **H.A. Stigge**, M.G. Bolek. THE INFLUENCE OF ANURAN HOST SPECIES ON SITE FIDELITY OF NORTH AMERICAN SPECIES OF *HALIPEGUS* (DIGenea: HEMIURIDAE).
- 1:30 (17)†** **S. Greiman**, V. Tkach, J.A. Vaughan. NATURAL AND EXPERIMENTAL TRANSMISSION OF *NEORICKETTSIA RISTICII* IN DIGENEANS *PLAGIORCHIS ELEGANS*.
- 1:45 (18)†** **M.J. Andres**, R.M. Overstreet. JUVENILE *ANISAKIS PHYSETERIS* FROM MESOPELAGIC LANTERNFISHES AND SHORTFIN SQUID IN THE GULF OF MEXICO.
- 2:00 (19)** **D.L. Medica**, P.E. Smouse, M.V. Sukhdeo. STAGE-SPECIFIC DEMOGRAPHIC MODELS OF *HAEMONCHUS CONTORTUS* NEMATODE TRANSMISSION INCORPORATING SEASONAL CYCLING AND DENSITY DEPENDENCE.

**2:15 (20)**      **T.J. Fayton**, R. Heard, R.M. Overstreet. LIFE HISTORY OF AN UNDESCRIBED SPECIES OF *PLAGIOPORUS* (DIGenea: OPECOELIDAE) FROM A KARST SPRING IN FLORIDA.

**2:30 (21)**      **T. Sparkes**. DISPERSAL AND TRANSMISSION IN THE ACANTHOCEPHALAN *ACANTHOCEPHALUS DIRUS*: LAB AND FIELD DATA.

**2:45-3:15 pm**                      **COFFEE BREAK**

**3:15 (22)<sup>†</sup>**      **A. Cooper**, E. Chomyshyn, C. Carrillo, L. Parrington, K. Mattison, B. Dixon. FLOW CYTOMETRY FOR THE DETECTION AND VIABILITY ASSESSMENT OF *CRYPTOSPORIDIUM* SPP. AND *GIARDIA DUODENALIS* IN FRESH PRODUCE AND ENVIRONMENTAL SAMPLES.

**3:30 (23)**      **M.G. Bolek**, S. Vhora, H. Stigge. TO STICK OR NOT TO STICK? LIFE CYCLE STRATEGIES PARAMPHISTOME METACERCARIAE DICTATE AMPHIBIAN HOST SPECIFICITY.

**3:45 (24)**      **D.K. Kvasager**, J.A. Vaughan. HAEMOSPORIDAN PARASITISM IN GRASSLAND SONGBIRDS OF NORTHWESTERN MINNESOTA.

**4:00 (25)**      **M.A. Muhammad**, M. Ayaz, M.J. Khan, S. Akhter, M. Naeem, A. Abbas, W. Zia, M. Asad. EVALUATION OF SINGLE SLIDE FECAL SAMPLES OF ZOO ANIMALS THROUGH MICRO FLOTATION TECHNIQUE.

**4:15 (26)**      **T.R. Olariu**, V. Bold, D. Vermesan, D. Teodorescu-Branzeu, C. Petrescu, G. Darabus, V. Dumitrascu. GIARDIASIS IN WESTERN ROMANIA: A 14-YEAR RETROSPECTIVE STUDY.

**4:30 (27)**      **T.R. Olariu**, G. Darabus, V. Dumitrascu, D. Teodorescu-Branzeu, C. Petrescu. PARASITIC INFECTIONS AMONG ROMANIAN INSTITUTIONALIZED CHILDREN AND THEIR MEDICAL STAFF.

## **4:30-6:30 pm    Student Research Workshop**

**Location: Potomac Salon E & F**

**Presiding:**      K.E. Luth, Wake Forest University

### **Time (Abstract No.)**

**4:30**              INTRODUCTION.

**4:45 (28)**      **L.E. Camp**. POPULATION GENETIC ANALYSIS OF *BAYLISASCARIS*.

**5:00 (29)**      **R.S. Williams**. CHEMISTRY OF THE *CRYPTOSPORIDIUM* OOCYST WALL.

**5:15 (30)**      **A.B. Mora**. EFFECTS OF NITROGEN POLLUTION ON AMPHIBIAN DISEASE DYNAMICS.

**5:30 (31)**      **K.E. Luth**, M.R. Zimmermann, G.W. Esch. CESTODE SAFARI: THE SEARCH FOR CRYPTIC SPECIES OF THE BASS TAPEWORM *PROTEOCEPHALUS AMBLOPLITIS* (PLATYHELMINTHES: CESTODA).

- 5:45 (32)**      **N. Ortega.** THE EFFECTS OF PRESCRIBED BURN ON PARASITE FAUNA.
- 6:00 (33)**      **M.R. Zimmermann,** K.E. Luth, G.W. Esch. POPULATION GENETICS OF *ECHINOSTOMA REVOLUTUM* ALONG THE MAJOR NORTH AMERICAN WATERFOWL FLYWAYS.
- 6:15 (34)**      **A.D. Bartelt,** T.J. Cook, A.J. Smith. HOST UTILIZATION AND DISTRIBUTION OF SEPTATE GREGARINES (APICOMPLEXA: EUGREGARINORIDA: SEPTATORINA) IN EIGHT SHORT-HORNED GRASSHOPPER SPECIES (ORTHOPTERA: ACRIDIDAE) IN THE SOUTHEASTERN UNITED STATES.
- 6:30**              CLOSING REMARKS, DISCUSSION.

## Friday Evening, 2012-07-13

**07:00 - 10:00 PM WELCOME RECEPTION – James River Salon C & D**

## Saturday Morning, 2012-07-14

**7:00 – 8:30 am**              ***Editorial Board Breakfast, Roanoke Room***

**8:30-10:30 am**              ***ASP PRESIDENT’S SYMPOSIUM***

***Location: James River Salon C***

**Presiding:**      J. Janovy. University of Nebraska-Lincoln.

**Theme:**          “Parasite Evolutionary Ecology”

**8:30**              INTRODUCTION.

**8:40 (35)**      **A.M. Kuris.** EVOLUTION TO PARASITISM AND EVOLUTION OF PARASITIC TROPHIC SYNDROMES.

**9:10 (36)**      **D.P. Hughes.** ZOMBIE ANTS: THE PRECISE MANIPULATION OF SOCIAL INSECT BEHAVIOR BY A FUNGAL PARASITE.

**9:40 (37)**      **R.F. Hechinger.** PARASITES AND THE METABOLIC THEORY OF ECOLOGY.

**10:10-10:30**      Questions, Closing Remarks.

**10:30-11:00 am**              **COFFEE BREAK**

**11:00 am-NOON**              ***Bueding and von Brand Lecture***

***Location: James River Salon C***



**Presiding:** D.S. Lindsay, Virginia Tech

**11:00** Introduction of 2012 Bueding and von Brand Lecturer  
A.G. Maule, Queen's University, Belfast

**11:10 (38)** **T.G. Geary.** "Adventures in Antiparasitic Drug Discovery: There and Back Again."



**Timothy Geary**  
*Bueding and von Brand  
Lecture 2012*

## Saturday Afternoon, 2012-07-14

### **1:00-2:45 pm Taxonomy, Systematics, Phylogeny I**

#### **Location: Potomac Salon E & F**

**Presiding:** J. Camp, Purdue University  
H. Eure, Wake Forest University

#### **Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

**1:00 (39)†** **S. Staicer,** J.M. Goessling, W. Lutterschmidt, A. Smith-Herron, T. Cook. PENTASTOMES (PENTASTOMIDA: CEPHALOBAENIDA) ISOLATED FROM THE ENDANGERED RATTLESNAKE, *CROTALUS UNICOLOR* FROM ARIDOK NATIONAL PARK, ARUBA.

**1:15 (40)** **S.M. Steele,** D.T. Clopton, R.E. Clopton. EXPERIMENTAL EXCYSTATION OF *BLABERICOLA MIGRATOR* AMONG ELEVEN SPECIES OF COCKROACHES.

**1:30 (41) †** **S.B. Weinstein,** A. Kuris. PARASITE ORIGINS ON THE TREE OF LIFE.

**1:45 (42)†** **R.C. Jadin,** S.A. Orlofske, J. Koprivnikar, P. Johnson. MOLECULAR PHYLOGENETICS REVEALS MULTIPLE INTERMEDIATE HOSTS ACROSS WIDELY DISTRIBUTED ECHINOSTOMATID PARASITES.

**2:00 (43)** **M.B. Mardock,** T.J. Cook. HOST UTILIZATION AND DISTRIBUTION OF SEPTATE GREGARINES (APICOMPLEXA: EUGREGARINORIDA: SEPTATORINA) PARASITIZING *ISCHNURA* SPP. (ZYGOPTERA: COENAGRIONIDAE) IN THE SEVEN BIOTIC PROVINCES OF TEXAS, U.S.A.

**2:15 (44)†** **E.T. Gendron,** D. Malone, E.S. Loker, S.V. Brant. DO INTERMEDIATE HOSTS PLAY A ROLE IN PARASITE POPULATION STRUCTURE? A PHYLOGEOGRAPHIC STUDY OF *TRICHOBILHARZIA QUERQUEDULAE*.

**2:30 (45)†** **E.L. Kasl,** W.F. Font, C.D. Criscione. UNDERSTANDING EVOLUTIONARY CHANGES IN LIFE CYCLE COMPLEXITY USING THE GENUS *ALLOGLOSSIDIUM* AS A MODEL.

**3:00-3:30 pm COFFEE BREAK**

**1:00-3:00 pm Biochemistry, Cell Biology, Chemotherapy, Vector Biology**

**Location: James River Salon D**

**Presiding:** J. Hillyer, Vanderbilt University  
D. Medica, The Pennsylvania State University

**Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

- 1:00 (46)** H. Eltaweel, **M. Tolba**, H. Sadaka, L. El-Zawawy, M. Osman. ZINC PVA VERSUS POTASSIUM DICHROMATE FOR PRESERVATION OF MICROSPORIDIAN SPORES.
- 1:15 (47)** **A.E. Garcia-Vedrenne**, G. Huelgas-Morales, A.M. Kuris, R.F. Hechinger. LIVING OUTSIDE THE SNAIL: IN VITRO MAINTENANCE OF TREMATODE LARVAE FROM THE MARINE SNAIL *CERITHIDEA CALIFORNICA*.
- 1:30 (48)** **M. García-Varela**, G.P. Ponce de León. PRESENCE OF MITOCHONDRIAL PSEUDOGENES AND THE DESCRIPTION OF A NEW SPECIES OF *PSEUDOCORYNOSOMA* (ACANTHOCEPHALA: POLYMORPHIDAE) BASED ON MORPHOLOGICAL AND MOLECULAR DATA.
- 1:45 (49)** **B.J. Johnson**, M.V. Sukhdeo. DROUGHT-INDUCED AMPLIFICATION OF WEST NILE VIRUS TRANSMISSION IN THE NORTHEASTERN UNITED STATES.
- 2:00 (50) †** **U. Chaudhry**, R. Muthusamy, M. Abbas, J. Gilleard. ORIGIN AND SPREAD OF BENZIMIDAZOLE RESISTANCE MUTATIONS IN THE PARASITIC NEMATODES *HAEMONCHUS CONTORTUS* AND *HAEMONCHUS PLACEI*: INSIGHT FROM GENETIC DATA.
- 2:15 (51)** **J.F. Hillyer**. INSIGHTS INTO THE CONTROL OF MOSQUITO HEART CONTRACTIONS.
- 2:30 (52)** **J.A. Vaughan**, J.O. Mehus, J.A. Bell, C.M. Brewer. MICROFILARIAE AND WEST NILE VIRUS IN SONGBIRDS - A TRUE-LIFE EXAMPLE OF MICROFILARIAL ENHANCEMENT OF ARBOVIRAL TRANSMISSION?
- 2:45 (53)** **O.M. Akanbi**, A. Omonkhua, C.M. Cyril-Olutayo. IN VIVO STUDY OF ANTIPLASMODIAL ACTIVITY OF *TERMINALIA AVICENNIOIDES* AND ITS EFFECT ON LIPID PROFILE IN MICE INFECTED WITH *PLASMODIUM BERGHEI*.

**3:00-3:30 pm COFFEE BREAK**

**1:00-3:00 pm Ecology I**

**Location: Potomac Salon G**

**Presiding:** R. Blaylock, University of Southern Mississippi  
W. Rossiter, Rutgers University

**Time (Abstract No.)**

† denotes student presentation in the Best Student Presentation Competition

- 1:00 (54) †**     **R. Bernot.** TREMATODES AND A CONTAMINANT AFFECT NUTRIENT CYCLING AND PRODUCTIVITY IN A FRESHWATER ECOSYSTEM.
- 1:15 (55)**        **N.F. Smith, J.H. Cohen.** PHOTOBHAVIOR OF MARINE CERCARIAE THAT UTILIZE DIFFERENT SECONDARY INTERMEDIATE HOSTS.
- 1:30 (56) †**     **S.A. Orlofske, R.C. Jadin, P.T. Johnson.** PREDATION ON PARASITES: EFFECTS OF PREDATOR TYPE, PARASITE SPECIES, AND ENVIRONMENTAL CONDITIONS.
- 1:45 (57)**        **D.J. Marcogliese, C. Blonar.** PARASITE COMMUNITY STRUCTURE IN SLIMY SCULPIN (*COTTUS COGNATUS*) AND LONGNOSE DACE (*RHINICHTHYS CATARACTAE*) FROM TRIBUTARIES EXPERIENCING DIFFERENT LEVELS OF OIL SANDS DEVELOPMENT IN THE ATHABASCA RIVER WATERSHED (ALBERTA, CANADA).
- 2:00 (58) †**     **S.R. Hopkins, J.M. Wojdak, J.A. Wyderko, L.K. Belden.** A SYMBIOTIC OLIGOCHAETE CAN PROTECT SNAILS FROM TREMATODE INFECTION.
- 2:15 (59) †**     **A.L. Arellano.** WHERE THE GREENER GRASS GROWS: CAN PARASITES SERVE AS ENVIRONMENTAL INDICATORS OF AQUATIC COMMUNITY CHARACTERISTICS IN HIGH AND LOW INTENSITY AGRICULTURE?
- 2:30 (60)**        **K.D. Lafferty, G. Strona.** FISHPEST: AN INNOVATIVE SOFTWARE SUITE FOR FISH PARASITOLOGISTS.
- 2:45 (61)**        **D. Zelmer.** PARASITES OF FLIER, *CENTRARCHUS MACROPTERUS*, FROM PRAIRIE AND CHANNEL HABITATS IN THE OKEFENOKEE SWAMP, GEORGIA.

**3:00-3:30 pm**

**COFFEE BREAK**

**3:30-5:30 pm    ASP Students' Symposium**

**Location: Potomac Salon E & F**

**Presiding:**        K.E. Luth, Wake Forest University  
                     M.R. Zimmermann, Wake Forest University

**Time (Abstract No.)**

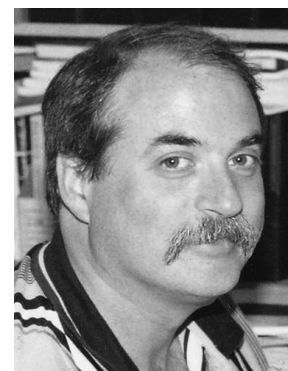
- 3:30 pm**        **K.E. Luth,** Introduction.
- 3:35 (62)**        **M. Bolek.** DISASSEMBLING THE IRON WHEEL OF PARASITE LIFE CYCLES AND GETTING A JOB!
- 3:55 (63)**        **V.J. McKenzie.** FROM TAPEWORMS TO MICROBES: VERSATILITY IS KEY TO A CAREER PATH IN PARASITOLOGY.
- 4:15 (64)**        **C.D. Criscione.** SHIFTING BALANCE THEORY AND THE 'EVOLUTION' OF AN ACADEMIC CAREER.

- 4:35 (65)**      **J. Koprivnikar.** JUMPING FROM THE POND TO THE LAKE: TRANSITIONING FROM GRADUATE STUDENT TO ACADEMIC.
- 4:55 (66)**      **N.J. Negovetich.** THERE AND BACK AGAIN: A PARASITOLOGIST'S TALE.
- 5:15**            **M.R. Zimmermann,** Question Session.

**5:30-6:30 pm    *The Steve Upton Party for ASP Students***  
**(sponsored by Susan and David Lovro)**

***Location: Potomac Salon G***

Dr. Steve J. Upton (6/14/1953-7/29/2010) was an active member of the ASP. His research focused on numerous coccidia and *Cryptosporidium* species. He taught a variety of courses including human parasitology and medical parasitology during his tenure at Kansas State University as a Professor of Biology. Dr. Upton published 225 original research papers, 11 book chapters and 3 books. In 1996, he was the recipient of the H.B. Ward Medal.



***Steve J. Upton***

**Saturday Evening, 2012-07-14**

**6:00-7:00 pm                      Auction Preview**

**7:00-9:00 pm                      22<sup>nd</sup> ANNUAL ASP STUDENT AUCTION\***

***Location: James River Salon A & B***

\* In 2005, Hurricane Dennis disrupted the annual meeting in Mobile. In the Program & Abstracts booklet the 17<sup>th</sup> Annual Student Auction was listed but never occurred. In 2006, ASP did not have its own meeting, members attended ICOPA in Glasgow. At the Merida meeting in 2007 the Annual Student Auction was listed as the 18<sup>th</sup>, when in fact it was the 17<sup>th</sup>. Thus, Auctions numbered 18-22 should have been 17-21. The Program and Abstracts Booklet for the 2012 Richmond meeting reflects this correction.

**Sunday Morning, 2012-07-15**

**8:30-10:15            *Associate Editors Symposium***

***Location: James River Salon A***

**Presiding:**      M. Sukhdeo, Rutgers University

**Time (Abstract No.)**

- 8:30 (67)**      **G.W. Esch, M. Sukhdeo.** Introduction, ASSOCIATE EDITORS SYMPOSIUM – 2012.
- 8:50 (68)**      **R. Carreno.** THE SYSTEMATICS OF OXYURID NEMATODES FROM INVERTEBRATES: INSIGHTS INTO THE EVOLUTION OF THE OXYURIDA.
- 9:10 (69)**      **S.A. Bullard, C.F. Ruiz.** MARINE FISHERIES, PARASITES, AND THE 2010 BP DEEPWATER HORIZON OIL SPILL.
- 9:30 (70)**      **M. Siddall.** OMICS.
- 9:50**              Questions, Closing Remarks.
- 10:15-10:30 am**              **COFFEE BREAK**

**9:00-11:45 pm**              **Genetics and Molecular Biology**

**Location: Potomac Salon E & F**

**Presiding:**      T. Geary, McGill University  
                     J. Porter-Kelly, Winston-Salem State University

**Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

- 9:00 (71)**      **V. Gelmedin, C. Dowling, J. Hawdon.** FUNCTION OF ACA-DAF-16 IN ARRESTED L1 AND L3 HOOKWORM LARVAE.
- 9:15 (72)†**      **M.E. Ogedengbe, J.R. Barta.** DNA BARCODING FOR SPECIES DELIMITATION AND PHYLOGENETICS OF SOME TISSUE COCCIDIA (TOXOPLASMATINAE: APICOMPLEXA).
- 9:30 (73)†**      **A. Gautam, S. Dangoudoubiyam, J.P. Dubey, W.J. Saville, D.K. Howe.** EXAMINATION OF THE SURFACE ANTIGEN (SNSAG) GENE FAMILY IN *SARCOCYSTIS NEURONA*.
- 9:45 (74)**      **A. Sinha, S. Banerjee, S. Ganguly, A.K. Sil, S. Sarkar.** FUNCTIONAL COMPLEMENTATION APPROACH TO STUDY PROTEIN DEGRADATION IN *GIARDIA LAMBLIA*.
- 10:00 (75)**      **J.P. Maia, E. Gómez-Díaz, S. Carranza, D.J. Harris.** MOLECULAR AND MICROSCOPIC SCREENING OF HEMOPARASITES IN REPTILES: A COMPARISON OF MULTIPLE DETECTION METHODS.
- 10:15-10:30 am**              **COFFEE BREAK**
- 10:30 (76)†**      **R. Al-Badri, J.R. Barta.** TRANSCRIPTOME ANALYSIS OF TWO IMMUNOLOGICALLY DISTINCT STRAINS OF *EIMERIA MAXIMA* DURING SPORULATION.
- 10:45 (77)**      **D. Zarlenga.** A SIMPLE METHOD TO IDENTIFY AND QUANTIFY GI NEMATODE EGGS USING A CAPILLARY SEQUENCER.

- 11:00 (78)<sup>†</sup>** **B. van Paridon**, C.V. Goater, D. Colwell, J. Gilleard. INVASION PATHWAY OF INTRODUCED LANCET LIVER FLUKE (*DICROCOELIUM DENDRITICUM*) INTO CATTLE AND WILDLIFE IN CYPRESS HILLS PARK, ALBERTA.
- 11:15 (79)** **A. Iqbal**, L. Parrington, D. Goldfarb, R. Slinger, B. Dixon. GENOTYPES AND SUBTYPES OF *CRYPTOSPORIDIUM* ISOLATES FROM DIARRHEIC PATIENTS IN THE CANADIAN ARCTIC (QIKIQTANI REGION).
- 11:30 (80)** **M.R. Youssefi**, S.H. Hosseini, R. Tabaripour, S. Miller. MOLECULAR CHARACTERIZATION OF *ECHINOCOCCUS GRANULOSUS* IN GOATS IN NORTH IRAN.

**9:00-11:45 pm**      **44<sup>th</sup> Coccidiosis Conference**  
**(sponsored, in part, by MERCK Animal Health)**

**Location: Potomac Salon G**

**Presiding:**      A.P. Sinai, University of Kentucky College of Medicine  
                       X. Suo, China Agricultural University

**Time (Abstract No.)**

**9:00 am**      Introduction.

**9:15 (81)**      **S. Fitz-Coy**. AVIAN COCCIDIOSIS: CURRENT COMMERCIAL PRACTICES FOR THE CONTROL OF THESE ILLUSIVE AGENTS.

**9:35 (82)**      **H. Lillehoj**, D.K. Kim. UNDERSTANDING SPECIES-DEPENDENT HOST RESPONSE TO *EIMERIA* SPP. USING COMPARATIVE TRANSCRIPTIONAL ANALYSIS.

**9:55 (83)**      G. Yin, X. Liu, **X. Suo**. A NOVEL MUCOSAL VACCINE BASED ON LIVE *EIMERIA* EXPRESSING CTB INDUCED SYSTEMIC IMMUNE RESPONSES IN CHICKENS.

**10:15-10:30 am**      **COFFEE BREAK**

**10:30 (84)**      L. Lai, B. Cowper, J. Bumstead, Y. Liu, D. Blake, T. Feizi, S. Matthews, **F. Tomley**. THE MOLECULAR BASIS FOR DISTINCT HOST AND TISSUE TROPISMS OF COCCIDIAN PARASITES.

**10:50 (85)**      T. Tomita, Y.F. Ma, B. Fox, D.J. Bzik, **L.M. Weiss**. IDENTIFICATION AND CHARACTERIZATION OF *TOXOPLASMA GONDII* CYST WALL PROTEINS.

**11:10 (86)**      B. Eller, B.C. Lynn, A. Data, **A.P. Sinai**. A CASE FOR HOST INVOLVEMENT IN THE GLYCOSYLATION OF *TOXOPLASMA* TISSUE CYSTS.

**11:30**      Questions, Closing Remarks.

**Sunday Afternoon, 2012-07-15**

**1:00-2:00      *ASP President's Address***

***Location: James River Salon C***

**Presiding:**      K.D. Lafferty, US Geological Survey  
                     J.C. Shaw, University of California Santa Barbara

**1:00**              Introduction of **Dr. Armand Kuris.**  
                     University of California Santa Barbara

**1:10 (87)**        **A.M. Kuris.** "Human Parasites: Who, What, When, Why and How"



**Armand M. Kuris**  
ASP President

***2:15-5:30 pm    Ecology II***

***Location: Potomac Salon G***

**Presiding:**      K.E. Luth, Wake Forest University  
                     A.W. Shostak, University of Alberta

**Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

**2:15 (88)†**        **M.F. Burwell, S.B. Weinstein, A.M. Kuris.** A DISTINCTIVE PARASITIC COPEPOD  
(HARPACTICOIDA: TISBIDAE) FROM CALIFORNIA *OCTOPUS BIMACULOIDES*.

**2:30 (89)†**        **J.P. Losee.** INFLUENCE OF VARIABILITY IN OCEAN CONDITIONS ON TROPHIC  
INTERACTIONS AND RECRUITMENT OF JUVENILE CHINOOK AND COHO SALMON  
INFERRED FROM TROPICALLY TRANSMITTED PARASITES.

**2:45 (90)†**        **M.S. Vhora, M.G. Bolek.** SEASONAL OCCURENCE AND COMMUNITY STRUCTURE OF  
HELMINTH PARASITES IN SOUTHERN LEOPARD FROGS, *RANA SPHENOCEPHALA*,  
FROM NORTH CENTRAL OKLAHOMA.

**3:00 (91)†**        **M.S. Vhora, M.G. Bolek.** HELMINTH COMMUNITY STRUCTURE IN NINE SPECIES OF  
SYMPATRIC ANURANS FROM NORTH CENTRAL OKLAHOMA.

**3:15 (92)†**        **M. Pickering, J.N. Caira.** SEASONAL DYNAMICS OF THE CESTODE FAUNA IN SPINY  
DOGFISH POPULATIONS OFF THE COAST OF RHODE ISLAND.

**3:30 (93)**        **W. Rossiter, M.V. Sukhdeo.** HABITAT-BASED SPATIAL CONSTRAINTS ON FOOD WEB  
STRUCTURE AND PARASITE LIFE CYCLES.

**3:45 – 4:00 pm              COFFEE BREAK**

**4:00 (94)**        **J. Detwiler, A. Zajac, D. Minchella, L. Belden.** ECHINOSTOME CRYPTIC DIVERSITY IN  
MUSKRAT DEFINITIVE HOSTS.

- 4:15 (95)**      **A.T. Neal.** DO BROKEN ASSUMPTIONS DRIVE *PLASMODIUM* SEX RATIOS TO STRAY FROM PREDICTIONS OF LOCAL MATE COMPETITION THEORY?
- 4:30 (96)**      **R. Carnegie,** E.M. Bureson. A PHENOTYPIC CHANGE IN *PERKINSUS MARINUS* WAS ASSOCIATED WITH INTENSIFICATION OF DISEASE IN OYSTER *CRASSOSTREA VIRGINICA*.
- 4:45 (97)**      **K.M. Hill,** R.B. Carnegie, N.A. Stokes, J.R. McDowell, K.S. Reece, E.M. Bureson. PHYLOGEOGRAPHY OF *BONAMIA EXITIOSA* (PHYLUM HAPLOSPORIDIA) THROUGH ANALYSIS OF INTERNAL TRANSCRIBED SPACER REGION RIBOSOMAL DNA SEQUENCES.
- 5:00 (98)**      **J.D. Shields,** C. Li, K.S. Reece, H. Wang, T.W. Dolan, M.J. Butler. ECOLOGICAL DETERMINANTS OF *HEMATODINIUM* EPIDEMICS IN THE AMERICAN BLUE CRAB, *CALLINECTES SAPIDUS*.
- 5:15 (99)**      **S. Sullivan,** H.J. Small, J. Shields. OVERWINTERING OF THE PARASITIC DINOFLAGELLATE, *HEMATODINIUM PEREZI* IN DREDGED BLUE CRABS.

## **2:15-5:30 pm    Taxonomy, Systematics, Phylogeny II**

### **Location: Potomac Salon E & F**

**Presiding:**      A. Choudhury, St. Norbert College  
                      R. Hathaway, Colorado College

#### **Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

- 2:15 (100)**      **J.J. Cielocha,** A. Yoneva, K. Jensen. SPERMATOZOON ULTRASTRUCTURE OF *ADELOBOTHRUM* SHIPLEY, 1900 (EUCESTODA: LECANICEPHALIDEA).
- 2:30 (101)†**      **D. Willsey,** F. Reyda, C. Healy. A NEW TAPEWORM SPECIES FROM *DASYATIS ZUGEI* (PALE-EDGED STINGRAY) FROM COASTAL MALAYSIAN BORNEO.
- 2:45 (102)**      **C. Turner,** K. Jensen, T. Ruhnke. EXAMINATION OF HOST SPECIES USAGE PATTERNS IN SPECIES OF THE SHARK CESTODE GENUS *PARAORYGMATOBOTHRUM*.
- 3:00 (103)†**      **R.P. Scheibel,** A. Jimenez. THE DISTRIBUTION AND SYSTEMATICS OF VIANNAIIDAE DURETTE-DESSET AND CHABAUD, 1981 OF NEW WORLD MARSUPIALS.
- 3:15 (104)†**      **C. Szmygiel,** B. Hanelt, A. Schmid-Rheasa, M.G. Bolek. IT'S ALL RELATED: CONSERVED MORPHOLOGICAL CHARACTERISTICS OF NON-ADULT STAGES OF HAIRWORMS (NEMATOMORPHA).
- 3:30 (105)†**      **B. Falk,** S. Perkins. DIVERSIFICATION AND DISPERSAL IN A WIDESPREAD LIZARD MALARIA PARASITE.

**3:45 – 4:00 pm**

**COFFEE BREAK**



- 4:00 (106)**     **S. Staicer**, J.M. Goessling, A. Smith-Herron, W.I. Lutterschmidt, T.J. Cook, H.K. Reinert, R.A. Odum. PENTASTOMES (PENTASTOMIDA: CEPHALOBAENIDA) ISOLATED FROM THE ENDANGERED RATTLESNAKE, *CROTALUS DURISSUS UNICOLOR* FROM ARIKOK NATIONAL PARK, ARUBA.
- 4:15 (107)**     **J.N. Caira**, K. Jensen. ON THE OCCASIONAL CHALLENGES OF MAINTAINING MONOPHYLETIC GENERA.
- 4:30 (108)<sup>†</sup>**     **V.M. Bueno**, F.P. Marques, D.J. Machado. SPECIES BOUNDARIES IN *RHINEBOTHROIDES* (CESTODA: RHINEBOTHRIIDEA) FROM FRESHWATER STINGRAYS IN SOUTH AMERICA.
- 4:45 (109)<sup>†</sup>**     **T.J. Katz**, J.N. Caira. REEVALUATION OF THE GENUS *CAULOBOTHRIUM* (CESTODA: TETRAHYLLIDEA) RESULTS IN DISCOVERY OF REMARKABLE MORPHOLOGICAL FEATURES.
- 5:00 (110)**     **T. Ruhnke**. PROGRESS AND OBSTACLES IN SPECIES LEVEL INVESTIGATIONS OF TWO CESTODE GENERA FROM SHARKS AND STINGRAYS.
- 5:15 (111)**     **A.J. Phillips**, J. Mariaux, B.B. Georgiev. A NEW GENUS AND SPECIES OF CESTODE (CESTODA: PARUTERINIDAE) FROM THE SQUIRREL CUCKOO, *PIAYA CAYANA* LESSON, 1830 (AVES: CUCULIFORMES), FROM PARAGUAY.

## **2:15-5:00 pm    Immunology**

### **Location: James River Salon A**

**Presiding:**     R.E. Kuhn, Wake Forest University  
                      K.K. Sapp, High Point University

### **Time (Abstract No.)**

<sup>†</sup> denotes student presentation in the Best Student Presentation Competition

- 2:15 (112)<sup>†</sup>**     **K.R. Price**, M. Guerin, J. Barta. A TECHNIQUE TO IMPROVE LIVE *EIMERIA* VACCINE EFFICACY.
- 2:30 (113)**     **R.H. Easy**, S.A. Adamo, D.K. Cone. STRESS, THE PARASITES FRIEND: STRESS EFFECTS ON IMMUNE FUNCTION ARE TIED INTO MOLECULAR NETWORKS.
- 2:45 (114)**     **A.E. Houk**, T. O'Connor, H.F. Penna, S.M. Gennari, A.M. Zajac. EXPERIMENTAL *CYTOISOSPORA CANIS* INFECTION IN BEAGLES.
- 3:00 (115)<sup>†</sup>**     **P. Sharma**. MOLECULAR EPIDEMIOLOGY OF *CRYPTOSPORIDIUM* ISOLATES FROM NORTH INDIAN PATIENTS.
- 3:15 (116)**     **F.O. Akinbo**, R. Omoregie. *PLASMODIUM FALCIPARUM* INFECTION IN HIV-INFECTED PERSONS ON HIGHLY ACTIVE ANTIRETROVIRAL THERAPY.
- 3:30 (117)**     **U. Ngenegbo**. GASTROINTESTINAL HELMINTHS AMONG PUPILS IN AN URBAN AND SUBURBAN COMMUNITIES IN NIGERIA.

**3:45 – 4:00 pm                      COFFEE BREAK**

- 4:00 (118)**     **O. Ukpai**, U.A. Amama. HIV SCREENING STATUS AND MALARIA IN NIGERIA: ENDEMICITY, SIGNS AND SYMPTOMS, KNOWLEDGE, ATTITUDE AND PRACTICES.
- 4:15 (119)**     **M.R. Youssefi**, S.H. Hosseini, M.J. Rasaee. PROTECTIVE EFFECT OF HYDATID CYSTS FLUID AND PROTOSCOLEX PEPTIDES IN TWO ANIMAL MODELS.
- 4:30 (120)**     **F. Khoshzaban**, F. Ghaffarifar. EVALUATION TREATMENT OF CUTANEOUS LEISHMANIASIS WITH GARLIC EXTRACT AND ITS FRACTION IN ANIMAL MODELS.
- 4:45 (121)**     **H.Z. Hezarjaribi**, F. Ghaffarifar, A. Dalimi. A SURVEY OF THE EFFECT OF IL-22 ON THE LESION ORIGINATED FROM LEISHMANIA MAJOR IN BALB/C MICE.

**4:00-5:30 pm    *Poster Display Boards delivered***

***Location: James River Salon C***

Authors may set up posters during this time.

**Sunday Evening, 2012-07-15**

**7:00 – 10:00 pm                      *Evening at the Lewis Ginter Botanical Garden***



Lewis Ginter  
Botanical Garden

**Monday Morning, 2012-07-16**

**8:00-11:15 am                      *Ecology III***

***Location: James River Salon A***

**Presiding:**     K. Herrmann, Minnesota State University  
                     R. Sorensen, Minnesota State University

**Time (Abstract No.)**

- 8:00 (122)**     **J.T. Detwiler**, C.D. Criscione. TESTING MENDELIAN INHERITANCE FROM FIELD-COLLECTED PARASITES ENABLES CORRECT INFERENCE OF REPRODUCTIVE MODE AND MATING SYSTEM.
- 8:15 (123)**     **G.J. Langford**, B. Willobee, L. Isidoro. LIFE CYCLE, HOST SPECIFICITY, AND SEASONAL OCCURRENCE OF *CYRTOSOMUM PENNERI* (NEMATODA: ATRACTIDAE) FROM LIZARDS IN POLK COUNTY, FLORIDA.

- 8:30 (124)**     **A.W. Shostak.** SEQUENTIAL AND CONCURRENT EXPOSURE OF FLOUR BEETLES TO PARASITES AND PESTICIDE.
- 8:45 (125)**     **S. Locke,** D.J. Marcogliese. A HOLARCTIC MOLECULAR SURVEY OF *DIPLOSTOMUM* SPECIES.
- 9:00 (126)**     **V.J. McKenzie.** CO-HABITATING AMPHIBIAN SPECIES HARBOR UNIQUE SKIN BACTERIAL COMMUNITIES IN WILD POPULATIONS.
- 9:15 (127)**     **B.L. Fredensborg,** J.J. Ramirez, L. Partida. SEASONAL AND SPATIAL VARIATION OF THE OYSTER PARASITE, *ACANTHOPARYPHIUM SPINULOSUM* IN THE LOWER LAGUNA MADRE, SOUTH TEXAS.
- 9:30 (128)**     **J.P. McLaughlin,** A.G. Jaramillo, J.C. Shaw, V.M. Vidal-Martinez, M.L. Aguirre-Macedo, J.E. Caselle, R.F. Hechinger. A.M. Kuris, K.D. Lafferty. METAZOAN PARASITES OF FISHES FROM AN INTERTIDAL SAND FLAT, PALMYRA ATOLL, EASTERN PACIFIC.
- 9:45-10:00 am**                     **COFFEE BREAK**
- 10:00 (129)**     **Y. Feng,** J. Ye, J. Ma, L. Xiao. ANTHROPONOTIC NATURE OF ENTERIC PROTISTS IN RHESUS MONKEYS IN A PUBLIC PARK IN GUIZHOU, CHINA.
- 10:15 (130)**     **F.A. Jimenez,** B. Byles, R.P. Scheibel, F.M. Catzeflis. THE ROLE OF COMPATIBILITY AND ENCOUNTER FILTERS IN THE STRUCTURE OF INFRACOMMUNITIES OF OPOSSUMS (MARSUPIALIA: DIDELPHIDAE) IN FRENCH GUIANA.
- 10:30 (131)**     **R. Monfort,** S. Boissinot. THE DETERMINANTS OF HELMINTH INFESTATION IN BABOONS.
- 10:45 (132)**     **R. Beechler,** A.E. Jolles, G.J. Van Dam, P.L. Corstjens, C. Seyler, V. Ezenwa, M.L. Steinauer. SCHISTOSOME INFECTION IN AFRICAN BUFFALO IN KRUGER NATIONAL PARK: EPIDEMIOLOGY AND COINFECTION PATTERNS.
- 11:00 (133)**     **M.A. Muhammad.** PRESENCE OF NEMATODE FOSSIL EVIDENCE IN CALCIFIED SEDIMENTARY ROCKS AT D.G. KHAN, SULEYMAN RANGE, PAKISTAN.

## **8:00-11:45 am                     *Host Parasite Interactions II***

***Location: James River Salon B***

**Presiding:**     V. Connors, University of South Carolina Upstate  
                      M.R. Zimmermann, Wake Forest University

### **Time (Abstract No.)**

- 8:00 (134)**     **I.I. Levin,** P.G. Parker. INFECTION WITH *HAEMOPROTEUS IWA* AFFECTS VECTOR MOVEMENT IN A HIPPOBOSCID FLY – FRIGATEBIRD SYSTEM.
- 8:15 (135)**     **J. Koprivnikar,** S. Orlofske, B. Melbourne, P.A. Walker, P.T. Johnson. ONE IS BETTER THAN TWO? ASYMMETRY IN ECHINOSTOME INFECTIONS OF TADPOLE KIDNEYS REDUCES HOST PATHOLOGY.

- 8:30 (136)**     **M. Tucker**, F. Lewis, J.D. Driver, W.O. Granath. STUDIES ON *SCHISTOSOMA MANSONI* CERCARIAL EMERGENCE FROM *BIOMPHALARIA GLABRATA* SNAILS.
- 8:45 (137)**     **S.E. Bush**, D. Kim, M.A. Aguilar, D.H. Clayton. EXPERIMENTAL EVOLUTION OF CRYPTIC COLORATION IN PARASITES.
- 9:00 (138)**     **J.A. Koop**, J.P. Owen, S.A. Knutie, S.M. Lavery, D. H. Clayton. DO ISLAND HOSTS HAVE INEFFECTIVE DEFENSES AGAINST INTRODUCED PARASITES? A TEST USING DARWIN'S FINCHES AND NEST FLIES.
- 9:15 (139)**     **P.J. Cosmann**, S.A. Arnott, W.A. Roumillat, A.E. Strand, I. de Buron. ASSOCIATIONS BETWEEN PARASITE BURDEN AND HEALTH IN SPOTTED SEATROUT, *CYNOSCION NEBULOSUS*.
- 9:30 (140)**     **J.L. Hein**, S.A. Arnott, W.A. Roumillat, I. de Buron. IMPACT OF THE INVASIVE PARASITE *ANGUILLICOLOIDES CRASSUS* ON HEALTH OF THE AMERICAN EEL, *ANGUILLA ROSTRATA*.
- 9:45-10:00 am**                     **COFFEE BREAK**
- 10:00 (141)**     **T.G. Geary**, X. Wang, J. Geary, J. Chehayeb, C. Mackenzie, M. Stevenson, Y. Moreno. NEMATODE SECRETOMICS: COMPARATIVE ANALYSIS.
- 10:15 (142)**     **T.W. Dolan**, M.J. Butler, J.D. Shields. THE INFLUENCE OF FISHING PRESSURE ON *HEMATODINIUM* OUTBREAKS IN THE AMERICAN BLUE CRAB, A SIMULATION STUDY.
- 10:30 (143)**     **S.M. Villa**, J. Koop, H.C. Proctor, D.H. Clayton. FEATHER MITE COMMUNITIES ON DARWIN'S FINCHES: THE ROLE OF HOST BEAK MORPHOLOGY.
- 10:45 (144)**     **S.C. Culloty**, E. O'Grady, J. Fermer, E. Morgan, C. Smith, D. Rachinskii, J. Ironside, T. Kelly. *UNIKARYON LEGERI* HAS A SIGNIFICANT IMPACT ON THE ECOLOGY OF THE COCKLE *CERASTODERMA EDULE*.
- 11:00 (145)**     **E. Thiele**, D.J. Minchella. APPLICATION OF A STRAIN-SPECIFIC MOLECULAR MARKER AND REAL-TIME QUANTITATIVE PCR IN THE DIAGNOSIS OF COINFECTION AND ASSESSMENT OF INTRASPECIFIC COMPETITION WITHIN A MOLLUSCAN INTERMEDIATE HOST.
- 11:15 (146)**     **U. Singh**, A. Mehta. AN EFFORT TO IMPLEMENT PUBLIC HEALTH AWARENESS AMONG COLLEGE STUDENTS TOWARDS THE MOST COMMON LIFE STYLE ON THE EARTH "PARASITISM".
- 11:30 (147)**     M.H. Elsayad, **M.M. Tolba**, M.A. Yehia, A.S. Ahmed, S. Abou Holw. HUMAN SUBCUTANEOUS DIROFILARIASIS, REPORT OF TWO CASES OF *DIROFILARIA REPENS* IN ALEXANDRIA, EGYPT.

## **8:45-11:00 am                     Taxonomy, Systematics and Phylogeny III**

**Location: Potomac Salon E & F**

**Presiding:**     J. Ceilocha, University of Kansas

**Time (Abstract No.)**

- 8:45 (148)**     **H.J. Small**, K.S. Reece, G.D. Stentiford, J. Xaio, K. Pagenkopp Lohan, K. Bateman, J.D. Shields. GLOBAL DIVERSITY AND DISTRIBUTION OF *HEMATODINIUM* SPP. - SIGNIFICANT PATHOGENS OF COMMERCIALY EXPLOITED CRUSTACEANS.
- 9:00 (149)**     **A. García Vásquez**, F.N. Morales-Serna, B. Mendoza-Garfias, Z.L. Hernández-Inda, G. Pérez-Ponce de León. SPECIES OF DACTYLOGYRIDS (MONOGENOIDEA), GILL PARASITES OF WILD AND CAGE CULTURED SNAPPERS (LUTJANIDAE) IN CHAMELA BAY, ON THE PACIFIC COAST OF MEXICO: PRELIMINARY RESULTS.
- 9:15 (150)**     **F.N. Morales-Serna**, A. García-Vásquez, B. Mendoza-Garfias, Z.L. Hernández-Inda, G. Pérez-Ponce de León. PARASITIC COPEPODS OF THE GENUS *CALIGUS* (SIPHONOSTOMATOIDA: CALIGIDAE) ON CARANGID AND LUTJANID TELEOSTS FROM A FISH FARMING AREA OFF WESTERN COAST OF MEXICO.
- 9:30 (151)**     **S.A. Nadler**, J. Park. PHYLOGENETICS OF MAJOR NEMATODE LINEAGES: HOW DIFFERENT ARE HYPOTHESES BASED ON NUCLEAR SSU RNA VERSUS COMPLETE MITOCHONDRIAL GENOMES?

**9:45-10:00 am**

**COFFEE BREAK**

- 10:00 (152)**     **S.V. Brant**, V. Flores, E.S. Loker. REVEALING SCHISTOSOME DIVERSITY IN SOUTH AMERICA (PATAGONIA): THE ENDEMIC GASTROPOD GENUS *CHILINA* SUPPORTS UNIQUE LINEAGES OF AVIAN SCHISTOSOMES.
- 10:15 (153)**     **S.L. Perkins**. TAXONOMIC REVISION OF HAEMOSPORIDA: ELIMINATION OF *PLASMODIUM FALCIPARUM*?
- 10:30 (154)**     **V. Tkach**. MOLECULAR PHYLOGENY AND EVOLUTION OF THE HYMENOLEPIDIDAE (CESTODA: CYCLOPHYLLIDEA) PARASITIC IN MAMMALS.
- 10:45 (155)**     **A.F. Ocegüera**, A.J. Phillips, G. Pérez-Ponce de León, M. Siddall. PHYLOGENETIC RELATIONSHIPS OF ARHYNCHOBDELLID LEECHES REVISITED.

**8:00-11:45 am**

***First International Nematomorpha Symposium***

***Location: James River Salon D***

**Presiding:**     M. Bolek, Oklahoma State University  
                     B. Hanelt, University of New Mexico

**Time (Abstract No.)**

**† denotes student presentation in the Best Student Presentation Competition**

- 8:00**             **M. Bolek**. INTRODUCTION. From Immune Systems to Ecosystems and Everything in Between.
- 8:15 (156)**     **M.C. Chiu**, C.G. Huang, W.J. Wu, S.F. Shiao. ABOUT *CHORDODES FORMOSANUS*: A GENERAL INTRODUCTION TO THE NEWLY DISCOVERED SPECIES FROM TAIWAN.

- 8:30 (157)<sup>†</sup>** **A.C. Begay**, A. Schmidt-Rhaesa, C. Looney, R. Zack, B. Hanelt. NEW SPECIES OF *GORDIONUS* (NEMATOMORPHA: GORDIIDA) FROM WASHINGTON STATE.
- 8:45 (158)<sup>†</sup>** **R.T. Sedam**, W.L. Gordy, J.D. Niforatos, B. Hanelt. HANGING UP ON THE CALL FOR LOVE: BEHAVIORAL MODIFICATION OF MALE *ACHETA DOMESTICUS* CRICKETS INFECTED WITH *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA).
- 9:00 (159)** J.D. Niforatos, E. Maldonado, T. Sedam, **B. Hanelt**. LOOKING FOR LOVE IN ALL THE RIGHT PLACES? HOW HAIRWORMS (NEMATOMORPHA: GORDIIDA) FIND POTENTIAL MATES.
- 9:15 (160)** **E.M. Maldonado**, J. Niforatos, B. Hanelt. ALTERATION OF FAT BODY AND OVARY DEVELOPMENT IN THE FEMALE *CRICKETACHAETA DOMESTICUS* INFECTED WITH THE HAIRWORM *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA).
- 9:30 (161)<sup>†</sup>** **C. Szmygiel**, R. Shannon, L.M. Hodges, B. Hanelt, M. Papes, A. Schmidt-Rhaesa, M.G. Bolek. USING GORDIID CYSTS TO DISCOVER THE HIDDEN BIODIVERSITY AND POTENTIAL DISTRIBUTION OF HAIRWORMS (NEMATOMORPHA).
- 9:45-10:00 am** **COFFEE BREAK**
- 10:00 (162)** **B. Hanelt**, M.A. Forys. DEFENDING THE ATTACKER: CHARACTERIZING THE IMMUNE SYSTEM OF *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA) USING NEXT GENERATION SEQUENCING.
- 10:15 (163)** **F.M. Zanca**. DIVERSITY OF GORDIIDA (NEMATOMORPHA) IN THE DIAMANTE RIVER BASIN AND THEIR EPIBIONTS.
- 10:30 (164)** **A. Schmidt-Rhaesa**, A.C. Begay, B. Hanelt. MOLECULAR MARKERS HELP IN RECOGNIZING SPECIES BOUNDARIES IN THE GENUS *GORDIONUS* (NEMATOMORPHA).
- 10:45 (165)** **M. Bolek**, C. Szmygiel, E. Rogers, B. Hanelt, A. Schmid-Rhaesa. DISCOVERING THE HIDDEN BIODIVERSITY OF GORDIIDS (PHYLUM NEMATOMORPHA): WHERE ARE WE AND WHAT ARE THE NEXT STEPS?
- 11:00 (166)** **T. Sato**, K. Watanabe, N. Tokuchi, M. Kanaiwa, K.D. Lafferty. NEMATOMORPHS ALTER CROSS-ECOSYSTEM ENERGY FLOW VIA HOST MANIPULATION.
- 11:15** **B. Hanelt**. Question/Poster Session.

**8:00-10:30 am** **Authors complete set up for poster session**

**Monday Afternoon, 2012-07-16**

**12:00-1:30 pm** **Poster Session, coffee and snacks**

**Location: James River Salon C**

All authors must stand with your posters from 12:00-1:30.

## CELL BIOLOGY

- 167 A.L. Sereno-Uribe**, C.D. Pinacho-Pinacho, G. Pérez-Ponce de León, L. Zambrano, M. García-Varela. MOLECULAR AND MORPHOLOGICAL DIFFERENTIATION OF *CLINOSTOMUM* LEIDY, 1856 (DIGenea: CLINOSTOMIDAE) FROM NEOTROPICAL REGION OF MEXICO.

## CHEMOTHERAPY AND DRUG RESISTANCE

- 168 F. Ghaffarifar**. THE EFFECT OF CANTHARIDIN ON INDUCING APOPTOSIS IN *LEISHMANIA MAJOR*.
- 169 R. Valipour Nouroozi**. EVALUATE THE GLUCANTIME SUSCEPTIBILITY OF *LEISHMANIA TROPICA* ISOLATES OF IZEH CITY.
- 170 R. Valipour Nouroozi**. EVALUATE THE EFFECT OF POLY METHYL METHACRYLATE NANOPARTICLES PLUS GLUCANTIME IN VISCERAL LEISHMANIASIS TREATMENT IN GOLDEN HAMSTER.
- 171 A.H. Sharief**, E.A. Khalil, A. Kharazmi, S.A. Omer, M.E. Ibrahim. *LEISHMANI DONOVANI*: AN IN VITRO STUDY OF ANTIMONY-RESISTANT AMPHOTERICIN B-SENSITIVE ISOLATES.

## ECOLOGY

- 172 N. Kintsurashvili**, A. Schmidt-Rhaesa, O. Gorgadze. GEORGIAN FRESHWATER HAIRWORMS (NEMATOMORPHA: GORDIIDAE) – RESULTS OF FAUNISTIC STUDY.
- 173 E.F. Bauer**, C.M. Whipps. TROPHICALLY CASCADING ENEMY RELEASE: TESTING THE CONNECTION BETWEEN SMALLMOUTH BASS PARASITE BURDEN AND CONSUMPTION OF INVASIVE ROUND GOBY IN THE ST. LAWRENCE RIVER.
- 174 C. Achioro**. FIRST ECOTOXICOLOGICAL EVALUATIONS IN NEMATOMORPHA: CAN *CHORDODES NOBILLII* BE CONSIDERED A GOOD BIOINDICATOR?
- 175 R. Adams**, J. Loudon, D. Van Gerven, V. McKenzie. A PALEOPARASITOLOGICAL STUDY OF 1,500-YEAR-OLD HUMAN MUMMY COPROLITES FROM SOUTHERN SUDAN.
- 176 A. Claxton**, K. Jacobson. LARGE SCALE PATTERNS OF SUBYEARLING CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) HABITAT USE IN THE COLUMBIA RIVER ESTUARY INFERRED FROM PARASITE ASSEMBLAGES.
- 177 Wyderko**, F. Benfield, J. Maerz, K. Cecala, L. Belden. QUANTIFYING *METAGONIMOIDES OREGONENSIS* INFECTION IN STREAM SALAMANDERS.
- 178 S.A. Zemmer**, J.G. Da Silva Neto, E.F. Benfield, L.K. Belden. THE DISTRIBUTION AND PREVALENCE OF *METAGONIMOIDES OREGONENSIS* (TREMATODA: HETEROPHYIDAE) IN SOUTHWESTERN VIRGINIA AND NORTHWESTERN NORTH CAROLINA.
- 179 J.L. Hein**, S.A. Arnott, W.A. Roumillat, I. de Buron. SPATIAL AND TEMPORAL PATTERNS OF INFECTION OF THE AMERICAN EEL, *ANGUILLA ROSTRATA*, BY THE INVASIVE PARASITE, *ANGUILLICOIDES CRASSUS*, IN ESTUARIES OF SOUTH CAROLINA.

- 180 **M. Rangel**, B.L. Fredensborg. SUITABILITY OF THREE SNAIL SPECIES AS CANDIDATES FOR USING TREMATODES AS INDICATORS OF ECOSYSTEM HEALTH IN A SOUTH TEXAS ESTUARY.
- 181 **E. Quintero**, B.L. Fredensborg. FITNESS COSTS OF LARVAL TREMATODES IN TWO CLOSELY RELATED POECILIIDS WITH DIFFERENT REPRODUCTIVE STRATEGIES.
- 182 **R. Salas-Montiel**, S. Contreras-Mirón, L. García-Prieto, D. Osorio-Sarabia, A. Ocegüera-Figueroa. DESCRIPTION OF THE SPERMATOPHORE OF THE BLOOD-FEEDING LEECH *HAEMENTERIA OFFICINALIS* AND ITS PREVALENCE, ABUNDANCE AND INTENSITY IN A WILD POPULATION FROM GUANAJUATO, MEXICO.
- 183 **R. Hernandez**, K. Lowe, B.L. Fredensborg. SPECIALIZED PARASITE IS NOT RESTRICTED TO USE OF CLOSELY RELATED HOSTS.

## GENETICS AND MOLECULAR BIOLOGY

- 184 **F.S. Maghsoodloorad**, N. Hosseinzade Sardarabadi, A. Haghighi, L. Gachkar, K. Sharifi Sarasiabi, E. Nazemalhosseini Mojarad. AMINO ACID MUTATION IN *PLASMODIUM VIVAX* DHFR AND DHPS GENES IN THE BORDER OF SISTAN AND BALUCHESTAN PROVINCE, IRAN.
- 185 **E.J. Choi**, K.H. Pyo, Y.S. Hwang, J. Lee, S. Woo, I.G. Hwang, H.J. Lee, E.H. Shin. PCR DETECTION OF WATERBORNE PROTOZOA IN ENVIRONMENTAL WATER.
- 186 **K. Abernathy**, S. Peoples, M. Woodard, J. Odera, J.M. Porter-Kelley, MICRORNAS IN *LEISHMANIA BRAZILIENSIS*.
- 187 **B. Hannible**, J.M. Porter-Kelley. CHARACTERIZATION OF LB-MIR-1 IN *LEISHMANIA BRAZILIENSIS*.
- 188 **M.E. Alvarado**, M. Wasserman. CALCIUM BINDING PROTEINS WITH EF-HAND DOMAINS IN *GIARDIA INTESTINALIS*.

## HOST-PARASITE INTERACTIONS

- 189 **J. Sheehan**, C. Lange, U. Habal, F. Reyda. PATHOLOGY CAUSED BY *LEPTORHYNCHOIDES THECATUS* (ACANTHOCEPHALA) IN *MICROPTERUS DOLOMIEU* (SMALLMOUTH BASS).
- 190 **C.M. Umberger**, E.J. McElroy, W.A. Roumillat, I. de Buron. EFFECTS OF THE PARASITIC NEMATODE, *PHILOMETROIDES PARALICHTHYDIS*, ON THE SWIMMING AND BURYING PERFORMANCE OF THE SOUTHERN FLOUNDER, *PARALICHTHYS LETHOSTIGMA*.
- 191 **B.J. Fazzone**, P.J. Cosmann, I. de Buron, W.A. Roumillat, V.A. Connors. SEATROUT HEART INFECTION BY *CARDICOLA* SP.: ARE SMALL FISH IN MORE TROUBLE?
- 192 **M.C. Curran**, M.B. Sherman. PREVALENCE OF THE PARASITIC ISOPOD *PROBOPYRUS PANDALICOLA* IN DAGGERBLADE GRASS SHRIMP *PALAEMONETES PUGIO* IN FOUR MARSH CREEKS NEAR SAVANNAH, GEORGIA.
- 193 **J. Philips**. MITES OF NORTH AMERICAN STRIGIFORM BIRDS.
- 194 **P.A. O'Leary**, O. Pung. BEHAVIORAL ANALYSIS OF A DIGENETIC TREMATODE CERCARIA (*MICROPHALLUS TURGIDUS*) IN RELATION TO THE MICROHABITAT OF GRASS SHRIMP (*PALAEMONETES* SPP.).



- 195 E. Walther**, J. Carlson, A. Cornel, R. Sehgal. AVIAN MALARIA IN CALIFORNIA: HOST-VECTOR LINKAGES AND DISEASE DYNAMICS IN A SONGBIRD COMMUNITY.
- 196 B.K. Wijayawardena**, D.J. Minchella, J.A. DeWoody. TRANSPOSABLE ELEMENT DYNAMICS IN *SCHISTOSOMA MANSONI* STRAINS.
- 197 A. Simmons**, T. Yeargins, M. Griffin, R. Jones, K. Stanford, S. Barnes, D. Scott, A.C. Rosypal, D.S. Lindsay. PREVALENCE OF ENCYSTED APICOMPLEXAN PARASITES IN MUSCLE OF RAPTORS FROM NORTH CAROLINA.
- 198 M. Mudasser**, A. Maqbool, A.E. Houk, D. Hawley, D.S. Lindsay. PREVALENCE OF APICOMPLEXAN PARASITES IN THE MUSCLES OF HOUSE FINCHES (*CARPODACUS MEXICANUS*).

## IMMUNOLOGY

- 199 Y. Hwang**, K. Pyo, M. Kim, E. Choi, J. Lee, S. Woo, E. Shin. CHRONIC INFECTION OF *TOXOPLASMA GONDII* IN THE BRAIN INDUCES M2 MICROGLIA PHENOTYPE BY REDUCING INDUCIBLE NITRIC OXIDE SYNTHASE.
- 200 K. Pyo**, M. Kim, Y. Hwang, J. Lee, S. Woo, E. Shin. IMMUNE CHARACTERISTICS IN TUMOR-BEARING BALB/C AND BALB/C NU/NU MICE AFTER THE TREATMENT OF *TOXOPLASMA GONDII* LYSATE ANTIGEN.
- 201 P.M. Callahan**, **M.K. Larson**, R.C. Bender, C.J. Bayne. RESISTANCE TO *SCHISTOSOMA MANSONI* IS CORRELATED WITH THE NUMBERS OF SPREADING GRANULOCYTES IN *BIOMPHALARIA GLABRATA*.

## LIFE CYCLES AND EPIDEMIOLOGY

- 202 P.F. Armstrong**, J. Payne, J. Gunderson. OCCURRENCE OF *MECISTOBOTHRIUM BREVISPIKE* METACESTODES IN BIVALVES.
- 203 D.N. Aribodor**. PREVALENCE AND ASSOCIATED RISK FACTORS OF INTESTINAL HELMINTH INFECTIONS AMONG 5-14 YEAR OLDS IN ANAMBRA STATE, NIGERIA.
- 204 M.K. Kim**, K.H. Pyo, Y.S. Hwang, E.J. Choi, J. Lee, S. Woo, I.G. Hwang, H.J. Lee, E.H. Shin. EFFECT OF TEMPERATURE ON THE EMBRYONATION OF *ASCARIS SUUM* EGGS IN ENVIRONMENTAL CHAMBER.
- 205 A.H. Sharief**, M.M. Mukhtar, T.B. Higazi. DETECTION OF ANTIBODIES TO *LEISHMANIA DONOVANI* IN ANIMALS IN A KALA-AZAR ENDEMIC REGION IN EASTERN SUDAN: A PRELIMINARY REPORT.
- 206 W.S. Buzetti**, S.C. Paulan, A.G. Souza, D.T. Silva, H.F. Pena, S.M. Gennari. OCCURRENCE OF PARASITIC CO-INFECTION IN DOGS FROM A RURAL SETTLEMENT.

## TAXONOMY, SYSTEMATICS AND PHYLOGENY

- 207 F.M. Zanca**, L.C. de Villalobos. TWO NEW AFRICAN SPECIES OF THE GENUS *CHORDODES* (GORDIIDAE: NEMATOMORPHA).
- 208 E.A. Martínez-Salazar**, R. Rosas-Valdez, T.R. Gregory, J. Violante-González. SYSTEMATICS AND GENOME SIZE OF *INFIDUM SIMILIS* TRAVASSOS, 1916 (DIGENEA).

- 209 **J. Koltek**, R. Carreno, D. Ordosch, D. Hamill. OXYURID NEMATODES FROM COCKROACHES (*BLATTARIA*) IN SOUTHERN FLORIDA WITH REVISED MORPHOLOGICAL CHARACTERS FOR *EURYCONEMA PARADISA* AND *PROTRELLOIDES PARADOXA*.
- 210 **A.H. Sharief**, E.A. Khalil, S.A. Omer. INNOVATIVE SERUM-FREE MEDIUM FOR IN VITRO CULTIVATION OF PROMASTIGOTE FORMS OF *LEISHMANIA* SPECIES.
- 211 **N. Odell**, K. Jensen. TETRAPHYLLIDEAN TAPEWORMS OF ELECTRIC RAYS (TORPEDINIFORMES) OFF THE PACIFIC COAST OF COSTA RICA.
- 212 **R. Devkota**, S.V. Brant, A. Thapa, E.S. Loker. SCHISTOSOME SHARING: THE ELEPHANT SCHISTOSOME *BIVITELLOBIKHARZIA NAIRI* ALSO INFECTS THE GREATER ONE-HORNED RHINOCEROS (*RHINOCEROS UNICORNIS*) IN CHITWAN NATIONAL PARK, NEPAL.
- 213 **A. Daigler**, F. Reyda. A NEW SPECIES OF CESTODE FROM THE *HIMANTURA WALGA* (DWARF WHIPRAY) OF BORNEO.
- 214 **E.S. Loker**, S.V. Brant. INTRODUCING A NEW MUSEUM FOR PARASITES – THE PARASITE DIVISION OF THE MUSEUM OF SOUTHWESTERN BIOLOGY AT THE UNIVERSITY OF NEW MEXICO IN ALBUQUERQUE.
- 215 **R.S. Seville**, D. Duszynski, L. Couch, L. Schmidt, D. Moser, K. Visnak, Z. Roehrs. RECONSTRUCTION OF THE COCCIDIA OF THE WORLD WEBSITE TO ENHANCE ACCESSIBILITY, USABILITY, AND UTILITY.

## VECTOR BIOLOGY

- 216 **R. Valipour Nouroozi**. EVALUATION OF CHANGES IN NUMBER OF *ANOPHELES SUPERPICTUS* LARVA AT MARGINS OF IZEH CITY MIANGHAN LAKE DURING 20 YEARS, FROM 1970 TO 1990.

**1:45 – 2:45 pm** **H.B. Ward Medal Lecture**

**Location: James River Salon D**

- Presiding:** C. Healy, Royal Ontario Museum, University of Toronto
- 1:45** Introduction of 2012 H. B. Ward Medal Recipient.  
R. Fayer, USDA, ARS, Beltsville Agricultural Research Center
- 1:55 (217)** **L.X. Xiao**. “My Humble Experience with Parasites.”



**Lihua X. Xiao**  
H. B. Ward Medal

**2:45 PM - 4:30 PM** **ASP Awards and Business Meeting,**

**Location: James River Salon D**

## ASP AWARDS

### CLARK P. READ MENTOR AWARD LECTURE

- Presiding:** S.A. Bullard, Auburn University

**Time (Abstract No.)**

**2:00** Introduction of 2012 C.P. Read Mentor Award  
C. Criscione, Texas A&M University  
M. Steinauer, Oregon State University

**2:10 (218)** **W.F. Font.** "Mentoring Then and Now."

**ASHTON CUCKLER NEW INVESTIGATOR AWARD**

**Presiding:** C. Davis, Western Kentucky University

The recipient of the 2012 New Investigator Award  
is **Dr. Jillian T. Detwiler**,  
Postdoctoral Researcher, Texas A&M University.

**WILLIS A. REID JR., STUDENT RESEARCH GRANT AWARDS**

**Presiding:** S. Seville, University of Wyoming

**BRAYTON H. RANSOM TRUST AWARD**

**Presiding:** Ralph Eckerlin, President of Ransom Trust

**Dr. William Campbell** is receiving the Brayton H. Ransom Trust  
Award in recognition of his many contributions to the field of  
parasitology.

**BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS**

**Presiding:** K.C. Jacobson, NOAA Fisheries

**ASP BUSINESS MEETING**

**Presiding:** A.M. Kuris, University of California Santa Barbara

*Thank you for attending this year's ASP meeting and have a safe trip home.  
See you **June 27-30, 2013** at our next meeting in **Quebec City, CANADA!***



**William F. Font**  
Mentor Award



**Jillian Detwiler**  
New Investigator Award

## Abstract Listings

### (1)

#### WHAT IS THE EFFECT OF THE PARASITIC ISOPOD *PROBOPYRUS PANDALICOLA* ON THE STARVATION RATE OF DAGGERBLADE GRASS SHRIMP *PALAEMONETES PUGIO* AT TWO DIFFERENT TEMPERATURES?

M.B. Sherman and M.C. Curran, Savannah State University

Daggerblade grass shrimp *Palaemonetes pugio* are prevalent in estuaries along the East Coast of the United States and are an integral part of the estuarine food web. *Probopyrus pandalicola* is a bopyrid isopod that parasitizes *P. pugio* and decreases the energy available to its host by feeding on the hemolymph of the shrimp. The parasite also causes both male and female shrimp to be sexually castrated. The purpose of this study was to determine the effect of *P. pandalicola* on the starvation rate of *P. pugio* at two different temperatures. Trials were conducted between September 2009 and June 2011. For each trial, 25 unparasitized, 25 parasitized, and 25 deparasitized shrimp were used. Mean initial lengths and weights were recorded for all shrimp, as well as mean cyst counts of the trematode *Microphallus turgidus*. Each shrimp was placed into individual aquaria and starved until 100% mortality occurred. Starvation rates were compared using a non-parametric statistical test. The mean number of trematode cysts, which ranged from  $0.41 \pm 0.08$  to  $1.05 \pm 0.12$ , had no effect on shrimp survival times during any of the trials. The bopyrid isopod did have a significant effect on shrimp survival times, but only in the warmer trials (25°C) when parasitized shrimp survived a significantly shorter amount of time ( $21.8 \pm 0.81$  d) than unparasitized shrimp ( $25.2 \pm 0.96$  d). The bopyrid did not have a significant effect on shrimp survival times in the colder trials (20°C), for which shrimp survived longer ( $29.9 \pm 0.85$  d). Therefore, cooler temperatures may slow the metabolism of the shrimp and reduce the effect of the bopyrid parasite on its host. Additional studies will be conducted to determine the specific temperature at which the parasite no longer has an effect.

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### (2)

#### HELMINTHS OF *MICAELAMYS NAMAQUENSIS* AND *AETHOMYS CHRYSOPHILUS* (RODENTIA: MURIDAE) FROM NORTHWESTERN BOTSWANA

L.E. Reid, M.L. Thies and T.J. Cook, Department of Biological Sciences, Sam Houston State University

Two species of Botswanan rodents, *Micaelamys namaquensis* (Namaqua rock rat) and *Aethomys chrysophilus* (veld rat), were collected from the Koanaka Hills region of Ngamiland Province in northwestern Botswana in July 2009. The gastrointestinal tracts of 40 specimens (20 *M. namaquensis* and 20 *A. chrysophilus*) collected from 3 microhabitats were examined for helminths. Prevalence and intensity were calculated to potentially reveal correlations between parasite prevalence and host sex, habitat range, and environmental factors. Gastrointestinal tracts were removed in the field, preserved in 95% ethanol, and returned to SHSU for subsequent analyses. Helminths were removed and stored in 70% ethanol for preservation. Cestodes were stained with hematoxylin and eosin and nematodes were viewed under wet mounts of glycerin and ethanol. Helminths were examined with an Olympus BX51 microscope and digital images of all specimens were captured with an Olympus DP 72 digital camera. Nematodes had the highest prevalence of infection in *A. chrysophilus* at 70%, with a lower prevalence in *M. namaquensis* at 65%. Prevalence of cestodes in *A. chrysophilus* was 10%, while the prevalence of cestode infection in *M. namaquensis* was 5%.

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### (3)

#### LANDSCAPE ECOLOGY OF AMPHIBIAN HELMINTHS IN THE SHEYENNE NATIONAL GRASSLANDS, ND

K. Gustafson, Oklahoma State University

Worldwide reports of amphibian declines have increased the urgency for understanding factors that influence the distribution and abundance of amphibian populations. Declines have been associated with habitat loss and fragmentation, reduced habitat quality, and infectious diseases, including impacts from parasites. The goal of this study was to identify landscape-level patterns of amphibian parasitism and how local and landscape characteristics influence host-parasite interactions. Here, I used field observations, geographic information systems, and statistical models to identify factors that influence amphibian breeding populations. Of the 5 anuran species found breeding in the grassland, 218 northern leopard frogs (*Rana pipiens*) and 110 wood frogs (*Rana sylvatica*) were collected and examined for helminths. I then identified spatial patterns of infection by modeling helminth species prevalence/abundance in relation to amphibian distributions and the landscape in which these hosts occurred. The distributions of helminths were influenced by several factors, including the life stage of the amphibian host, landscape structure, and host habitat preferences. Leopard frogs were important hosts for maintaining adult trematodes, whereas wood frogs were important reservoirs for nematodes. Metamorphic frogs were commonly infected with larval trematodes, whereas juveniles and adult frogs were more commonly infected with nematodes and trematodes. The distributions of trematode species were less predictable than the distributions of direct life cycle nematodes. The spatial scale of this study was not large enough to detect strong patterns of helminth species that were distributed to frogs by mobile hosts, such as birds, mammals, and invertebrates. In contrast, amphibian nematodes showed strong dependencies on host distributions. Both *Rhabdias* spp. showed strong positive relationships with the breeding populations of their specific amphibian host. In areas of high leopard frog occupancy, *Oswaldocruzia pipiens* had a lower prevalence in both leopard frogs and wood frogs, suggesting leopard frogs may be diluting the *O. pipiens* population. Additionally, wood frogs had a higher prevalence of *Cosmocercoides* sp. in areas with high Canadian toad occupancy, suggesting these toads are important for maintaining *Cosmocercoides* populations.

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### (4)

#### FITNESS BENEFITS OF A DIVISION OF LABOR IN PARASITIC TREMATODE COLONIES: DEFENSE AGAINST COMPETITORS?

M.M. Lloyd and R. Poulin, University of Otago

A reproductive division of labor has recently been discovered within polyembryonic larval colonies of two species of parasitic trematodes infecting snail hosts. In these colonies, one larval morph expands the colony through asexual reproduction while the other morph never reproduces. As in other polyembryonic species using a division of labor (parasitoid wasps, one species of sea anemone), the non-reproducing morph appears specialized for defense against competing colonies. In this study, we first assessed competition between larvae of the trematodes *Philophthalmus* sp. (which possesses reproducing and non-reproducing morphs) and the most common co-infecting species, *Maritrema novaezealandensis*, by quantifying colony success within snail hosts. Colonies of either species that did not compete within their host were more successful (i.e. produced more transmission stages) than colonies that were competing in a shared host. Secondly, we cultured larvae of both species in vitro, alone or together, to study the interaction more closely and to measure any advantage obtained by the colony from the non-reproducing morphs. This was done by manipulating the presence and abundance of *M. novaezealandensis* as well as

the presence of the non-reproducing 'defensive' morph. *Philophthalmus* colonies with both reproducing and non-reproducing morphs but without *M. novaezealandensis* larvae were most successful. This implies the non-reproducing larvae provide a fitness benefit to *Philophthalmus* sp. colonies even in the absence of competition, though the nature of this advantage remains unclear.

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## (5)

### COMPATIBILITY OF *FASCIOLOIDES MAGNA* MIRACIDIA AND FOUR SNAIL SPECIES: MIRACIDIAL CHOICE AND SNAIL RESPONSE

**B.P. Rolfsen**, Eastern Illinois University

This study was designed to assess the factors involved in intermediate host finding and host-parasite compatibility in the deer liver fluke (*Fascioloides magna*). The study used a panel of four sympatric snails (*Lymnaea caperata*, *Lymnaea elodes*, *Lymnaea exilis*, and *Physa* sp.) which display a range of susceptibility to the trematode (from *L. caperata* which is the natural intermediate host, to experimentally susceptible *L. elodes*, to resistant *L. exilis* and *Physa* sp). Miracidial host finding was tested by observing single miracidium infections for 30 min. time periods to record number of contacts, attachment time, infection success, and whether the miracidium was harmed. Miracidia attached to susceptible *L. caperata* more often ( $\chi^2=6.6561$ ,  $p=.0359$ ) and for longer periods of time ( $\chi^2=8.5290$ ,  $p=0.0141$ ) than to resistant *L. exilis* or *Physa* sp. Miracidia exposed to a physid snail were harmed more often than those exposed to the lymnaeids ( $\chi^2=5.4000$ ,  $p=0.0251$ ). Subsequently, miracidia were exposed to snail mucus *in vitro* to assess its toxicity. Following the pattern seen with intact snails, mucus from *Physa* sp. was 100% toxic to miracidia at 1:3 and 1:30 dilutions with CBSS within one hour compared to CBSS control. This effect decreased to 12.2% at a 1:300 dilution. Mucus from *L. caperata*, *L. elodes*, and *L. exilis* showed no difference from CBSS for up to 4 hours. This study showed that miracidia do play an active role in locating and attacking a preferred host. However, the fact that mucus from *Physa* sp. served as a barrier to infection implied that snail components were at least as important in the host-parasite relationship.

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## (6)

### PARASITE COMMUNITY STRUCTURE IN 5 SPECIES OF DAMSELFLIES (ODONATA: ZYGOPTERA) FROM TEAL RIDGE, STILLWATER OKLAHOMA

**C.M. Wiles**, Oklahoma State University

Few ecological studies exist on parasite community structure in insects and compared to other invertebrate and vertebrate groups, insects have been largely ignored in ecological studies on parasite community structure. This is surprising because some insects such as odonates have become model systems for studies on host parasite interactions, and there is a desperate need for descriptive studies on their parasite community structure. In this study we examined 372 individual teneral and/or adults of 5 species of damselflies (*Argia apicalis*, *Enallagma civile*, *Ischnura hastata*, *Ischnura verticalis*, and *Lestes disjunctus australis*) that varied in their development time in the water, temporal and flying season, size and phylogenetic relationships. All damselflies were collected from Teal Ridge a semi-permanent wetland located in Stillwater, Oklahoma during the fall and summer of 2010-2011. The parasite compound community of this odonate assemblage consisted of at least 7 taxa: 4 gregarines, 2 helminths, and 1 mite. A total of 441 individual parasites were recovered of which 59% were gregarines, 35% were mites and 6% were helminths. In the 3 most commonly collected damselfly species, the nematode *Serpinema trispinosus* was considered a generalist and infected all 3 species of damselflies. In contrast, a majority of mites, *Arrenurus* sp. (93%) and gregarines (87%) infected *E. civile*, and were considered specialists.

Average parasite species richness was low among the 3 species of damselflies ranging from  $0.17 \pm 0.38$  (0-1) for *I. hastata* to  $0.29 \pm 0.50$  (0-2) for *E. civile*. However, in each case average parasite species richness was higher for female damselflies than males. There was no relationship in damselfly size and parasite abundance, intensity, or species richness among any of the damselfly species examined. However, *I. hastata* which begins flying in the late afternoon had the lowest parasite abundances and species richness among all damselflies sampled.

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## (7)

### REVEALING THE MECHANISTIC DETERMINANTS OF HOST SPECIFICITY: USING THE PARASITE *SCHISTOSOMA MANSONI* AND THE SNAIL *BIOMPHALARIA OBSTRUCTA* AS A MODEL SYSTEM

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The majority of parasite species exhibit host specificity. In general, our mechanistic understanding of why a particular parasite can infect some host species but fails to infect others is poor. We address this question using the digenean *Schistosoma mansoni* as our model parasite. The larval development of *S. mansoni* occurs in certain species of snails of the genus *Biomphalaria*, but not in others. For example, the Neotropical snail *B. glabrata* supports *S. mansoni* development whereas the North and Central American species *B. obstructa* does not. A series of laboratory experiments is underway to explore the underlying reasons for *B. obstructa*'s lack of compatibility with *S. mansoni*. Snails were first exposed to *S. mansoni* miracidia and sectioned to determine if there is an epidermal barrier that prevents penetration of miracidia. Histological sections revealed that miracidia penetrated *B. obstructa* and although hemocytes could be observed near intramolluscan sporocysts, the sporocysts were not overtly encapsulated and persisted for at least 8 days of observation. The sporocysts did not develop normally however, and no exposed snails shed *S. mansoni* cercariae. Next we exposed *B. obstructa* to a parasite with a known ability to interfere with hemocytes of *B. glabrata*, namely *Echinostoma paraensei*. We showed that 67% of *B. obstructa* were capable of supporting cercariae-producing infections of this South American digenean. To avoid the complication of having viable predatory rediae of *E. paraensei* present in *B. obstructa*, yet still accruing this parasite's immunosuppressive benefits, we next exposed *B. obstructa* to irradiated *E. paraensei* miracidia. We then challenged these snails four days later with viable *S. mansoni* miracidia. None of the snails became infected with either parasite. Thus, unlike with schistosome-resistant populations of *B. glabrata*, *B. obstructa* snails can not be made more vulnerable by prior exposure to *E. paraensei*. Additional experiments are underway to determine if *B. obstructa*'s lack of compatibility to *S. mansoni* can be broken down by application of environmental stresses (such as heat shock) or by knock-down of specific known snail immune genes.

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## (8)

### A TALE OF ANTHROPOGENIC DISTURBANCE: HOW FOREST DEGRADATION AND HUMAN PROXIMITY TO NONHUMAN PRIMATE POPULATIONS INFLUENCE PARASITISM

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Novel human pathogens may emerge from wildlife reservoirs as a result of anthropogenic disturbances such as people encroaching upon previously uninhabited tropical forests, agriculture, deforestation, hunting, and climate change. Pathogen emergence pathways are difficult to dissect however due to the complex interactions between the environment, hosts, and their parasites. In order to understand the



causal pathways leading to disease emergence, parasites of the mantled howler monkey *Alouatta palliata aequatorialis* in Ecuador were investigated. Environmental disturbance indicators, proximity of humans to primate populations, parasite abundance, and parasite prevalence were determined to: 1) chronicle the full scale of endoparasitism in howlers by measuring abundance, prevalence, and diversity using three morphological techniques (i.e., fecal smear, flotation and sedimentation) and genetic methodologies (i.e. traditional PCR and DNA sequencing), and 2) address the impact of environmental degradation and human proximity on howler parasitism. Fecal samples were also obtained from local human populations and individuals responded to a demographic survey to evaluate risk factors associated with parasitism. In howlers, initial results suggest at least 3 species of protozoa, 3 nematodes, 1 platyhelminth, and 3 apicomplexan. Humans had reduced parasite diversity and abundance when compared to howlers, harboring 1 protozoan species, 2 platyhelminths, and 1 apicomplexan. Findings suggest that in older growth forests parasite diversity in primates was greater than logged areas. Conversely, primates proximal to human habitation had reduced parasite diversity. These results suggest that forest degradation and human proximity to primate populations influences parasite prevalence, abundance and species diversity. These results are useful in establishing the degree to which forest degradation and human proximity influence primate parasitism.

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## (9)

### ASSESSMENT OF *PLASMODIUM FALCIPARUM* CASE-BASED SURVEILLANCE AT THE TWO MAJOR UNIVERSITY TEACHING HOSPITALS SOUTH WESTERN NIGERIA: A COMPARATIVE STUDY

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Guidelines focusing on National core indicators tools and methodology for monitoring and evaluating of Roll Back Malaria in Nigeria, in conformity with other countries in Africa region has been developed. This study gives an insight on screened patients blood presented with *Plasmodium falciparum* focusing on diverse tools of surveillance ranging from age differences, gender status, education, level of awareness and individual therapeutic approach. Blood samples were collected from the fingers pricked of 200 patients (100 from each Hospital) who visited either of the two university teaching hospital (Obafemi Awolowo University (OAUTHC) and the University College Hospital (UCH), Nigeria) between August-December 2010 for Malaria parasitemia tests. Rapid Test Kit Global device was used in detection of the presence of *P. falciparum*. All data generated were presented with chi-square description statistical analysis using statistical package for social sciences (SPSS) version 15.0 for windows. Difference were shown to be statistically significant where  $p < 0.05$ . In the OAUTHC, higher infection rate was observed among age group <20 years (71.4%), 20-30(18.2%) > 40 (16.7%), higher prevalent rate noted among male which attribute 23 (49.2%), compare with female individuals of 15(31.3%), un-educated attributed 29(62.1%),educated 20(10%),semi-educated 43(37.2%) and non experience 8(25%). Non-drug compliance individual 7(57.1%); Patients on malaria medication 70(38.6), local herb users 8(25%). 84(38.1%) shows higher level of awareness to *P. falciparum* while non-awareness 7(42.9%), indifference 9(33.3%), frequently infected individuals 22(40.9%), non-frequent infections 30(36.7%), rarely infected 36(36.17%), no response 12(41.7%). Means of protection; 22(31.8%) used insecticides, 36(55.6%) mosquito net, 40(22.5%) none. At the UCH, 12 positive results were recorded out of 100 patients tested, higher infection rate was observed among age group <20(19%), 20-30(13%), >40(4.0%), A higher prevalent rate was recorded among the female which attributed 9(12.2%), compare with male individuals 3(11.5%). Semi-educated with higher prevalent rate showed 36(25%), uneducated 21(4.8%), educated 43(4.7%). patients who were on malaria medication showed 65(13.8%), Non-drug compliance individuals 27(11.1%), local-drugs/herbs users showed no attack, insecticides means of protection constituted 39(15.4%), mosquito net 18(11.1%), non-protective users 43(9.3%), level of awareness 84(38.1%), non-awareness 7(42.9%), indifference 9(33.3%). Frequent infected individuals showed 10(20%), non-frequent



54(14.8%) and rarely infected 36(5.6%). Development of reliable information on infection risks is highly needed at the OAUTHC in comparison with the alternate hospital. Technology to prevent, monitor, diagnose and efficient treatment of malaria mostly among lower age group needs to be adapted and to be applied through local and national Malaria Control Programme.

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(10)

TWO MANIPULATIVE TREMATODE PARASITES MODIFY THE PHYSIOLOGY AND BEHAVIOR OF CALIFORNIA KILLIFISH (*FUNDULUS PARVIPINNIS*)

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**A. Sih**, University of California Davis

The trematode parasites *Euhaplorchis californiensis* (EUHA) and *Renicola buchanani* (RENB) infect California killifish (*Fundulus parvipinnis*) as second intermediate host. Infected killifish exhibit conspicuous behaviors. Infection is associated with a 10 to 30 fold increase in predation by the parasites' shared final host. Our aim is to further understand the extent to which infection modifies the killifish's behavioral and physiological phenotype. We conducted a series of laboratory assays on wild-caught killifish, quantifying hormone profiles (11-ketotestosterone, estradiol, and cortisol) and killifish behavioral type (activity, boldness, and sociability), and examined whether these traits were associated with the intensity of EUHA and RENB infection. We discuss the results from these studies, and put them in the context of previous studies identifying changes in neurotransmitter activity in response to EUHA infection. We also discuss future plans for exploring these relationships using controlled infections.

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(11)

ANTI-PARASITE DEFENSE IN THE CALIFORNIA FIDDLER CRAB, *UCA CRENULATA*: BEHAVIOR AND SEX DIFFERENCES

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Although anti-parasite behaviors are a host's first line of defense against pathogens, they are relatively understudied despite being effective ways to prevent and resist infection. The California fiddler crab (*Uca crenulata*) is host to several helminth parasites, most notably the trematode *Probolocoryphe uca*. Crabs exposed to *P. uca* exhibit increased mortality, thus anti-parasite behaviors may be important to host fitness. In addition, sex differences in host morphology and ecology could also affect infection rates in crab hosts. Fiddler crabs exhibit extreme sexual dimorphism; while females possess two small claws for feeding and grooming, males have one while the other claw is enlarged for use as an ornament and weapon. I predicted that crabs exposed to *P. uca* would exhibit anti-parasite behaviors to reduce infection. Due to differences in claw morphology, I also expected that males would be less effective at grooming and ingesting parasites than females, resulting in higher parasite abundances. To test these hypotheses I exposed crabs to *P. uca* larvae, scored various behaviors, and dissected them for parasites. To quantify behavioral efficacy in reducing infection, crabs were either behaviorally impaired (chilled) or unimpaired and exposed to *P. uca* larvae, followed by dissection for parasites. Exposed crabs were 10 times more likely to feed and groom themselves than were unexposed controls. Although males groomed twice as often as females, they harbored twice as many *P. uca* trematodes, consistent with the prediction that males are less able to behaviorally remove parasites.

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(12)

PARASITES OF RESIDENT AND MIGRATORY DOUBLE-CRESTED CORMORANTS  
(*PHALACROCORAX AURITUS*)

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Parasites used as biomarkers are valuable for tracking the movement of hosts during migration. Here, we document helminthic communities among many locations within a host species ubiquitous in North America, the Double-crested cormorant (*Phalacrocorax auritus*). We assessed over 200 *P. auritus* intestines collected from Alabama, Mississippi, Minnesota, and Vermont and documented disease and parasites. Abnormal tissues, body condition, and parasitic eukaryotes were documented in immature and adult males and females. Digenean trematodes and nematodes (Anisakidae and Capillariidae) were common. Cestodes were also frequently documented. Community parameters (abundance, richness, and relative biomass) of parasite assemblages were compared for location, age, and sex. The seasonality of parasitic infections for resident and migrant *P. auritus* in breeding and wintering colonies is addressed considering few habitats support the persistence of most parasite species. Understanding changes (and the lack thereof) of parasitic communities could elucidate shifts in the geographic distribution associated of migratory waterbirds.

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(13)

A NEW APPROACH FOR MONITORING AND MEASURING SCHISTOSOMIASIS TRANSMISSION  
IN AFRICA: EXPOSURE OF SENTINEL MICE COUPLED WITH GENOTYPING OF RECOVERED  
ADULT WORMS

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E.S. Loker, University of New Mexico

We lack quantifiable and spatially and temporally explicit estimates of the force of schistosome transmission from snails to their definitive hosts in natural transmission foci in Africa. To address this problem, we have devised floating cages that hold laboratory mice that can be placed in contact with water from lakes or streams for defined intervals, in defined localities. Following exposure of such “sentinel mice”, they are taken to the lab and six weeks later perfused to determine if they have adult schistosomes. Individual adult worms are then available for genotyping using two available panels of microsatellite primers. With this approach we can determine if some localities are more potent transmission foci than others, infer rates of acquisition of adult worms including at different times of the day or year, and learn if mice become infected with worms representing relatively few genotypes or if extensive mixing of genotypes occur. We can also learn how long some snails may persist in shedding cercariae in natural habitats. A similar approach can be devised to use with indigenous rodent species to assess their ability to serve as reservoir hosts. Our preliminary results involving habitats both along the shore of Lake Victoria and along the course of Asao stream in west Kenya reveal considerable heterogeneities among sampling sites in the numbers of worms acquired by the sentinels. This approach also revealed that mice placed in the water between 10 in the morning and 2 in the afternoon were considerably more likely to become infected than mice placed in the water either before or after this time interval. The total number of worms acquired per mouse varied considerably but in some locations was as high as 7 worms per hour. We will report results of genotyping of these worms and hope to learn if, when mice acquire large numbers of worms, the worms are genetically identical, indicative of having been acquired from the same actively shedding snail, or not.

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(14)

DAVID AND GOLIATH: EXAMINATION OF ADDITIONAL COMPLEXITY IN THE GENUS  
CALLIOBOTHRIUM (CESTODA: TETRAPHYLLIDEA) IN SMOOTHHOUND SHARKS OF THE  
GENUS MUSTELUS (CARACHARHINIFORMES: TRIAKIDAE)

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Previous molecular work on 6 of the 12 described species of the small, non-lacinate form of the cestode genus *Calliobothrium* confirmed that they represent 2 distinct clades: 1 including species with an accessory piece between the bases of the axial hooks and the other including species that lack an accessory piece. When compared with a recently generated comprehensive phylogeny of the sharks, these clades were found to be consistent with what now appears to be 2 robust clades of smoothhound sharks of the genus *Mustelus*. The present study focuses on species of the large form of *Calliobothrium* that co-occur with species of the small form in at least 7 species of smoothhound sharks. In addition to size, species of the large form of *Calliobothrium* differ from both clades of the small form in their possession of lacinate proglottids and 3, rather than 1, sucker in their apical bothridial pad. A preliminary phylogenetic analysis of 28S rDNA and 18S rDNA data supports the independent monophyly of the small and large form relative to one another. In combination, these data suggest that establishment of a new genus for species of the small form is warranted (given that type species of *Calliobothrium* is of the large form). Sequence data for a subset of species of the large form were generated to explore whether they exhibit phylogenetic substructure and host associations like those seen in species of the small form.

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(15)

COMPARISON OF PCR AND IFA FOR DETECTION OF BLASTOCYSTIS IN FOOD ANIMALS

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*Blastocystis* is one of the most common human intestinal parasites found in developed and developing countries and also in a wide range of animals. It has been found not only in individuals with gastrointestinal symptoms but also in apparently healthy and asymptomatic individuals, so the pathogenic potential of *Blastocystis* is controversial with numerous conflicting reports regarding its ability to cause disease. Diagnosis has traditionally relied on light microscopy of fecal smears, which has low sensitivity, or on culture methods that are time-consuming and not available in most diagnostic laboratories. Therefore, a diagnostic test was needed that was simple, rapid, and accurate. A new commercially available test kit (Boulder Diagnostics) was evaluated in the present study to examine feces from 48 dairy cattle for the presence of *Blastocystis* and to compare those findings with results obtained by PCR. Of 8 PCR positive specimens 7 were available for testing from cattle and all were found positive by IFA. All 38 PCR negative samples were also found negative by IFA, again indicating the accuracy and practicality of this new test kit. Neither *Cryptosporidium* nor *Giardia* were recognized by the IFA reagents. Similar testing for detection of *Blastocystis* in pigs will be reported.

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(16)

THE INFLUENCE OF ANURAN HOST SPECIES ON SITE FIDELITY OF NORTH AMERICAN  
SPECIES OF HALIPEGUS (DIGenea: HEMIURIDAE)

H.A. Stigge and M.G. Bolek, Oklahoma State University

The preferential site selection of helminths within their definitive hosts is well documented. However, factors that influence this site selection remain poorly understood. In North America, species of *Haliplus* infect the buccal cavity or eustachian tubes of amphibians and demonstrate conserved site fidelity. Studies on green frogs indicate that *H. eccentricus* is always found in the eustachian tubes of their amphibian host; whereas *H. occidualis* always resides under the tongue. However, our field work on bullfrogs indicates that the site fidelity of *H. occidualis* is more variable than previously thought. During our field studies, we always recovered *H. occidualis* from the stomach of bullfrogs, and these hosts were never infected with worms under their tongues. In order to investigate this variation in site fidelity, we established this life cycle in the laboratory. Laboratory reared snails were exposed to eggs from worms recovered from the stomach of naturally infected bullfrogs. Cercariae were collected from snails and exposed to laboratory reared microcrustaceans. Infected microcrustaceans were then fed to Woodhouse's toads, eastern gray treefrogs, and bullfrogs. Adult gravid worms appeared under the tongue of toads and treefrogs; whereas gravid worms never appeared under the tongue of bullfrogs but instead remained in the stomach. The site fidelity of *H. occidualis*, within bullfrogs, was further tested by transplanting gravid worms from under the tongue of experimentally infected treefrogs into the mouths of uninfected bullfrogs and treefrogs. Gravid worms remained under the tongue of treefrogs for over 8 weeks. In contrast, gravid adults did not remain in the buccal cavity of bullfrogs for more than 7 days, and the worms moved from the buccal cavity into the stomach. These results clearly indicate that the site fidelity of *H. occidualis* is dependent on the species of amphibian host. In addition, our study suggests a mechanism that may play an important role in the diversification of species in this genus of hemiurids that infects amphibians worldwide.

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**(17)**

**NATURAL AND EXPERIMENTAL TRANSMISSION OF *NEORICKETTSIA RISTICII* IN DIGENEANS *PLAGIORCHIS ELEGANS***

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*Neorickettsia* are obligate intracellular bacterial endosymbionts of digeneans. These endosymbionts pass through all stages of digenean life cycles via vertical transmission. Importantly, they may also be passed to the vertebrate hosts of digeneans including humans, via horizontal transmission. Despite the role of these bacteria as pathogens in domestic animals, wildlife and humans, there is much to learn about their diversity, digenean host ranges and fundamental biology. We have screened digenean cercariae from snails collected in eastern North Dakota for the presence of *Neorickettsia*. DNA was extracted from pooled cercariae and the 16S ribosomal RNA and/or citrate synthase genes were amplified by PCR and sequenced. *Neorickettsia risticii* was found in multiple digenean taxa, including schistosomatids. We have developed a model system using *Neorickettsia risticii*-infected digeneans of the genus *Plagiorchis* that were originally obtained from locally collected snails and propagated in the laboratory. For the first time, we were able to sustain neorickettsial infection through all stages of digenean life cycle in laboratory. Quantitative aspects of vertical transmission of *Neorickettsia* are presented. This study was supported by the grant R15AI092622 from the National Institutes of Health and the grant DEB 1021431 from the National Science Foundation.

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**(18)**

**JUVENILE *ANISAKIS PHYSETERIS* FROM MESOPELAGIC LANTERNFISHES AND SHORTFIN SQUID IN THE GULF OF MEXICO**

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Midwater lanternfishes (Myctophidae) and the broadtail shortfin squid, *Illex coindetti*, comprise an important link in the mesopelagic foodweb as second- and third-order consumers, and they serve as important second intermediate and paratenic hosts for anisakid nematodes. *Anisakis physeteris* is a typical anisakid. Its primary first intermediate host is typically a crustacean, and the final host is a vertebrate (a physeteroid cetacean). Mattiuccia et al. (2008) suggested that the low prevalence of juvenile *A. physeteris* infecting pelagic fishes in the Atlantic Ocean and Mediterranean Sea was the consequence of squid serving as the main intermediate host for that species. Thus, we examined myctophids and *I. coindetti* for *A. physeteris* in the Gulf of Mexico (GOM) to determine which host was more important in the lifecycle. Eight species of myctophids and *I. coindetti* were collected from 33 locations in the GOM from the NOAA R/V *Pisces* at a depth range of 50-476 m and examined for nematodes. From each location, we examined all myctophids and a maximum of 10 specimens of *I. coindetti*. Based on morphological data and subsequent sequencing of the ribosomal DNA internal transcribed spacer (ITS) ITS-1, 5.8S, ITS-2, and 28S regions, we found that *A. physeteris* infected 2 of 8 myctophid species as well as *I. coindetti*. The most heavily infected myctophid, *Lobianchia gemellari*, and *I. coindetti* both had approximately 20% prevalence of infection and approximately 1 juvenile per infected host. Juveniles of *A. physeteris* infecting *L. gemellari* were smaller than the other anisakids (*Anisakis brevispiculata*, *Anisakis typica*, *Hysterothylacium* sp. and *Raphidascaris* sp.) collected from that host, and they appeared brownish and degenerating. Juveniles infecting *I. coindetti* were large, redish-white, and apparently healthy. The similar prevalence of infection of *A. physeteris* in *L. gemellari* and *I. coindetti* probably indicates that the 2 hosts forage at a similar trophic level, but the infection in the lanternfish seems to be a short-term or dead-end one.

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## (19)

### STAGE-SPECIFIC DEMOGRAPHIC MODELS OF *HAEMONCHUS CONTORTUS* NEMATODE TRANSMISSION INCORPORATING SEASONAL CYCLING AND DENSITY DEPENDENCE

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*Haemonchus contortus* is the most pathogenic nematode of sheep, and development of drug resistance has made it increasingly difficult to control. *H. contortus* populations have a seasonal cycle, both within the host and on the pasture, and development of these stages is dependent on parasite density. Determining which stages of the life cycle are most vulnerable to control may provide alternative control strategies. Matrix models have been extensively applied in the study of population demography. These models can use field data with minimal modification, and can be executed with standard mathematical software. A benefit of this type of model is that sensitivity and elasticity analyses of the model can identify the most vulnerable components of the organism's life history, which may serve as targets for control. Our objective is to develop a stage-structured demographic matrix model of the life cycle and epidemiology of this problematic parasite. There are now large amounts of data available on the biology of *H. contortus*, and this species represents an ideal exemplar for the development and deployment of such a model. The growth, development, survival and reproduction of parasitic nematodes are subject to the effects of population density at various stages of the life cycle. This model is the first to incorporate density dependence and seasonality at multiple stages of the life cycle, within the vertebrate host and on the pasture, and the growth of the model parasite population over a period of four years corresponds to yearly dynamics of natural *H. contortus* populations. Parasite reproduction and development were damped, based on the survival and development of various components of the life cycle. The largest reduction in parasite population growth rate ( $\lambda$ ) was observed when the development of eggs to larvae was damped, relative to egg numbers ( $\lambda=1.30$ ), as compared to the absence of density dependence ( $\lambda=2.75$ ). These results indicate that control strategies targeted at reducing developing stages on pasture may help suppress *H. contortus* infections in sheep.

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(20)

LIFE HISTORY OF AN UNDESCRIBED SPECIES OF *PLAGIOPORUS* (DIGENEA: OPECOELIDAE)  
FROM A KARST SPRING IN FLORIDA

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During a survey of the digenean parasite assemblages from karst springs in the panhandle of Florida, we collected adult opecoelids from the gall bladders of 2 fishes, *Gambusia holbrooki* and *Notropis harperi*, and found digenean larval stages consistent with Opecoelidae in the pleurcerid snail *Elimia floridensis*, which was infected with sporocysts containing microcercous cercariae. The opecoelid belongs in *Plagioporus* because it has a short excretory bladder that extends to near the posterior margin of the posterior testis, and it appears to represent an undescribed species. Emerging cercariae were exposed to 34 distinct macroinvertebrate taxa collected from the spring under laboratory settings. Cercariae were observed to encyst only in the hemocoel of the oligochaetes *Chaetogaster* spp., which we observed living as commensals with *E. floridensis* in the spring. This is the first report of a species of *Plagioporus* utilizing an oligochaete as a second intermediate host. Comparison of ribosomal DNA, including the internal transcribed spacer region ITS1, ITS2, and partial 28S gene, from sporocysts (n=6) and adults (n=6) revealed that the stages were conspecific.

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(21)

DISPERSAL AND TRANSMISSION IN THE ACANTHOCEPHALAN *ACANTHOCEPHALUS DIRUS*:  
LAB AND FIELD DATA

**T. Sparkes**, DePaul University

In acanthocephalans, eggs are typically dispersed in the feces of definitive hosts. A recent laboratory-based study provided support for the hypothesis that some female acanthocephalans (*Acanthocephalus dirus*) carry eggs into the environment prior to dispersal. Here, we examined the potential occurrence of this relationship in nature. Using 6 field surveys, we searched the sediment of a local stream to determine whether the bodies of *A. dirus* females could be located. We recovered the bodies of both mature and immature female *A. dirus* individuals. All of the mature females contained mature eggs with 1 female carrying approximately 10,000 eggs. Using a lab-based behavioral experiment, we also showed that target hosts (sediment-dwelling isopods) were more likely to attempt to feed on the bodies of gravid females than immature females. These results are consistent with the interpretation that eggs can be dispersed from the bodies of female *A. dirus* in nature and that the behavior of target hosts could facilitate transmission.

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(22)

FLOW CYTOMETRY FOR THE DETECTION AND VIABILITY ASSESSMENT OF  
*CRYPTOSPORIDIUM* SPP. AND *GIARDIA DUODENALIS* IN FRESH PRODUCE AND  
ENVIRONMENTAL SAMPLES

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Up to a quarter of the reported gastrointestinal illnesses in Canada are caused by infections with the food and waterborne parasites *Cryptosporidium* spp. and *Giardia duodenalis*. In a recent study on leafy greens, we detected these organisms in 5.9 and 1.8% (respectively) of samples. One possible route of such fresh produce contamination is through agricultural use of composted materials such as manure. These organisms are typically identified by microscopy and/or polymerase chain reaction (PCR). However, the sensitivity of microscopy is limited as only small volumes can be examined at one time while requiring considerable expertise. Likewise, detection by PCR does not distinguish between live and dead (oo)cysts and may be affected by PCR inhibitors in environmental samples. To overcome these limitations, a flow cytometry method was developed for quantifying viable *Cryptosporidium* and *Giardia* in relatively large sample volumes of livestock manure and fresh produce. Raspberry, cattle and chicken manure samples were spiked with live and heat-killed (oo)cysts. Viable *Cryptosporidium* and *Giardia* (oo)cysts were detected simultaneously in both sample types, although dead (oo)cysts clustered with background debris in manure samples. SytoX Blue (Invitrogen) was evaluated as an alternative to the standard propidium iodide (PI) dye commonly used for determining viability of (oo)cysts. Viability results using SytoX Blue correlated closely to results obtained using the traditional PI method, SytoX being preferable to PI for complex samples as the tight emission/excitation spectrum enabled (oo)cyst detection despite autofluorescent debris. In addition, the availability of SytoX in multiple colors facilitated multiplex detection of several genera in a single flow cytometry assay. This novel method will enable high-throughput detection and viability assessment of (oo)cysts in clinical, environmental and produce samples, providing a means for comprehensive surveillance of products along the farm-to-fork continuum.

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## (23)

### TO STICK OR NOT TO STICK? LIFE CYCLE STRATEGIES PARAMPHISTOME METACERCARIAE DICTATE AMPHIBIAN HOST SPECIFICITY

**M.G. Bolek, S. Vhora and H. Stigge**, Oklahoma State University

*Megalodiscus temperatus* and *Allasostomoides parvus* are North American paramphistomes that infect amphibians and reptiles. Both species have similar life cycles and involve *Planorbella trivolvis* snails as the first intermediate host and the formation of metacercariae on either amphibian skin for *M. temperatus* or on amphibian skin and invertebrates for *A. parvus*. Amphibians become infected with these worms when they ingest their shed skin or invertebrate hosts containing metacercariae. Although very similar in their life cycles, these species differ drastically in their host specificity at the definite host level. *Megalodiscus temperatus* is a generalist reported from 24 amphibian species; whereas *A. parvus* has narrower host specificity and is reported from 2 amphibian species. In order to investigate these differences in host specificity, we conducted large scale field surveys and controlled experimental hosts specificity studies in amphibian hosts. Our surveys indicated that *M. temperatus* infected 7 species of anurans, whereas *A. parvus* only infected 1 species of anuran. In the laboratory both *M. temperatus* and *A. parvus* formed metacercariae on all amphibian species exposed. However, differences existed in the length of time that metacercariae of these 2 species remained on the skin of their amphibian hosts. Metacercariae of *M. temperatus* remained on skin of all anuran species exposed; whereas metacercariae of *A. parvus* dropped off the skin of all amphibian species exposed within minutes to hours. As a result, all anuran species that ingested their shed skin became infected with *M. temperatus*, but not with *A. parvus*. However, when metacercariae of *A. parvus* were feed to anurans, all individuals became infected. Our data suggest that paramphistome species specific differences in the ability of metacercariae to remain

attached to amphibian skin may have consequences on anuran colonization and host specificity among amphibian paramphistome trematodes.

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(24)

HAEMOSPORIDAN PARASITISM IN GRASSLAND SONGBIRDS OF NORTHWESTERN MINNESOTA

D.K. Kvasager and J.A. Vaughan, University of North Dakota

Native grasslands in the northern Great Plains provide vital breeding habitat for many bird species. Yet native prairie is increasingly being turned over to agriculture. As grassland habitats become more fragmented, it is important to acquire baseline information on potentially harmful parasitic diseases affecting grassland species. This study examined grassland songbirds for 3 genera of hemosporidian parasites: *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*. Sampling was conducted at 5 study sites within Pennington, Polk and Red Lake counties in northwest Minnesota during 2009, 2010 and 2011. A total of 150 birds were captured using mist nets. Most were Savannah Sparrows (50%), followed by Bobolinks (18%), and Clay-colored Sparrows (12%). A small amount of blood was collected from each bird. A portion was thinly smeared on a slide, stained and examined for parasites using microscopy. The remaining blood was extracted for DNA, which was then subjected to nested PCR, electrophoresis and sequencing. PCR detected more infections than did microscopy. Sixty-eight (45%) of the 150 bird blood samples were positive for either *Haemoproteus* or *Plasmodium* and 35 (23%) were positive for *Leucocytozoon*. A third of all infected birds contained at least 2 species of parasites. DNA sequencing indicated that *Plasmodium* infections were generally more prevalent than *Haemoproteus* infections. *Plasmodium* infection in a juvenile Bobolink indicated that active transmission occurred within the study area. By microscopy, the prevalence of hemosporidian infection was similar among adult Savannah Sparrows (58%), Bobolinks (47%), and Clay-colored Sparrows (59%). The species composition of hemosporidians within infected Savannah Sparrows and Bobolinks were divided equally between *Leucocytozoon* (46% of infections) and *Plasmodium*/*Haemoproteus* (56% of infections). However, infections in Clay-colored Sparrow were composed mostly of *Plasmodium*/*Haemoproteus* (90% of infections). Hemosporidian parasitism is common among the grassland songbirds of northwest Minnesota.

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(25)

EVALUATION OF SINGLE SLIDE FECAL SAMPLES OF ZOO ANIMALS THROUGH MICRO FLOTATION TECHNIQUE

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A. Abbas, Universidad de Salamanca, España  
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Fecal samples are evaluated for the detection of adult parasites, larvae, ova or the segments of the tapeworms. All relevant techniques require a considerable amount of feces obtained from the animals. If, in any case, there is less amount of fecal sample questions arise regarding how it can be evaluated. To evaluate a minute amount of fecal sample as low as 0.5-1.0 gram or the fecal material of only one slide, when it is positive or not, can be examined by a newly developed technique called Micro-Floatation Technique. The fecal samples used in the Direct Smear Method, present on the glass slide can also be used in this technique. The samples obtained from the zoological garden were evaluated. Among the positive zoo animals like Kiwi, Black Asian bear, Jackals, Moufflin Sheep, Black buck, Chinkara deer, spotted deer,



lion and monkeys fecal samples showed a low infestation of oocysts, cryptosporidium cyst, larva of strongyles and nematodaris.

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(26)

GIARDIASIS IN WESTERN ROMANIA: A 14-YEAR RETROSPECTIVE STUDY

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**V. Bold**, Timis County Public Health Authority, Romania

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**G. Darabus**, Faculty of Veterinary Medicine, Timisoara, Romania

**V. Dumitrascu**, Victor Babes University of Medicine and Pharmacy, Timisoara, Romania

Parasitic diseases have a worldwide distribution and represent an important public health problem. *Giardia lamblia* is found worldwide but in high prevalence in the developing countries. The aim of the present study was to evaluate the prevalence of *G. lamblia* infection in Timis County, Western Romania. Information regarding giardiasis reported by family doctors between January 1993 and December 2006 was retrospectively investigated. Epidemiological data were extracted from the Statistics Department database of the Timis County Public Health Authority. Population was grouped into 4 categories by age: 0-1 year, 1-14 years, 15-64 years and  $\geq 65$  years. During the 14-year period, 102098 cases of *Giardia lamblia* infection were reported (average number of cases/ year = 7293). 75.2% of the cases were from urban areas of the county. Of the total number of cases with giardiasis, 50423 (49.4%) were aged 1-14 years, 44385 (43.5%) were aged 15-64 years, 5627 (5.5%) were  $\geq 65$  years and 1663 (1.6%) were aged 0-1 year. A decline in the prevalence of giardiasis was observed over the past 6 years of the studied period, from 11.997 total cases in 2001, to 8.351 cases in 2006. *Giardia lamblia* infection occurs at all ages but is more frequent in those aged 1-14 years. The prevalence of the disease was higher in the urban areas of the county. Giardiasis is reported annually in Timis County and still represents an important public health problem.

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(27)

PARASITIC INFECTIONS AMONG ROMANIAN INSTITUTIONALIZED CHILDREN AND THEIR MEDICAL STAFF

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Intestinal parasitic infections are characterized by high prevalence and a variety of clinical manifestation, especially frequent in institutionalized children. The aim of the present study was to evaluate the prevalence of digestive parasitosis in a Romanian Pediatric Care Unit. We have also followed the clinical symptoms for the patients with parasitosis. Complete physical and stool examinations were performed. Stool examinations were performed using the iodine staining for the identification of protozoan cysts and the Willis-Hung method for the identification of helminth eggs. We investigated 147 institutionalized children aged 2 to 10 years. Parasitic infections were determined in 25 cases (17%). *Giardia lamblia* (16.3%), *Blastocytis hominis* (3.4%), *Entamoeba coli* (0.7%) and *Enterobius vermicularis* (2.7%) were diagnosed. We have determined associations of two (28%) and more than two parasites (4%) in children. We have also evaluated 46 adults, members of the medical staff, working in this unit. Parasitic infections were diagnosed in 15 cases (32.6%). *Giardia lamblia* (26.1%), *Blastocytis hominis* (6.5%), *Entamoeba coli* (4.3%) and *Enterobius vermicularis* (2.2%) were identified in adults. Association of two parasites was

observed in 20% of the positive cases among the medical staff. Clinical examinations were conducted to investigate the presence of symptoms in patients with parasitic infections. Respiratory infections (72%), weight loss (48%), nervous disorders (32%), diarrhoea (36%) and cutaneous manifestations (16%) were the most frequent symptoms in children. Abdominal pain (26.6%), diarrhoea (20%) and weight loss (13.3%) were observed in adults. Parasitic diseases were diagnosed in children and their medical staff. Clinical signs and association of parasites were noted in both groups.

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(28)

POPULATION GENETIC ANALYSIS OF *BAYLISASCARIS*

L.E. Camp, University of California-Davis

Studies of the genetic variation and structure of parasite populations are becoming more common. At present, most investigations focus on parasites that directly impact human health, such that population genetic structure is unknown for most parasites. In the absence of information about potential genetic variation of natural parasite populations, limited information of one or a few isolates is typically assumed to be representative for the entire species. Characterizing genetic variation of parasite populations is valuable because it influences features such as infectivity, pathogenicity, and the ability of a parasite to spread among host populations. I intend to address population genetic questions with *Baylisascaris procyonis*, the raccoon roundworm. Raccoons are widely distributed and abundant throughout much of the United States and *B. procyonis* is present (sometimes at high prevalence) in many raccoon populations. While many aspects of the *B. procyonis* system have been described, molecular studies have been limited. I am interested in regional and local patterns of genetic diversity and specifically if the urbanization of raccoon hosts influences the genetic structure of parasite populations. I intend to analyze populations of *B. procyonis* from multiple regions of the U.S., as well as locally within northern California in order to address these questions.

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(29)

CHEMISTRY OF THE *CRYPTOSPORIDIUM* OOCYST WALL

R.S. Williams, University of Texas of the Permian Basin

*Cryptosporidium* is a protozoan parasite that is responsible for significant loss of neonatal calves on dairy farms, and is also a significant zoonotic threat in both developed and developing countries. Over 150 distinct genomic variations of *Cryptosporidium* are known, with each variation exhibiting varying degrees of host species specificity. *Cryptosporidium* oocysts are capable of passing through an "incorrect" potential host unaffected, remaining infective when later introduced into the "correct" host. However, the biochemical mechanisms underlying host specificity have not been elucidated. A recent biochemical analysis of the oocyst wall identified a mix of fatty acids, straight-chain hydrocarbons, fatty alcohols, and proteins that were present in the oocyst wall, with the non-protein components having carbon chains in the range of 12 to 34 carbons in length. However, most of the chemical species identified have melting points below 640C, some significantly so. This appears to be in conflict with reports that *Cryptosporidium* oocysts remain infective after exposure to temperatures as high as 730C. While only 9 proteins have previously been reported in GenBank as being associated with the oocyst wall, there is some evidence for at least 12 distinct oocyst wall proteins. The objectives of the present study are to extend previous work by isolating and sequencing previously unidentified oocyst wall proteins, as well as to attempt to resolve the apparent conflict in reported melting points as compared to the reported upper temperature limit of viability of the oocyst.

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(30)

EFFECTS OF NITROGEN POLLUTION ON AMPHIBIAN DISEASE DYNAMICS

A.B. Mora, University of California, Riverside

Amphibian populations are experiencing dramatic worldwide decline: up to 50% of all species are threatened with extinction. Habitat destruction, climate change, pollution, disease, and competition with invasives are among the many suspected contributors. Causes of these declines are multifactorial and complex, thus more work is needed to understand their combined effects. Nitrogen pollution is one such factor that could have multiple deleterious effects on amphibian populations. Contaminants such as nitrate and ammonia are toxic to aquatic animals and have been shown to impair immune function. Further, nitrogen deposition is associated with increased abundance of macroparasites that cause severe pathology in amphibian hosts. I will outline an investigation of the relationship between nitrogen pollution and disease dynamics in native and invasive frog species. I propose that nitrogen pollution adversely affects amphibian populations in several ways: it indirectly increases macroparasite abundance, decreases amphibian immune response, and further exacerbates the ability of more robust invasive species to outcompete and depredate native populations.

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(31)

CESTODE SAFARI: THE SEARCH FOR CRYPTIC SPECIES OF THE BASS TAPEWORM  
*PROTEOCEPHALUS AMBLOPLITIS* (PLATYHELMINTHES: CESTODA)

K.E. Luth, M.R. Zimmermann and G.W. Esch, Wake Forest University

The bass tapeworm (*Proteocephalus ambloplitis*) is an obligate endoparasite that cycles through 3 hosts: a microcrustacean first intermediate host (IH) (either *Cyclops* spp. or *Hyalella knickerbockeri*), a centrarchid fish second IH, and a small or largemouth bass (*Micropterus dolomieu* or *M. salmoides*, respectively) definitive host (DH). The life cycle can also be completed by excluding the second IH if a DH consumes an infected first IH. In the northern United States, adult *P. ambloplitis* are found in DHs during the summer mo while, in the southern portion of the country, adult parasites are found in DHs during the winter mo. This regional dichotomy in the cestode's life cycle suggests that the parasites found in these different regions may be cryptic species. Alternatively, differences in the life cycle may be due to differing biotic, abiotic, or both, factors such as the presence or absence of IHs, DH hormone levels, or water temperature. Furthermore, the life cycle of this Nearctic species differs from its Palearctic congeners, all of which possess a life cycle with only 2 hosts and no parenteric developmental stage. The goal of the proposed study is to sample fish hosts from as many different lentic bodies of water in as many states in the United States as possible to identify the driving force(s) behind the life cycle dichotomy of adult parasites in DHs. A suite of ecological factors (both biotic and abiotic) will also be monitored and recorded at each sampling site, and *P. ambloplitis* specimens will be collected and preserved for molecular and morphological analyses. Ecological data, coupled with sequence data, should help explain this intriguing regional discrepancy in the bass tapeworm's life history pattern. Follow-up studies employing the molecular data obtained in the current study should provide an explanation concerning why morphologically similar Palearctic congeners of the Nearctic parasite (here described) group distantly from *P. ambloplitis*, and how the population genetic structure of this autogenic parasite compares to an allogenic group of trematode parasites being studied by a co-author.

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(32)

## THE EFFECTS OF PRESCRIBED BURN ON PARASITE FAUNA

**N. Ortega**, University of South Florida

In forming management plans for the monitoring or controlling infectious wildlife diseases, the natural ecology behind the mechanistic forces that lend to fluctuating or emerging diseases must be investigated. One such naturally occurring process that possesses the ability to alter the dynamics of natural ecosystems is fire. Fire and disease occur naturally but are also highly manipulated by humans. Currently, the Southwest Florida Water Management District conducts periodic compartmental burns at Flatwoods Park in Hillsborough County, Tampa, FL; due to location, size, and accessibility, this site is ideal for a continued effort in understanding the relationship between fire and pathogens. My project aims to gather information on the impact fire could have on host-pathogen interactions as a result of the fires killing and thereby reducing soil parasites. The objective is to determine if prescribed burns alter soil-dwelling parasitic nematode abundance and composition in soil. Additionally, I will determine if abundance and composition of these parasites are altered in herpetofauna. A Before-After-Control-Impact (BACI) design will be used to assess the effects of the prescribed burns. The results of changes in soil parasites due to fire, coupled with known beneficial ecological alterations of habitat and biodiversity during prescribed burns, could better address necessary measures for managing wildlife diseases.

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### (33)

#### POPULATION GENETICS OF *ECHINOSTOMA REVOLUTUM* ALONG THE MAJOR NORTH AMERICAN WATERFOWL FLYWAYS

**M.R. Zimmermann, K.E. Luth and G.W. Esch**, Wake Forest University

*Echinostoma revolutum* (Digenea: Echinostomatidae) is a parasite distributed across the United States and Canada in over 40 definitive hosts. Prominent definitive hosts for the parasite are Canada Geese (*Branta canadensis*), which acquire the parasite via consumption of infected snails. Geese migrate from their northern breeding grounds to their southern wintering grounds along 4 major migratory routes, the Atlantic, Mississippi, Rocky Mountain, and Pacific flyways. High site fidelity is observed in Canada Geese in both the breeding and wintering grounds, suggesting little mixing between populations. Parasite collections in each of the flyways will allow for comparison of their population genetics across a longitudinal gradient. It is predicted that the genetic diversity of *E. revolutum* will differ in each of the flyways due to longitudinal separation in both the breeding and wintering grounds of the definitive host. Comparisons of the population genetics of the parasites may also lead to the identification of cryptic species and potentially clarify some aspects of species diversity, speciation, and population dynamics among the echinostomes.

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### (34)

#### HOST UTILIZATION AND DISTRIBUTION OF SEPTATE GREGARINES (APICOMPLEXA: EUGREGARINORIDA: SEPTATORINA) IN EIGHT SHORT-HORNED GRASSHOPPER SPECIES (ORTHOPTERA: ACRIDIDAE) IN THE SOUTHEASTERN UNITED STATES

**A.D. Bartelt and T.J. Cook**, Sam Houston State University  
**A.J. Smith**, Texas Research Institute for Environmental Studies at Sam Houston State University

Septate gregarines (Apicomplexa: Eugregarinida: Eugregarinorida: Septatorina) are obligate, unicellular

endoparasites known from every invertebrate phylum, but are most common in insects, and global diversity is estimated to be around one million species. As part of our long-term goal of comprehensive discovery and systematic revision of the Nearctic Eugregarinorida, we will survey the gregarine fauna of eight species of grasshoppers (Orthoptera: Acrididae) representing five genera and three subfamilies. Host species were chosen based on taxonomic relationships to see if gregarine species infect only closely related hosts (i.e. from the same genus or subfamily) or one species of gregarine was only found infecting one host species. Hosts were also selected within areas of habitat overlap to see if ecological factors such as space or location are affecting mechanisms of host use. Time will also be considered as an ecological factor with collecting occurring across summer and fall months. Thus our sampling strategy is designed to examine patterns of host utilization and distribution. We suggest that observed similarities in gregarine assemblages in closely related grasshopper taxa, despite broad geographical separation, provides evidence of a strong coevolutionary influence on assemblage structure; whereas similarities in gregarine assemblages in geographically close or ecologically similar habitats provides evidence for ecological fitting. Attempts at cross infection will be conducted in a laboratory setting to observe the strictness of possible co-speciation or if spatial barriers are preventing infection in host species that are not as taxonomically related. I intend to present this idea-driven talk during the student research symposium.

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### (35)

#### EVOLUTION TO PARASITISM AND EVOLUTION OF PARASITIC TROPHIC SYNDROMES

**A.M. Kuris**, University of California Santa Barbara

While all parasitic groups have evolved from a free-living antecedent, the nature of the ancestral relationships are unclear. Most frequently discussed possibilities are mutualism and commensalism, but there is scant phylogenetic evidence to support either of those hypotheses. Other possibilities include predation, micropredation, saprophagy and decomposition. There are 7 distinct infectious adaptive syndromes, 5 of which are speciose: parasitoids, macroparasites (=typical parasites), pathogens, parasitic castrators and trophically transmitted parasites, and two uncommon infectious syndromes: trophically transmitted parasitic castrators and trophically transmitted pathogens. These functional groups can be distinguished by just three dichotomies. Few if any intermediate conditions exist, suggesting that evolution to these syndromes is rapid and very infrequent, envisioned as an ephemeral and steep adaptive ridge in an adaptive landscape, the appearance of an evolutionary wormhole. The ecologies of these adaptive syndromes differ considerably, concerning aggregation, crowding, host behavior modification and relative size. Recent work indicates that they play different roles in ecological dynamics at all hierarchical levels: population, community and ecosystem.

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### (36)

#### ZOMBIE ANTS: THE PRECISE MANIPULATION OF SOCIAL INSECT BEHAVIOR BY A FUNGAL PARASITE

**D.P. Hughes**, Center for Infectious Disease Dynamics Department of Entomology and Biology Penn State University

Parasites can (and often do) spectacularly manipulate the behavior of the hosts they infect in ways that enable transmission to the next host. Here I give an overview of our work on a now well developed example of complex manipulation where microbial fungi alter worker ant behavior in tropical and temperate forests. From a brief review of the natural history of the phenomenon I reconstruct the evolution of this complex manipulation including fossil evidence of manipulation before highlighting our studies into the proximate mechanisms of complex control. We show how manipulation of ant behavior has evolved multiple times. Our recent work in the Amazon has revealed how complex adaptive manipulation restricts parasites to a narrow range of host taxa as revealed by beta analysis of fungal and

ant diversity across 3 plots using a database of over 30,000 ants. The peculiar nature of social insect societies with central place foraging ecology and effective behavioral defense further restricts behaviorally manipulating fungi leading to chronic infections that are stable year to year. We have identified a trade off between short distance behaviorally induced transmission vs long range environmental transmission using a metapopulation model of disease spread that integrates the effect of hyperparasites in the system. In an interesting reversal the high specificity of the behaviorally manipulating fungus has lead to major shift in fungal biology as ant behavior (foraging ecology) shapes core features of fungal biology. We are now exploring the metabolome of the fungus to examine correlated changes.

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**(37)**

**PARASITES AND THE METABOLIC THEORY OF ECOLOGY**

**R.F. Hechinger**, University of California, Santa Barbara

Metabolic ecology emphasizes the transfer and use of energy by individuals and in ecological interactions. Energetics can provide a universal currency for ecology, spanning individuals to ecosystems. The metabolic theory of ecology (MTE) puts metabolic ecology into practice. MTE is operationally powerful because we can get to energetics with the use of a few, easily obtained variables. MTE capitalizes on the scaling of individual metabolic rate with body (or cell) size and temperature. Metabolic rate takes us straight to energetics. Parasites have bodies and they have energy metabolism. Parasites also comprise the bulk of species diversity and parasites impact most free-living species. However, MTE research has not typically considered parasites or parasitism. Nevertheless, considering parasites can inform and enhance MTE. We can also use MTE in parasitology. I will cover several areas where parasitology and MTE bear on one another. Individual energy metabolism provides the starting point. Here, parasites may differ from free-living species, maximizing power instead of efficiency. Scaling upwards, I will then present an MTE framework for parasite assemblages within individual hosts. We can immediately apply this framework to observed infrapopulations/communities. This may facilitate a better understanding of parasites and their impacts on hosts. Progressing to larger scales, I will then examine how considering parasites simultaneously with free-living species permits us to develop and test new MTE theory. I will particularly focus on improved MTE theory for species abundance that applies to all life forms in food webs. Building upon this, we can use MTE to examine the energetic importance of parasites in entire ecosystems. I will conclude by mentioning a few of the promising avenues for future research that involves parasitology and MTE.

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**(38)**

**BUEDING AND VON BRAND LECTURE**

**ADVENTURES IN ANTIPARASITIC DRUG DISCOVERY: THERE AND BACK AGAIN**

**T.G. Geary**, McGill University

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**(39)**

**PENTASTOMES (PENTASTOMIDA: CEPHALOBAENIDA) ISOLATED FROM THE ENDANGERED RATTLESNAKE, *CROTALUS UNICOLOR* FROM ARIDOK NATIONAL PARK, ARUBA**



**S. Staicer** and **J.M. Goessling**, Department of Biological Science, Sam Houston State University  
**W. Lutterschmidt** and **A. Smith-Herron**, Sam Houston State University, Texas Research Institute for  
Environmental Studies

**T. Cook**, Department of Biological Science, Sam Houston State University

During a routine biodiversity survey in Aridok National Park Aruba in the summer of 2010, three specimens of the endangered Rattlesnake, *Crotalus unicolor* were collected and necropsied for parasites. A total of 39 larvae and one adult of an unknown pentastome were taken from the upper to middle respiratory tract. Specimens were excised, fixed in 10% formalin, and stored for transport in 70% Ethanol. The adult and larvae were examined with an Olympus SZX16stereo microscope, and pictures were taken with an Olympus SDF Plapo camera. To aid in identification, the cephalothorax was removed, dehydrated in an ethanol series, cleared in xylene, and mounted with Damar Balsam. Measurements of the oral cadre, and 2 pairs of hooks of the cephalothorax were obtained. A total of seven morphological characters were selected for measurement to identify the adult specimen: total adult body length, adult body width at the widest point, estimated annulus number, adult mouth length, adult mouth width, adult pharynx width, and hook dimensions. This pentastomid provides a new host and location record.

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## (40)

### EXPERIMENTAL EXCYSTATION OF *BLABERICOLA MIGRATOR* AMONG ELEVEN SPECIES OF COCKROACHES

**S.M. Steele**, **D.T. Clopton** and **R.E. Clopton**, Peru State College

An experimental excystation assay was used to test the potential species isolating effect of host excystation signaling among gregarines. Oocysts of a single gregarine species, *Blabericola migrator*, were tested for activation, excystation, and sporozoite motility using intestinal extracts from 11 species of cockroaches representing a cohesive phylogeny of seven genera, three subfamilies, and two families of Blattodea. Sporozoite activation, excystation, and motility were observed for all excystation assay replications using intestinal fluid from hosts in the family Blaberidae, but delayed or delayed excystation was observed for all excystation assay replications using intestinal fluid from hosts in the family Blattellidae. The study results illustrate a trend toward a generalized host excystation signal among gregarines that is conserved across the host clade at a subfamily or family level, but is unlikely to play a significant role as a species isolating mechanism among gregarine sibling species.

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## (41)

### PARASITE ORIGINS ON THE TREE OF LIFE

**S.B. Weinstein** and **A.M. Kuris**, University of California, Santa Barbara

Perhaps half of extant species are parasites and most major metazoan lineages have parasitic members. Because of this diversity it is unclear how many times parasitism, as a trophic strategy, has evolved. We used existing phylogenies of metazoan groups with parasitic members to estimate the minimum number of transitions from free living to parasitic trophic strategies. The extant species diversity in parasitic clades was compared to that of their non-parasitic sister clades to test the hypothesis that the evolution of parasitism leads to adaptive radiations. A single transition to parasitism is seen in many highly specious parasitic clades such as the parasitoid hymenoptera, Trematoda+Cestoda+Monogenea, and unionid mussels. In other groups, such as the nematodes, lice, and copepods, the diversity of parasitic species can be traced to multiple origins of parasitism. Although the majority of parasite species are found in groups containing large parasitic clades, the majority of transitions to parasitism are not found in these same

groups. Some groups, such as the Diptera, contribute disproportionately to the total number of transitions from free living to parasitic trophic strategies. Overall, the origin of parasitism appears to be a rare occurrence that does not, in general, lead to adaptive radiations.

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## (42)

### MOLECULAR PHYLOGENETICS REVEALS MULTIPLE INTERMEDIATE HOSTS ACROSS WIDELY DISTRIBUTED ECHINOSTOMATID PARASITES

**R.C. Jadin** and **S.A. Orlofske**, Department of Ecology and Evolutionary Biology, University of Colorado Boulder  
**J. Koprivnikar**, Department of Biology, Brandon University, Canada  
**P. Johnson**, Department of Ecology and Evolutionary Biology, University of Colorado Boulder

Echinostomatid trematodes are a diverse and widespread group of parasites that are increasingly the focus of investigations owing to their effects on sensitive amphibian hosts. However, the evolutionary relationships, cryptic diversity, and biogeography of these parasites remain largely unexplored. Our objectives were to assess diversity of echinostomatid parasites across hosts and a wide-geographic range. Our geographic sampling included California (8 sites), Arizona (1 site), Wisconsin (1 site), and Manitoba, Canada (2 sites). We obtained DNA from 19 individuals of multiple life stages of echinostomatid parasites (i.e., cercaria, metacercaria, and redia) from two snail (*Helisoma trivolvis* and *Lymnaea* sp.) and two anuran (*Pseudacris regilla* and *Rana catesbeiana*) intermediate host species. We conducted standard PCR on this DNA using a nuclear gene fragment (internal transcribed spacer region of ribosomal DNA, ITS 1). Novel sequences were combined with previously published material on genbank for Bayesian phylogenetic analyses of Echinostomatids. We find that *Echinostoma* and *Echinoparyphium* species are widely distributed across North America. Additionally, these species use multiple intermediate snail and anuran hosts. Finally, we not only found at least two echinostome species at a single site using the same snail host species but also found two echinostome species in the same individual snail. Building on these preliminary results, we plan to incorporate additional molecular markers (ITS 2 and CO1), increase our sampling of diverse snail and anuran hosts, and broaden our geographic range in order to better characterize biogeographic and host use patterns.

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## (43)

### HOST UTILIZATION AND DISTRIBUTION OF SEPTATE GREGARINES (APICOMPLEXA: EUGREGARINORIDA: SEPTATORINA) PARASITIZING ISCHNURA SPP. (ZYGOPTERA: COENAGRIONIDAE) IN THE SEVEN BIOTIC PROVINCES OF TEXAS, U.S.A.

**M.B. Mardock** and **T.J. Cook**, Sam Houston State University

Septate gregarines (Apicomplexa: Eugregarinorida: Septatorina) are obligate, unicellular endoparasites known from every invertebrate phylum, but are most common in insects. The damselfly genus *Ischnura* (Odonata: Zygoptera: Coenagrionidae) is a cosmopolitan genus comprising 14 species across the United States, 10 of which occur across various habitat preferences and environmental conditions in Texas. Among damselflies, *Ischnura* remains under-sampled with gregarines known only from a single species. *Ischnura verticalis* is the type host for *Domadracunculus janovyi* Clopton, 1995, and *Steganorhynchus dunwoodyi* Percival et al, 1995 but is also a reported host for *Actinocephalus carrilynnae* Richardson and Janovy 1990, *Nubenocephalus nebraskensis* Clopton, Percival, and Janovy 1993, *Hoplorhynchus acanthotholius* Percival, Clopton, and Janovy 1995, and *Nubenocephalus secundus* Hays et al, 2007. As part of our long-term goal of comprehensive discovery and systematic revision of the Nearctic Eugregarinorida, we surveyed the gregarine fauna of ten species of *Ischnura* from each of the seven biotic



provinces in Texas. We report additional information of gregarine diversity in a previously under sampled taxon.

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(44)

DO INTERMEDIATE HOSTS PLAY A ROLE IN PARASITE POPULATION STRUCTURE? A  
PHYLOGEOGRAPHIC STUDY OF *TRICHOBILHARZIA QUERQUEDULAE*

E.T. Gendron, D. Malone, E.S. Loker and S.V. Brant, The University of New Mexico

Understanding parasite distribution and population dynamics is an important and understudied area within Parasitology. Host influence on parasite diversification and distribution is not clearly understood, especially in heteroxenous systems, yet is a key component of understanding parasite evolutionary ecology. Determinants of gene flow, dispersal ability of larvae and degree of host specificity, remain largely unknown. How does the intermediate host, typically with more restricted dispersal abilities, contribute to gene flow within parasite populations when the definitive host is vagile? Avian schistosomes, which represent an amazing diversification within the blood fluke family Schistosomatidae, cycle through aquatic snail intermediate hosts which have restricted dispersal abilities and water birds, which are highly vagile as their definitive hosts. Within Schistosomatidae, *Trichobilharzia* is the most speciose genus infecting primarily ducks and two families of snails worldwide. In an effort to understand how population structure relates to patterns and mechanisms of diversification, we reconstructed the phylogeography of *Trichobilharzia querquedulae*, using mitochondrial ND4 gene region and created a haplotype map of subpopulations across its known range. *Trichobilharzia querquedulae*, found throughout North America infects three species of dabbling ducks and uses physid snails as an intermediate host. Is there evidence of population structure in a species with a highly vagile avian host? We predicted that there would be high gene flow and a homogenization of genetic diversity, driven by the definitive host. We also predicted that the haplotype map would reveal hidden genetic diversity between intrapopulations, possibly due to the dispersal constraints of the intermediate host. Our phylogeographic analysis showed no population structure within *T. querquedulae* based on host, either definitive or intermediate, or geography. Haplotype maps provided a finer resolution of genetic diversity, which proved to be higher than expected. These findings aid in understanding the role that each host plays in parasite distribution and population dynamics of a widespread and diverse genus of schistosomes.

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(45)

UNDERSTANDING EVOLUTIONARY CHANGES IN LIFE CYCLE COMPLEXITY USING THE  
GENUS *ALLOGLOSSIDIUM* AS A MODEL

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Life cycle complexity (number and host species needed to complete development) can influence parasite transmission, gene flow, and mating systems, and thus, is a key determinant of parasite ecology and evolution. Before comparative approaches can be used to understand how different life cycle patterns impact parasite ecology and evolution, it is first necessary to elucidate the phylogenetic patterns of changes in life cycle complexity. Many digeneans have a 3-host life cycle, where worm sexual reproduction occurs in a vertebrate final host, but some species exhibit a 2-host pattern where sexual maturity occurs in what is typically considered the second intermediate host. In the genus *Alloglossidium*, 2- and 3-host life cycles are present and a variety of final hosts are used (catfish, crustacean, or leech). Thus, this genus provides a model system to study the evolution of life cycle complexity. Previous studies on this genus have led to 3 hypotheses about the origin of changes in life cycle pattern: 1) an ancestral 3-host life cycle

underwent 2 independent losses of the vertebrate host, 2) the 3-host pattern was derived from an ancestral 2-host (leech final host) life cycle, and 3) a single transition led from a 3-host to a 2-host pattern, with subsequent host switching from crustaceans to leech final hosts. These hypotheses were based on deductive reasoning (1, 2) or a phylogeny generated from morphological and life history data (3). Here we use mtDNA and nuclear DNA data to conduct an independent test of the evolutionary changes in life cycle complexity. Using representative *Alloglossidium* species with different life cycles we present a reconstruction of relationships within the genus and assess support for the 3 previous hypotheses. In particular, our data suggest multiple origins of changes in life cycle complexity. We discuss the broader context of these results in terms of Dollo's law of irreversibility, developmental changes, host use, and the potential to do subsequent comparative ecological/evolutionary studies using the genus *Alloglossidium*.

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**(46)**

**ZINC PVA VERSUS POTASSIUM DICHROMATE FOR PRESERVATION OF MICROSPORIDIAN SPORES**

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Human microsporidiosis is an emerging opportunistic disease. Preservation of the biological properties of microsporidian spores is frequently required in research work. We compared zinc PVA and potassium dichromate solutions for preservation of microsporidian spores separated from human faecal samples. After 0, 1, 2 and 4 months of storage, morphological features and staining characters of the spores were assessed by light microscopy in modified trichrome stained smears and their viability percentages were calculated using acridine orange/ethidium bromide mixture. Also, spore infectivity was evaluated by faecal spore shedding [number of spores per oil immersion field /mouse (S/OIF/M)] and intestinal spore load [number of microsporidia infected epithelial cells/villous / mouse(IC/V/M)] in mice orally inoculated with the preserved spores. Friedman Chi<sup>2</sup> test was used to analyze the effect of storage duration on spores viability and infectivity. In case of significance ( $P < 0.05$ ), Wilcoxon signed ranks Z test was used for further analysis. Results revealed that morphological features and staining characters of the spores were maintained in both solutions throughout the study period. In PVA and potassium dichromate, viability percentages of the spores decreased from 89% and 86% at the beginning of preservation to 69 and 66% at the 4<sup>th</sup> month of preservation ( $P > 0.05$ ). In mice orally inoculated with PVA preserved spores, the reductions in fecal spore shedding ( $9.11 \pm 4.7$  S/OIF/M after 4 months of preservation compared to  $11.68 \pm 4.2$  S/OIF/M at 0 month of preservation) and intestinal spore load ( $5.43 \pm 3.5$  IC/V/M after 4 months of preservation compared to  $7.17 \pm 2.3$  IC/V/M at 0 duration) were not statistically significant denoting adequate preservation of infectivity in Zinc PVA. Baseline infectivity deteriorated significantly after four months of preservation in potassium dichromate solution as shown by reduction in fecal shedding from  $9.38 \pm 4.3$  to  $5.01 \pm 2.4$  S/OIF/M and spore load from  $6.23 \pm 1.6$  to  $2.73 \pm 1.6$  IC/V/M.

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**(47)**

**LIVING OUTSIDE THE SNAIL: IN VITRO MAINTENANCE OF TREMATODE LARVAE FROM THE MARINE SNAIL *CERITHIDEA CALIFORNICA***

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The development of *in vitro* systems that permit the maintenance and cultivation of marine trematode rediae and sporocysts would greatly facilitate studies of trematode biology. We evaluated methods for the *in vitro* maintenance of digeneans that infect the marine snail *Cerithidea californica* as first intermediate host. Initial observations using several commercially available media indicated that Leibovitz's L-15 medium (modified for marine invertebrates) performed best for the rediae of two trematode species, *Euhaplorchis californiensis* (Heterophyidae) and *Himasthla* sp. B (Echinostomatidae). We then evaluated the impacts of several factors on mean survival time, monitoring motility, tegument integrity, and color. The treatments were: a) Use of the modified L-15 medium vs. balanced salt solution, b) Temperature variation (constant 15°C, constant 19°C, or diurnal fluctuation), and c) Incorporation of tissue fragments from the host *tunica propria*. The trematodes appeared to perform equally well in all treatments in which the L-15 medium was employed. The optimized medium permitted maintenance of rediae for an average of 23 days ( $\pm 12$  d) to at least 60 days, at which time the experiment was terminated. Additionally, survivorship varied substantially (up to eight-fold) between rediae originating from different host individuals. Notably, cercariae also survived in the optimized medium, generally maintaining normal swimming for up to 4 days, with some retaining activity for up to 25 days. Further development of this technique can provide a valuable tool to better understand the biology and ecology of these organisms, including investigations of social structure, and interspecific and intraspecific competition.

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(48)

PRESENCE OF MITOCHONDRIAL PSEUDOGENES AND THE DESCRIPTION OF A NEW SPECIES OF *PSEUDOCORYNOSOMA* (ACANTHOCEPHALA: POLYMORPHIDAE) BASED ON MORPHOLOGICAL AND MOLECULAR DATA

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*Pseudocorynosoma* is currently composed of 5 species that use waterfowl as definitive hosts and amphipods as intermediate hosts, with a distribution ranging from North to South America. In the current study, specimens identified as *P. constrictum* type species and *P. anatarium* were collected from several waterfowl species of the genera *Anas* and *Bucephala* respectively. However other specimens from *Pseudocorynosoma* sp., were collected from the ruddy duck (*Oxyura jamaicensis*). In the current study DNA sequences from the large subunit, including the domains D2 + D3 of the rDNA (LSU) and of the cytochrome c oxidase subunit I (cox1) were generated. Our sequences were aligned with other species of Polymorphidae available in the genbank data set. Maximum likelihood, maximum parsimony and Bayesian Inference analyses were performed for the combined data sets (LSU + cox 1) and each data set alone. All the phylogenetic analyses showed that the specimens of *Pseudocorynosoma* sp., from ruddy duck represented a monophyletic clade with strong bootstrap support and Bayesian posterior probabilities. The morphological evidence, in combination with the genetic divergence estimated with two genes, the reciprocal monophyly in all the phylogenetic analyses, suggested that the specimens of *Pseudocorynosoma* sp., from ruddy duck represent a new species. *Cox 1* pseudogenes sequences were detected and placed in a clade in the phylogenetics trees. The presence of pseudogenes only in *P. anatarium* represent the second record in acanthocephalans.

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(49)

DROUGHT-INDUCED AMPLIFICATION OF WEST NILE VIRUS TRANSMISSION IN THE NORTHEASTERN UNITED STATES

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The purpose of this study was to examine the influence of inter-annual variations in temperature and precipitation on seasonal mosquito abundances, the ability of local mosquito communities to maintain and transmit WNV (vector community competence), and the prevalence of WNV in the northeastern United States. Vector and virus surveillance took place within Middlesex County in New Jersey (USA) over two transmission seasons (2010/2011). It was discovered that drought conditions occurring during the 2010 season resulted in significant increases in the number of blood-fed *Culex spp.* mosquitoes collected per week ( $85.5 \pm 56.6$ ) and in the ability of local vector communities to transmit WNV ( $0.45 \pm 0.08\%$ ), measured as vector community competence, when compared to the milder 2011 season ( $40.9 \pm 36.5$ ;  $0.35 \pm 0.08\%$ ). These increases correlated to increases in weekly WNV infection rates during the 2010 season ( $18.44 \pm 8.5/1000$ ) compared to the 2011 season ( $8.3 \pm 3.5/1000$ ). Additionally, the positive influence of drought on the amplification of WNV was also confirmed at the state level where early seasonal (June-July) increases in temperature and decreases in precipitation were strongly correlated ( $r = 0.78$ ;  $0.63$  respectively) with increases in yearly WNV infection rates over a nine-year period (2003-2011). These data provide concrete evidence that early seasonal drought conditions positively impact the transmission dynamics of WNV at both the local and regional levels.

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**(50)**

**ORIGIN AND SPREAD OF BENZIMIDAZOLE RESISTANCE MUTATIONS IN THE PARASITIC NEMATODES *HAEMONCHUS CONTORTUS* AND *HAEMONCHUS PLACEI*: INSIGHT FROM GENETIC DATA**

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The parasitic nematode species *Haemonchus contortus* and *Haemonchus placei* are highly pathogenic parasite species of ruminants worldwide. Although these parasites have strong host preferences, they can infect multiple host species and co-infections have been reported. *H. contortus* is most commonly found in sheep and goats, whereas *H. placei* is most common in cattle. Anthelmintic resistance is now widespread in *H. contortus* populations worldwide. In contrast, the extent of anthelmintic resistance in *H. placei* is currently unknown. The two parasite species are phylogenetically close and experimental co-transplantation of adult parasites can result in hybridization between two species. Hence this provides a potential mechanism by which resistance genes from *H. contortus* could pass into *H. placei* populations. *H. contortus* and *H. placei* are sympatric in many regions of the world especially where large and small ruminants share the same pasture. However control of parasitic nematodes in ruminants is heavily dependent upon the prophylactic use of broad spectrum anthelmintics drugs. Resistance to the all major class of anthelmintics has been observed in parasitic nematodes of livestock. There are three different mutations (P200, P198 and P167) in the isotype-1  $\beta$ -tubulin gene that have been associated with benzimidazole (BZ) resistance in *H. contortus*. Although the understanding of the mechanisms and genetics of anthelmintic resistance is now progressing there are many aspects that remain poorly understood. In particular it is still unclear how resistance originates and spreads in parasite populations in the field. In the present study, we have shown that co-infection and interspecies hybridization does occur in natural field populations of these two parasite species and we are currently investigating if this leads to introgression of BZ resistance mutations between species.

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**(51)**

**INSIGHTS INTO THE CONTROL OF MOSQUITO HEART CONTRACTIONS**

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Mosquitoes propel hemolymph by the contractile action of a dorsal vessel that extends the length of the insect and is subdivided into an abdominal heart and a thoracic aorta. Hemolymph enters the heart through 7 pairs of incurrent valves, called ostia, and is propelled in anterograde (toward the head) and retrograde (toward the tip of the abdomen) directions prior to being released into the hemocoel through distal excurrent openings. In previous ASP meetings we have described potent immune responses that occur in the peristial regions of the heart, and these data suggest that the manner and direction in which the heart contracts might influence a mosquito's ability to overcome a systemic infection. Thus, we have begun to investigate various factors that may affect heart contraction rates and contraction directionalities. Here, we will present our bioinformatic identification of several potentially myotropic neurohormones in the mosquito, *Anopheles gambiae*. Specific emphasis will be placed on the neurohormone corazonin, a peptide originally discovered in the cockroach, *Periplaneta americana*, because of its cardioacceleratory effect but later shown to have little myotropic activity in other insect species. In *A. gambiae*, corazonin is encoded by a single gene but is alternatively spliced. Both splice variants share the same developmental expression pattern, with peaks in transcription in second instar larvae and during the pupa to adult transition. Functional experiments where various amounts of synthetically produced corazonin were injected into mosquitoes showed that increasing corazonin levels in the hemocoel does not affect heart physiology. Similarly, partial knockdown of corazonin transcription has little effect on heart contraction rates or contraction directionalities. Thus, while corazonin has been shown to have cardioacceleratory activity in some insects, its function in mosquitoes remains unknown.

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**(52)**

**MICROFILARIAE AND WEST NILE VIRUS IN SONGBIRDS - A TRUE-LIFE EXAMPLE OF MICROFILARIAL ENHANCEMENT OF ARBOVIRAL TRANSMISSION?**

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In nature, the vertebrate reservoirs of arboviruses also harbor a wide range of hematozoan parasites. One type of hematozoan - i.e., microfilariae (mf) - has been shown in laboratory studies to enhance the infectivity of arboviruses to mosquitoes. Soon after being ingested, mf penetrate the mosquito midgut. If the host blood also contains virus (i.e., vertebrate is dually-infected), some of the virus can enter the mosquito hemocoel directly, circumventing the normal route of arboviral infection within the mosquito midgut epithelia. Mf-mediated movement of virus into the mosquito hemocoel can enhance arboviral transmission by 1) transforming otherwise virus-incompetent mosquito species into virus-competent species; and 2) accelerating virus development, allowing mosquitoes to transmit virus sooner than normal. This phenomenon is termed microfilarial enhancement of arboviral transmission. There are four requirements that must be met in order for this phenomenon to occur in nature. We investigated two of these requirements as they apply to the enzootic transmission of West Nile virus. To do this, we determined 1) the potential prevalence of dually-infected robins and grackles in eastern North Dakota, 2) the temporal overlap between mf in the blood of songbirds and the feeding activities of local mosquitoes, and 3) the ability of mf of different songbird species to penetrate the midguts of mosquitoes. We concluded that mf infections may play a role in the natural transmission of some arboviruses and that the potential interaction between arboviruses and hematozoan parasites deserves closer scrutiny.

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**(53)**

**IN VIVO STUDY OF ANTIPLASMODIAL ACTIVITY OF *TERMINALIA AVICENNIOIDES* AND ITS EFFECT ON LIPID PROFILE IN MICE INFECTED WITH *PLASMODIUM BERGHEI***



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*Terminalia avicennioides* has been used traditionally in the treatment of malaria, but the actual curable dosage and its effect on some biochemical parameters have not been studied. This work studies the antiplasmodia activity of *T. avicennioides* and its effect on the lipid profiles in mice infected with *Plasmodium berghei*. Mice used for this study were grouped into five. The first group was not infected with the malaria parasite, the second group was infected with the parasite but not treated with antimalaria drugs, the third group was infected with the parasite and treated with 5mg/kg body weight of artesunate, while the fourth and fifth groups were infected with malaria parasite and treated with 100 and 200mg/kgbw of *T. avicennioides* respectively. The parasitaemia was monitored for five days upon treatment. The animals were sacrificed on the fifth day and the blood was collected. The serum was used to assess the biochemical parameters. The rate of parasite clearance in animal treated with antimalaria drugs was compared with those without treatment. As the parasite density increases in the negative control per day, there was a sharp reduction in the parasite density in the treated groups. The rate of parasite clearance was significantly higher ( $p < 0.05$ ) in those treated with 200mg/kgbw of *T. avicennioides* than those treated with 100mg/kgbw of *T. avicennioides* and 5mg/kgbw of artesunate. The mean total cholesterol was significantly lower ( $p < 0.05$ ) in the group treated with 200mg/kgbw of *T. avicennioides* than in the normal control and the group treated with 5mg/kgbw of artesunate. HDL was significantly higher in those treated with 200mg/kgbw than in the normal, negative and positive control. The mean LDL level was significantly higher in the positive control than negative control and in the group treated with 100mg/kgbw. This study shows that *T. avicennioides* have higher antiplasmodial activity than artesunate which is one of the first line drugs in the treatment of malaria in Nigeria. It is also capable of boosting HDL levels in malaria-infected organisms.

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## (54)

### TREMATODES AND A CONTAMINANT AFFECT NUTRIENT CYCLING AND PRODUCTIVITY IN A FRESHWATER ECOSYSTEM

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Parasites are ubiquitous members of ecological communities, but have only recently been recognized as key players in broad ecological interactions and ecosystem dynamics. Likewise, organisms in natural systems are exposed to an increasing array of potential chemical contaminants including manufactured nanomaterials with unknown ecological consequences. Many trematodes infect snails as intermediate hosts, often altering snail body and excretory elemental ratios. We explored the effects of trematodes on benthic ecosystem processes through their effects on snail nutrient recycling and grazing in the presence of realistic concentrations of a potential contaminant, nanosilver. Specifically, we investigated the relationships among the prevalence of the trematode *Trichobilharzia*, their host snails (*Physa acuta*), and ecosystem processes with and without nanosilver. In an outdoor mesocosm experiment, we measured periphyton productivity, N:P ratio, algal community structure, and snail populations across a range of trematode prevalence. Trematode prevalence negatively affected benthic algal productivity and altered algal elemental composition, but the relationships were altered in the presence of 0.03µg/L nanosilver. Specifically, algal N:P ratios were linearly and positively dependent on trematode prevalence in the presence of nanosilver, but nonlinearly related in the absence of nanosilver. Nanosilver reduced periphyton productivity by 20% likely due to its antibacterial properties. *Physa* biomass was reduced in highly infected mesocosms. However, nanosilver stimulated *Physa* egg production resulting in 27% more

snail individuals after 28 days of exposure compared to mesocosms without nanosilver. Thus, greater trematode prevalence reduced algal productivity and altered algal N:P elemental composition, but the effects depended on the presence of nanosilver. Overall, these results indicate that trematodes modify ecosystem processes and the net result of these parasite-ecosystem interactions is affected by anthropogenic chemical pollution.

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## (55)

### PHOTOBHAVIOR OF MARINE CERCARIAE THAT UTILIZE DIFFERENT SECONDARY INTERMEDIATE HOSTS

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For parasitic larvae, light can serve as an important exogenous cue allowing them to locate specific microhabitats, thereby increasing the probability of encountering their next host. Here, photoresponses of two species of marine cercariae were tested under two types of light fields in order to determine whether light plays an initiating and orienting cue for swimming behavior. *Euhaplorchis* sp. and *Probolocoryphe lanceolata* initially parasitize the same species of benthic snail, but then utilize different second intermediate hosts located in pelagic and benthic habitats, respectively. In a laboratory experiment that simulated downwelling light, dark-adapted *Euhaplorchis* cercariae swam slowly in darkness but ascended quickly towards light at quantal intensities over  $4.0 \times 10^{15}$  photons  $\text{m}^{-2} \text{s}^{-1}$ . Their swimming speed increased significantly with increasing light intensity, exceeding  $1.5 \text{ mm s}^{-1}$  under the highest light levels. In a horizontal trough, they oriented towards the directional light source, confirming that light plays both an initiating and orienting role in phototactic behavior resulting in ascent in the water column in order to locate a fish host. In contrast, *P. lanceolata* cercariae exhibited haphazard vertical swimming in darkness, but exhibited direct downward swimming upon exposure to light intensities  $>4.0 \times 10^{14}$  photons  $\text{m}^{-2} \text{s}^{-1}$ . Such downward swimming can quickly bring cercariae to the benthic environment, facilitating their contact with crabs. They also swam significantly faster (up to  $1.08 \text{ mm s}^{-1}$ ) during the light stimulus compared to darkness. In contrast to *Euhaplorchis*, *P. lanceolata* cercariae did not swim in response to a directional light source, suggesting that while light initiated their descent, their orientation may be controlled by another factor, such as pressure or gravity. These light-mediated behavioral responses support the use of light in selecting for microhabitats frequented by potential hosts; an adaptive benefit that may enhance transmission success.

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## (56)

### PREDATION ON PARASITES: EFFECTS OF PREDATOR TYPE, PARASITE SPECIES, AND ENVIRONMENTAL CONDITIONS

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Parasites can contribute significantly to biomass flow and networks of aquatic food webs. Direct predation on free-living infective stages, such as trematode cercariae, influences these processes and interactions. How specific parasite traits, predator traits, and the environmental context influence predation risk is an important consideration. Our objectives were to 1) compare parasite consumption by vertebrate and invertebrate predators that varied in size, 2) quantify the vulnerability of four trematode species that differed across a body size gradient, and 3) evaluate the effect of a light or dark environment on consumption. Because trematode species have variable circadian shedding patterns, they are not continuously available to predators and may vary in predation risk as a function of light conditions,

particularly for visual predators. We assessed the consumption of cercariae using short-term laboratory experiments quantifying the number of parasites removed by the predators. We observed strong and complex interactions between the factors tested by our laboratory study. First, consumption differed based on the predator species. Damselfly nymphs consumed 30-50% of two parasite species of intermediate size (770-1080  $\mu\text{m}$ ) but less than 4% of cercariae smaller (530  $\mu\text{m}$ ) or larger (1180  $\mu\text{m}$ ). Damselflies also consumed more parasites in the light compared to the dark, but damselfly body length did not influence consumption. Mosquitofish consumed between 10-90% of cercariae. Small mosquitofish (~10 mm) consumed over 80% of each parasite taxa, but their consumption was reduced by more than half in the dark treatments. Large mosquitofish (~30 mm) showed similar consumption rates in the light and dark treatments, but overall consumption correlated positively with parasite body size. None of the parasite taxa infected damselflies, but two species *Ribeiroia ondatrae* and an echinostome (morphotype: magnacauda) infected mosquitofish. Collectively, we show that diverse traits can influence parasite consumption with implications for biomass and energy flow in food webs.

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**(57)**

**PARASITE COMMUNITY STRUCTURE IN SLIMY SCULPIN (*COTTUS COGNATUS*) AND LONGNOSE DACE (*RHINICHTHYS CATARACTAE*) FROM TRIBUTARIES EXPERIENCING DIFFERENT LEVELS OF OIL SANDS DEVELOPMENT IN THE ATHABASCA RIVER WATERSHED (ALBERTA, CANADA)**

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The effects of oil sands operations on parasite community structure were assessed in slimy sculpin (*Cottus cognatus*) and longnose dace (*Rhinichthys cataractae*) from the Steepbank and Firebag rivers, two tributaries of the Athabasca River (Alberta, Canada) experiencing different degrees of oil sands development. Fish (152 sculpin, 90 dace) were collected from three locations on each tributary, and parasite abundance, diversity, and community structure were examined in relation to explanatory variables including host species, location within watershed, water chemistry, sediment characteristics, as well as contaminant levels in water and sediment. Parasite species richness differed significantly between sculpin ( $S=1.7 \pm 0.9$ ) and dace ( $2.7 \pm 0.8$ ), but not between rivers, nor among sites along individual rivers. Sculpin and dace fundamentally differed in the composition of their parasite communities. Sculpin parasite communities were dominated by *Diplostomum* sp., *Tetracotyle* sp., and *Rhabdochona cotti*; other parasites found were *Gyrodactylus* sp., *Bucephalus* sp., *Ornithodiplostomum* sp., *Hysteromorpha* sp., *Ichthyobronema hamulatum*, *Raphidascaris acus*, and glochidia. Conversely, dace communities were dominated by *Gyrodactylus stunkardi*, *Ornithodiplostomum* sp., and *Bucephalus* sp.; other parasites found were *Tetracotyle* sp., *I. hamulatum*, and *Rhabdochona canadensis*. Multivariate Analysis of Similarity found significant among-site differences in parasite community structure for both sculpin and dace. Most notably, parasite community structure changed gradually from upstream to downstream for both species on both tributaries. However, a modified mantel test failed to find any significant correlation between these changes and contaminant levels in water or sediment. The only subset of environmental data that was significantly correlated to parasite community structure was water chemistry.

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**(58)**

**A SYMBIOTIC OLIGOCHAETE CAN PROTECT SNAILS FROM TREMATODE INFECTION**

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**J.A. Wyderko** and **L.K. Belden**, Virginia Tech



A wide range of non-host species are known to consume the free-living stages of endohelminth parasites, and such ambient biodiversity may be important to the transmission of infectious diseases. *Chaetogaster limnaei*, an episymbiont of many mollusk species, has long been considered a predator of aquatic trematodes, but the relationships between predator, parasite, and host are complex and poorly understood. In order to determine whether *C. limnaei* can protect its snail host against second-intermediate trematode infection, we used field data regarding natural *C. limnaei*-snail-trematode co-occurrence to parameterize laboratory studies in which we manipulated both the intensity of *C. limnaei* infestation and trematode abundance. Natural *C. limnaei* infestation was highly variable, both spatially and temporally, with a mean infestation intensity of 3.96 (+ 0.56; 1 SE) worms per snail in July 2011. In laboratory studies, the presence of *C. limnaei* reduced second-intermediate *Echinostoma trivolvis* infection in *Helisoma trivolvis* snails, where the magnitude of the protective effect increased with increasing *C. limnaei* infestation intensity. The *C. limnaei* population also increased with increasing cercarial density, and such population growth may be important over the long-term in the natural pond environment. This study emphasizes the importance of considering disease dynamics at the community level, and suggests that non-host species can be important components of disease systems.

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## (59)

### WHERE THE GREENER GRASS GROWS: CAN PARASITES SERVE AS ENVIRONMENTAL INDICATORS OF AQUATIC COMMUNITY CHARACTERISTICS IN HIGH AND LOW INTENSITY AGRICULTURE?

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Agriculture takes a toll on the quality of wildlife habitat, however some agricultural practices aim to reduce environmental impacts and few studies have addressed whether these practices actually improve habitat for wildlife. Wetland associated fauna and their parasites offer discrete biological communities to compare across different land use types. We examined host community and parasite infracommunity structure from 55 wetlands associated with either high or low intensity agriculture in northeastern Colorado. In June-August 2011, we performed standardized surveys of wetlands in chemically intensive, large conventional farms in Morgan County (MC, n=20) versus smaller, less chemically intensive, farms in Boulder County (BC, n=35). At each wetland, we conducted visual encounter surveys to estimate diversity and abundance of vertebrates, used dipnet sweeps and seine hauls to characterize larval amphibian, fish and invertebrate communities, measured wetland area, and characterized shore vegetation. Woodhouse's toads (*Bufo woodhousii*) were hand-collected haphazardly for dissection from 4 MC and 5 BC sites (n=21-25 per site) and *Physa acuta* snails were collected (n=30 per site) from 11 MC and 6 BC sites. Parasites recovered from toads included *Echinostoma* sp., *Manodistomum syntomentera*, *Fibricola* sp., *Opalina*, *Nychotherus*, unidentified cestodes, and nematodes; parasites recovered from snails included larval echinostomes, *Chaetogaster limnaei*, and unidentified nematomorphs and ciliates. Despite the low levels of parasite diversity in this system, there were differences in the diversity and abundance of potential trematode vertebrate hosts between the low versus high intensity agricultural sites. The use of parasites as indicators of wetland community functioning has the potential to elucidate the effects of different types of agriculture on aquatic communities; however, in the premontane prairie landscapes of Colorado, parasite diversity may be too low to easily draw conclusions.

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## (60)

### FISHPEST: AN INNOVATIVE SOFTWARE SUITE FOR FISH PARASITOLOGISTS

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Fish Parasite Ecology Software Tool (FishPEST) integrates fish parasite information from scientific literature, internet databases, and museum collections with phylogenetic, biogeographical, and ecological host data coming from Fishbase. Users do not need to download software and are free to use FishPEST without fee or login. FishPEST has three sections, namely Parasite Niche Modeler (PaNic), Parasite Cooccurrence Modeler (PaCo), and Parasite List Generator (PaL). PaL creates lists of known parasites per host, lists of known hosts per parasite, and lists of host/parasite records. PaL is innovative in its input and output. It allows users to filter the internal database according to parasite (taxon, area of distribution) and host features (phylogeny, habitat, ecology), making it easy to test biogeographic, coevolutionary, and ecological hypotheses. Additionally PaL can create presence-absence matrices to be used for further analyses. PaL provides basic statistical information for each generated list. While there are many ways to generate lists of known parasites or hosts, it is, as yet, not been possible to systematically propose probable lists of parasites or hosts. PaNic generates a list of probable hosts for a parasite while PaCo generate lists of probable parasites for a host. These tools are based on complex and flexible algorithms. FishPEST can be accessed at <http://purl.oclc.org/fishpest>.

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## (61)

### PARASITES OF FLIER, *CENTRARCHUS MACROPTERUS*, FROM PRAIRIE AND CHANNEL HABITATS IN THE OKEFENOKEE SWAMP, GEORGIA

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Flier (*Centrarchus macropterus*: Centrarchidae) were collected from a channel habitat, a prairie habitat, and from a boundary between the 2 habitat types in March of 2009, and examined for parasites. Flier from the prairie site had a significantly lower abundance of *Pterocleidus acer*, and a significantly higher abundance of *Hysterothylaceum* juveniles. Patterns of infracommunity similarity showed a distinct break between the 2 habitat types, with fish collected from the boundary site clustering with either channel or prairie communities, suggesting that the small home range of flier restricts the exposure of individuals to parasites.

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### DISASSEMBLING THE IRON WHEEL OF PARASITE LIFE CYCLES AND GETTING A JOB!

**M. Bolek**, Oklahoma State University

Over the last decade the field of parasitology has regained its popularity in the scientific community. However, studies on parasite life cycles and their diversity have lagged far behind other more popular areas of parasitology. In fact, based on recent publications one might conclude that parasitologists have almost abandoned studies on parasite life cycles. However, understanding life cycle strategies of parasites is critical for our interpretations of parasite community structure, life cycle evolution, and the spread of diseases through populations. The difficulty in studying parasite life cycles can be summarized in a statement by Wendell Krull in a letter to Miriam Rothschild where he stated "Experiences with life-cycles are unique in one way: I do not think the average biologist or even some parasitologists have any idea of the amount of confining work that is necessary in completing one." Due to these challenges, the scientific community as a whole has avoided this area of parasitology. As a result, the common perception of parasite life cycles is that of rigid iron wheels, with little or no room for plasticity. However, over the last decade I and now my students at Oklahoma State University have attempted to disassemble this common misperception of the iron wheel of parasite life cycles. This endeavor has been an evolving experience supported by lessons from my mentors, ASP colleagues, friends, wife, my students and our beloved

parasites. In this presentation, I will share some of my experiences which have provided me with the opportunity for a rich and rewarding academic carrier.

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**(63)**

**FROM TAPEWORMS TO MICROBES: VERSATILITY IS KEY TO A CAREER PATH IN PARASITOLOGY**

**V.J. McKenzie**, University of Colorado

Students seeking an advanced degree in parasitology these days may feel the pressure surrounding the competition for the shrinking pool of academic jobs. While academic shrinkage is a real phenomenon in general, the opportunities to pursue a career as a scientist studying parasitology are very present and may lurk in unexpected places. The very nature of parasites requires scientists to become inter-disciplinary and there is a growing job market for people with inter-disciplinary skills. I will share my own experiences along the path to a job where I can call myself a parasitologist, in the hopes that it offers some insight into the process for students of parasitology. My journey into parasitology began as an undergraduate at the University of Connecticut, studying shark tapeworms in Dr. Janine Caira's lab. I also completed a Master's degree with Dr. Caira and studied parasites of reptiles and amphibians in Guatemala in collaboration with Jonathan Campbell from the University of Texas at Arlington. I sought further training in Dr. Robin Overstreet's lab at the Gulf Coast Research Laboratory during my Master's work. For a PhD, I joined the lab of Dr. Armand Kuris at the University of California Santa Barbara and studied tropical land use and amphibian parasites. Upon graduating, I accepted a teaching postdoctoral position at the University of Colorado (CU) where I developed a parasitology course. Next, I spent a year working as a disease ecologist at the National Ecological Observatory Network (NEON) in Boulder, Colorado. In 2009, I started a tenure track faculty position at CU. My main current research agendas include studying amphibian populations in Colorado and the effects of land use change, invasive species, and disease as well as a newer direction to investigate the role that microbial symbionts play in the host response to pathogens. A key factor in entering the job market is to be versatile and have multiple ways of describing yourself so that you can emphasize different aspects of your research depending on the jobs you are pursuing.

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**(64)**

**SHIFTING BALANCE THEORY AND THE 'EVOLUTION' OF AN ACADEMIC CAREER**

**C.D. Criscione**, Texas A&M University, Department of Biology

Sewall Wright's shifting balance theory states that adaptive evolution results from the interaction of natural selection, genetic drift, migration, and mutation. In particular, he proposed an adaptive landscape with multiple fitness peaks (trait combinations associated with higher fitness), some being higher than others. With gradual mutational changes, the path of phenotypic evolution via natural selection would traverse from fitness valleys (low fitness) to fitness peaks. Yet, these peaks may be local maxima and not the global maximum. Once on a local peak, there is no way to reach the global maximum via selection as 'one would have to hike back through valleys of lower fitness' to reach the phenotypic peak with greater fitness. Wright postulated that genetic drift (random fluctuations in allele frequencies due to sampling effects in finite populations) could drive selectively disadvantageous changes in phenotypes and thus 'help' populations move across the landscape and possibly run into peaks with higher fitness. In analogy, my own career path has crossed several fitness valleys and peaks in academia, where academic fitness is measured via teaching, pubs, service, awards, grants and jobs. Because an adaptive trait is one that evolved via selection, it is incorrect to say an individual has adapted to academia. Thus, I will refer to the Academic 'adaptive' landscape as the 'acclimation' landscape, where acclimation is analogous to the selective process, stochastic events parallel the mechanism of drift, and the learning of new methods and theory are mutational events. My path from undergrad (herpetology) to MS (parasitology) to PhD

(population genetics) to postdoc (molecular epidemiology/genetics) to Assistant Professor (integrating previous interests) was certainly a product of directional choices (acclimation process). However, I can say for sure that I would not have reached higher fitness peaks if it were not for many key stochastic (if not downright lucky) events in my career. I will recap events that have led to my current research program and position.

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**(65)**

**JUMPING FROM THE POND TO THE LAKE: TRANSITIONING FROM GRADUATE STUDENT TO ACADEMIC**

**J. Koprivnikar**, Brandon University

The pursuit of a tenure stream academic position is one potentially fraught with peril and stress but graduate students who know what they want, as well as what their prospective employers are looking for, may increase their chances of a successful professional and personal transition. Graduate students in the field of parasitology face additional challenges in an academic environment increasingly favoring the replacement of organismal expertise with broader research disciplines. Consequently, those seeking a faculty position must be prepared to market themselves generally and flexibly. It is also critical to recognize that academic institutions value research, teaching, and service in order to plan appropriately. Nonetheless, these multiple aspects of a faculty position vary amongst institutions and graduate students should take this into consideration. Knowing what type of position you really desire will help to create a good professional and personal fit. Transitioning from the relatively small community of the graduate student “pond” to the larger academic “lake” means greater competition and new suite of interactions with previously unencountered “species”. However, phenotypic plasticity and niche differentiation are strategies that can be successfully employed by many organisms, including graduate students.

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**(66)**

**THERE AND BACK AGAIN: A PARASITOLOGIST'S TALE**

**N.J. Negovetich**, Angelo State University, San Angelo, TX

Being a parasitologist requires knowledge of most if not all aspects of biology. In many cases, an adequate education in parasitology can enable one to cross the traditional boundaries of research that are delineated by the various scientific fields. In this talk, I will trace my research path that began in the streams and marshes of west-central Indiana, continued in the Piedmont Triad (Winston-Salem, North Carolina), detoured through the City on the Bluff (Memphis, TN), and is now becoming established at the edge of the Southern Great Plains in West Central Texas (San Angelo, TX). This path included two major transitions: (1.) transition from ecological parasitology to virology, and back again, and (2.) moving from a temperate zone with abundant water to an arid region where water is sparsely distributed. Each transition presented their own set of problems as they relate to my research interests and expertise. As such, the difficulties and benefits of the transitions will be discussed as I summarize the main research projects to which I have contributed.

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**(67)**

**EDITOR'S SYMPOSIUM - 2012**

**G.W. Esch**, Wake Forest University  
**M. Sukhdeo**, Rutgers University

For the fifth consecutive year, three Associate Editors of the Journal of Parasitology will present talks regarding their personal research activities. Michael Sukhdeo will chair the symposium and lead a Q and A session at the end. Gerald Esch will provide introductory remarks. Dr. Ramon Carreno, of Ohio Wesleyan University will begin the symposium with a discussion on the systematics of oxyurid nematodes. Ramon's presentation will be followed by a paper from Dr. Ash Bullard of Auburn University. Ash will attempt to relate the ramifications of the BP Deepwater Horizon oil spill down in the Gulf of Mexico with possible changes in host/parasite interactions in the vicinity of the accident. Dr. Mark Siddall of the American Museum of Natural History will speak to our members about leech biology. More specifically, he will deal with information regarding their phylogeny, evolution of bioactive compounds in salivary secretions, and the salivary transcriptome itself.

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**(68)**

**THE SYSTEMATICS OF OXYURID NEMATODES FROM INVERTEBRATES: INSIGHTS INTO THE EVOLUTION OF THE OXYURIDA**

**R. Carreno**, Ohio Wesleyan University

The oxyurid nematodes (pinworms) reveal the evolution of an interesting host-parasite system that includes both invertebrate and vertebrate definitive hosts for these nematodes. There is a vast diversity of morphological forms among those species that parasitize invertebrates. Recent morphological analysis of several genera reveals the need for a revision of many species for which numerous characters are either lacking or are inadequately described. Molecular phylogenetic analysis is revealing interesting patterns. Analysis of small- and large subunit ribosomal RNA gene sequences indicates that the genus *Thelastoma* is paraphyletic. Within the Thelastomatoidea, the Thelastomatidae appear to be paraphyletic, and members of the Protrelloidiidae and Hystrignathidae are nested in a clade containing species traditionally grouped in the Thelastomatidae. These findings indicate a preliminary pattern depicting the phylogeny of the Thelastomatoidea that will eventually be integrated with similar data for the Oxyurida parasitizing vertebrates.

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**(69)**

**MARINE FISHERIES, PARASITES, AND THE 2010 BP DEEPWATER HORIZON OIL SPILL**

**S.A. Bullard**, and **C.F. Ruiz**, Department of Fisheries and Allied Aquacultures, Auburn University

Fish parasites comprise a large portion of marine biodiversity but so far have been underutilized as Gulf of Mexico (GoMex) bioindicators. Shifts in parasite diversity, prevalence, and intensity resulting from the 2010 BP Deepwater Horizon Oil Spill (DHOS) could indicate spill-related changes to water quality, abundances and immunological health of free-living organisms, or the GoMex food web. Ectoparasites with direct life cycles (no intermediate host or food-web mediated transmission) may be sentinels for acute spill effects, as they are typically small, have high surface area to volume ratios, and remain immersed in seawater. Endoparasites with indirect life cycles (intermediate host[s] required) involving food-web mediated transmission may be sentinels for detecting chronic spill effects, as they reside in a host where they are less vulnerable to toxins and have larvae requiring predator/prey transmission.

Environmental perturbations affecting food-web structure (chronic effect) may impact endoparasites more than ectoparasites. A ratio of the numbers of ectoparasite species to endoparasite species per fish species per geographic locality has been informative regarding oil pollution events: a relatively smaller ratio signals acute environmental effects (i.e., ectoparasites die; endoparasites survive), a relatively larger ratio signals chronic environmental effects (i.e., ectoparasites recolonize hosts as water normalizes; endoparasites are extirpated as food-web links are broken by loss of intermediate hosts). To test these ideas, in collaboration with the Louisiana Department of Wildlife and Fisheries, we have routinely sampled the parasites of Gulf killifish *Fundulus grandis* from 8 reference sites (4 oiled, 4 non-oiled) in Barataria Bay (Grand Isle, Louisiana) every 3rd month since the oil spill. To date, five collection events comprising 800 fish each have been logged (100 individual fish from each reference site per collection event). So far, 32 parasite species have been tentatively identified from approximately 400 fish necropsied. Our pending results may provide critical new insights about parasites as bioindicators in an exemplar Gulf of Mexico salt marsh while providing insights on the environmental “ripple effects” of the DHOS. The parasitological data is being complemented by synergistic studies of toxicological aspects (PAH concentrations in sediments and fish) and microbiological aspects (microbial community profiles from water, sediment, and fish) across all of our study sites. This work is supported by grants from the Marine Environmental Science Consortium of Alabama, Gulf of Mexico Research Institute, and National Science Foundation.

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OMICS

M. Siddall, AMNH, CPW@79, NY

The ability to gather massive amounts of genetic information from study organisms is accelerating at a pace not previously anticipated. In less than 25 years we have gone from laborious techniques requiring difficult isolation procedures of things like whole mitochondrial genomes to a situation where we are now “drinking from a fire hose” in terms of genomic and transcriptomic information, and are now more challenged by downstream bioinformatics. It is now cheaper to resequence a human’s genome than it is to archive and back-up the information. The growth and advancement of genetic sequencing will be presented, including new technology that promises massive genome genome sequencing projects on wholly self-contained USB drive. More importantly, the challenges and the potential held by various “omics” (genomics, transcriptomics, phylogenomics, saliomics, etc) will be explored in terms of how much more informative they can be when approached from a comparative and evolutionary standpoint instead of a focus on model organisms or systems.

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FUNCTION OF ACA-DAF-16 IN ARRESTED L1 AND L3 HOOKWORM LARVAE

V. Gelmedin, C. Dowling and J. Hawdon, George Washington University Medical Center

Hookworms and other soil-transmitted nematodes are infectious through cutaneous penetration or ingestion of the non-feeding and developmentally arrested third larval (L3) stage. The developmental arrest in the L3 stage is obligate. Host-derived stimuli that L3 larvae sense during invasion are necessary to re-initiate feeding and development. Knowledge about the mechanism of recovery from arrest during transition from the free-living to the parasitic stage is still limited. Recently, we discovered that hookworms are also able to arrest in the L1 stage. Contrary to L3 arrest, L1 arrest is facultative and induced by starvation. Arrest at other stages of development than L3 has been reported from other nematodes, but not from hookworms. The non-parasitic, related nematode *Caenorhabditis elegans*



undergoes facultative arrest at both the L1 and the dauer stage, in response to starvation and overcrowding, respectively. The insulin/ insulin-like growth factor signaling pathway (IIS) and the transcription factor FoxO/DAF-16 regulate arrest in both cases. To better understand the role of developmental arrest in the hookworm life cycle, we focused on recovery from arrest and the re-initiation of development. We used quantitative RT-PCR and *in vitro* cultivation techniques to study hookworm L1 and L3 arrest and the role of IIS. In addition, we used *C. elegans* as surrogate to dissect the function and regulation of hookworm DAF-16 in L1 and L3 recovery. Our results indicate that the role of DAF-16 in arrest recovery differs between hookworm stages, as well as from its recovery in *C. elegans*.

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## (72)

### DNA BARCODING FOR SPECIES DELIMITATION AND PHYLOGENETICS OF SOME TISSUE COCCIDIA (TOXOPLASMATINAE: APICOMPLEXA)

**M.E. Ogedengbe**, Department of Pathobiology Ontario Veterinary College University of Guelph Canada  
**J.R. Barta**, University of Guelph, Canada

The evolutionary history of apicomplexan parasites and their biodiversity has only started to be explored despite their roles in some of the most serious parasitic diseases of humans and animals. Morphological and biological characterization has been shown in some cases to be inadequate for delimiting species and inferring phylogenetic relationships. Molecular evolutionary and biodiversity studies have relied largely on nuclear rDNA or ribosomal ITS sequences. Mitochondrial sequences (e.g. CytB or COI) have been used extensively for haemosporinid parasites but their use in identification and phylogenetic studies of other apicomplexan parasites has been limited by a paucity of suitable PCR primers. Our objectives were to assess the utility of mitochondrial COI sequencing (DNA barcoding) for differentiating tissue coccidia (Toxoplasmatinae) belonging to the genera *Toxoplasma*, *Hammondia*, *Neospora* and *Cystoisospora*. Prior to this study, no PCR primers were available to amplify the COI gene from parasites other than haemosporinids, piroplasms or *Eimeria* spp. All available COI sequences from apicomplexan parasites were aligned using MUSCLE within Geneious v.5.0. Regions of similarity were examined to generate a series of degenerate primers likely to bind broadly within the Apicomplexa. Four new primers, COI\_400F, COI\_1202R, COI\_10F and COI\_500R, were then used to amplify and sequence partial (500-800bp) COI sequences from many coccidia. Bayesian phylogenetic analysis followed by tests of species delimitation suggests that partial COI sequences are well suited for species delimitation and inferring phylogenetic relationships among some tissue coccidia (Toxoplasmatinae). Genetic distance data showed more reliable discrimination among species than the 18S rDNA locus and thus COI offers a better genetic marker for identifying and differentiating coccidia.

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## (73)

### EXAMINATION OF THE SURFACE ANTIGEN (SNSAG) GENE FAMILY IN *SARCOCYSTIS NEURONA*

**A. Gautam** and **S. Dangoudoubiyam**, M.H. Gluck Equine Research Center, Department of Veterinary Science, University of Kentucky  
**J.P. Dubey**, USDA-ARS, Beltsville  
**W.J. Saville**, College of Veterinary Medicine, The Ohio State University  
**D.K. Howe**, M.H. Gluck Equine Research Center, Department of Veterinary Science, University of Kentucky

*Sarcocystis neurona* is a protozoan parasite whose complex life cycle progresses through multiple developmental and life cycle stages that differ morphologically and molecularly. The *S. neurona* merozoite surface is covered by multiple related proteins, which are orthologous to the surface antigen

(SAG) gene family of *Toxoplasma gondii*. Expression of the SAG surface antigens in *T. gondii* and another related parasite *Neospora caninum* is life cycle stage-specific and seems necessary for parasite transmission and persistence of infection. In the present study, expression of the *S. neurona* merozoite surface antigens (SnSAGs) was evaluated in the sporozoite and bradyzoite stages. Western blot was used to compare SnSAG expression in merozoites versus sporozoites, while immunocytochemistry was performed to examine expression of the SnSAGs in merozoites versus bradyzoites. These analyses revealed that SnSAG2, SnSAG3 and SnSAG4 are expressed by sporozoites, while SnSAG5 appeared to be downregulated in this life cycle stage. In *S. neurona* bradyzoites, SnSAG2, SnSAG3, SnSAG4 and SnSAG5 were either absent or expression was greatly reduced. Additionally, an effort was made to identify new SnSAGs in the draft sequence of the *S. neurona* genome. Multiple searches revealed several potential new SnSAG genes, and bioinformatic analyses of the sequences revealed characteristics consistent with the SAG gene family. Preliminary studies to characterize these new putative SnSAGs have been initiated. Polyclonal antibodies against one new putative SnSAGs, SnSAG.156, are being utilized to confirm that this gene is expressed and the protein is localized to the parasite surface. As well, ELISA using recombinant SnSAG.156 indicated that infected horses produce antibodies against this protein. Studies are underway to characterize in detail the proteins encoded by other putative SnSAG genes. The information acquired about the stage-specific expression of the SnSAGs together with identification of new SnSAG paralogues should provide a better understanding of the parasite, its complex life cycle, and its pathogenesis during infection of host animals.

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**(74)**

**FUNCTIONAL COMPLEMENTATION APPROACH TO STUDY PROTEIN DEGRADATION IN  
*GIARDIA LAMBLIA***

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**S. Ganguly**, National Institute of Cholera and Enteric Diseases  
**A.K. Sil**, University of Calcutta  
**S. Sarkar**, Bose Institute

The differently diverged protist *Giardia lamblia* switches between two morphological forms, trophozoite and cyst, and protein turnover is crucial for this transition. However, little is known about protein degradation machinery of *G. lamblia*. Eukaryotic protein degradation occurs in two major cellular locations: the proteasome and the vacuole/lysosome. Towards understanding both systems of protein degradation of *G. lamblia*, we have characterized candidate proteins that may be facilitating either vacuolar or proteasomal protein degradation. These studies were conducted in the genetically facile yeast *Saccharomyces cerevisiae* as *G. lamblia* is refractory to genetic manipulations. The lipid phosphatidylinositol 3-phosphate (PtdIns3P) is a key regulator that controls protein trafficking to the lysosome and proteins containing FYVE and PX domains are effectors of this lipid. The *G. lamblia* genome encodes one FYVE and five PX domains. Sequence analysis revealed that while key residues are conserved in the *G. lamblia* domains, they are significantly diverged from similar domains of higher eukaryotes. All of the genes encoding these domains are expressed in both trophozoites and cysts. Both in vitro biochemical studies and in vivo cellular localizations indicate that the FYVE domain binds to PtdIns3P. However, similar studies indicate that the ligand affinity of the PX domains appears to be less precise. We have also identified a component of the proteasomal lid subunit that is likely to act as a receptor for binding to ubiquitin tags of proteins destined for proteasomal degradation. This *G. lamblia* protein is able to bind to ubiquitin in vitro and can functionally complement the phenotype resulting from deletion of the yeast orthologue. However, a domain of the yeast protein that is crucial for regulating ubiquitin binding is truncated in the *G. lamblia* orthologue. Thus, our studies indicate that while many of the protein components of the machinery involved in protein degradation in higher eukaryotes are present in *G. lamblia*, their regulation is likely to be different.

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**(75)**



## MOLECULAR AND MICROSCOPIC SCREENING OF HEMOPARASITES IN REPTILES: A COMPARISON OF MULTIPLE DETECTION METHODS

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Microscopy has been traditionally used in screening for parasites, but conventional and quantitative PCR (qPCR) have been shown to be more sensitive and are increasingly being used in parasitological studies. Hemogregarines are intraerythrocytic apicomplexan parasites and the most common hemoparasites of reptiles. Among these, the genus *Hepatozoon* is the most abundant, yet little is known about its prevalence, infection intensity and distribution in natural reptile populations. In this study we compare different methods, namely microscopy, conventional PCR and qPCR, for the detection and quantification of hemoparasites in reptiles. We examined blood smears, blood drops and tail tissues from two lizard species from a single location in Portugal. Preliminary results through microscopy showed high prevalence and similar parasitemia levels between these species. Then, using hemogregarine-specific PCR and qPCR assays for a segment of the 18S rRNA gene, we compared the three detection methods. Preliminary results show that qPCR is more sensitive than the other methods and that this assay is consistently repeatable, can quantify parasitemia levels and can distinguish mixed infections. These results show the potential of molecular methods to detect and quantify parasites in tissue and blood samples, providing important information on their prevalence, intensity and distribution.

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## TRANSCRIPTOME ANALYSIS OF TWO IMMUNOLOGICALLY DISTINCT STRAINS OF *EIMERIA MAXIMA* DURING SPORULATION

**R. Al-Badri** and **J.R. Barta**, Dept. of Pathobiology, Ontario Veterinary College, University of Guelph

*Eimeria maxima* is an economically important parasite that impacts the health of chickens globally. Most *Eimeria* spp. of chickens elicit a species-specific, protective immune response in birds after one or a few exposures to the parasites. In most cases, *E. maxima* elicits complete protective immunity against further challenge by the same species after a single exposure to 100 or fewer oocysts. As a means of attempting to determine the specific differences that may account for their lack of immunologically cross-reactivity, the transcriptomes of two immunologically distinct strains of *Eimeria maxima* (GS and M6 strains) were compared during sporulation. Four distinct periods (at 18h, 22h, 38h of sporulation as well as fully sporulated) were chosen to sample the major developmental stages of sporulation of these parasites. Bulk parasite RNA was extracted from sporulating oocysts of each strain at the 4 time points. One µg of bulk RNA from each time point was pooled for each of M6 and GS and then the mRNA was selected from each of the two pools using oligo-dT selection. The resulting mRNA samples were used as templates for production of cDNA libraries that were then used to generate 100 bp paired-end reads using an Illumina pyrosequencer. More than 80Gbp of sequence data was obtained in total. De novo assembly (SOAPdenovo, kmer = 49) was used to generate scaffolds and contigs that were then examined for differential expression using two methods (cufflinks and DESeq). Only a few dozen contigs/scaffolds demonstrated significant differential expression but, of those, a few coded for proteins with homology to a family of GPI anchored surface antigens of *Eimeria tenella*, suggesting that variation of these surface antigens may explain, at least in part, the immunological distinctiveness of these two strains.

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## A SIMPLE METHOD TO IDENTIFY AND QUANTIFY GI NEMATODE EGGS USING A CAPILLARY SEQUENCER

**D. Zarlenga**, USDA, ARS, ANRI Animal Parasitic Diseases Lab

Classic approaches for discerning GI nematodes from fecal eggs require cultivation to infective L3 followed by morphological examination. Over the years, a plethora of molecular techniques have surfaced, the majority of which are now predicated upon real-time PCR or PCR amplification followed by gel analysis. While adequate for diagnosis, most techniques fall short of quantifying mixed infections without substantial numbers of controls and/or standard curves. The goal of the work presented herein, was to develop a simple and rapid test for differentiating and quantifying mixed infections of GI nematodes, using fluorescently-labeled PCR products and a capillary-based sequencer. Prior sequence data indicate that the ITS2 region of common cattle GI nematodes is sufficiently distinct in length to delineate among infecting genera. As such, conserved PCR primers that span the ITS2 and bind to the 3'-end of the 5.8S rRNA (forward) and the 5'-end of the 18S rRNA (reverse) were synthesized one of which was fluorescently-labeled with FAM. DNA from egg samples or infective L3 was isolated, PCR amplified, diluted directly in HI-DYE sequencing buffer containing LIZ 500 standard, then loaded onto an ABI 3100 sequencer adapted for size fragment analysis. Tests were first performed on monospecific infections to validate the ability to differentiate *Haemonchus*, *Ostertagia*, *Cooperia*, *Trichostrongylus* and *Oesophagostomum* using this technology. Secondly and as proof of principle, L3 from *Ostertagia ostertagi* and *Cooperia punctata* were mixed in 10% increments, and the DNA isolated and analyzed for relative infection levels using Gene Marker V1.85. Using the chosen primer set, amplified DNA gave the following size fragments: *Haemonchus* 364 bp; *Ostertagia* 371 bp; *Cooperia* 374 bp; *Trichostrongylus* 369 bp, and; *Oesophagostomum* 355 bp using primers 1244 and 1246. Analysis of environmentally-derived samples from animals infected with *Haemonchus* and *Cooperia* coincided well with coproculture and PCR data. Quantified peak intensities using predefined mixes of *Cooperia* and *Ostertagia* gave a linear response in the range of 10%-90%. Data showed that primer design is critical for quantitative analysis. Preliminary information suggests that size fragment analysis is both diagnostic and quantitative on a relative scale. The methodology is scalable for large sample numbers. Ongoing work is continuing to validate the technology for quantifying parasite mixtures.

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## INVASION PATHWAY OF INTRODUCED LANCET LIVER FLUKE (*DICROCOELIUM DENDRITICUM*) INTO CATTLE AND WILDLIFE IN CYPRESS HILLS PARK, ALBERTA

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**D. Colwell**, Agriculture and Agri-Food Canada, Lethbridge Research Centre, and University of Calgary

**J. Gilleard**, University of Calgary

Once an invasive parasite is introduced into a host population, eradication via chemical or physical treatment is impractical, or takes years to develop. Thus, identification of invasion pathways is the most effective control strategy for many introduced parasites. But we rarely know the history of invasion of these parasites, nor do we know how they spread within multi-host communities. Characterizing genetic structure of invasive populations is a key step to resolving the route of invasion as well as critical epidemiological questions. Modern genetic fingerprinting tools provide a powerful approach to do so. *Dicrocoelium dendriticum* invaded southeastern Alberta, Canada, in approximately 1990 and is now present in most cattle, elk, and deer in the region. It is not known whether this invasion occurred directly from European sources, or via stepwise migration from earlier invasion sites in eastern North America, or both. We use two genetic marker systems (Amplified Fragment Length Polymorphism and cytochrome oxidase 1 gene sequences) to characterize the population structure and genetic variability of European and North American populations of adult *D. dendriticum* to distinguish these alternatives. Preliminary results

from flukes collected in Alberta show little variation between hosts at both markers, consistent with a bottlenecking event such as a recent and single introduction. Little prior genetic information is available for *D. dendriticum*, making results from this study important for establishing levels of genetic sub-structuring and overall variation in these populations from a variety of geographic locations.

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GENOTYPES AND SUBTYPES OF *CRYPTOSPORIDIUM* ISOLATES FROM DIARRHEIC PATIENTS IN THE CANADIAN ARCTIC (QIKIQTANI REGION)

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Little is known regarding the species and molecular types of *Cryptosporidium* found in humans in the Canadian Arctic. The present study used genotyping and subtyping for the molecular characterization of *Cryptosporidium* isolates from diarrheic patients in Nunavut (Qikiqtani Region), Canada, in order to determine the possible sources of infection, with the aim of reducing the risk of transmission in this region. *Cryptosporidium* spp. positive stool samples were initially identified by real-time PCR. Genomic DNA from the stool samples was then analysed by a nested-PCR targeting the small subunit ribosomal RNA (SSU rRNA) gene and a portion of the 60 kDa glycoprotein (gp60) gene to determine the *Cryptosporidium* genotypes and subtypes respectively. PCR products were purified and sequenced in both directions, and consensus sequences were aligned with target sequences in GenBank. Sequencing of the SSU rRNA amplicons revealed that *C. parvum* was the most frequently detected species, while sequencing of the gp60 amplicons identified the presence of the zoonotic *C. parvum* IIa subtype. Further work is required to determine the potential for zoonotic, and possibly foodborne, transmission in this region, or whether anthroponotic transmission, through either the fecal-oral route or sewage-contaminated drinking water, is more likely.

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MOLECULAR CHARACTERIZATION OF *ECHINOCOCCUS GRANULOSUS* IN GOATS IN NORTH IRAN

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*Echinococcus granulosus* of carnivores and its metacestode in herbivores and human have been recognized as the most important helminth zoonoses and of great economic and public-health significance in worldwide. *E. granulosus* shows a wide range of intra-specific variation in relation to host specificity, epidemiology, morphology, biology and genetics. It has ten intra-specific strains based on G1-G10 alleles. Three strains of *E. granulosus* (G1, G3 and G6), have been found in infected sheep in Iran, however there is a little known about the genotypes of *E. granulosus* in goats in Iran or worldwide. To determine the *E. granulosus* alleles, 160 goats in the Mazandaran province, north of Iran were screened and twenty nine fertile hydatid cysts were collected for genetic analysis. Cysts contents were aspirated and examined under light microscope to confirm the presence of protoscolex and checked for viability using the Eosin

exclusion test and by observing flame cell activity. Protoscoleces were washed with PBS (pH 7.2) and genomic DNA was extracted from 50 µl of protoscoleces using a DNA purification kit (Roche). The mitochondrial cytochrome C oxidase subunit 1 of *E. granulosus* genome was used for sequence analysis. A region of 440 bp of mitochondrial COI gene was amplified using following primers: J3- Forward 5'-TTTTTGGCCATCCTGAGGTTTAT-3' and J4.5-Reverse 5'-TAACGACATAACATAATGAAAATG-3'. DNA sequencing was performed for samples in two directions using the same forward and reverse primers employed in the PCR. The sequence chromatograms were analyzed using the Chromas version 3.1 software and compared to those registered in the Gen Bank using the 'Basic Local Alignment Search Tool' (BLAST). The nucleotide sequences obtained were also aligned using the ClustalW method of MegAlign (DNA Star) program, using the sequences of the different genotypes of *E. granulosus* and the microvariants of the G1 genotypes deposited in the GenBank. The sequence analysis data showed that all samples belonged to common sheep strain, G1 strain, and the two microvariants of G1<sup>4</sup> and G1C. This is the first report of G1<sup>4</sup> and G1C microvariants identification of G1 strain of *E. granulosus* in goats and also showed that goats can serve as an intermediate host for *E. granulosus* strain that infects sheep. There is now considerable evidence demonstrating the importance of determining the nature and extent of strain genotypic variation in *Echinococcus*. The use of morphology, solely, is not efficient for determination of genetic diversity. The genotypes are important regarding the host specificity and life cycle of *E. granulosus*. An initial step in controlling the life cycle of *E. granulosus* and minimizing infections is to determine the genotype. The sheep strain (G1 genotype) of *E. granulosus* is the most widely distributed strain around the world. It has been found to be dominant strain both in human and animals. Limited surveys have been done on the genotypes of *E. granulosus* originating from goats around the world. Present study used mitochondrial COX 1 gene as one of the best targets for discriminating between strains and detection of variants of *Echinococcus* for characterization of goat isolates in Iran. This study showed that the sheep strain (G1) was found in 100% of the isolated sequences. This revealed the fact that goats can serve as intermediate host for the sheep strain and may play an important role in the epidemiology of hydatidosis in Iran especially north of Iran and should be targeted in control programs.

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### AVIAN COCCIDIOSIS: CURRENT COMMERCIAL PRACTICES FOR THE CONTROL OF THESE ILLUSIVE AGENTS

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The coccidian parasites of poultry invade the intestines and cecae of their hosts. Birds of all ages are susceptible to one or more species of coccidia, unless immune from previous exposure. The *Eimeria* species have had predictable behaviors or patterns which have been described and accepted. The pathology and pathogenicity of the coccidia species were considered characteristic traits of each species; *Eimeria praecox* is believed to be relatively and *E. necatrix* is highly pathogenic. The highly pathogenic *E. necatrix* is the least prevalent or even extinct from broiler chicken houses. Many of the commonly used anticoccidial drugs are demonstrating efficacy against many field isolates. This has allowed pharmaceuticals to maintain the major share of the prevention and controlled market for coccidiosis. However, there is a re-vitalized interest in vaccines for the control of coccidiosis. This has brought a boom in the development of both live and killed vaccines for the control of the disease. Poultry production practices may also have influenced the host parasite relationship; densities in which birds are grown, multiple uses of bedding material and strategic uses of pharmaceuticals. A recent practice is to vaccinate and use an anticoccidial. All species of *Eimeria* are antigenic and may offer protection to different strains within the species, but no protection across species. There are reports of poor protection or variability in protection within strains of *E. maxima* (Norton and Hein, 1976, Long and Millard, 1979, Fitz-Coy, 1993, Smith, A. L. et al. 2002, Jenkins et al. 2004). Some vaccines have used multiple *E. maxima* antigens to enhance the antigenic capabilities of the product. Recently uncharacteristic patterns or behaviors are being reported; such uncharacteristic patterns or behaviors are for example the cryptic and variant organisms within the species. But the question that has not been answered is how prevalent or wide-spread are these variant organisms.

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UNDERSTANDING SPECIES-DEPENDENT HOST RESPONSE TO *EIMERIA* SPP. USING  
COMPARATIVE TRANSCRIPTIONAL ANALYSIS

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Beltsville Agricultural Research Center, USDA

Understanding comparative host immune response to different species of *Eimeria* will lead to enhanced insights on the nature of pathology caused by various coccidian species. To accomplish this, we investigated relative expression levels of immune- and non-immune-related mRNAs in chicken intestinal intraepithelial lymphocytes experimentally infected with 3 major species of coccidia, *Eimeria acervulina*, *E. maxima*, or *E. tenella* using a 9.6K cDNA microarray. Based on a cutoff of > 2.0-fold differential expression compared with uninfected controls, relatively equal numbers of transcripts were altered by the three *Eimeria* infections at 1, 2, and 3 days post-primary infection. By contrast, *E. tenella* elicited the greatest number of altered transcripts at 4, 5, and 6 days post-primary infection, and at all time points following secondary infection. When analyzed on the basis of up- or down-regulated transcript levels over the entire 6 day infection periods, approximately equal numbers of up-regulated transcripts were detected following *E. tenella* primary (1,469) and secondary (1,459) infections, with a greater number of down-regulated mRNAs following secondary (1,063) vs. primary (890) infection. On the contrary, relatively few mRNA were modulated following primary infection with *E. acervulina* (35 up, 160 down) or *E. maxima* (65 up, 148 down) compared with secondary infection (*E. acervulina*, 1,142 up, 1,289 down; *E. maxima*, 368 up, 1,349 down). With all three coccidia, biological pathway analysis identified the altered transcripts as belonging to the categories of "Disease and Disorder" and "Physiological System Development and Function". Sixteen intracellular signaling pathways were identified from the differentially expressed transcripts following *Eimeria* infection, with the greatest significance observed following *E. acervulina* infection. Taken together, this new information will expand our understanding of host-pathogen interactions in avian coccidiosis and contribute to the development of novel disease control strategies. Keywords: *E. acervulina*, *E. maxima*, *E. tenella*, microarray, innate immunity

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A NOVEL MUCOSAL VACCINE BASED ON LIVE *EIMERIA* EXPRESSING CTB INDUCED  
SYSTEMETIC IMMUNE RESPONSES IN CHICKENS

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Most pathogens invade their hosts through mucosal surfaces and mucosal vaccination is considered ideal for the control of mucosal infections, such as cholera, rotavirus and enterotoxigenic *E. coli* (ETEC) diarrhea. Delivery of vaccines to mucosal surfaces makes immunization practice safe and acceptable, and eliminates needle-associated risks. The B sub-unit of CT (CTB) is a highly efficient carrier molecule for chemically or genetically conjugated antigens for eliciting mucosal and systemic antibody responses. In this study, we developed a recombinant (transgenic) *Eimeria tenella* strain expressing CTB under the control of the actin promoter with codon usage optimized for expression in *E. tenella*. A double expression-cassette plasmid, pMIC-EYFP/ACTss-CTB was constructed for the transfection of *E. tenella*, the EYFP coding region is flanked by the promoter of microneme 1 (MIC, 779 bp) and 3' region of actin (632 bp); while the CTB is flanked by the promoter of actin (ACT, 1128 bp) and 3' region of actin, a signal sequence (ss, 85 bp) derived from dense granule protein 8 (GRA8) of *Toxoplasma gondii* and a 30 bp myc tag sequence ligated in-frame with the CTB codon region. The fluorescent oocysts collected from chicken faeces were sorted using flow-activated cell sorting (FACS) and propagated several passages in



chickens. Lysates of the transgenic oocysts were analyzed by Western blotting with anti-myc monoclonal antibody, and the result showed that CTB was expressed successfully in the transgenic apicomplexan parasite. Mucosal immunization of chickens with transgenic oocysts resulted in the production of antibody responses against CTB antigen and the oocyst antigen. Furthermore, chickens immunized with the transgenic oocysts developed a higher IgG response to the oocyst antigen than those immunized with wild type oocysts. The results demonstrate a positive step for the development of *Eimeria*-based vector vaccines against mucosal pathogens. The study is supported by the National Natural Science Foundation of China (Project numbers: 30871862 and 30671579), the National High Technology Research and Development Program of China (2011AA10A209), and The Yangtze River Scholar and Innovation Research Team Development Program (Project No. IRT0945).

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**(84)**

**THE MOLECULAR BASIS FOR DISTINCT HOST AND TISSUE TROPISMS OF COCCIDIAN PARASITES**

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The phylum Apicomplexa includes many parasites of significant medical and veterinary importance and despite their shared ancestry they exhibit markedly different host and tissue tropisms. *In extremis*, the single species *Toxoplasma gondii* invades and infects virtually any nucleated cell from any warm-blooded vertebrate, whilst the >1800 species of *Eimeria* described to date infect epithelial or endothelial cells (usually of the intestine) and with few exceptions are limited to a single vertebrate, or invertebrate, host. Apicomplexan protozoa establish infection by rapid and forced invasion of host cells starting with non-specific attachment, followed by gliding across cellular surfaces to find a particular niche, then deployment of the parasite cell entry machinery. The process of initial host cell recognition and attachment is governed by the regulated deployment of surface microneme proteins (MICs), which are therefore likely to be major determinants of the host and tissue tropism of each parasite. Structural and functional data are now available for several coccidian MICs, providing insights into their receptor specificities and modes of recognition in atomic detail. This talk will summarise our recent analyses of MICs from *Toxoplasma gondii* and *Eimeria tenella* with an emphasis on the carbohydrate-binding properties of two distinct families of MICs – the microneme adhesive repeats (MAR) containing proteins that interact with sialic acid and the apple domain containing proteins that bind glycans terminating in galactose.

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**(85)**

**IDENTIFICATION AND CHARACTERIZATION OF *TOXOPLASMA GONDII* CYST WALL PROTEINS**

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*Toxoplasma gondii* forms tissue cysts during initial infection which persist in the host and are involved in disease relapses. A prominent characteristic of these cysts is the cyst wall which protects the parasites

from environmental stress including the immune system. Identifying cyst wall components should help elucidate mechanism(s) of parasite persistence. To identify cyst wall proteins two approaches were utilized: (1) a proteomic analysis of cyst wall preparations and (2) the development of cyst wall specific monoclonal antibodies (mABs). Using various cyst wall specific mABs the corresponding antigens were purified by immunoprecipitation from parasite lysates. The purified antigens were analyzed by mass spectrometry and corresponding genes identified using EPICdB and Toxodb (EuPathdB). mAB SalmonE stained the cyst wall uniformly, but not the tachyzoite parasitophorous vacuole and the identified protein was designated TgCST250. The localization of TgCST250 was verified by a polyclonal antibody raised against expressed recombinant protein. TgCST250 is highly glycosylated and reacts with DBA. A knockout (KO) of TgCST250 was performed in *T. gondii* PruΔKU80. Although the TgCST250 KO did not lose its ability to differentiate into bradyzoites, the number of brain cysts in mice was greatly reduced and KO cysts were much more fragile than wild type cysts suggesting a defect in cyst wall formation. A second cyst wall protein reacting with mAb PufferM has also been characterized. Using our proteomic approach the gene corresponding to mAb PufferM, TgCST88 has been identified and we are in the process of evaluating the phenotype of KO parasites. [Supported by NIH AI39454 and 5T32AI070117-03].

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A CASE FOR HOST INVOLVEMENT IN THE GLYCOSYLATION OF *TOXOPLASMA* TISSUE CYSTS

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Despite their central role in the pathogenesis of *Toxoplasma gondii* little is known about the composition and functions of proteins associated with the cyst and cyst wall. The tissue cyst is defined by the presence of a heavily glycosylated cyst wall with additional glycoproteins present in the tissue cyst matrix. Lectins and monoclonal antibodies against glycan moieties indicate the presence of both sialic acid and complex N-linked glycans in the tissue cyst wall and/or matrix. The detection of these moieties in the tissue cyst is surprising in light of the fact that the *Toxoplasma* genome does not encode any of the enzymes needed for the synthesis, activation or transfer of sialic acid or for that matter the enzymatic machinery to synthesize complex N-glycans. This presents the possibility that *Toxoplasma* may acquire these modifications from the host cell. This view is not new as work primarily from the Schwarz laboratory has suggested that host glycans (complex N-linked) may be usurped by the parasite. We now have data that strongly implicate not only host sugars but more critically host enzymes in the modification of the tissue cyst wall and matrix. Using host cell mutants with specific defects in the sialylation pathway we are now dissecting the mechanistic basis underlying the sialic acid modification of *Toxoplasma* proteins particularly those associated with the tissue cysts. These findings suggest a mechanisms whereby *Toxoplasma* may redirect host ER and Golgi vesicles followed by fusion with PVM to deliver the requisite modifying enzymes to the vacuole. We believe these events that happen at a slow rate in tachyzoite vacuoles are greatly accelerated during differentiation accounting for the rapidity with which tissue cyst wall glycosylation occurs. We believe that the subversion of host activities resulting in the decoration of the tissue cyst with host glycans may have a role in the relative immunological invisibility of tissue cysts that appear to be disguised as immunological self. Confirmation of this pathway may also contribute to the vast host range of the parasite whereby host specific modifications can be promoted.

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ASP PRESIDENT'S ADDRESS

## HUMAN PARASITES: WHO, WHAT, WHEN, WHY AND HOW

A.M. Kuris, University of California, Santa Barbara

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#### A DISTINCTIVE PARASITIC COPEPOD (HARPACTICOIDA: TISBIDAE) FROM CALIFORNIA *OCTOPUS BIMACULOIDES*

M.F. Burwell, S.B. Weinstein and A.M. Kuris, University of California, Santa Barbara

Cephalopods are parasitized by copepods, usually as ectoparasites on the skin, attached to the gills, or in the mantle cavity. The California two spot octopus, *Octopus bimaculoides*, was collected from the intertidal zone and near shore subtidal habitats near Santa Barbara, California and individuals were comprehensively sampled for parasites. Dissection of *O. bimaculoides* revealed numerous parasitic copepods of the family Tisbidae, subfamily Cholidiinae. Previously described Cholidiinae have only been collected from deepwater octopuses at hydrothermal vents or from soft substrate habitats. There is only one report of their larval stages. The cholidiine copepodid larvae from *O. bimaculoides* were embedded in the connective tissue surrounding the branchial hearts, oviducal gland and underlying the mantle. Copepodid larvae were abundant and included several copepodid stages. This supports the hypothesis that this copepod subfamily includes an endoparasitic larval development stage. Here we describe their morphology, host response, and their descriptive parasite ecology; reporting prevalence, intensities and organ site use. The discovery of abundant cholidiine copepods in a California shallow water octopus considerably broadens the geographic and habitat range of these parasites and provides an opportunity to increase our knowledge of their life cycle and impact on their hosts.

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#### INFLUENCE OF VARIABILITY IN OCEAN CONDITIONS ON TROPHIC INTERACTIONS AND RECRUITMENT OF JUVENILE CHINOOK AND COHO SALMON INFERRED FROM TROPHICALLY TRANSMITTED PARASITES

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Relationships between the marine survival of Pacific salmon and physical and biological processes in the ocean have been well documented, however the mechanisms responsible for these relationships are unclear. This study examined the trophically transmitted parasite communities of Chinook (*Oncorhynchus tshawytscha*) and coho (*O. kisutch*) salmon to better understand how interannual variability in food web processes affects salmonids in the marine environment. Juvenile salmon used in this study were caught off the Oregon and Washington coast during an 8-year period (2002 to 2009) of variable salmon survival and ocean conditions based on the Pacific Decadal Oscillation (PDO), sea surface temperature and upwelling strength prior to salmon ocean entry. A total of nine marine macroparasite species were recovered from the stomachs, intestines and body cavities of 406 juvenile coho and 354 juvenile Chinook salmon. The acanthocephalan *Rhadinorhynchus trachuri* and a tetraphyllid cestode were more abundant in “warm” ocean years (positive PDO) associated with relatively low adult salmon returns. *Anisakis simplex*, and the trematodes *Parhemius merus* and *Lecithaster gibbosus* were more abundant in “cold” ocean years (negative PDO) associated with high numbers of returning adults. Relationships between trophically transmitted parasites, ocean climate, and corresponding adult returns, suggests that variability in ocean conditions alter salmon trophic interactions and may affect salmon survival.



SEASONAL OCCURENCE AND COMMUNITY STRUCTURE OF HELMINTH PARASITES IN SOUTHERN LEOPARD FROGS, *RANA SPHENOCEPHALA*, FROM NORTH CENTRAL OKLAHOMA

M.S. Vhora and M.G. Bolek, Oklahoma State University

From May to September 2011, 74 southern leopard frogs, *Rana sphenoccephala*, were collected from Teal Ridge, Payne County, Oklahoma U.S.A. Sixty-nine (93%) of 74 frogs was infected with 1 or more helminth species. The component community consisted of 11 helminth species, including 1 larval and 1 adult cestode, 2 larval and 3 adult trematodes, and 1 juvenile nematode and 3 adult nematodes. Of the 1,790 helminths recovered, 51% (911) were nematodes, 47% (842) were cestodes, and 2% (37) were trematodes. Seasonally, the average monthly temperature was lowest in May and highest in July, whereas monthly precipitation was highest in May and lowest during the first week of September. A significant positive correlation existed for percent of all helminths acquired by skin contact and monthly precipitation ( $r = 0.95$ ,  $P < 0.01$ ); whereas a significant negative correlation existed for seasonal precipitation and percent of helminths acquired through frog diet ( $r = -0.95$ ,  $P < 0.01$ ). In addition, statistically significant differences existed in the total abundance of helminths acquired by skin contact or through frog diet among monthly component communities of southern leopard frogs ( $H$  corrected = 23.56,  $P < 0.0001$  for skin contact helminths;  $H$  corrected = 19.07,  $P = 0.0008$  for helminths acquired by diet). Our results indicate that seasonal abiotic conditions have a major influence on the avenues for and constraints on the transmission of helminths with life cycles associated with water/moisture or terrestrial intermediate hosts. Thus, abiotic factors, such as precipitation or the lack of, are important factors in structuring helminth communities in amphibian hosts, and these may vary seasonally

HELMINTH COMMUNITY STRUCTURE IN NINE SPECIES OF SYMPATRIC ANURANS FROM NORTH CENTRAL OKLAHOMA

M.S. Vhora and M.G. Bolek, Oklahoma State University

Oklahoma has a diverse anuran fauna; however, little information is available on the helminth communities that they harbor. This study documented the helminth community structure from 363 anurans representing nine species from four families. Frogs and toads were collected from March 2010 to September 2011 from four locations in Stillwater, Payne County, Oklahoma. Complete necropsies were performed, and a total of 2,996 larval and adult trematodes, 10,370 juvenile and adult nematodes, and 1,166 larval and 2 adult cestodes were recovered. Of the four collection locations, two had sympatric frog species and were used to compare helminth community structure. Communities differed in composition among host species. Host diet, size and habitat were important factors in structuring helminth communities among this amphibian assemblage. Larger host species had greater mean abundance, mean intensity, and species richness of helminths ( $H$  corrected = 85.68,  $P < 0.0001$ ;  $H$  corrected = 17.44,  $P = 0.004$ ;  $H$  corrected = 90.86,  $P < 0.0001$ ; respectively) than smaller host species. Aquatic anurans were dominated by digenetic trematodes with complex life cycles or helminths that utilized aquatic intermediate/paratenic hosts, whereas the parasite communities of terrestrial anurans were dominated by nematodes and cestodes which were acquired directly from the soil or through feeding on terrestrial intermediate hosts. Semi-terrestrial and arboreal frogs had fewer adult digenetic trematodes and direct life cycle nematodes than did aquatic and terrestrial anurans. Although, helminth species composition varied at the local (pond) level in amphibian species that were sampled from multiple locations, the life cycle strategies of their helminths did not. Our work strongly suggests that the habitat of the amphibian host is the strongest predictor of its helminth community composition.

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SEASONAL DYNAMICS OF THE CESTODE FAUNA IN SPINY DOGFISH POPULATIONS OFF THE COAST OF RHODE ISLAND

M. Pickering and J.N. Caira, University of Connecticut

Seeking patterns in the structure of parasite communities across space and/or time is of much interest in parasite community ecology. This study records trends in measures of infection (prevalence, intensity, and abundance) of the cestode community of the spiny dogfish, *Squalus acanthias*, across seasons in the northwest Atlantic Ocean. Between February 2007 and October 2009, seasonal collections of *S. acanthias* were made off the coast of Rhode Island, USA and each shark was examined for intestinal cestodes. In total, 1,848 individual cestodes were recovered from the 217 sharks examined. These consisted of 343 specimens of the trypanorhynch *Gilquinia squali*, 1,472 specimens of the tetraphyllidean *Trilocularia gracilis*, and 33 specimens of a second tetraphyllidean, *Phyllobothrium squali*. Measures of infection differed for the 3 cestode species. Season and host size were found to have a significant effect on both prevalence and abundance of *G. squali*, while only season affected infection intensity; infections were highest and heaviest in winter and spring, and larger sharks were more likely to be infected. All three measures of infection in *T. gracilis* were significantly affected by season but showed the opposite pattern than that seen in *G. squali*; all three infection measures were highest in summer and fall. The rarest species was *P. squali*, which exhibited comparatively low infections overall; prevalence and intensity were significantly higher in the fall. Differences seen in the infection measures among these three species likely reflect differences in their life history strategies.

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HABITAT-BASED SPATIAL CONSTRAINTS ON FOOD WEB STRUCTURE AND PARASITE LIFE CYCLES

W. Rossiter and M.V. Sukhdeo, Rutgers University

While habitat space is often discussed in the context of food webs, few studies explicitly ask if habitat heterogeneity within a given community can influence trophic structure. We examine a high resolution riverine food web that considers abundance, biomass and feeding interactions and includes microbes, plankton and parasite components in addition to the more typical macroscopic groups. We ordinate species' (node) locations in the food web across three habitat dimensions and ask if habitat type acts as a constraint on the species they interact with. We find that species are more "centered" (i.e. occur in multiple habitat types) than would be expected at random, and the distances between species is best described by a Poisson distribution. Distances between interacting species are shorter than would be predicted under a null model derived from the Poisson distribution. Additionally, host-host distances are significantly shorter than the overall observed distances, and the life cycles of parasites involve species that are extremely overlapping in their distribution across habitats. These findings suggest that species-species interactions are significantly constrained by habitat, and that parasites with complex life cycles are particularly sensitive to these constraints.

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ECHINOSTOME CRYPTIC DIVERSITY IN MUSKRAT DEFINITIVE HOSTS

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**A. Zajac**, Virginia Tech  
**D. Minchella**, Purdue University  
**L. Belden**, Virginia Tech

Many trematode groups have a long history of systematic revision, which can make parasite identification a difficult task. However, increasing interest in host-parasite interactions and ecology in natural wildlife systems has heightened the need for accurate identification of both larval and adult wildlife parasites. Here, we highlight some of the systematic issues associated with trematodes of muskrats, with a focus on echinostomes. Then we demonstrate the utility of using both morphological and molecular tools to identify these parasites. Morphological examinations of specimens from 63 muskrats collected in Virginia suggested that at least four genera of trematodes were present in the gastrointestinal tract including *Echinostoma*, *Wardius*, *Quinqueserialis*, and *Notocotylus*. For the latter three groups, the 28S region verified this assessment. For echinostomes, ND1 sequences of a subset of 69 worms revealed at least five genetic lineages were present. However, a particular lineage, *Echinostoma trivolvis* lineage b, predominated in both prevalence and intensity of infection. Molecular markers provided a more accurate estimate of echinostome diversity in the muskrats and generated sequences that further support the idea that *Echinostoma trivolvis* is a species complex. Future studies will focus on whether there are differences in host specificity among the *Echinostoma trivolvis* lineages. In addition, this study has provided initial sequences that will help verify the life cycles of *Wardius*, *Quinqueserialis* and especially *Notocotylus*, by allowing us to match larval types and adult forms.

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DO BROKEN ASSUMPTIONS DRIVE *PLASMODIUM* SEX RATIOS TO STRAY FROM  
PREDICTIONS OF LOCAL MATE COMPETITION THEORY?

**A.T. Neal**, University of Vermont

Malaria parasites (*Plasmodium* and related genera) often produce significantly female-biased gametocyte sex ratios. Prior research has attributed these biased sex ratios to Local Mate Competition (LMC) resulting from the parasite's divided population structure within the insect vectors during mating. However, if there is not a positive linear relationship between the number of zygotes produced during mating and the probability of transmission from vector to vertebrate host, the assumptions of LMC are not fulfilled and the equilibrium sex ratio may stray from the predictions based on LMC theory. I developed a model that incorporates biologically reasonable deviations from the assumptions of LMC theory to determine the resulting equilibrium sex ratio. I then determined the sex ratio, gametocytemia, and fecundity of single- and multiple-clone infections of the lizard malaria parasite *Plasmodium mexicanum* to determine whether standard LMC theory or the new model better accounts for the variation in sex ratios observed for malaria parasites. The model predicts a range of possible equilibrium sex ratios, with the specific ratio influenced by gametocyte density, number of coexisting clones, male gametocyte fecundity, and the shape of the relationship between number of zygotes and transmission success. The average sex ratio of *P. mexicanum* infections, regardless of the number of clones or whether infections were naturally occurring or experimentally induced, was 44% male. There was no effect of clonal diversity or any consistent effect of gametocytemia on sex ratio. Male gametocytes produce few gametes on average (2-3, though the proportion that was successful at mating may be lower), and male gamete production was correlated with sex ratio in natural single-clone infections. With such low fecundity, the sex ratios observed (and lack of relationship with both number of clones and gametocytemia) are consistent with either LMC theory or the new model. Data from other species will be compiled and the implications for LMC theory will be discussed.

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## A PHENOTYPIC CHANGE IN *PERKINSUS MARINUS* WAS ASSOCIATED WITH INTENSIFICATION OF DISEASE IN OYSTER *CRASSOSTREA VIRGINICA*

**R. Carnegie** and **E.M. Bureson**, Virginia Institute of Marine Science

The great intensification of oyster diseases caused by parasites *Haplosporidium nelsoni* and *Perkinsus marinus* in the 1980s in Chesapeake Bay devastated an already beleaguered oyster fishery, prompting long consideration of a non-native oyster introduction before ultimately leading to the rise of intensive *C. virginica* aquaculture based on disease-resistant domesticated stocks. The intensification of disease has been attributed to a multi-year drought, which favored the parasites by raising salinities. For directly transmissible *P. marinus*, higher prevalence and intensities increased transmission efficiencies, favoring continued increased abundance. Comparison of contemporary histological materials with archival slides pre-dating the intensification generated surprising observations, however, that altered our view of this event. Relative to earlier samples, contemporary *P. marinus* cells are much smaller, infect oysters at far greater intensities, and display few of the large multinucleate schizonts that are fundamental to the described *P. marinus* life cycle; contemporary cell division occurs primarily in a binary mode. We also know from field trials that these intense infections emerge sooner after initial challenge with *P. marinus* than in earlier years. This transition in *P. marinus* presentation was first apparent in samples from 1986, the same year that *P. marinus* activity sharply intensified. The phenotypic change and disease intensification followed a 25-year period in which *P. marinus* was largely absent from mesohaline waters of Chesapeake Bay, a disappearance linked to depopulation of oyster beds caused by the emergence of *H. nelsoni* in 1959. We hypothesize that these changes represent a selective response by *P. marinus* to the introduction of *H. nelsoni* and the resulting diminution of oyster populations: the *P. marinus* that would thrive in the transformed environment being one that could generate very high intensities of infection very rapidly so as to more effectively be transmitted in an environment in which hosts were now scarce.

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## PHYLOGEOGRAPHY OF *BONAMIA EXITIOSA* (PHYLUM HAPLOSPORIDIA) THROUGH ANALYSIS OF INTERNAL TRANSCRIBED SPACER REGION RIBOSOMAL DNA SEQUENCES

**K.M. Hill, R.B. Carnegie, N.A. Stokes, J.R. McDowell, K.S. Reece** and **E.M. Bureson**, Virginia Institute of Marine Science

*Bonamia exitiosa*, a parasite of oysters first described in association with catastrophic *Ostrea chilensis* mortality in New Zealand, has since been observed in various oyster hosts around the world—from Australia and New Zealand, Europe and North Africa, Argentina, and the eastern and western coasts of North America. This distribution is unusually broad for a haplosporidian, and the potential for this parasite to cause significant impacts in new hosts and locations prompted research into its origins and dispersal. Gene genealogies were constructed using internal transcribed spacer (ITS) region ribosomal DNA (rDNA) sequence data to look more closely at intraspecific diversity, with the objective of generating hypotheses concerning *B. exitiosa* dispersal. Analysis of 410 cloned PCR amplicons, from nine hosts in ten geographic locations, revealed *B. exitiosa* population structure in the form of four well-defined clusters of sequences. Three of these corresponded to geographic regions (temperate Atlantic and Pacific waters of the Southern Hemisphere; the coast of California; and the Atlantic coast of the Americas), with the fourth being cosmopolitan in distribution. The Southern Hemisphere cluster comprising sequences from New Zealand, Australia, and South America may plausibly reflect natural dispersal of the parasite via rafting with oyster hosts, whereas the California cluster may reflect a limited anthropogenic introduction. The wide geographic distribution of *B. exitiosa* in the cosmopolitan and Atlantic coast groups could reflect both natural and anthropogenic dispersal with one host, *Ostrea stentina*, which is now recognized as distributed from the eastern Americas to the Mediterranean and New Zealand—that is, in most regions where *B. exitiosa* has been found to occur. This analysis highlights the utility of ITS region rDNA

sequencing for examining the distribution of *B. exitiosa*. Development of a molecular clock and sequence data from additional loci will enable even greater resolution of this parasite's phylogeography.

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ECOLOGICAL DETERMINANTS OF *HEMATODINIUM* EPIDEMICS IN THE AMERICAN BLUE CRAB, *CALLINECTES SAPIDUS*

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*Hematodinium perezii* is a parasitic dinoflagellate that infects blue crabs along the eastern seaboard of the USA. The prevalence of this parasite can approach 100% in focal outbreaks that occur in the summer and fall. These coincide with molting periods of the host. We have been studying the infection dynamics of *Hematodinium* in blue crabs from small embayments in Virginia. The bays have long residence times that may contribute to the outbreaks. We developed a quantitative PCR assay to detect dinospores of *Hematodinium* in environmental samples. The dinospore abundance in water samples was significantly correlated with prevalence of infection in crab hosts from high salinity embayments. In several bays, crab abundance is negatively correlated with prevalence of infection. We are modeling the blue crab - *Hematodinium* system to gauge how physiographic features, fishing pressure and host factors contribute to outbreaks of disease. There is circumstantial evidence that overexploitation has contributed to the emergence of disease in several marine fisheries, but the effect of fishing pressure on disease has received little attention. We want to understand how fishing pressure and declining water quality combine with the physiography of small coastal estuaries to promote outbreaks of disease in blue crabs.

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OVERWINTERING OF THE PARASITIC DINOFLAGELLATE, *HEMATODINIUM PEREZII* IN DREDGED BLUE CRABS

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The parasitic dinoflagellates *Hematodinium* spp. have caused significant mortality in many species of marine crustaceans. One species, *H. perezii*, occurs in blue crabs along the eastern seaboard of the USA. Epizootics can reach 100% during outbreaks with most of the diseased crabs dying from the infection. The mode of transmission is unknown and the life cycle has only recently been established *in vitro*. Prevalence of the parasite is bimodal peaking in early summer and fall, and declining markedly in early winter. The rapid decline in infections in the winter samples begs the question of whether the parasite overwinters in crabs. We report observations on the prevalence of the parasite from winter dredge surveys carried out in 2011 and 2012. Crabs were examined via hemolymph smears, histology, and PCR diagnosis for the presence of *H. perezii*. Active infections were observed in winter samples in 2011 and 2012, indicating the parasite can overwinter in blue crabs. In previous years, prespore stages indicative of heavy infections were observed in infected crabs in mid spring and early summer samples; thus, there is evidence that overwintering occurs and that it provides a source of infected animals for transmission to occur in the spring.

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## SPERMATOOZON ULTRASTRUCTURE OF *ADELOBOTHRIMUM* SHIPLEY, 1900 (EUCESTODA: LECANICEPHALIDEA)

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Spermatozoon ultrastructural characters have shown to be informative in phylogenetic studies among cestode orders. Detailed comparative data exist on the sperm ultrastructure of most cestode orders, though information for the Lecanicephalidea is very limited. The only previous data on lecanicephalidean sperm ultrastructure came from a specimen of the genus *Tetragonocephalum* from *Himantura* sp. (Justine, 2001). Mature spermatozoa of *Tetragonocephalum* were described as possessing a crested body, parallel cortical microtubules, and a single axoneme. Based on these data, Levron et al. (2010) suggested lecanicephalideans to have Type IV spermatozoa and postulated a spiral nucleus. One specimen each, of 2 species of *Adelobothrium* were collected from eagle rays (*Aetobatus* spp.) in Vietnam and fixed for transmission electron microscopy (TEM). The 2 posterior-most proglottids with well-developed external seminal vesicles were cut from the strobila of each individual and processed for TEM: proglottids were embedded in Spurr's resin; ultrathin sections were cut on an ultramicrotome, mounted on copper grids, double stained with uranyl acetate and lead citrate, and observed with TEM. Sperm ultrastructure was identical for both species of *Adelobothrium* and generally consistent with previous observations of *Tetragonocephalum*. However, preliminary data suggest the nucleus to be parallel to the axoneme. *Adelobothrium* is only the second genus of lecanicephalidean for which sperm ultrastructure has been determined. Given that variation within orders has been documented for other cestode groups studies focusing on additional lecanicephalidean taxa will provide a more comprehensive perspective on sperm ultrastructure in this order. Moreover, details of spermiogenesis remain to be documented for lecanicephalideans.

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#### A NEW TAPEWORM SPECIES FROM *DASYATIS ZUGEI* (PALE-EDGED STINGRAY) FROM COASTAL MALAYSIAN BORNEO

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The study is part of a large, ongoing survey of parasites, including cestodes, from elasmobranchs in Borneo. In this study, examination of four individual *Dasyatis zugei* resulted in collections of several cestode species, including specimens representing a new genus and species of a rhinebothriidean cestode. Examination of specimens with both light microscopy and scanning electron microscopy revealed the presence of several unique characteristics. These features include the arrangement of loculi on the bothridia. A combination of longitudinally- and transversely-oriented septa occur on each bothridium, resulting in a combination of vertically- and horizontally-oriented loculi, a feature not previously observed among rhinebothriidean cestode genera. Other morphological features were measured and used to distinguish this species from other known species of this recently discovered genus, such as the dimensions of the bothridia, number of loculi per bothridium, microthrix patterns, and terminal proglottid features. This study, like similar ones from the Borneo survey work, indicates that every time an elasmobranch species is examined for the first time parasitologically, such as *D. zugei*, new cestode species are discovered.

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## EXAMINATION OF HOST SPECIES USAGE PATTERNS IN SPECIES OF THE SHARK CESTODE GENUS *PARAORYGMATOBOTHRIUM*

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The shark cestode genus *Paraorygmatobothrium* was erected by Ruhnke (1994) for three species. Since then, the genus has grown to include 22 species. Host specificity has also been a key assumption in the taxonomy of this genus. Collections from a variety of localities world-wide have revealed substantial undescribed species diversity within the genus. Thus far, analysis of the cytochrome c oxidase I (COX1) region has been conducted for 76 individual samples of *Paraorygmatobothrium*. These samples have been collected from 17 shark species of the order Carcharhiniformes. Sharks were taken from the Northwestern Atlantic Ocean, the Gulf of Mexico, the Gulf of California, and the waters off Northern Australia, Malaysian Borneo, and Senegal. An alignment of 471 nucleotide positions was completed for the samples of *Paraorygmatobothrium*, in addition to the outgroup taxa *Thysanocephalum thysanocephalum* and *Phyllobothrium lactuca*. At least 17 species have been putatively identified using COX1, and only two are known to science. Seven of the new species were collected from two or more host species. This pattern of host use by species of *Paraorygmatobothrium* is contrary to previous assumptions of host specificity for the group.

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## THE DISTRIBUTION AND SYSTEMATICS OF VIANNAIIDAE DURETTE-DESSET AND CHABAUD, 1981 OF NEW WORLD MARSUPIALS

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Members of Viannaiidae, infect a variety of New World mammals, including marsupials and hystricognath rodents. Characters used in their identification and classification include the synlophe and disposition of bursal rays. Systematic position of Viannaiidae remains unclear in that two groups have been proposed as closely related: Ornithostrongylidae, parasites from American and Old World mammals and birds, or, alternatively, Herpetostrongylidae, which parasitizes reptiles and marsupials in Sahul (Australia and Papua New Guinea). To test these two competing hypotheses, species traditionally included in Viannaiidae were surveyed from several localities ranging from southern Illinois to Argentina. The three genera were found infecting a wide diversity of opossums in this range, however, species from the genus *Travassostrongylus* were not found north of Veracruz, Mexico. These records show a widespread distribution, especially for *Hoineffia simplicispicula* and *Viannaia philanderi*. Our investigations in French Guiana and Bolivia show that species of *Viannaia* are able to infect most species of opossums. Some species of *Travassostrongylus* show a restricted distribution in their associations, including *Travassostrongylus callis* and two undescribed species of *Travassostrongylus*. The patterns appear to be consistent in both French Guiana and Bolivia. In addition, the phylogenetic analysis of 18S, ITS, COB, and 16S for Trichostrongylina reveals that Viannaiidae is paraphyletic. While *Viannaia* and *Hoineffia* form a tight monophyletic group, *Travassostrongylus* is recovered as the sister group for species in Herpetostrongylidae. Both *Viannaia* and *Hoineffia* are monodelphic and share an almost identical synlophe, while *Travassostrongylus*, *Nicollina* and *Herpetostrongylus* are didelphic. We propose to redefine Viannaiidae based on the monodelphic condition and the presence of three ventral synlophe ridges. Further classification and definition of *Travassostrongylus* and its related taxa necessitates a larger sampling scheme that includes parasites from Australasian hosts.

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IT'S ALL RELATED: CONSERVED MORPHOLOGICAL CHARACTERISTICS OF NON-ADULT STAGES OF HAIRWORMS (NEMATOMORPHA)

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Estimates suggest that only 15% of hairworm species have been described globally. One reason for the lack of knowledge on the diversity of hairworm species is the lack of reliable ways of collecting adult hairworms over large geographical areas. However, a recent study suggests that non-adult cyst stages of hairworms may be the most commonly encountered life stages of hairworms in the environment, and therefore may be a useful tool for discovering the hidden biodiversity of this group. Unfortunately, little information is available on the morphological characteristics of non-adult stages of hairworms. To address this issue, we examined the morphological characteristics of non-adult stages of 9 species of hairworm from 4 North American and 2 African genera (*Chordodes*, *Gordius*, *Paragordius*, and *Neochordodes*). Observations were made on the oviposition behavior of adult worms and morphological characteristics were recorded for egg strings, larvae and cysts using differential interference contrast microscopy and/or scanning electron microscopy. In addition, we constructed molecular phylogenetic hypotheses for multiple genera of hairworms using partial *cox1* and 18S sequence data. Our results indicate that oviposition behavior and egg string, larva, and cyst morphology was conserved within genera of *Gordius* and *Paragordius*; whereas no differences were observed among any of these morphological characteristics among genera of *Chordodes* and *Neochordodes*. Our molecular phylogenies demonstrated 3 evolutionary lineages among hairworms. Genera of *Gordius* and *Paragordius* were monophyletic whereas the genus *Neochordodes* was nested within species of *Chordodes* supporting the paraphyly of this genus. These results indicate that morphological characteristics of non-adult of hairworms may be useful in differentiating some but not all genera of hairworms. More importantly, morphological characters of non-adult stages of gordiids appear to be phylogenetically conserved among hairworm lineages.

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DIVERSIFICATION AND DISPERSAL IN A WIDESPREAD LIZARD MALARIA PARASITE

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Few studies have assessed patterns of low-level divergence in the malaria parasites of genus *Plasmodium* (Sporozoa: Haemosporidia), and we have a generally poor understanding of diversification in this group. We attempt to shed light on this process by studying the phylogeography of the lizard parasite *Plasmodium floridense*. We collected samples of this parasite from across its range in southeastern North America and the Caribbean, and sequenced these at both mitochondrial and nuclear loci. We inferred several reciprocally monophyletic clades that correspond to populations of *P. floridense* on each major island. We observed morphological differences between some of these clades, suggesting that these are reproductively isolated and each is a separate species. We also found evidence of bidirectional dispersal between Florida and Cuba, which suggests multiple overwater dispersal events in their lizard hosts. We discuss these results in the context of molecular dating and overall diversification processes in malaria parasites.

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PENTASTOMES (PENTASTOMIDA: CEPHALOBAENIDA) ISOLATED FROM THE ENDANGERED  
RATTLESNAKE, *CROTALUS DURISSUS UNICOLOR* FROM ARIKOK NATIONAL PARK, ARUBA

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H.K. Reinert, The College of New Jersey  
R.A. Odum, Toledo Zoological Society

Due to the inadvertent road mortality of three *Crotalus durissus unicolor*, we had the opportunity to necropsy and inspect their viscera (with permission of the Aruba Veterinairie Dienst and Parke Nacional Arikok). Upon necropsy, we found a total of 39 larvae and one adult of an unknown pentastome in the upper to middle respiratory tract. The parasites were excised, fixed in 10% formalin, and stored for transport in 70% Ethanol. The adult and larvae were examined with an Olympus SZX16 stereo microscope, and pictures were taken with an Olympus SDF Plapo camera. To aid in identification, the cephalothorax was removed, dehydrated in an ethanol series, cleared in xylene, and mounted with Damar Balsam. Measurements of the oral cadre, and 2 pairs of hooks of the cephalothorax were obtained. A total of seven morphological characters were selected for measurement to identify the adult specimen: total adult body length, adult body width at the widest point, estimated annulus number, adult mouth length, adult mouth width, adult pharynx width, and hook dimensions. These observations provide a new host and location record for pentastomes.

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ON THE OCCASIONAL CHALLENGES OF MAINTAINING MONOPHYLETIC GENERA

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K. Jensen, University of Kansas

The advantages of circumscribing and maintaining monophyletic genera are many. Typically, such genera are relatively easy to diagnose because the shared history of their members generally manifests itself in morphological similarities, some of which may be unique. Furthermore, the evolutionary cohesion of monophyletic groups makes them appropriate subjects of coevolutionary and other macroevolutionary studies. However, in a number of cases, the application of molecular methods to cestode systematics has produced rather puzzling results, calling into question the monophyly of morphologically cohesive genera. Of particular note are the tetracyllidean genus *Platybothrium* and the litobothriidean genus *Litobothrium*, each of which currently contains species that are remarkably uniform relative to one another, but distinctive relative to other genera. However, in both cases, results from molecular phylogenetic analyses suggest these genera include morphologically strange forms deeply nested among their members. While the molecular data applied in these cases may simply be failing to accurately reflect evolutionary history, in both cases subtle morphological features provide additional support for these otherwise heretical placements. This leads one to ponder if the grouping of such aberrant forms within otherwise uniform genera may, in fact, be the result of simple genetic mutations manifesting themselves as complex changes in phenotype. In which case, if the monophyly of such genera is to be maintained, a standardized method for recognizing such taxa, without reducing the utility of the generic diagnosis should be established. One suggestion is the inclusion of a separate section in the diagnosis which would serve to draw attention to such intrageneric heteromorphisms, and also to provide the diagnostic morphological information required for recognition of the aberrant form. However, this solution for retaining generic monophyly should be implemented only after a substantial and diverse array of molecular data have been found to repeatedly corroborate such morphologically divergent affinities.

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SPECIES BOUNDARIES IN *RHINEBOTHROIDES* (CESTODA: RHINEBOTHRIIDEA) FROM  
FRESHWATER STINGRAYS IN SOUTH AMERICA

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Members of the rhinebothriidean cestode genus *Rhinebothroides* are parasites of freshwater stingrays of the family Potamotrygonidae, endemic to South America. To date, six species are recognized as valid but eight nominal species are available. Most species are currently diagnosed using morphometric and meristic characters that have failed to take account of intraspecific variability. Furthermore, the widespread distribution of some species, as well as their apparent relaxed host specificity, a pattern that differs from that documented for marine tetraphyllideans, suggests the genus actually includes species complexes that require taxonomic refinement. This study aimed at revising the taxonomy of one of these complexes, the *Rhinebothroides freitasi* complex, which potentially includes three other nominal species (*R. campbelli*, *R. circularisi*, *R. venezuelensis*). A combination of molecular and morphological data was used to shed light on taxonomic issues in this complex. Within this framework, molecular data were generated for the markers 28S rRNA, ITS1, and COI for 57 specimens of *Rhinebothroides* collected from approximately 30 species of stingrays throughout the major river basins of Brazil. This extensive biogeographic and host sampling also allowed the compilation of morphological data for ~400 specimens within the *R. freitasi* complex, thereby providing a robust assessment of intraspecific morphological variability. A phylogenetic analysis of the molecular data using POY 4, which also included 26 taxa representing diversity of marine and freshwater lineages of tetraphyllideans, yielded evidence for five major clades within *Rhinebothroides*. Four of these clades are morphologically congruent with currently valid species in the genus; one of them shows features present in one of the 2 previously synonymized species. As a result, the following five species of *Rhinebothroides* are considered to be valid: *R. glandularis*, *R. freitasi*, *R. moralarai*, *R. scorzai*, and *R. venezuelensis*.

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### REEVALUATION OF THE GENUS *CAULOBOTHRIMUM* (CESTODA: TETRAPHYLLIDEA) RESULTS IN DISCOVERY OF REMARKABLE MORPHOLOGICAL FEATURES

T.J. Katz and J.N. Caira, University of Connecticut

The tetraphyllidean genus *Caulobothrium* is currently poorly understood. A recently published phylogenetic analysis, based on molecular data for one described and five undescribed species, supports the monophyly of the genus, but includes a number of morphologically diverse taxa. The present study was undertaken in an attempt to formally circumscribe the morphological identity of the genus. Material of all six species included in the molecular study was examined, specifically *Caulobothrium opisthorchis* and *Caulobothrium* n. sp. 1 from *Myliobatis californicus* off Baja, *Caulobothrium* n. sp. 2 and *Caulobothrium* n. sp. 3 from *Pteromyiaeus bovinus* off Senegal, *Caulobothrium* n. sp. 4 from *Pastinachus solocirostris* off Malaysia, and *Caulobothrium* n. sp. 5 from *Pastinachus atrus* off Australia. Specimens of each species were studied using light microscopy of whole mounts and histological sections, as well as scanning electron microscopy. The resulting defining characteristics of the genus *Caulobothrium* include a conspicuously narrow cirrus sac, the presence of a previously overlooked apical sucker in the anterior-most loculus, resulting in establishment of defined anterior regions of each bothridium (features not found in most rhinebothriideans), and a cephalic peduncle of varying lengths. *Caulobothrium* n. sp. 2, although it clustered deeply among the other *Caulobothrium* species in the tree resulting from the molecular analysis, was found to possess a peculiar longitudinal groove along the dorsal and ventral length of each proglottid. Curiously, this prominent groove, which penetrates relatively deeply into the proglottid, resembles a structure found in a recently described lecanicephalidean species, also from a myliobatid host. This structure stained positively with Periodic acid-Schiff (PAS), indicating the presence of mucopolysaccharides, suggesting it may serve in attachment to the host spiral intestine. Our findings

indicate that the genus *Caulobothrium*, although likely monophyletic, is composed of an assortment of remarkably morphologically diverse species.

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PROGRESS AND OBSTACLES IN SPECIES LEVEL INVESTIGATIONS OF TWO CESTODE  
GENERA FROM SHARKS AND STINGRAYS

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Substantial un-described species diversity exists within the cestode fauna of elasmobranch fishes, especially within the genera *Anthocephalum* and *Paraorygmatobothrium*. The study of morphology and molecules for species of these genera has yielded both success and frustration. In different ways, both serve as case studies of species level taxonomy and systematics. In this talk, species concepts are considered as they apply to tapeworms. Issues with the problematic nature of the boundaries of new and existing species are also considered. Examples of how DNA sequence data is employed in the study of cestode species level questions will also be presented. Elasmobranch cestode species have been assumed to be quite host specific. That assumption will be examined.

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A NEW GENUS AND SPECIES OF CESTODE (CESTODA: PARUTERINIDAE) FROM THE  
SQUIRREL CUCKOO, *PIAYA CAYANA* LESSON, 1830 (AVES: CUCULIFORMES), FROM  
PARAGUAY

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J. Mariaux, Muséum d'Histoire Naturelle

B.B. Georgiev, Bulgarian Academy of Sciences

A new genus and species of cyclophyllidean cestode is described from 18 specimens (five scolices, 13 fragments of strobilae only) collected from the intestines of three Squirrel Cuckoos, *Piaya cayana* Lesson, 1830 (Aves: Cuculiformes: Cuculidae), taken from two localities in Paraguay in 1984 and 1985. The new genus appears to belong to the Paruterinidae and is most similar to *Francobona similis* (Ransom, 1909) Georgiev and Korniyushin, 1994, but differs in its possession of a fan-shaped, lobed ovary rather than an irregular ovary, an atrial pore that opens dorsally to the cirrus sac rather than an atrial pore that opens posteroventrally to the cirrus sac, and a uterus that is symmetrical rather than asymmetrical and irregularly-shaped. In addition to *F. similis*, only a few other paruterinids have been found parasitizing members of Cuculidae, as most parasitize other bird families. Cestodes of other families (i.e., Dilepididae and Davaineidae) also parasitize cuckoos; the majority of the records come from three cuckoo subfamilies that are predominately arboreal. Interestingly, the two cuckoo subfamilies that have not yet been found to host cestodes consist primarily of ground-dwelling cuckoos. Thus, host habitat may be a contributing factor to the lack of cestode records from the latter two subfamilies, but incomplete sampling cannot be ruled out as a factor for the 24 species in these subfamilies are particularly poorly sampled. Broader and deeper sampling of cuckoos is required for these host associations to be more clearly understood.

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A TECHNIQUE TO IMPROVE LIVE *EIMERIA* VACCINE EFFICACY

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Host-specific *Eimeria* spp. are of great economic burden to poultry production due to performance loss and cost of parasite control attributed to coccidiosis. The genetically limited lifecycle of *Eimeria* spp. and birds' ability to readily generate protective immune responses permits the use of live vaccination for coccidiosis control; however, few methods to improve vaccine efficacy under different rearing conditions have been developed. Live *Eimeria* vaccination stimulates immunity from the first small dose of vaccine oocysts and is enhanced through fecal-oral cycling. Without adequate cycling, only limited immunity may develop and chickens risk coccidiosis when challenged. Cycling is influenced by environmental management. Young table-egg hens (pullets) are frequently reared in a cage system with mesh floors to allow feces to fall away from the birds. To promote cycling, producers can cover the mesh to retain feces for the first 10 days; yet coccidiosis can occur when birds are transferred to the laying barn (due to inadequate cycling). We tested the ability of durable fibre trays covering part of the mesh floor (lasting ~5 weeks) to improve fecal-oral cycling. Pullets were gavaged orally with live vaccine and reared with 0, 20, 40 or 60% of the cage floors covered by trays from hatch to 6 weeks, then subsequently challenged with *Eimeria* spp. Total oocyst output between birds housed with or without coverage differed significantly. Pullets on 40% coverage shed significantly fewer oocysts than the other birds (>99% reduction compared to no coverage). No difference was found between 20 and 60% coverage. Lesion scores at 6 DPI mirrored oocyst output results. Increased access to oocysts using 40% cage coverage with fibre trays over 5 weeks allowed for improved vaccine efficacy in live *Eimeria* vaccinated caged pullets.

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**STRESS, THE PARASITES FRIEND: STRESS EFFECTS ON IMMUNE FUNCTION ARE TIED INTO MOLECULAR NETWORKS**

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**D.K. Cone**, Saint Mary's University

When animals (e.g. fish) are attacked by viral, bacterial or parasitic infection there is differential regulation of molecules involved in the innate immune system. Different stressors, such as handling or crowding, also alter the expression of genes involved in the innate immune system. Immune responses and stress responses can conflict when they occur simultaneously, leading to immunosuppression. In this study we use the cricket model to examine some of the molecular underpinnings of these interactions. We examine the effect of both the immune response and stress response on the expression of heat shock protein 90 (Hsp90), glutathione-s-transferase (GST) and nitric oxide (NO) synthase gene expression using quantitative PCR. We examine the effects on gene expression in the fat body, a tissue important for both the stress and immune responses in crickets. Hsp90 is a protective chaperone molecule and increases in response to heat stress 100 fold compared to control animals. GST is part of a class of enzymes involved in detoxification of oxidative stress products. It is upregulated 50 fold, compared to non-injected animals, when crickets are injected with paraquat, a toxic pesticide. Following an immune challenge with heat killed *Serratia marcescens* Hsp90 is upregulated 21 fold at 3 hours and 100 fold at 12 hours and drops to 60 fold at 24 hours compared to non-challenged animals. There is a 2 fold upregulation of GST at 3 hours but no change at 1, 6, 12 or 24 hours. The enzyme NO synthase, which produces NO, is upregulated 5 fold at 24 hours compared to non-injected controls. The effects of acute stress, and acute stress in combination with an immune challenge, on gene expression will be discussed.

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**EXPERIMENTAL CYSTOISOSPORA CANIS INFECTION IN BEAGLES**

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We originally characterized the responses of beagle puppies to experimental inoculation with an isolate of *Cystoisospora canis* obtained from dogs from Blacksburg, Virginia. Our attempts to infect 2 beagle puppies with 50,000 sporulated *C. canis* oocysts of this isolate that had been stored at 4 C for 3 years were not successful. Therefore, we obtained oocysts of *C. canis* from a naturally infected dog from São Paulo, Brazil. Oocysts were sent to the Center for Molecular Medicine and Infectious Diseases, Blacksburg, Virginia. Oocysts were sporulated in 2% (v/v) sulfuric acid. Sporulated oocysts were concentrated by sugar flotation and 50,000 oocysts were fed to each of five 6 week-old female beagle puppies. The prepatent period was 9 (N=3) or 10 (N=2) days and the patent period was 7 (N=1), 8 (N=1) and 10 (N=3) days. Diarrhea was observed after 9 days in 2 dogs and was present in all dogs on day 10 PI. Feces were loose to normal appearing from these days up until day 17 PI when they became formed again in all dogs. Oocyst numbers in individual dogs peaked between 10 and 12 days post-inoculation. One dog was treated with Albion® (sulfadimethoxine) 12 days after inoculation due to severe bloody diarrhea. The size of oocysts collected from these dogs averaged 37.6 x 28.6 µm. After sporulation, oocysts contained 2 sporocysts each with 4 sporozoites. *Caryospora*-like oocysts were occasionally observed that contained 1 sporocyst with 8 sporozoites. This work was supported by a grant from IDEXX laboratories to DSL and AMZ.

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### MOLECULAR EPIDEMIOLOGY OF *CRYPTOSPORIDIUM* ISOLATES FROM NORTH INDIAN PATIENTS

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Cryptosporidiosis is a significant cause of diarrheal illness in both developed and developing countries and its infection has been documented in both immunocompetent and immunocompromised populations. Many species/genotypes of *Cryptosporidium* infect a wide range of hosts including humans, domestic and wild animals. Different species/genotypes are morphologically indistinguishable and molecular techniques have become the key to detection and source tracking. Thus, present study was designed to study genetic diversity of *Cryptosporidium* isolates from humans in North India. *Cryptosporidium* oocysts were detected in stool samples by bright field microscopy (100X) of Ziehl-Neelsen stained faecal smears. DNA was extracted with Qiagen Kit and all samples were genotyped by SSU rRNA based PCR-RFLP tool which differentiates all known *Cryptosporidium* species/genotypes causing infection in humans. With this technique ~850 bp fragment was amplified by nested PCR and species or genotypes were differentiated by banding patterns in restriction analysis of secondary PCR products with enzymes SspI and VspI. *C. hominis* and *C. parvum* isolates were sub-typed by sequence analysis of nested PCR amplified GP60 gene. For subtype families, sequences were searched for similarity by BLAST analysis and aligned with reference sequences retrieved from GeneBank by multiple sequence alignment (ClustalW, BioEdit7.0.5.3). Fifty-three faecal samples were found to be positive for *Cryptosporidium* oocysts. RFLP analysis revealed 39 isolates as *C. hominis* and 13 isolates as *C. parvum*, one sample failed amplification. GP60 based sequencing of *C. hominis* and *C. parvum* divided them into 8 subgenotype families and 17 subtypes. GP60 based sequencing could detect 7 cases of mixed infections with *C. hominis* and *C. parvum*/*C. meleagridis* and showed the presence of *C. meleagridis* in 6 HIV positive patients which were indistinguishable in RFLP.

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## PLASMODIUM FALCIPARUM INFECTION IN HIV-INFECTED PERSONS ON HIGHLY ACTIVE ANTIRETROVIRAL THERAPY

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*Plasmodium falciparum* infection is endemic in most tropical countries and will definitely infect Human Immunodeficiency Virus persons living in this region at one time or the other during the course of their infection. This study was conducted to determine the prevalence of malaria in HIV-infected patients on highly active antiretroviral therapy (HAART) in Benin City, Nigeria. A total of 285 (84 males and 201 females) adults attending the hospital were enrolled in this study. Blood specimens were collected from each participant and processed for CD4 counts, *Plasmodium falciparum* detection and haemoglobin concentration using standard procedures. A total of 6 (2.11%) out of 285 Human Immunodeficiency Virus infected patients on HAART treatment had malaria and anaemia. CD4 count <200cells/ $\mu$ l was significantly associated with *Plasmodium falciparum* infection (OR=11.610; 95%CI=2.059, 65.477;  $p<0.0039$ ). An overall prevalence of 2.11% of asymptomatic malaria was observed in this study. Malaria parasitaemia was associated with CD4 counts <200cells/ $\mu$ l and anaemia. Measures to reduce malaria infection and anaemia among HIV patients on highly active antiretroviral therapy are advocated.

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## GASTROINTESTINAL HELMINTHS AMONG PUPILS IN AN URBAN AND SUBURBAN COMMUNITIES IN NIGERIA

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Prevalence and intensity of gastrointestinal helminthic infections was compared among six hundred (600) Nigerian Primary School pupils in the urban and suburban areas in some communities in Nigeria, between November 2010 and February 2011. Selected pupils were instructed on how to collect the samples for examinations. These samples were collected the same day and about the same time of processing them for infections, using normal saline and iodine stained smears of the samples. Worm burden estimation was also performed using the cellophane stick smear technique. Pupils with peri-anal itching were examined using modified cellulose adhesive tapes for ova of *Enterobius vermicularis*. The overall prevalence of gastrointestinal helminths was 65%. The pupils in the Suburban were more infected (75%) than those in the urban (35%). *Ascaris lumbricoides* was the most frequently seen parasites (54%), while the *Enterobius vermicularis* was the least seen (2%). Hookworm infection was second with (30%). Other Nigerian researchers showed that hook worm infection was more during the rainy seasons in Nigeria. Relatively therefore, this may have affected the low prevalence observed in this study, since this study was conducted in the dry season. Other researchers in Nigeria have also reported *A.lumbricoides* as the most frequently encountered parasite. The distribution of infection by sex was not statistically significant, whereas a statistically significant difference was noted for the prevalence of infection by location of schools and the type of toilet facilities used by the pupils. Most pupils are healthy carriers of these infections and are reservoir hosts of transmission of these infections to their mates. Good hygiene practices, should be included as a course or a subject of study into the curricula of all the rural/suburban areas of West African primary schools course works. Most pupils get infected out of ignorance and most suffer to even lose their lives out of severe consequences of these infections when they are heavy. It may be recommended that Governments and Non Governmental Organizations must assist in the provisions of anti-worm tablets for school pupils regularly.

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## HIV SCREENING STATUS AND MALARIA IN NIGERIA: ENDEMICITY, SIGNS AND SYMPTOMS, KNOWLEDGE, ATTITUDE AND PRACTICES

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HIV/AIDS has become one of the most devastating diseases humanity has ever faced. Malaria is a serious parasitic disease responsible for approximately 1-3 million deaths annually. HIV screening status and prevalence of malaria were determined among undergraduates of a Nigerian University. A total of 315 students made up of 136 males and 179 females voluntarily gave their blood samples for this study. HIV screening was done using Determine HIV 1/2, Unigold, and Stat-pak kits while thick and thin Giemsa stained blood films were used for the examination for malaria parasites. Of this number, 296 (93.97%) had malaria while 9 (2.86%) had a positive HIV screening status. Indeterminate HIV cases stood at 0.95%. Malaria-HIV co-infection was 3.81%. Gender wise, more males (4.41%) than females (1.68%) were infected for HIV and more males (94.86%) than females (93.30%) were infected for malaria though infection was not statistically significant ( $p > 0.05$ ). Age related infection was highest in the age group 21-25 years for both malaria and HIV. Some symptoms associated with malaria were headache, weakness, fever (24.13%), cough (11.11%), vomiting (13.02%), nausea (19.37%), sweating (35.24%), loss of appetite (18.41%), while those of HIV were continuous fever (24.13%), rashes (1.27%), cough (11.11%), weakness (15.56%), loss of weight (0.95%). Factors that affected students' attitude toward HIV and malaria tests were fear, distance and lack of time. Mosquito bites (81.90%), uncleanness (21.90%), presence of breeding sites (3.17%) were some attributable causes of malaria while those of HIV were ignorance (54.29%), premarital sex (2.22%), sharing of shaving sticks (91.75%), skin piercing and tattooing (1.90%), use of sharp objects (0.95%) and blood transfusion (0.63%). Some preventive measures taken against malaria were the use of insecticides (13.5%), anti-malaria drugs (66.03%), insect repellents (0.32%), mosquito nets (49.52%); and for HIV they were the use of screened blood for transfusion (56.20%), avoiding the sharing of sharp objects (97.78%), needles and syringes (91.11%), abstinence from sex with non spouse (8.89%), use of condom (62.22%) and proper information (96.51%). Sources of information for HIV and malaria were stickers (46.35%), television (94.92%), radio (95.56%), teachers in school (12.06%) and seminars/workshops (27.30%).

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## PROTECTIVE EFFECT OF HYDATID CYSTS FLUID AND PROTOSCOLEX PEPTIDES IN TWO ANIMAL MODELS

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Hydatidosis or cystic echinococcosis is a zoonotic disease caused by cestoda of the genus *Echinococcus* (Family *Taeniidae*). In spite of control programs, the parasite still has a very wide geographical distribution. There is clear evidence for the emergence or re-emergence of human cystic *Echinococcosis* in parts of China, central Asia, and Eastern Europe. Dogs, as definitive hosts, are pivotal in the transmission of the hydatid cyst. Substantial efforts have been made to control of *E. granulosus* in the world, with limited success. Vaccination can provide an adjunct to improved, integrated control. Dog vaccination can provide an acceptable and cost effective complementary control method. Present study aimed to determine the immunogenicity of hydatid cyst fluid and protoscoleces under 30 kDa proteins provide protection in *E. granulosus* experimentally infected mice as experimental intermediate host and dogs as definitive hosts. After separation of hydatid cyst fluid and protoscoleces from liver cysts, 1.5 cc of fluid and sonicated protoscoleces were centrifuged (5000 × g) by using Millipore filter at 4 °C for 10 minutes. After protein measurement by Bradford method, the filtered solution was lyophilized. Present study was

performed on 27 mice and 9 dogs in 3 different groups. 1<sup>st</sup> group treated with less than 30 KDa antigens of hydatid cyst fluid, 2<sup>nd</sup> group received less than 30 KDa antigens of protoscolex and 3<sup>rd</sup> group as control received PBS. All the injections were along with incomplete Freund's adjuvant. 2 weeks later animals were immunized for second time and after 2 weeks from the last injection, they were challenged to *E. granulosus*. Dogs 35 days and mice 5 month post challenge were euthanized. Number and size of hydatid cysts in mice and number of worms in dogs were measured and compared in different experimental groups. During experiment detection of serum antibody was done using ELISA method. Average number of worms recovered in immunized dogs was less than control. According to the growth rate of adult worms in different groups, the total length and the length of terminal segment in the control group was significantly more than immunized groups ( $p < 0.001$ ). The number of worms in the group which received 30 kDa fluid antigens was less than the group which received under 30 kDa protoscolex antigens, and the control group. It has also been shown that the total and terminal segment length of worms in Group I was smaller than other groups. In mice, the ones which were immunized with hydatid cyst fluid produced higher antibody in comparison to protoscolex immunized and control mice ( $P < 0.05$ ). Results of present study showed that protective immunity in vaccinated mice was 100%. Control of cystic echinococcosis is one of the most important issues in an endemic area, although not the only one. The potential use of a vaccine in dogs, as a definitive host, is more effective because could reduce the biomass of *E. granulosus*. Results of present study showed that less than 30 kDa proteins of hydatid cyst fluid and protoscoleces especially fluid can be used as a new protective protein for immunization which could render final and intermediate hosts resistant to challenge with *E. granulosus* infection.

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### EVALUATION TREATMENT OF CUTANEOUS LEISHMANIASIS WITH GARLIC EXTRACT AND ITS FRACTION IN ANIMAL MODELS

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Leishmaniasis is one of the six most common parasitic infections in tropical regions. There are different therapeutic modalities. However therapeutic resistance has developed and resulted in numerous problems. So evaluation of other therapeutic modalities is performed extensively. We compared the therapeutic response of cutaneous leishmaniasis with Glucantime and Garlic extract and it'R10 in animal model. The therapeutic response of cutaneous leishmaniasis to Glucantime and Garlic extract and R10 in animal model was studied in BALB/c, outbred SW mice and C57BL/6 mice. These three races were divided in four groups according to receiving either one of these three agents or no treatment (control). The therapeutic response was evaluated according to parasitic load before and after treatment and also with measuring the size of the lesions.

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### A SURVEY OF THE EFFECT OF IL-22 ON THE LESION ORIGINATED FROM *LEISHMANIA MAJOR* IN BALB/C MICE

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**Z. Sharifi**, **S. Ghaffarifar**, **G. Shahpari**,

IL-22 is the family member of IL-10 that is created by Th17, Th22, NK cells and recently the role of IL-22 in protection and inherent defense mechanisms, in the control of bacterial and viral infection, homeostasis and repair tissue has been demonstrated. So in this research the effect of IL-22 treatment on lesion originated from *Leishmania major* in BALB/c mice has been survived. The experimental methods: 24



female BALB/c mice for 8 weeks old at least  $2 \times 10^6$  Promastigotes of *Leishmania major* Iraninan standard strain MR HO/IR/75/ER in stationary phase through 100 microliter subcutaneous challenged and in three of eight groups of mice has been injected by 5ng/ml and 10ng/ml (IM) with recombinant IL-22. Immunity cellular and humoral with assessment cytokines IL-4, IFN- $\gamma$ , culture spleen lymphocyte cells and survey of IgG2a, IgG Total with Elisa method and MTT method and clinical study measuring the wound healing and lifespan of mice and death registration was done. The study conclusion indicated that the growth of ulcer especially has been reduced in IL-22 groups and the greatest effect in IL-22(5ng) group. IL-22(5ng) has caused the increased production of, IFN- $\gamma$  and the reduced IL4. The LSD test has shown that, IFN- $\gamma$ , IgG Total with  $P < 0.05$  significant in IL22-5ng groups rather than other groups and IL4 with  $P < 0.05$  nonsignificant in IL22-5ng but significant with other groups. IgG2a in IL22-5ng with  $P < 0.05$  is not significant with IL22-10ng groups but significant with other groups. MTT IL-22, 5ng is significant with other groups. We can infer that increasing IFN- $\gamma$  and reducing IL-4 by IL-22, 5ng has caused the protective immunity in *L. major*, so if it is used with the anti-leishmania drug combined may have effective results in treatment.

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**TESTING MENDELIAN INHERITANCE FROM FIELD-COLLECTED PARASITES ENABLES  
CORRECT INFERENCE OF REPRODUCTIVE MODE AND MATING SYSTEM**

**J.T. Detwiler, and C.D. Criscione, Texas A&M University**

Cryptic aspects of parasite population biology, e.g., mating systems, are increasingly being inferred from polymorphic and co-dominant genetic markers such as microsatellite loci. Underlying the use of such co-dominant markers is the assumption of Mendelian inheritance. The failure to meet this assumption can lead to artifactual statistics and erroneous population inferences. Here, we illustrate the importance of testing the Mendelian segregation and assortment of genetic markers and demonstrate how field-collected samples can be utilized for this purpose. To examine the reproductive mode and mating system of hermaphroditic parasites, we developed microsatellites for the cestode, *Oochoristica javaensis*. Among loci, we found a bimodal distribution of  $F_{IS}$  (a fixation index that quantifies the deviation from Hardy-Weinberg equilibrium within subpopulations) values where loci were either highly negative (close to -1) or highly positive ( $\sim 0.8$ ). By conducting tests of Mendelian segregation from natural crosses, we determined that loci with negative  $F_{IS}$  values were in fact duplicated loci that were amplified by a single primer pair. Genetic crosses also provided linkage data and indicated that the duplicated loci most likely arose via tandem duplications rather than whole genome/chromosome duplications. By correcting for the duplicated loci, we were able to correctly infer that *O. javaensis* has a sexual reproductive mode, but the mating system is highly inbred. We discuss the feasibility of this approach in other parasite systems.

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**(123)**

**LIFE CYCLE, HOST SPECIFICITY, AND SEASONAL OCCURRENCE OF *CYRTOSOMUM PENNERI*  
(NEMATODA: ATRACTIDAE) FROM LIZARDS IN POLK COUNTY, FLORIDA**

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The nematode *Cyrtosomum penneri* is a commonly encountered gastrointestinal parasite of the Brown Anole (*Anolis sagrei*). The life cycle of *C. penneri* has not been elucidated, and no experimental infections have been conducted on this nematode to establish its host specificity. Therefore, we conducted experimental infections to fully elucidate the life cycle of *C. penneri* and determine the ability of the nematode to establish infections in sympatric lizards from Polk County, Florida. In addition, we collected nematodes from Brown Anoles on the campus of Florida Southern College from 2010-11 to establish

seasonal occurrence of *C. penneri*. Our experimental infection experiments strongly suggest *C. penneri* was only transmitted during copulation, which was supported by our seasonal occurrence data; Brown Anoles with a snout-vent length  $\leq 34$ mm (i.e., non-reproductive individuals) were never infected. Our host specificity experiments yielded unexpected results; for example, we found *C. penneri* obtained from *A. sagrei* were unable to infect *Anolis carolinensis* (a closely related lizard), yet successfully and consistently infected *Hemidactylus tursicus* (a distantly related lizard).

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SEQUENTIAL AND CONCURRENT EXPOSURE OF FLOUR BEETLES TO PARASITES AND PESTICIDE

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The response of flour beetles *Tribolium confusum* to sublethal levels of 2 environmental stressors was studied. Parasitism (a single exposure to the cestode *Hymenolepis diminuta*) and a physical stressor (the natural pesticide diatomaceous earth, DE) were applied sequentially (DE, then parasitism) and concurrently (DE immediately following exposure to parasites). Treatment with DE and parasitism did not increase mortality over exposure to DE alone. Parasite abundance increased about 50%, from 3.0 to 4.5 parasites per host examined, in beetles exposed to DE before infection. Parasite abundance in concurrent treatment was at least 40% higher in mated beetles (5.3) than in unmated beetles (3.0 in virgin males; 3.8 in virgin females). Parasitism resulted in about 20% fewer eggs retained in the oviduct of beetles, but made no difference in the number of eggs that accumulated in the culture medium, or on the surface seeking behavior of beetles. Mating status of beetles increased their surface-seeking behavior in all treatments. DE exposure in concurrent treatment increased surface seeking behavior, and also resulted in a 4- to 6-fold increase in host eggs numbers that accumulated in the culture medium. Although prior DE exposure increased parasite numbers in beetles, parasitism and pesticide otherwise appeared to act as independent stressors.

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A HOLARCTIC MOLECULAR SURVEY OF *DIPLOSTOMUM* SPECIES

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Metacercariae of digenetic trematodes belonging to the cosmopolitan genus *Diplostomum* are common in the eyes and central nervous system of freshwater fishes. Metacercariae are pathogenic and have been implicated in losses of wild and farmed fish. Diversity and taxonomy within *Diplostomum* are poorly known, as are host-parasite relationships at all life cycle stages, particularly the metacercaria, which cannot be identified to species morphologically. We obtained sequences from the barcode region of cytochrome c oxidase 1 (CO1, ~500 bp) from 1360 specimens collected across North America, Europe and China. We sequenced ribosomal spacers (ITS) in a subset of these specimens in order to support CO1-based species delineation and link our data with previous studies. Twenty-four species were detected. As in a previous study conducted in the St. Lawrence River, lens-infecting species showed low host specificity and species inhabiting other tissues infected a smaller number of closely related fishes. The most widely distributed species, *Diplostomum paracaudum*, was found in snails and fish collected 8000 km apart in Europe and China. No species occurred in both the Palearctic and Nearctic. An intermediate level of divergence in both ITS and CO1 between European samples of *Diplostomum pseudospathaceum* and a North American species suggests recent speciation.

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CO-HABITATING AMPHIBIAN SPECIES HARBOR UNIQUE SKIN BACTERIAL COMMUNITIES IN WILD POPULATIONS

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All species of plants and animals harbor microbial symbionts but we know very little about the specificity of microbial communities to their hosts. Pond-dwelling larval amphibian communities are a unique system to address host-specificity of skin microbial communities because multiple species can share the same habitat and microbial inocula from the environment. Four pond habitats in Colorado were sampled where multiple amphibian species were present. In total, 32 amphibian individuals were sampled using sterile, cotton tipped swabs, belonging to three different species: northern leopard frogs (*Lithobates pipiens*), western chorus frogs (*Pseudacris triseriata*), and tiger salamanders (*Ambystoma tigrinum*). To examine bacterial communities, we surveyed the 16S small subunit ribosomal gene using universal bacterial primers, followed by bar-coded pyrosequencing. Using bioinformatic tools including the UniFrac algorithm and QIIME, we analyzed sequence data across samples to compare the composition and relative abundance of different bacterial phylotypes. Analysis of similarity was performed to test whether host species and/or pond location were significant predictors of bacterial community variation. Results of the pyrosequencing allowed us to compare 745 sequences from each sample. We found that the three amphibian species differed with respect to the diversity of bacterial phylotypes present; *L. pipiens* had the highest diversity of bacteria and *A. tigrinum* the lowest. Host species was a highly significant predictor of bacterial community similarity while pond location was not significant. These results indicate that innate species differences drive the composition and abundance of skin bacterial communities on amphibians, even when different species co-habitate in the same water body. In light of recent discoveries that some bacteria on amphibian skin have demonstrated antifungal activity, these findings regarding host specificity of bacterial communities may play a role in the species-specific resistance to fungal pathogens.

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SEASONAL AND SPATIAL VARIATION OF THE OYSTER PARASITE, *ACANTHOPARYPHIUM SPINULOSUM* IN THE LOWER LAGUNA MADRE, SOUTH TEXAS

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The American oyster (*Crassostrea virginica*) is a commercially important resource for the state of Texas, and for the Gulf of Mexico, generating more than \$60 mio per year in revenue. In 1966 Little et al. discovered mature metacercariae of the trematode, *Acanthoparyphium spinulosum* in *C. virginica* collected from Port Isabel, South Texas. This species may pose a public health risk since several studies elsewhere demonstrate that echinostome trematodes may infect humans who ingest raw infected oysters. Unfortunately, no studies have been published on *A. spinulosum* in *C. virginica* in the region in the past 30 years. Our first objective was therefore to obtain baseline spatial and seasonal data on *A. spinulosum* and other macroparasites from oysters in Laguna Madre. Secondly, we conducted a three-month field experiment to evaluate the effect of oyster density on the recruitment of *A. spinulosum*. For our first objective, clusters of oysters were randomly collected from two tidal levels every three months, dissected and examined for macroparasites. We found that 96.7 - 100% of oysters were infected with *A. spinulosum* and with the cestode *Tylocephalum* sp. at both tidal levels. Oysters at the mid-tidal level harbored a significantly higher mean abundance of *A. spinulosum* than those at the low tidal level ( $84.5 \pm 8.2$  versus  $15.8 \pm 1.6$ ) reflecting the intertidal distribution of the first intermediate host, *Cerithidea pliculosa*. Oyster density did not significantly change the accumulation of metacercariae in oysters during our field

experiment. The very high prevalence and abundance of *A. spinulosum* in oysters from Laguna Madre stress the potential risk of infection to recreational oyster harvesters in the South Texas region.

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**METAZOAN PARASITES OF FISHES FROM AN INTERTIDAL SAND FLAT, PALMYRA ATOLL,  
EASTERN PACIFIC**

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**A.V.M. Vidal-Martinez and M.L. Aguirre-Macedo**, CINESTAV  
**J.E. Caselle, R.F. Hechinger and A.M. Kuris**, University of California, Santa Barbara  
**K.D. Lafferty**, United States Geological Survey

We conducted an extensive survey of parasites of fishes occurring on the intertidal sand flats of Palmyra Atoll, Line Islands, Eastern Pacific. Due to its remote location, and the absence of commercial and subsistence fishing for 60 years Palmyra Atoll is a relatively pristine and trophically intact system. Parasitological analyses were performed on more than 500 individual fish, comprising over 40 species. All metazoan parasites occurring in each fish were identified and counted. Over 75,000 individual parasites were recovered, comprising over 90 species, including copepods, isopods, monogenes and adult and larval digenes and nematodes. Here we present data on the prevalence and intensity of various taxa (e.g. monogenes), trophic strategies (e.g. micropredators, trophically transmitted parasites) and using parasites to improve resolution in food webs.

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**ANTHROPONOTIC NATURE OF ENTERIC PROTISTS IN RHESUS MONKEYS IN A PUBLIC PARK  
IN GUIZHOU, CHINA**

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**J. Ye**, Centers for Disease Control and Prevention  
**J. Ma**, East China University of Science and Technology  
**L. Xiao**, Centers for Disease Control and Prevention

Despite their close relatedness to and, in some areas, frequent contacts with humans, the identity and public health significance of enteric parasites in non-human primates are not clear. In this study, we characterized enteric protists in rhesus monkeys in a public park in Guizhou, China. A total of 411 fecal specimens were analyzed by PCR for *Cryptosporidium* spp., *Giardia duodenalis* and *Enterocytozoon bienersi*, which were found in 47 (11.2%), 32 (7.8%), and 118 (28.7%) specimens, respectively. Within *Cryptosporidium*, the anthroponotic *C. hominis* was the dominant species, being found in 40 specimens, and belonging to six subtypes. *Cryptosporidium parvum* was found in six specimens, all belonging to the anthroponotic IIc subtype family. Only the human-pathogenic Assemblages A and B were found within *G. duodenalis*, with the former all belonging to the anthroponotic A-II subtype. The *E. bienersi* detected were mostly (110/118) belonging to group I, which most human-pathogenic *E. bienersi* genotypes belong to. Thus, rhesus monkeys in close contact with humans are mostly infected with anthroponotic *Cryptosporidium* spp., *Giardia duodenalis*, and *E. bienersi*; therefore, serving as potential reservoirs of human-pathogenic protists.

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## THE ROLE OF COMPATIBILITY AND ENCOUNTER FILTERS IN THE STRUCTURE OF INFRACOMMUNITIES OF OPOSSUMS (MARSUPIALIA: DIDELPHIDAE) IN FRENCH GUIANA

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A total of 102 extant species of didelphid marsupials occur in the New World. In several localities of French Guiana, a maximum of 12 species may occur in sympatry. These species belong to four lineages that correspond with the subfamily Caluromyinae and the tribes Marmosini, Thylamini, Didelphini and Metachirini (in Didelphinae). Most species are locally abundant and occupy different strata in primary and secondary forests. Their phylogenetic affinities, as well as their habitat segregation, allow evaluating the role of compatibility and encounter filters in the structure of their infracommunities. The parasite fauna for six species consists of 21 species of digeneans, cestodes, nematodes and acanthocephalans. From these, four species of nematodes occur in relatively high prevalence and abundance in all species of marsupials. These include *Aspidodera raillieti*, *Trichuris reesali*, *Travassostrongylus paraquintus* and *Spirura guianensis*. Prevalence and abundance of concurrent species of helminths was significantly different, since some parasites were exclusively present in a maximum of two or three species of opossums. The analysis of prevalence and abundance using canonical multivariate analyses reveals a similar structure in the helminth infracommunities of syntopic species of opossums. The analyses of these values under a phylogenetic contrast assist at determining that although the compound community may be essentially the same, the structure of the infracommunities correlates with the habitat segregation of the marsupials in the field.

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#### THE DETERMINANTS OF HELMINTH INFESTATION IN BABOONS

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The prevalence of intestinal parasites in natural populations is highly variable. The ecology and behavior as well as the genetic make-up of populations can all affect the rate of infection, yet the relative importance of ecological and genetic factors remain unclear. We addressed this issue by performing a four-year survey of parasite infestation in baboons in Awash National Park, Ethiopia. Awash national park hosts populations of olive baboons (*Papio anubis*) and *hamadryas* baboons (*Papio hamadryas*), as well as hybrid populations that are phenotypically intermediate between olive and *hamadryas* baboons. We analyzed 342 fecal samples over a 4 year period (2008-2011) using the fecalyzer fecal flotation method or a modified McMaster flotation method. Several species of helminthes were detected including *Trichuris* sp., *Schistosoma* sp., *Enterobius* sp., *Strongyloides* sp., *Trichostrongylus* sp., and hookworm. Olive baboon populations had a much higher prevalence of intestinal parasite than the *hamadryas* and the hybrids and this was true every year. In addition, the average number of eggs found in olive baboons was always higher than in the other two populations. This is likely to reflect the higher humidity of their habitat and/or their proximity to humans. Hybrid baboons had a moderate prevalence (~40%) but the number of parasite eggs was always very small. The prevalence in *hamadryas* baboons varied considerably from one year to another and apparently correlates with period of intense drought. Although *hamadryas* are adapted to extremely dry habitats, the droughts of 2009 and 2011 were so severe that the *hamadryas* have modified their ecology and came closer to human habitats, possibly increasing their exposure to worm eggs. Our results strongly suggest that ecological factors constitute the main determinant of parasitic worm infestation in baboons.

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## SCHISTOSOME INFECTION IN AFRICAN BUFFALO IN KRUGER NATIONAL PARK: EPIDEMIOLOGY AND COINFECTION PATTERNS

**B.R. Beechler** and **A.E. Jolles**, Oregon State University  
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**C. Seyler**, Oregon State University  
**V. Ezenwa**, University of Georgia  
**M.L. Steinauer**, Oregon State University

We investigated the epidemiology of schistosomes in African buffalo including their coinfection dynamics with other pathogens. We conducted a survey (seroprevalence and fecal exam) for schistosomes in African buffalo in Kruger National Park. Animals were tested for schistosomiasis using a further optimized version of the serum CAA UCP-LF assay. We found strong geographical differences in the prevalence of schistosomes. In an area where schistosome prevalence was high, we measured incidence over 6 months. We found that prevalence in younger animals was lower than in older animals, but young individuals were more likely to have higher burdens than older animals, possibly due to the long lifespan of schistosomes and acquired anti-immunity or premunition. We evaluated two host condition measures for correlations with schistosome infection severity. Body condition score (short-term measure) did not correlate with schistosome infection. However animals that were schistosome positive had reduced horn width (long-term measure) compared to those that were negative. We also investigated pathogen community structure to determine the associations between schistosomes and common buffalo pathogens (trichostrongyles, coccidia, rift valley fever virus, *Brucella abortus*, and *Mycobacterium bovis*). We found positive correlations between schistosome prevalence and Rift Valley fever seropositivity, which likely is due to shared exposure risk because of the similarity of the habitat of both disease vectors (mosquitos and snails). We also found a positive correlation between schistosome burdens and prevalence and intensity of trichostrongyles (measured by fecal egg count). It is likely that this correlation is not due to host exposure similarities, but to interactions in host susceptibility. We also found that 51.2% of buffalo initially infected with schistosomes had cleared their infections six months later suggesting the presence of host anti-adult schistosome immunity. Only 15.9% of those animals acquired schistosomes. Future research will investigate patterns of incidence over a longer time span and further investigate the dynamics between schistosomes and trichostrongyles.

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## PRESENCE OF NEMATODE FOSSIL EVIDENCE IN CALCIFIED SEDIMENTARY ROCKS AT D.G.KHAN, SULEYMAN RANGE, PAKISTAN

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Nematodes are not commonly observed as fossils in sedimentary rocks. In the Suleyman range sedimentary rocks are common. Evidence of nematode fossils has been observed embedded in sedimentary calcified rock that dates back to several millions years ago, exact age is to be determined. This is the first ever evidence of nematode fossils in sedimentary rocks in the Suleyman Range of Pakistan.

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### (134)

## INFECTION WITH HAEMOPROTEUS IWA AFFECTS VECTOR MOVEMENT IN A HIPPOBOSCID FLY – FRIGATEBIRD SYSTEM

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**P.G. Parker**, University of Missouri - St. Louis, St. Louis Zoo

Studying haemosporidian parasites in their arthropod hosts in natural settings has proved challenging.



Here we explore the effects of a haemosporidian parasite, *Haemoproteus iwa*, on a Hippoboscid fly vector, *Olfersia spinifera*. *Olfersia spinifera* is an obligate ectoparasite of the Great Frigatebird, *Fregata minor*, living exclusively among bird feathers for all of its adult life. There is considerable evidence from mosquito – *Plasmodium* research that haemosporidian parasites can negatively impact their arthropod vectors. This study examines the movements of *O. spinifera* between Great Frigatebird hosts. Movement, or host-switching, is inferred by analyzing host (frigatebird) microsatellite markers run on host DNA amplified from the vector. Using the most variable microsatellite markers, we are able to identify host genotypes in bloodmeals that do not match the host from which the fly was collected. We analyzed fly bloodmeal – host genotype mismatch using a logistic regression model, and the best-fit model included the *H. iwa* infection status of the fly and the bird host sex. Uninfected flies are more likely than infected flies to have a bird genotype in their blood meal that was different from their current bird host and flies collected from females were more likely than those collected from males to have a bird genotype in their blood meal that was different from that of their current host. Reduced movement of infected flies suggests that there may be a cost of parasitism for the fly. Parasite virulence reducing vector movement has been shown theoretically to be evolutionarily stable if that virulence contributes to a higher success of infection.

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ONE IS BETTER THAN TWO? ASYMMETRY IN ECHINOSTOME INFECTIONS OF TADPOLE KIDNEYS REDUCES HOST PATHOLOGY

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**S. Orlofske** and **B. Melbourne**, University of Colorado at Boulder

**P.A. Walker**, Brandon University

**P.T. Johnson**, University of Colorado at Boulder

While parasite aggregation on/within hosts is a well-established tenet of parasite ecology, asymmetric parasite distribution between paired organs or structures (e.g. eyes, limbs, gills) has not been commonly reported and is not well understood. Here, we report a consistent, right-side bias in the distribution of echinostome metacercariae within the kidneys of American bullfrog, Pacific chorus frog, and wood frog tadpoles but not western toad larvae. The right kidney was generally larger in volume than the left kidney across these species, regardless of host infection. However, the disparity in kidney sizes was generally smaller than the disparity in infection between the two kidneys and was not a significant predictor for all amphibian species. In spite of this, the degree of parasite aggregation in the right kidney was a significant positive predictor of host condition and development among experimentally infected Pacific chorus frogs. A similar result was seen for wood frog tadpoles but only at high infection intensities. Given the documented pathologies arising from echinostome infection in larval amphibians, we suggest that the general aggregation of these metacercariae into the larger host kidney represents an adaptive strategy. Amphibian hosts may limit damage via cyst aggregation and/or the parasite may enhance transmission to the definitive host by increasing host longevity, but such hypotheses require a further examination of ecological and mechanistic aspects.

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STUDIES ON *SCHISTOSOMA MANSONI* CERCARIAL EMERGENCE FROM *BIOMPHALARIA GLABRATA* SNAILS

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**J.D. Driver** and **W.O. Granath**, University of Montana

Studies were conducted on living and fixed samples of *Schistosoma mansoni*-infected *Biomphalaria glabrata* snails in order to determine sites of cercarial emergence (shedding). Using 3 means of

evaluations/observations, we attempted to determine the relative contributions of different snail tissues that were involved in shedding. The three methods of observations were (1) direct microscopical observations of shedding snails, (2) microscopic analysis of 5 µm serial sections (H&E stained) of actively shedding snails and (3) scanning electron microscopical (SEM) observations of snails that were fixed while actively shedding. For this analysis there were advantages and disadvantages to using each method, but the cumulative picture that emerged was that there were three tissues of the snail that contributed most prominently to cercarial release (mantle collar, pseudobranch, and headfoot). Based on histological analysis of cercarial accumulations in presumably shedding sites in these three tissues, 58% of the cercariae could be seen in the mantle collar, 30% in the pseudobranch, and 12% in the headfoot. Other anterior structures were involved to a much lesser extent. SEM observations clearly showed cercariae emerging either body first, tail first, or likely emerging *en masse* from blebs, especially from the mantle collar. Future studies will aim to visualize emerging cercariae more effectively and to better quantify cercarial emergence over time from these important tissues.

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EXPERIMENTAL EVOLUTION OF CRYPTIC COLORATION IN PARASITES

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**D. Kim, M.A. Aguilar**  
**D.H. Clayton**, University of Utah

Over macroevolutionary time feather lice, which are permanent parasites of birds, have evolved cryptic coloration. A recent comparative study of ours showed that louse color matches feather color in lice because it helps them avoid preening, which is the host's main form of defense. Here we report the results of an experimental evolution study to test whether lice transferred to different color hosts will evolve cryptic coloration in microevolutionary time. Our study involved Rock Pigeons (*Columba livia*) and their feather lice (Phthiraptera: Ischnocera). Rock Pigeons are an ideal host to test hypotheses about cryptic coloration because Rock Pigeons vary in color from white to black. Lice were transferred to white and normal colored Rock Pigeons that could and could not preen. After ten generations, we quantified the color of the lice on each bird. Lice on white birds were significantly lighter than lice on normal colored Rock Pigeons, but only if the birds could preen. Our results experimentally demonstrate the evolution of cryptic coloration in lice. Furthermore, our results confirm that preening is the selective force driving lice to match the color of the host's feathers

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DO ISLAND HOSTS HAVE INEFFECTIVE DEFENSES AGAINST INTRODUCED PARASITES? A TEST USING DARWIN'S FINCHES AND NEST FLIES

**J.A. Koop, J.P. Owen, S.A. Knutie, S.M. Lavery, and D. Clayton**, University of Utah

Introduced parasites and pathogens are a major threat to host populations, particularly those in isolated island ecosystems. Island hosts are inherently at risk due to small population sizes, and no prior exposure to introduced parasites. Host populations that are unable to rapidly evolve effective defenses may decline or go extinct. While this Ineffective Defense Hypothesis (IDH) is intuitively appealing, it has rarely been tested directly. We conducted an experimental test of IDH using Darwin's finches and a recently introduced parasitic nest fly, *Philornis downsi*. We manipulated parasite abundance in nests of medium ground finches (*Geospiza fortis*) using a fumigant, then quantified finch behavioral and immunological responses. We also monitored host fledging success to test the effectiveness of any defenses. Neither nestlings nor adult males showed evidence of behavioral or immunological responses to *P. downsi*. In



contrast, we found a significant effect of *P. downsi* on maternal behavior and immunology. However, these maternal responses were not effective; none of the parasitized nests fledged offspring, whereas all fumigated nests fledged at least one offspring. Our results are consistent with IDH, in that medium ground finches have no effective behavioral or immunological defenses against the introduced parasite.

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ASSOCIATIONS BETWEEN PARASITE BURDEN AND HEALTH IN SPOTTED SEATROUT,  
*CYNOSCION NEBULOSUS*

P.J. Cosmann, S.A. Arnott, W.A. Roumillat, A.E. Strand and I. de Buron, College of Charleston

Spotted seatrout are commonly infected by three species of parasites in South Carolina estuaries: the myxosporeans *Kudoa inornata* (in skeletal muscle) and *Henneguya cynoscioni* (in the bulbus arteriosus), and the digenean *Cardicola* sp. (in the ventricle). We hypothesized that these parasites negatively affect their host's health. To investigate this, we quantified the burden of each parasite species in wild-caught spotted seatrout over the course of one year using histology, and assessed host health in terms of body weight and liver weight (measures of energy storage), and spleen weight (a measure of immune response). The prevalence of infection was 91% for *K. inornata*, 29% for *H. cynoscioni*, and 86% for *Cardicola* sp., with 27% of fish being concomitantly infected by all three parasites ( $N=117$ ). Using general linear models to control for the effects of body length, sex, and season, we found that *Cardicola* sp. was associated with reduced body weight and that *K. inornata* was associated with reduced liver weight. All three species were associated with changes in spleen weight, with *Cardicola* sp. being associated with enlarged spleens in all seasons, while the effect of *K. inornata* and *H. cynoscioni* on spleen weight depended on season. The decline in body and liver weights with increased parasite burden is interpreted as being due to the elevated energetic costs of resisting infection, whereas spleen enlargement is likely due to up-regulation of the immune system and/or increased hemopoiesis caused by infection by *Cardicola* sp.

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IMPACT OF THE INVASIVE PARASITE *ANGUILLICOLOIDES CRASSUS* ON HEALTH OF THE  
AMERICAN EEL, *ANGUILLA ROSTRATA*

J.L. Hein, S.A. Arnott, W.A. Roumillat, and I. de Buron, College of Charleston

There are serious concerns regarding global eel populations. Reports show that harvests of the American eel (*Anguilla rostrata*) have been in decline since 1979, and fishery-independent surveys of South Carolina eel populations have shown a decline since at least 2001, when surveys began. The invasive parasite, *Anguillicoloides crassus*, is considered one potential reason for the decline. This nematode is endemic to East Asia, where it infects the swim bladder of Japanese eels without causing serious pathology to the host. It was first recorded in wild-caught American eels from Winyah Bay, SC in 1995, and has since been found along most of the Atlantic Coast. There is little information regarding the health impacts of infection on the American eel, but studies of the European eel, *Anguilla anguilla*, which has also become infected, show that they suffer serious pathological effects. The goal of this project was to examine the health effects of *A. crassus* on American eels. Eels were collected for one full year (2011) in South Carolina estuaries. Health of the eels was evaluated using haematocrit ( $n=34$ ), splenosomatic and hepatosomatic indices ( $n=421$ ), as well as swimbladder damage ( $n=421$ ). The validity of using vent coloration as a non-invasive diagnostic tool of infection was tested, since it has been found to be a useful tool in European eels.

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NEMATODE SECRETOMICS: COMPARATIVE ANALYSIS

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**X. Wang**, South China Agricultural University  
**J. Geary**, Michigan State University  
**J. Chehayeb**, McGill University  
**C. Mackenzie**, Michigan State University  
**M. Stevenson**, McGill University  
**Y. Moreno**, Harvard University

Nematode parasites establish successful infections at least in part through their ability to influence the host. Proteins secreted by the parasites are key contributors to the molecular negotiation that leads to the success or failure of an infection. We have characterized the secretome composition of multiple nematodes, including both parasitic and free-living species (*B. malayi*, *H. polygyrus*, *M. incognita*, *D. immitis*, *A. suum* and *C. elegans*). Proteins appear to be secreted through classical pathways, but exosome-mediated release appears to be responsible for many of the secreted proteins. A limited set of proteins appears to constitute the basic nematode secretome, with species-, infection site- and clade-selective modifications. Identifying proteins likely to be important for different kinds of parasites may be made easier by comparative analyses that highlight proteins of known function that are secreted by only some kinds of organisms.

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THE INFLUENCE OF FISHING PRESSURE ON *HEMATODINIUM* OUTBREAKS IN THE AMERICAN BLUE CRAB, A SIMULATION STUDY

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**J.D. Shields**, Virginia Institute of Marine Science

The American blue crab, *Callinectes sapidus*, is beset by epizootics of *Hematodinium perezii*, a parasitic dinoflagellate that causes high mortality. Focal outbreaks can approach 100% prevalence. Juvenile crabs are more susceptible to infection than mature crabs, possibly due to their molting frequency, and recent studies have shown that infected crabs may be more susceptible to predation. Blue crabs are also cannibalistic, with up to 30% of the diet of larger crabs consisting of smaller instars. Therefore, density-dependent cannibalism has the potential to modulate epidemics through differential mortality of infected juvenile crabs. Overlying this complex system is an intensive seasonal fishery for the adult blue crab, which alters the population structure of the host by removing over 60% of legal size crabs annually. Thus, the fishery may increase the relative number of susceptible individuals both directly, by removing low-prevalence adults, and indirectly, by releasing juveniles from density-dependent cannibalism. To better understand the impact fishing has on these disease dynamics, we developed a simple stage-structured model of blue crab population dynamics with Susceptible-Infectious-Susceptible disease dynamics, and simulated different levels of fishing pressure on the population. Preliminary results support the hypothesis that higher fishing pressure may lead to greater instability in the system.

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FEATHER MITE COMMUNITIES ON DARWIN'S FINCHES: THE ROLE OF HOST BEAK MORPHOLOGY

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**D.H. Clayton**, University of Utah

Although bird's beaks are primarily tools for feeding, they also play an important role in preening, which is the first line of defense against ectoparasites. The beaks of Darwin's finches are among the most thoroughly studied, with different beaks specialized for different feeding niches. However, nothing is known about how this beak morphological diversity impacts the ectoparasites of Darwin's finches. We examined the role of beak morphology in four species of ground finches (*Geopiza* spp.) in relation to their feather mite diversity. We netted 111 finches on Santa Cruz Island in the Galapagos and dust-ruffled them for mites. Five common genera of feather mites were present. The prevalence of mites was 65.8%. Mite intensity did not vary among species in relation to bill length, width, or depth. However, we did find that across all four finch species, individuals with beak overhangs of intermediate length had the fewest mites. This correlation is consistent with previous studies of other groups of birds showing a relationship between beak overhang length and ectoparasite diversity. The adaptive significance of beak morphology in Darwin's finches should be re-assessed with both feeding and preening in mind.

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**UNIKARYON LEGERI HAS A SIGNIFICANT IMPACT ON THE ECOLOGY OF THE COCKLE  
CERASTODERMA EDULE**

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**T. Kelly**, University College Cork

*Unikaryon legeri* is a microporidian, a hyperparasite that infects the trematode *Meiogymnophallus minutus*, and in turn infects the cockle. The cockle is the second intermediate host of this trematode. Both the trematode and the cockle have a similar range in Europe. The cockle is an important commercial species but in recent years has suffered significant mortalities. The reasons for these mortalities are unclear but studies to date suggest a complex aetiology. Through field and laboratory based studies and mathematical modelling of the data generated, we examined the relationship between the microsporidian, its host and the cockle. We investigated the distribution of the microsporidian, the trematode and the cockle spatially and temporally. The population genetics of this microsporidian were investigated. *M. minutus* can be found in very large numbers in the cockle with the microsporidian and the trematode being most prevalent over the summer months. A threshold number of trematodes is required before the microsporidian is observed. We describe the complex relationship that exists between the hyperparasite, its host the trematode and the cockle and discuss how this relationship may ultimately impact on the biology and ecology of the cockle.

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**APPLICATION OF A STRAIN-SPECIFIC MOLECULAR MARKER AND REAL-TIME QUANTITATIVE  
PCR IN THE DIAGNOSIS OF COINFECTION AND ASSESSMENT OF INTRASPECIFIC  
COMPETITION WITHIN A MOLLUSCAN INTERMEDIATE HOST**

**E. Thiele and D.J. Minchella**, Purdue University

In natural populations of the human parasite *Schistosoma mansoni*, the distribution of parasites among snail intermediate hosts is generally overdispersed, such that a small proportion of hosts harbor the majority of parasite genotypes. Among those few infected hosts, a majority contain multiple parasite genotypes, creating circumstances in which co-infecting parasites are faced with potential competition over limited host resources. Such parasite competition has been the subject of much theoretical modeling, particularly concerning how coinfection influences the evolution of parasite exploitation strategies. Empirical investigations of parasite-parasite competition often hinge on the untested assumption that co-exposure produces co-infection. However, exposure to multiple parasite strains may not result in infection by multiple strains and to assume that it does can obscure true effects of parasite-parasite competition. Here we describe a real-time quantitative PCR method to both distinguish the presence of multiple infecting strains, as well as quantify the relative larval output of each co-infecting strain. We applied the method to an empirical investigation of intraspecific parasite competition between strains of *S. mansoni* within the intermediate snail host, *Biomphalaria glabrata*, assessing the effects on parasite infectivity and productivity and the concomitant effects on host fitness. Overall, there was no effect of parasite competition on snail life history traits relative to single-strain infections. In contrast, there was an effect of co-infection on both parasite infectivity and productivity that could be ascribed to the effects of resource competition.

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**AN EFFORT TO IMPLEMENT PUBLIC HEALTH AWARENESS AMONG COLLEGE STUDENTS  
TOWARDS THE MOST COMMON LIFE STYLE ON THE EARTH "PARASITISM"**

**U. Singh and A. Mehta**, Seminole State College

Parasitic diseases have been under attention in recent years because of their role as an opportunistic infection in immunocompromised patients and as neglected tropical diseases. In the United States, there is a largely hidden burden of diseases caused by a group of chronic and debilitating parasitic infection. In light of these findings, we proposed that the study of parasites might be one of the most exciting and rewarding experiences that college students could gain in an academic setting. Thus, we introduced a new curriculum "Parasitology and Human Disease" for the first time in our college, in the biological sciences division. This course meets the need of students with interests in medicine and other allied healthcare fields. Our course included a broad survey of parasites of humans and animals as well as how all these parasites impact human lives. The students gained hands-on laboratory experience in identifying different parasites. At the end of semester, we received very positive feedback from all our students as part of their course evaluation. A few of these included such as this course was an eye opener that how these parasites can impact human lives; this course was the best one ever taken in the educational career of the student. Thus, we conclude that we were able to maximize our efforts to generate much enthusiasm among students for parasitism using a new curriculum based approach.

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**HUMAN SUBCUTANEOUS DIROFILARIASIS, REPORT OF TWO CASES OF *DIROFILARIA*  
*REPENS* IN ALEXANDRIA, EGYPT**

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The zoonotic filariae, *Dirofilaria immitis* and *Dirofilaria repens*, have become increasingly recognized world wide as inadvertent human pathogens. Humans are accidental dead end hosts of dirofilariae because adult worms mostly do not reach maturity in the heart or skin. Human infection presents with either subcutaneous nodules or lung parenchymal disease that may be asymptomatic. Some subcutaneous lesions are commonly recognized as malignant tumors requiring invasive investigations and surgery before a correct diagnosis is made. The aim of this paper is to present two cases, the first case was an adult male referred to the surgical outpatient clinic of the Medical Research Institute hospital complaining of a painful abscess like nodule in the right arm, the second case was a woman from the same locality of the first case (Ezbet Mohsen in Alexandria, Egypt) referred to the dermatologist with a nodule on the right side of the chest. One worm was extracted from each nodule, identification of the collected worms depended on parasitological, histological and SEM studies, morphologically through measuring the length of the worms, the thickness of the cuticle, and the longitudinal ridges on the circumference of the cuticle. The two cases were diagnosed as dirofilariasis (*D. repens*) as locally acquired infection.

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GLOBAL DIVERSITY AND DISTRIBUTION OF *HEMATODINIUM* SPP. - SIGNIFICANT PATHOGENS OF COMMERCIALY EXPLOITED CRUSTACEANS

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**G.D. Stentiford**, Centre for Environment, Fisheries and Aquaculture Science  
**J. Xaio**, First Institute of Oceanography  
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**J.D. Shields**, Virginia Institute of Marine Science

*Hematodinium* species are parasitic dinoflagellates known to infect a growing number of marine crustacean genera, many of which support important commercial fisheries. Affected hosts undergo dramatic pathological alterations to their organs, tissues and hemolymph, eventually leading to death. Until recently, there has been little effort to document the number of *Hematodinium* species, or strains, or to determine their host and geographic distributions. These data, however, may shed light upon potential transmission routes between distant crustacean populations. Such studies have been hampered partially by a lack of specific comparative work on isolates from different geographical regions, but more so by an absence of knowledge on the pathological, ultrastructural, and molecular characteristics of the type species, *Hematodinium perezii*, from its type hosts and locations within Europe. However, molecular and morphological characterization of the rediscovered type-species of *H. perezii* from both type host, *Liocarcinus depurator* and *Carcinus maenas*, has revealed a close relationship to *Hematodinium* isolates known to infect crustaceans from North America and Asia. Furthermore, our SSU rRNA phylogeny suggests the existence of a closely related, yet distinct clade containing *Hematodinium* sp. SSU sequences from other commercially important host species from the Northern Hemisphere. Additional phylogenies based on the LSU, HSP90, Cob, and Cox1 genes support the existence of a second *Hematodinium* species, currently unnamed, infecting these hosts. Identification of *Hematodinium* species (and genotypes of *H. perezii*) is largely dependent upon geographical location, rather than host species. However this is not exclusive, as both of these *Hematodinium* species can be found infecting multiple species from the same location, as is the case in the English Channel.

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SPECIES OF DACTYLOGYRIDS (MONOGENOIDEA), GILL PARASITES OF WILD AND CAGE CULTURED SNAPPERS (LUTJANIDAE) IN CHAMELA BAY, ON THE PACIFIC COAST OF MEXICO: PRELIMINARY RESULTS

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The snappers (Pisces: Lutjanidae) are one of the most abundant species in the tropics and subtropics. Particularly, the spotted rose snapper, *Lutjanus guttatus* Steindachner, 1869 and Pacific red snapper *Lutjanus peru* Nichols & Murphy, 1922 possess a high commercial value in the Mexican Pacific coast and they are subjected to aquaculture activities. Therefore, we are studying the diversity of dactylogyrids on these host species off Western coast of Mexico. A total of 68 individual fish belonging to *L. guttatus* (n=24) and *L. peru* (n=43) were collected from Chamela Bay on the Pacific coast of Mexico. Dactylogyrid specimens collected were subjected to proteolytic digestion and image analysis of the opisthaptor sclerites were used to obtain tissue-free, accurate measurements which were subjected to statistical analysis. Five species of Dactylogyrids were found, *Haliotrematoides plectridium* (n=175), *Haliotrematoides spinatus* (n=46), *Haliotrematoides guttati* (n=3), *Euryhaliotrematoides perezponcei* (n=277) and *Euryhaliotrematoides* sp. ( $\pm 211$ ). The most frequent species were *Euryhaliotrematoides perezponcei* (20%), and *Haliotrematoides plectridium* (20%) both being found in *L. guttatus* and *L. peru*. All host-parasite associations, represents new geographical records. Certainly, these results are based on morphology as the major species distinction criterion; however, currently we are running molecular analysis in order to improve our understanding on the diversity of these organisms.

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**PARASITIC COPEPODS OF THE GENUS *CALIGUS* (SIPHONOSTOMATOIDA: CALIGIDAE) ON CARANGID AND LUTJANID TELEOSTS FROM A FISH FARMING AREA OFF WESTERN COAST OF MEXICO**

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Wild juvenile snappers, *Lutjanus guttatus* and *Lutjanus peru*, are captured and grown in sea cages in coastal waters of Jalisco, Mexico. These activities could potentially promote the transmission of parasitic copepods between wild and farmed fishes. Particularly of sea lice that can be difficult to control. Therefore, we are investigating the presence of parasitic copepods on farmed lutjanids and on wild fishes adjacent to sea cages. Preliminary results about *Caligus* species are presented herein. A total of 87 individual fish were captured and examined during 2011. Samples of wild fishes included 17 specimens of *L. guttatus*, 25 *L. peru*, 9 *Caranx caballus* and 7 *Caranx hippos*. Samples of farmed fishes included 9 *L. guttatus* and 20 *L. peru*. Eleven species of *Caligus* (*C. confusus*, *C. aff. coryphaenae*, *C. aff. diaphanus*, *C. aff. hoplognathi*, *C. mutabilis*, *C. robustus*, *C. sclerotinosus*, *C. serratus*, *C. spinosus*, *C. aff. tylosuri* and *Caligus* sp.) plus a few undetermined larval stages of sea lice were detected. The highest number of *Caligus* species (7) was found in *C. caballus*, of which *C. serratus* and *C. spinosus* were the most prevalent (55 and 44%, respectively). Of these 7 species, 6 were also found on *C. hippos* (*C. confusus* was the most prevalent, 57%). Wild lutjanids shared *C. mutabilis* and *C. sclerotinosus* being the first species the most prevalent (29% on *L. guttatus* and 8% on *L. peru*). Except for *L. peru*, all host species shared *C. serratus*. The only copepod detected on farmed lutjanids was *C. sclerotinosus* with a prevalence of 11% on *L. guttatus* and 20% on *L. peru*. This survey suggests that *C. confusus*, *C. serratus* and *C. spinosus* are the most frequent parasitic copepods and its transmission could increase if finfish aquaculture is to be intensified. To the extent of our knowledge, all host-copepod associations here reported are new records, except for *C. confusus* and *C. robustus* previously reported on *C. hippos*.

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## PHYLOGENETICS OF MAJOR NEMATODE LINEAGES: HOW DIFFERENT ARE HYPOTHESES BASED ON NUCLEAR SSU RNA VERSUS COMPLETE MITOCHONDRIAL GENOMES?

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**J. Park**, Chungbuk National University

Phylogenetic hypotheses for Nematoda have almost exclusively been based on nuclear ribosomal DNA genes, mainly SSU rRNA. Since the publication of the first phylum-wide SSU tree based on 53 species, the number of near-complete SSU sequences has increased to over 1200. However, with respect to major lineages and their relationships defined in the earliest SSU trees, relatively little has changed despite increased taxon sampling and improvements in analytical methods. For some, this stability in major lineages defined by SSU has resulted in their acceptance as near confirmed representations of evolutionary history, and rejection of alternatives represented by other genes, despite known caveats of phylogenies based on any single locus. An alternative source of sequence data for nematode phylogenetics is complete mitochondrial genomes (cmtDNA), a distinct "locus" of non-recombining DNA. The diversity of currently sampled cmtDNA for Nematoda permits comparison with phylogenies based on nuclear SSU sequences. Similarities between SSU and cmtDNA trees include the division of Nematoda into clades corresponding to classes Chromadorea and Enoplea, and the close relationship between parasitic Strongylida and free-living Rhabditoidea. Although several major clades are in common to rDNA and cmtDNA trees, there are strongly supported relationships that conflict. With respect to parasites of vertebrates, differences include the lack of monophyly for representatives of clade III (e.g., Ascaridida, Oxyurida, Spirurida) in cmtDNA trees. Evaluations of alternative trees (representing the conflicting gene tree) are often significantly worse interpretations of these datasets. This indicates that there are strongly supported, but different relationships supported by these different loci. Such differences are not unexpected because these results are based on only two independent loci and each has known shortcomings for tree inference. Greater confidence in estimates of evolutionary history for Nematoda will require evaluation of more single-copy nuclear genes.

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## REVEALING SCHISTOSOME DIVERSITY IN SOUTH AMERICA (PATAGONIA): THE ENDEMIC GASTROPOD GENUS *CHILINA* SUPPORTS UNIQUE LINEAGES OF AVIAN SCHISTOSOMES

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Our current knowledge of the trematode family Schistosomatidae from South America is rudimentary in all respects: the identity and diversity of species present, their life cycles, patterns of host use, and evolutionary affinities. For the past several decades, many of the reports from South America relating to schistosomes (other than *Schistosoma*) detailed outbreaks of cercarial dermatitis. These studies linked the outbreaks not only to the snail host *Chilina*, but also to other families of snails including those from marine waters. The diversity of snails contributing to outbreaks of cercarial dermatitis suggests that there is a wealth of diversity to be discovered in Argentina, and South America. We collected freshwater snails of the monotypic genus *Chilina* (Chilinidae) from Argentina in search of schistosome infections. Chilinidae is unusual among the freshwater pulmonate (Hydrophila) families for being confined to a single continent. We collected six known species of *Chilina* (720 individuals) from 14 localities. From these samples we found three distinct groups of schistosomes based both on morphology of the cercariae and the genetic analyses of three genes (one mitochondrial and two nuclear). Interestingly, we found that each *Chilina* species we examined hosted at least one schistosome species. Coupling this new information with our current genetic dataset of schistosomes, phylogenetic analyses revealed that the three *Chilina*-



borne schistosome species do not group with any recognized clade, but represent lineages unique to South America and *Chilina* spp. While there has been previous work on schistosomes in South America, currently there are no reports linking genetic diversity to morphology, especially for the cercariae, which are often difficult to identify to genus and certainly to species by morphology alone. The framework incorporating both morphological and molecular data that is emerging for Nearctic and Palearctic avian schistosomes will be particularly useful for unraveling the complex of schistosome species that likely exploits the diverse avian fauna of South America.

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**TAXONOMIC REVISION OF HAEMOSPORIDA: ELIMINATION OF *PLASMODIUM FALCIPARUM*?**

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The malaria parasites, family Haemosporida, have had a complicated and unstable taxonomic history. Previous classifications have relied heavily on the vertebrate hosts used along with life history characteristics and basic morphological characters. Molecular sequence data have challenged many of the previous relationships and revealed that changes in vectors were correlated with the major cladogenic events. However, taxon sampling across the group has still remained scant and parasites from hosts such as bats and turtles have not been included in most analyses to date. Samples of haemosporids from South American freshwater turtles and West African bats were obtained and DNA sequences produced from both mitochondrial and nuclear genes. Phylogenetic analysis with maximum likelihood and Bayesian inferences revealed multiple instances of polyphyletic and paraphyletic genera, suggesting that major taxonomic revision within the family may be warranted. The caveats and consequences of these potential revisions will be discussed.

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**MOLECULAR PHYLOGENY AND EVOLUTION OF THE HYMENOLEPIDIDAE (CESTODA: CYCLOPHYLLIDEA) PARASITIC IN MAMMALS**

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Hymenolepididae is the largest family of the cyclophyllidean tapeworms and the whole class Cestoda. It is characterized by a great diversity of morphological characters, types of larvae and host associations. Life cycles of hymenolepidids may involve aquatic or terrestrial invertebrates while adult tapeworms are parasitic in birds or mammals. Their strobilae may consist of hundreds of proglottids or just a few segments. Their scolex may be armed with hooks or unarmed, with or without rostellum or its rudiment. Members of several hymenolepidid genera possess various egg-protecting structures. This diversity creates difficulties in understanding of the character evolution, their homology and relative systematic value. Molecular phylogenetic analyses of the family were absent until recent phylogenetic study including 33 species of mammalian hymenolepidids representing 15 genera (Haukisalmi et al., 2010). The present study uses partial sequences of nuclear 28S rRNA gene and includes a much broader selection of mammalian hymenolepid taxa from marsupials, insectivores, bats and rodents. Our analysis provides further support for some of the conclusions made by Haukisalmi et al. (2010) regarding potential evolutionary host switches, non-monophyly of several current hymenolepidid genera and multiple loss of rostellar armament in the course of hymenolepidid evolution. The greater diversity of analyzed taxa allowed additional host-switching events among hymenolepidids parasitic in rodents, marsupials and insectivores as well as evolutionary exchange with these parasites between mammals and birds. The current study has also shown a secondary transition to aquatic life cycles from the fully terrestrial circulation typical of the majority of mammalian hymenolepidids. Obtained phylogenetic trees have

demonstrated for the first time non-monophyly of the genus *Staphylocystis* and the lack of support for the sub-family Pseudhymenolepidinae previously recognized by several authors. This study was supported in part by the National Sciences Foundation grant No. 0818823.

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PHYLOGENETIC RELATIONSHIPS OF ARHYNCHOBDELLID LEECHES REVISITED

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Since the recognition that blood-feeding arhynchobdellid leeches (i.e. leeches without proboscis) do not form a monophyletic group, considerable efforts have been devoted to the understanding of the phylogenetic relationships of haematophagous representatives yet to the detriment of the study of their macrophagous counterparts. A broad phylogenetic analysis of Arhynchobdellida, including both bloodfeeders and macrophagous leeches, might provide clues to design more efficient strategies for anticoagulant screenings as well as to provide a general framework for classification. Phylogenetic analyses using Parsimony and Maximum Likelihood methods of 166 terminals representing most of the major lineages and more than 2000 aligned characters of one mitochondrial (COI) and two nuclear (18S rRNA and 28S rRNA) markers were conducted using TNT and RAxML, respectively. At least five lineages of macrophagous leeches were recovered (Haemopidae, Xerobdellidae, Cylicobdellidae, Erpobdelliformes and *Patagoniobdella*/*Semiscollex*/*Orchibdella*). Analyses of the tree topologies suggest alternative interpretations of the evolution of the feeding preferences of each group, contrasting particularly with previous studies that suggested a haematophagous last common ancestor of the group and attributed the numerous taxa to represent multiple independent switches of feeding behavior. In addition, we provide a general discussion of the evolution of jaws and their relationship with feeding preferences. We also show evidence that suggests that species of *Blanchardiella* actually lack jaws or any kind of sclerotized structures, a long controversy for leech systematists with impacts on the classification of South American macrophagous leeches. Finally, we propose several nomenclatural changes, both at family and genus level, in order to reconcile names with groups.

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ABOUT *CHORDODES FORMOSANUS*: A GENERAL INTRODUCTION TO THE NEWLY DISCOVERED SPECIES FROM TAIWAN

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*Chordodes formosanus* is a newly described *Hierodula*-parasitized horsehair worm in Taiwan and Japan. Its taxonomic status had been confused with the Japanese species, *C. japonensis*, which parasitize Chinese mantids, *Tenodera sinensis*. Nevertheless, the significantly longer filaments on the female crowned areoles and diverse cytochrome oxidase subunit I sequence support the isolated clade of *C. formosanus*. The different taxonomic status also reflects the narrow host ranges of these two horsehair worms. Although *T. sinensis* are always found sympatrically with *Hierodula* spp., none of them have been found to be parasitized with *C. formosanus*. The host specificity could probably be enhanced through the strong interaction between hosts and parasites. In the field, the infected hosts, *H. formosana*, showed unusual morphologies in particular the relative short wings in both sexes and reduced sensilla in males. These phenomena support the potential of parasites to influence their hosts' development. In spite of the limited mantid-final host, the cyst of *C. formosanus* has been found in three orders of aquatic insects,

including bloodworms, caddisflies, and stoneflies. Interestingly, inside the stoneflies we also found the cysts of other horsehair worms, *Acutogordius* sp., which parasitized in Orthoptera as a final host. The interaction between these two horsehair worms is still unknown. To know the possibility of competition during their paratenic host phase, more field survey of aquatic insects is worthy of further study.

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NEW SPECIES OF *GORDIONUS* (NEMATOMORPHA: GORDIIDA) FROM WASHINGTON STATE

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*Gordionus* is one of twenty extant genera within the phylum Nematomorpha, which consists of about 320 species. Fifty-six species of the genus *Gordionus* have been described from throughout the world, 7 of these from the contiguous United States. From 1998 to 2003, carabid beetles infected with hairworms were collected from 4 sites within the Hanford Nuclear Site and the Hanford Reach National Monument, Washington State. Pitfall traps with ethylene glycol were used to collect beetles; worms emerged partially from hosts. Thirty infected hosts were collected from 6 species and contained 2 new *Gordionus* species. Since the posterior end remained within the hosts, the morphological characters of this character-rich region were difficult to view using SEM. Species 1 had square-shaped polygonal areoles present in the anterior and posterior end. Interareolar structures are present in the two opposing sides of the areoles and postcloacal spines are present. Bristles are abundant in the anterior end and change direction in between areoles, and borders between bristles and areoles are present. Mid-body, canoe shaped areoles run parallel to the worm's longitudinal axis. Species 2 had square shaped areoles with polygonal-shaped neighbouring areoles. Interareolar structures are present mainly on opposing areoles; tubercles were present between areoles. Bristles, precloacal spines and adhesive warts are present. To confirm that these represent separate species, the mitochondrial barcoding region of *cox1* was sequenced and analyzed. In addition, we used the *cox1* gene to produce a phylogenetic hypothesis of the relationship of several *Gordionus* species. Including the new species presented here, known *Gordionus* diversity from the contiguous US has almost doubled over the last year, suggesting that there is much diversity to be described. Since many gordiids are collected in pitfall traps, usually as a byproduct of entomological collections, methods described here for microscopy and DNA extractions of worms fixed within the host by ethylene glycol will be of tremendous use.

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HANGING UP ON THE CALL FOR LOVE: BEHAVIORAL MODIFICATION OF MALE *ACHETA DOMESTICUS* CRICKETS INFECTED WITH *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA)

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Male crickets call in order to attract the attention of females. This calling performance is costly to the male because 1) it is energetically costly, and thus decreases the amount of energy allocated to reproduction, and 2) it attracts the attention of predatory species, which in extreme cases can decrease the cricket's reproductive potential to zero. These behaviors can also be detrimental to parasites, since the host is using

energy which the parasite itself could use and in cases of predation can also severely decrease the parasite's reproductive potential. Thus, a mechanism to interfere with the host's courtship behavior would greatly benefit parasites. Field work has suggested that such a mechanism may be found in male hairworm-infected crickets. The hairworm, *Paragordius varius*, infects crickets by being ingested as cysts within aquatic insects. Within 27 days, the 50µm long worm grows to 15–20cm. Hosts can be infected with up to a dozen worms. Early during development, the worms castrate the cricket hosts by completely absorbing the testes. In this study, we examined the relationship between infection and cricket calling behavior. To test whether infected crickets change their calling behavior, we recorded twenty adult male crickets' calling rates before and after *P. varius* infection. Individual control and experimental (infected) crickets were recorded at 2 days before and 2, 5, 10, 15, 20, and 30 days after infection. Each cricket's recording was done over the course of 8 hour periods during the scotophase. Each experimental cricket was dissected at the end of the experiment to determine infection status. Data shows that infected crickets ceased calling within one to two weeks, whereas controls continued calling throughout the trial. These data show that infection with *P. varius* causes *A. domesticus* hosts to put their calling display on hold. Although this behavioral change is thought to be beneficial to the parasite, it cannot yet be determined whether this change is due to the parasite-induced pathology or to an active parasite manipulation.

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LOOKING FOR LOVE IN ALL THE RIGHT PLACES? HOW HAIRWORMS (NEMATOMORPHA: GORDIIDA) FIND POTENTIAL MATES

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Behavioral parasitology usually involves the study of host manipulation by parasites, but few studies have investigated the behavior of the parasites themselves, especially their mating behavior. Freshwater gordiids or hairworms have a unique life cycle in which they complete their maturation within the definitive host, but delay mating until after being released by their host into water, where the free-living adult worms pair and mate. Since gordiids naturally occur singly in hosts and often rely on large and long river systems and areas with vast aquatic habitats, they must overcome the problem of release by the host distantly in space and time, which can result in worms finding themselves trapped in aquatic systems without mates. Despite this difficulty, gordiids are often found in mating knots consisting of several dozen individuals. To determine whether gordiids use chemical cues to find mates, we tested the attraction of worms to each other in an aquatic Y-maze. We used a field-collected species, *Gordius* sp., and a lab-reared species, *Paragordius varius*. In preliminary experiments, the only behavioral parameter measured was initial arm choice. However, in subsequent experiments, 3 additional behavioral parameters were measured: time spent in each arm over 10 minutes, first contact with the end of the maze, and final location after 10 minutes. *Gordius* sp. were only tested using the preliminary parameter, and males were found not to discriminate into which arm of the maze they moved. However, for *P. varius* males, the initial parameter tested significantly positive. Thus to better understand their behavior the additional 3 parameters were measured, and also showed significant differences, with the preference of choosing the side containing the female worm. In the future, female choice will also be tested. This study hints at the intriguing idea that some gordiids use chemical signals to find mates. In the future we hope to isolate the responsible chemicals.

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ALTERATION OF FAT BODY AND OVARY DEVELOPMENT IN THE FEMALE *CRICKETACHAETA DOMESTICUS* INFECTED WITH THE HAIRWORM *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA)

Unlike parasitoids, which kill their hosts, hairworms are inextricably linked to the health of the host until the very last moment of their symbiotic relationship. When hairworms have completed their development they rely on the host to move them to an aquatic environment. During their maturation, gordiids can grow to comprise more than half of their host's tissues suggesting that a large amount of damage is done to the host's organs although this damage is apparently not great enough to interfere with the host's ability to deliver the worms safely to water. To date however, the impact of the parasites on the host during development has never been quantified. In this study, the effect of the developing parasite, on the mass of the host's major organs was investigated. Four week old juvenile *Acheta domesticus* crickets were infected with *Paragordius varius* cysts. Infected *A. domesticus* were dissected 5, 10, 15, 20, 25, and 30 days post exposure (DPE). For each time point, a control group was sham infected in parallel. All exposed crickets were screened for infection, and only those exposed crickets harboring worms were used. For each cricket, gonads and fat body were removed, dried, and weighed. Data from infected hosts at each time point was compared to uninfected crickets. The mass of the fat body significantly decreased during the late stages of infection. Surprisingly however, the fat body significantly increased within the first 10 days of infection and was found to nearly double that of the control group. Few infected crickets showed ovary growth within 20 DPE, and ovaries completely disappeared by 30 DPE. Although the ultimate demise of the ovaries and the decrease in the fat body mass was expected, the doubling of the fat body during early infection was unexpected. One explanation is that worms stimulated the growth of the fat body; however, it is also possible that by diverting energy away from the production of eggs, the fat body grew more than controls. The impact of these changes on the host's biology will be discussed.

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**USING GORDIID CYSTS TO DISCOVER THE HIDDEN BIODIVERSITY AND POTENTIAL DISTRIBUTION OF HAIRWORMS (NEMATOMORPHA)**

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One reason for the lack of knowledge on the diversity and distribution of hairworm species is the lack of reliable ways to collect hairworms over large geographical areas. However, our recent studies indicate that cyst stages of hairworms may be the most commonly encountered gordiid life stage in the environment and can be used in generic and/or clade identification. These discoveries have given us the ability to investigate for the first time the biodiversity and distribution of these cryptic parasites. In this study, we sampled aquatic snails for the presence of hairworm cysts from 46 streams in Payne Co., Oklahoma where only a single species of gordiid (*Gordius robustus*) has been reported. Using this modified survey procedure, gordiid cysts were found at 70% (32/46) of sites examined throughout Payne Co., Oklahoma. Based on cyst morphology and/or arthropod host infections, we were able to identify 3 morphological types of gordiid cysts including *Paragordius varius*, *Gordius* spp. and *Chordodes/Neochordodes* spp. Based on our gordiid cyst presence data and in conjunction with environmental layers for Payne Co., we developed an ecological niche model using Maxent to identify areas suitable for snail gordiid infections. The ecological niche model for Payne County successfully predicted all localities of gordiid cysts in snails over a geographical area of 1,810 km<sup>2</sup>. To test the predictability of our ecological niche model, we projected our Payne Co. model onto Lancaster Co. Nebraska for which snail gordiid cyst presence data was available. The projected model was able to account for 85% of the presence occurrence points. To our knowledge, this is the first ecological niche model attempted on a small geographical extent (county level) that recovered known locations successfully.



DEFENDING THE ATTACKER: CHARACTERIZING THE IMMUNE SYSTEM OF *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA) USING NEXT GENERATION SEQUENCING

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Parasite immunologists more often study the immune system of the host, in reaction to the parasite, than the immune system of the parasite itself. Therefore the immune capabilities of parasites, especially against pathogens such as bacteria, are not well understood and remain little studied. Next-generation sequencing (NGS) has revolutionized the field of molecular biology, by enabling previously unimaginable scientific achievements and novel biological applications. NGS technologies allow fast sequencing of genomes and can take a snapshot of transcriptomes expressed under different conditions allowing large-scale comparative and evolutionary studies. Using these techniques, our aim was to characterize the immune system of the parasite *Paragordius varius*, and compare it to members of its sister phylum, the Nematoda. We were specifically interested in investigating the presence of key Toll-like receptor (TLR) signaling components, missing in nematodes but present in all other tested Eumetazoans. The lack of this pathway in nematodes was thought to indicate a divergence before the cooption of TLRs for immune signaling; however, with the recent discovery of these components within cnidarians, this notion has been reevaluated. Two *P. varius* groups were examined: 1) worms injected with a cocktail of bacteria to stimulate the production of immune factors, and 2) sham injected worms. 4-5-4 NGS was done producing 1.5 million reads with an average read length of about 400 base pairs. These aligned into 22,000 contigs with about 40,000 single sequences. More than 150 genes, associated with stress and an immune response, were identified along with the up regulation of bacterial defense response genes, and antimicrobial peptides. In addition, MYD88, NF- $\kappa$ B, and other genes of the Toll-like signaling pathway were found. The presence of these pathways in *Paragordius*, *Drosophila*, cnidarians, and vertebrates, and its absence in nematodes strongly supports the conclusion that nematodes lost these factors after branching off from the Nematoda/Nematomorpha ancestor.

DIVERSITY OF GORDIIDA (NEMATOMORPHA) IN THE DIAMANTE RIVER BASIN AND THEIR EPIBIONTS

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The Diamante River basin is one of the hydrogeological basins used for irrigation purposes (irrigation, industry, consumer population) located south of the Province of Mendoza, Argentina. So far, only two species of Gordiida were registered from the north of the province in Chacras de Coria: *Beatogordius irregularis* and *Paragordius varius*. The biodiversity of Gordiida in the Diamante River basin, the intraspecific variation and their epibionts are here studied. All the collection sites were georeferenced and temperature and pH were registered. All male specimens were fixed in ethanol 70° at the site of collection and the females were reserved the offspring's birth. The study was carried out under optical microscopy and scanning electron microscopy, with and without previous washes. Sections of the mid-body (5mm) of each specimen were cut. For identification under optical microscopy the gordiid tissues were removed with (OH) Na 5M during 3-5 minutes and then observed. In order to identify the gordiid species and their epibionts by scanning electron microscopy, all the pieces washed and not washed, were critical point dried and observed. Shannon index and density of epibionts were

calculated. The collection comprised 43 males, 15 *Pseudochordodes gordioides*, 13 *Pseudochordodes bedriagae*, 13 *Noteochordodes talensis*, 1 *Noteochordodes cymatium* and 1 *Neochordodes occidentalis*, and 2 females of *P. gordioides*. The specific diversity was –1,26. All the epibionts belong to the genus *Cocconeis* (Bacillariophyta). The morphology data of *P. gordioides* larvae are presented. The intraspecific variation and the importance of adding new characters like larval morphology and DNA sequence data in order to identify species of Gordiida will be discussed.

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**MOLECULAR MARKERS HELP IN RECOGNIZING SPECIES BOUNDARIES IN THE GENUS GORDIONUS (NEMATOMORPHA)**

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*Gordionus* is a difficult genus among freshwater horsehair worms (Gordiida, Nematomorpha), because on the one hand many species are differentiated by delicate morphological differences, on the other hand there is evidence for considerable morphological plasticity. We investigated whether molecular markers, the sequence of the barcode gene CO1, can help in resolving species boundaries. Two European species with broad distribution, *Gordionus violaceus* (Baird, 1853) and *G. wolterstorffii* (Camerano, 1888) were compared. Previous investigations have shown a broad range of cuticular patterns to be present, ranging from a “typical” *G. violaceus*-pattern to a “typical” *G. wolterstorffii*-pattern. Comparison of the CO1-sequences however showed a clear distinction between these two species. Almost similar patterns are present in North American *Gordionus* species. This study shows that molecular markers are of great help in cases where morphology has problems to resolve species boundaries.

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**DISCOVERING THE HIDDEN BIODIVERSITY OF GORDIIDS (PHYLUM NEMATOMORPHA): WHERE ARE WE AND WHAT ARE THE NEXT STEPS?**

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**E. Rogers**  
**B. Hanelt**, University of New Mexico  
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Approximately 350 species of gordiids have been described worldwide from 19 extant and 2 extinct genera; but estimates suggest that only 15% of the hairworm diversity has been documented globally. Our lack of knowledge of the biodiversity of gordiids stems from the facts that most hairworm species have been described based on random collections of single worms for which life cycles are unknown. However, over the last 5 years, our team has developed novel and unique collecting and culturing techniques for gordiids that overcome these shortfalls. First, our studies on the distribution of gordiids by using cyst stages indicate that nematomorph cysts in aquatic snails are the most common stages of gordiids to detect in the environment and are extremely easy to collect over large geographical areas. Second, cysts can be identified to genus/clade and can produce adult worms in the laboratory when fed to appropriate arthropod hosts. Third, our recent discovery of the ability of gordiid cysts from North American and African species of hairworms to survive freezing and produce viable adult worms when fed to laboratory reared hosts indicates that this technique will enable us to collect cyst stages of gordiids anywhere in the world and establish their life cycles in the laboratory. I will discuss our advances in these novel techniques along with their pitfalls which should allow us, for the first time, to move forward in discovering the hidden diversity of gordiids globally and test hypotheses on their distribution and biodiversity.



NEMATOMORPHS ALTER CROSS-ECOSYSTEM ENERGY FLOW VIA HOST MANIPULATION

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Manipulative parasites modify energy flow among organisms via alteration of their hosts' phenotypes, which potentially affect structure, dynamics, or functioning of food webs. However, less is known about the magnitude and scale of the effects of host manipulation on food webs and ecosystem functions. Here, we show that a nematomorph parasites (known as horsehair or Gordian worms; Phylum: Nematomorpha) can modify cross-ecosystem energy flow in forest-stream ecosystems. In a Japanese headwater stream, we quantified camel crickets and grasshoppers (Orthoptera) were 20 times more likely to enter a stream if infected by nematomorph parasites, corroborating evidence that nematomorphs manipulate their hosts to seek water where the parasites emerge as free-living adults. Endangered Japanese trout (*Salvelinus leucomaenis japonicus*) readily ate these infected orthopterans, which, due to their abundance, accounted for 60% of the annual energy intake of the trout population. This parasite-mediated energy flow commonly occurred through Japanese mountainous streams; on average, 46% of the trout diets were occupied by the infected orthopterans when the nematomorphs manipulated their orthopteran hosts. Finally, our molecular analysis (18S rRNA and COI genes) revealed that diverse nematomorph species (~7 species) and even nematode species (~8 species) drive the parasite-mediated energy flow. Given the nematomorphs inhabit throughout the world, we expect their effects we presented here may be widespread in many other regions.

MOLECULAR AND MORPHOLOGICAL DIFFERENTIATION OF *CLINOSTOMUM* LEIDY, 1856 (DIGenea: CLINOSTOMIDAE) FROM NEOTROPICAL REGION OF MEXICO

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*Clinostomum* Leidy, 1856 (Clinostomidae) is a genus of endoparasite of fish eating birds distributed worldwide. The infective larval stage of this parasite is commonly found encysted in several species of fish in the Neotropical region of Mexico. In the current study DNA sequences from internal transcribed spacers ITS-1, 5.8S and ITS-2 (ITS) and of the cytochrome c oxidase subunit I (cox1) from metacercaries and adults of 10 localities from Gulf of Mexico and Pacific Sea slopes from Mexico were generated. Our sequences were aligned with sequences from *C. marginatum* and *C. complanatum* download from Genbank. The genetic divergence estimated among specimens of *Clinostomum* sp., from Mexico ranged from 0.0 to 0.07 % for ITS and from 0.4 to 0.08% for cox 1, whereas the genetic divergence among the populations of *Clinostomum* sp., from Mexico and *C. marginatum*, *C. complanatu* ranged from 5 to 9 % for ITS and from 15 to 17% for cox 1. Maximum likelihood, maximum parsimony and Bayesian Inference analyses were performed for the combined data sets (ITS + cox 1) and each data set alone. All the phylogenetic analyses showed that the specimens of *Clinostomum* sp., from Mexico represented a monophyletic clade with strong bootstrap support and Bayesian posterior probabilities. The morphological evidence, in combination with the genetic divergence estimated with two genes, the

reciprocal monophyly in all the phylogenetic analyses, suggested that the specimens of *Clinostomum* sp., from Mexico represent a new species.

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THE EFFECT OF CANTHARIDIN ON INDUCING APOPTOSIS IN *LEISHMANIA MAJOR*

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*Leishmania major* is causative agent of cutaneous leishmaniasis. Leishmaniasis is most public health problem in developing countries. There are no effective vaccines against leishmaniasis. Resistance and relapse have been reported after chemotherapy. Cantharidin is vesicant that produces in the hemolymph of *Meloidea* beetles. Several study show that cantharidin can induce apoptosis in cancer cells. In the present study, the effect of cantharidin in inducing apoptosis in *Leishmania major* promastigotes and macrophages infected with *Leishmania major* was investigated by MTT test and flow cytometry *in vitro*. MTT test indicated that cantharidin with concentrations 0.5µg/mL and 50µg/mL had 14.26% and 49.86% cytotoxicity on the promastigotes after 72h respectively. Flow cytometry results showed 14.29% cytotoxicity (as 13.12% apoptosis, 1.12% late apoptosis and 0.05% necrosis) and 68.51% cytotoxicity (as 5.28% apoptosis, 63.23% late apoptosis and 0% necrosis) in promastigotes due to 0.5µg/mL and 50µg/mL cantharidin after 72h respectively. By MTT assay, cytotoxicity induced by 50µg/mL and 5µg/mL cantharidin on the infected macrophages with *L. major* amastigotes was 3.56% and 19.95% after 48h respectively, flow cytometry results were 44.44% (as 31.05% apoptosis, 3.31% late apoptosis and 10.08% necrosis) and 61.81% (as 43.42%apoptosis, 1.27% late apoptosis and 17.11% necrosis) respectively. We concluded that cantharidin induces apoptosis in the *Leishmania major* promastigotes and infected macrophages with amastigotes in a time and dose dependent manner.

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EVALUATE THE GLUCANTIME SUSCEPTIBILITY OF *LEISHMANIA TROPICA* ISOLATES OF IZEH CITY

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The protozoan parasite leishmania is distributed worldwide and has a number of clinical manifestations including cutaneous, mucocutaneous and visceral leishmaniasis. Available drugs against leishmaniasis are limited in number and each has various short comings. Leishmaniasis is controlled mostly through the use of chemotherapy. Pentavalent antimonials have long been the mainstay treatment but resistance to this class of drugs is increasing throughout the endemic regions in many parts of the world. The aim of this survey was evaluate the Glucantime susceptibility of *Leishmania tropica* isolates of Izeh city. 5 different isolates of Izeh city *Leishmania tropica* were collected and detected by PCR from 2008 to 2010. For each isolate, 10 balb/c mice were inoculated with each isolate by tail base inoculation. After emergence of a lesion, treatment with equal dose of Glucantime began. The times of lesion emergence, convalescence and length of treatment was recorded precisely. Outcomes of this study don't show any significant difference in susceptibility to Glucantime among *Leishmania tropica* isolates of Izeh city considered in this study. With few exceptions, treatment failure has not been reported from Iran up to now. Initially, susceptibility measurements were made in the promastigote stage but it is clear that this form of the parasite is not relevant to studying susceptibility to antimonial drugs and possibly to other drugs. However, recent studies have clearly demonstrated that *in vitro* intracellular testing of Glucantime susceptibility in infected macrophages is in good agreement with clinical responses.

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EVALUATE THE EFFECT OF POLY METHYL METHACRYLATE NANOPARTICLES PLUS GLUCANTIME IN VISCERAL LEISHMANIASIS TREATMENT IN GOLDEN HAMSTER

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Nanoparticles consist of macromolecular materials and can be used therapeutically or prophylactically, for example, as adjuvants in vaccines or drug carriers, in which the active principle (drug or biologically active material) is dissolved, entrapped, or encapsulated, or to which the active principle is absorbed or chemically attached. Poly methyl methacrylate proved to be by far the most optimal and suitable material. VL (kala azar or dumtum fever) is caused by *L. donovani* and *Leishmania infantum* in the Old World. *L. infantum* mainly affects young children and has a greater tendency to cause lymph node enlargement. The course of the disease and outcome depend on the general health status of the patient at the time of infection. The goal of this research was to evaluate the effect of Poly Methyl Methacrylate Nanoparticles with glucantime in visceral leishmaniasis treatment in golden hamsters. 10 golden hamsters infected with *L. infantum* and then divided in two groups of 5, one group as test and one group as control. After signs of disease emerge and the infection is demonstrated using ELISA, the test group was treated by glucantime plus PMMA nanoparticles and the control group only treated with glucantime. In this study, the 5 hamsters in test group after 4 weeks of beginning the treatment, only 1 hamster remained alive, spleen and bone marrow examination did not show any amastigotes. However, in the control group, 3 hamsters remained alive after 4 weeks that spleen and bone marrow examination showed amastigotes in 2 of the hamsters. PMMA is a material with a good safety record that has been used in humans for more than 50 years. PMMA nanoparticle adjuvant achieved good antibody responses and good protection against challenge with a number of antigens.

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LEISHMANI DONOVANI: AN IN VITRO STUDY OF ANTIMONY-RESISTANT AMPHOTERICIN B-SENSITIVE ISOLATES

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A rise in VL cases and especially those unresponsive to antimonial therapy has brought the question of *Leishmaniasis* into focus in the Sudan. This study came to evaluate drug sensitivity of clinically antimony-unresponsive *Leishmania donovani* isolates from Eastern Sudan in an *in vitro* culture system against sodium stibogluconate (Pentostam) and Amphotericin B. Eight isolates, six from antimony-resistant and two from clinically responsive patients were included in the study. Parasites were tested as promastigotes and four of them were selected to be tested as amastigotes using a murine macrophage-like cell line. The results indicated that the conventional promastigotes and amastigotes-screening assays did not correlate with the clinical picture of patients. *In vivo* unresponsiveness does not necessarily mean primary parasite resistance. Amphotericin B could be a suitable second line drug in patients unresponsive to pentostam and without concomitant diseases, if close hospital monitoring is available. Promastigotes sensitivity testing concentrations are virtually incomparable with the *in vivo* clinically curable doses and the amastigotes/macrophage test concentrations.

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GEORGIAN FRESHWATER HAIRWORMS (NEMATOMORPHA: GORDIIDA) – RESULTS OF FAUNISTIC STUDY

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Caucasus (and Georgia) is situated between the Black and Caspian seas on the border of Europe and Asia. The region is isolated from other mountainous areas by seas and plains, and this high degree of isolation may be responsible for unusually high levels of endemism. This diversity and level of endemism has led to the recognition of this area as one of the world's 34 biodiversity hot spots. Biodiversity of Georgian hairworm remains greatly understudied. Until recently, only four species have been described. From the neighboring countries, Armenia and Azerbaijan, even fewer records are known. We recently started a study of Nematomorpha in Georgia. Specimens are studied by light microscopy and by scanning electron microscopy. Our collection sites are located in three locations in Eastern Georgia: Mtskheta-Mtianeti, Shida Kartli, and Tbilisi. Our findings include new records for Georgia including one genus (*Gordionus*) which was previously unknown from Georgia and one new species (*Chordodes parabipilus* Kintsurashvili, Schmidt-Rhaesa & Gorgadze, 2011). During our studies we have revealed two host insect associations: *Chordodes anthophorus* with *Mantis* sp. and *Gordionus violaceus* with *Carabus septemcarinatus*. We continue to expand our studies in other regions in Georgia and expect a higher number of new species records and new species.

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TROPHICALLY CASCADING ENEMY RELEASE: TESTING THE CONNECTION BETWEEN SMALLMOUTH BASS PARASITE BURDEN AND CONSUMPTION OF INVASIVE ROUND GOBY IN THE ST. LAWRENCE RIVER

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Enemy release has been proposed to explain the lack of parasites in species that have been translocated from their native habitats. Round goby (*Neogobius melanostomus*) have become ubiquitous and highly abundant in the St. Lawrence River where it became established in 2005. This Ponto-Caspian fish species has been used as an example of an introduced species that has experienced release from its parasites, in the Great Lakes. Round gobies now compose a significant portion of the diet of many native piscivores of the St. Lawrence River, but have been especially exploited by smallmouth bass (*Micropterus dolomieu*). This system was chosen to test the hypothesis that consumption of a superabundant invasive prey species may lead to depauperate parasite abundance and diversity in bass. Round gobies in the Great Lakes are known to harbor fewer parasites than in their native range, and as smallmouth bass consume more gobies they are less likely to be exposed to trophically transmitted parasites that occur in native prey. Furthermore, as bass exploit gobies in different foraging habitats they may be exposed to different, and possibly fewer parasites than in habitats with native prey species. Here, 118 smallmouth bass were collected at four sites over 37.5 km of the St. Lawrence River (Grindstone Island to Chippewa Bay) and examined for parasites. Stomach contents of the sampled fish were also examined to determine presence of round gobies. Thirteen species of parasites have been encountered with five having prevalence greater than 10% at any one site. These were the copepods, *Ergasilus centrarchidarum* and *Achtheres pimelodi*, the acanthocephalans *Leptorhynchoides thecatus* and *Neoechinorhynchus tenellus*, and a species of *Trichodina*. Both diet and parasite diversity differed between sample sites. Parasite diversity and abundance appear to be negatively correlated with the prevalence of goby in the diet of smallmouth bass.

Stable isotope analyses are currently underway to determine relative goby consumption between fish and refine these observations on parasite burdens and diet.

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FIRST ECOTOXICOLOGICAL EVALUATIONS IN NEMATOMORPHA: CAN *CHORDODES NOBILII* BE CONSIDERED A GOOD BIOINDICATOR?

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The present study was carried out based on the hypothesis that environmental stress affects Gordiida infective capacity as well as their numbers in their aquatic habitat. The need to find Neotropical native bioindicators is also considered in this study. For the first time, assay protocols were designed to evaluate the effect of pollutants in the free-living stages of *Chordodes nobilii*, in order to determine if this Nematomorpha species is a good bioindicator of contamination in freshwater environments. Endpoints compatible with their life cycle were selected, and for two of them, an index which evaluates the infective capacity of parasites was put into practice for the evaluation of the effect of environmental and anthropic variables. Sensitivity of *C. nobilii* to temperature, pesticides and referent toxics was determined. From the results obtained during the experimental period, it was possible to conclude that preparasitic stages of *C. nobilii* present not only a high sensitivity to the used toxics but also a wide range of thermic tolerance under laboratory conditions. Therefore, the protocols designed for such end could be carried out and were repeatable and reliable and have subsequently been validated for the ecotoxicological evaluation of Gordiida species. Finally, it can be considered that *C. nobilii* presents many of the necessary characteristics to be considered a bioindicator species. Studies to correlate the presence of this species in different habitats according to water quality are being held in Argentina. The results obtained together with the ecological value of *C. nobilii*, which links aquatic and terrestrial ecosystems occupying different levels in the trophic web, strengthen the idea of considering this species as a diagnostic organism for ecotoxicological evaluations and as a contamination bioindicator.

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A PALEOPARASITOLOGICAL STUDY OF 1,500-YEAR-OLD HUMAN MUMMY COPROLITES FROM SOUTHERN SUDAN

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In this paleoparasitological study, presence of parasite eggs was examined in ancient fecal samples (coprolites) from 47 individual 1500-year-old, human mummies from two cemetery sites along the Nile in ancient Nubia (today's southern Sudan), for which cultural and health status had previously been studied. Coprolites were removed from within the bodies of individual mummies, thus ensuring their origin. Fecal matter was re-hydrated for 72 hours at room temperature (0.5 g in 10-ml sodium nitrate with a specific gravity of 1.20, followed by centrifugation, and 0.5 g in 10 ml of 0.5% trisodium phosphate) and a total of 10 wet-mounted slides per sample were scanned at 10x magnification. Eggs of 6-7 different parasite species were identified by their morphological features, including *Schistosoma mansoni*, *Schistosoma haematobium*, a potential third *Schistosoma* species, hookworm (*Necator americanus*), pinworm (*Enterobius vermicularis*), roundworm (*Ascaris* sp.), and an unidentified species of tapeworm. Half (51%) of the mummies were infected with at least one parasite species, and 30% were infected with at least one of the *Schistosoma* species. The latter finding is consistent with previous immunological evidence for *S. mansoni* in this mummy population, although the present study found *S. mansoni* eggs in fecal samples from several individuals in which no immunological response had been detected. The highest number of *S. mansoni* eggs was found in young individuals, between 4-20 years of age at the time



of death, the age category previously assessed as having the poorest health status. Furthermore, hookworm eggs were found only in mummies identified as female. In conclusion, 1500-year-old Nubian mummies exhibited evidence of infection with multiple helminth parasites, which offers a view into the role of disease in an ancient population of humans. This study can also help elucidate epidemiological patterns of these parasites that still burden local populations of present-day peoples living on the banks of the Nile River.

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LARGE SCALE PATTERNS OF SUBYEARLING CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) HABITAT USE IN THE COLUMBIA RIVER ESTUARY INFERRED FROM PARASITE ASSEMBLAGES

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There has been increased interest in clarifying the role of the Columbia River estuary in supporting juvenile endangered and threatened salmon as they migrate to the Pacific Ocean. To infer habitat use and identify areas of potential restoration, parasite assemblages of subyearling Chinook salmon (n = 405) were examined throughout the Columbia River estuary (river kilometers [RKM] 20, 110, and 230) in May and July of 2010. From the gastrointestinal tract, swim bladder, and kidney, we recovered 6899 individuals of 14 parasite species. Overall, large scale differences in parasite assemblages reflected changes in diet composition as salmon migrated through the estuary. *Salvelinema walkeri* (Nematoda) and three trematodes *Plagioporus shawi*, *Deropegus aspina*, and *Nanophyetus salmincola*, which use intermediate hosts in freshwater habitats, were most prevalent at RKM 110 (prevalence range 30-55%). Farther upstream (RKM 230), these parasites were not recovered in May and prevalence was low in July (0-15%). This suggests feeding on freshwater amphipods and larval insects required for transmission of some parasites is restricted to the middle reach of the estuary. In contrast, prevalence of *Hysterothylacium aduncum* (Nematoda) near the river mouth (RKM 20) varied from 36% in May to 63% in July compared to the range of 0 – 10% in both freshwater reaches in the estuary. In July, prevalence of *Contracaecum* sp. and *H. aduncum* was 0% and 3% respectively at RKM 230 in the Upper Columbia River Summer and Fall stock group. Prevalence of both parasites in this group increased at the river mouth to 28% and 45% respectively indicating that this endangered upriver stock is feeding and rearing in the estuary. In summary, a generally uninfected group of salmon at the most upriver reach, high prevalence of parasites dependent on freshwater invertebrates in the middle reach, and restriction of parasites that use estuarine amphipods to the lower estuary, provide evidence that the Columbia River estuary provides feeding and rearing habitats for Chinook salmon before they enter the ocean.

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QUANTIFYING *METAGONIMOIDES OREGONENSIS* INFECTION IN STREAM SALAMANDERS

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Relatively little is known about transmission dynamics for most wildlife helminths, including the trematodes. The complex life cycles of trematodes, typically involving three hosts that can vary dramatically in their use of the landscape and response to environmental conditions, makes understanding transmission dynamics in these natural systems more challenging. Trematodes are common in freshwater streams, as snails are obligate first intermediate hosts. *Metagonimoides oregonensis* (Family: Heterophyidae) in the southeastern U.S. uses stream-dwelling *Pleurocera proxima* snails as a first intermediate host, stream salamanders as a second intermediate host, with metacercariae

encysting in the muscle tissue, and raccoons as a definitive host. We are examining host-parasite interactions in this system, and to understand the role of various stream salamander species as important hosts, we examined 289 salamanders collected from 23 sites in North Carolina in 2009. All salamanders were cleared and stained and their abdomens were examined for the presence of *Metagonimoides oregonensis* metacercariae. Six plethodontid salamander species were represented in the samples, including *Desmognathus quadramaculatus* (n=69), *Eurycea wilderae* (n=160), *Desmognathus ocoee* (n=31), *Desmognathus monticola* (n=3), *Eurycea guttolineata* (n=7), and *Gyrinophilus porphyriticus* (n=19). There were clear patterns of varying prevalence and intensity of infection among the species. *Desmognathus quadramaculatus* had higher prevalence and intensity of infection than any of the other species. This was not linked to body size, as there was no correlation between body size and intensity of infection among the species. *Desmognathus quadramaculatus* may be a more important host in the maintenance of the life cycle of *M. oregonensis* than the other stream-dwelling salamanders in this region.

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THE DISTRIBUTION AND PREVALENCE OF *METAGONIMOIDES OREGONENSIS* (TREMATODA: HETEROPHYIDAE) IN SOUTHWESTERN VIRGINIA AND NORTHWESTERN NORTH CAROLINA

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Emerging infectious diseases (EIDs) increasingly threaten human health and economies, as well as global biodiversity. Most human EIDs originate in wildlife, but we know little about the ecological mechanisms that regulate host-pathogen interactions in wildlife systems. Digenetic trematodes are parasitic flatworms with complex multi-host life cycles; they cause numerous human diseases (e.g. schistosomiasis) and can have significant negative impacts on wildlife. Identifying the factors that are important in trematode-host interactions can advance our understanding of parasitism and the dynamics of infectious disease. *Metagonimoides oregonensis* (family: Heterophyidae) is a North American trematode that infects raccoons as definitive hosts, and stream snails (*Pleurocera* spp.) and amphibians as intermediate hosts. Other than the basic life-cycle, little else is known about this parasite. During the summer of 2011, we surveyed snails from 26 streams to examine the distribution and prevalence of *M. oregonensis* in southwestern Virginia and northwestern North Carolina. With the exception of one stream, *M. oregonensis* was present at all sites, ranging in prevalence from 1-20% of snails infected. In addition to *M. oregonensis*, we found cercariae from at least four other families of trematodes ranging in prevalence from 0-38%. These included: (1) *Sanguinicola fontinalis*, a blood fluke of dace; (2) a virgulate-type cercariae, likely of the family Lecithodendriidae, which infects aquatic insects as second-intermediate hosts and birds as definitive hosts; (3) a cotylomicrocercous-type cercariae, likely of the family Opecoelidae, which infects aquatic insects as second-intermediate hosts and fish as definitive hosts; and (4) a monostome-type cercariae, possibly from the family Notocotylidae. There is increasing evidence that community diversity is a key factor in disease dynamics, and future research within the *M. oregonensis* system will focus on how stream community composition of both parasites and hosts may impact trematode infection rates.

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SPATIAL AND TEMPORAL PATTERNS OF INFECTION OF THE AMERICAN EEL, *ANGUILLA ROSTRATA*, BY THE INVASIVE PARASITE, *ANGUILLICOIDES CRASSUS*, IN ESTUARIES OF SOUTH CAROLINA

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Serious concerns have been raised regarding American eel populations nationwide and reports of eel



populations in South Carolina estuaries have shown a decline since at least 2001. The invasive parasite, *Anguillicoloides crassus*, infects the eel swimbladder and is considered one potential reason for this decline. This nematode is endemic to East Asia, where it infects the Japanese eel. It was first seen in the United States in 1995 and has since been reported along the Atlantic Coast however, we have no information regarding the status of infection and impacts of this parasite on eel populations in South Carolina. Our goal was to survey and compare the presence of *A. crassus* in American eel populations in two National Estuarine Research Reserves (the ACE and North Inlet NERRs) and two anthropogenically impacted areas (Winyah Bay and the Cooper River). Eels were collected for one full year (2011) to determine prevalence, mean intensities and mean abundances of *A. crassus* at each site and according to salinity and season and differences in infection between pristine and impacted areas. All populations of eels were found to be heavily infected. Results are mapped using GIS technology to help visualize patterns of infection.

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SUITABILITY OF THREE SNAIL SPECIES AS CANDIDATES FOR USING TREMATODES AS INDICATORS OF ECOSYSTEM HEALTH IN A SOUTH TEXAS ESTUARY

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The usefulness of digenean trematodes as indicators of estuarine ecosystem health has successfully been demonstrated in a few studies where the abundance and diversity of hosts were reflected in the prevalence of infection in snail first intermediate hosts. Since trematodes are ubiquitous and the most abundant metazoan parasites in aquatic ecosystems, their role as indicators of ecosystem health should be generally applicable to a wide variety of aquatic ecosystems. In this study, we searched for suitable gastropod first intermediate hosts from the intertidal as well as subtidal habitats in the coastal Laguna Madre, from the Northwestern Gulf of Mexico. Several hundred *Cerithidea pliculosa* were collected from intertidal mudflats associated with mangroves on several occasions, while hundreds of *Cerithium lutosum*, and *Neritina virginea* were collected from subtidal seagrass beds. To study the spatial variation of trematode infections in *C. lutosum* and *N. virginea*, three 50 m transects were placed perpendicular to the shore. In addition, random samplings were made in two seagrasses *Halodule wrightii* and *Thalassia testudinum*. In the laboratory, the snails were dissected and inspected for trematode larval stages. The results showed that *C. pliculosa* and *C. lutosum* both serve as first intermediate host to several species of trematodes and often with a moderate to high prevalence of infection while *N. virginea* showed no infections. *C. lutosum* in shallow near-shore water displayed a higher prevalence and diversity of trematodes in comparison to those in deeper water indicating a preference for the shoreline by wading birds. In the seagrass habitat, while *H. wrightii* and *T. testudinum* showed the same prevalence, *H. wrightii* harbored significantly more species than *T. testudinum* suggesting that a higher diversity of birds use *H. wrightii* for foraging and/or roosting. Comparisons of the two seagrass species from several sites in Laguna Madre are currently in progress to verify the observed pattern.

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FITNESS COSTS OF LARVAL TREMATODES IN TWO CLOSELY RELATED POECILIIDS WITH DIFFERENT REPRODUCTIVE STRATEGIES

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The Red Queen Hypothesis predicts that genetic recombination via sexual reproduction allows organisms to maintain a high genetic diversity and, in theory, enable hosts to become moving targets that stay one

step ahead of co-evolving parasites. In contrast, parthenogenetic organisms have no genetic recombination and they should serve as easy targets for parasite specialization and suffer from heavier parasite loads than sexual species. Parthenogenesis should therefore be disadvantaged over evolutionary time if parasites significantly affect host fitness. We previously found that the sexually reproducing sailfin molly, *Poecilia latipinna* harbored significantly more parasites compared to its close parthenogenetic relative, *P. formosa* in contrast to what ecological theory would predict. In this study, we investigated the fitness cost of infection on host reproduction in *P. latipinna* and *P. formosa* by counting the number of embryos produced in relation to the number of trematodes in the eyes, gills, heart, and brood sac. At least 30 females of both species were collected from irrigation canals in the Rio Grande Valley, by seining in March/April and again in October of 2011 to compare the effects of parasites on brood size when parasites are least abundant (spring) in comparison to when they are most abundant (late summer). In the spring sample, brood size was positively related to body mass and negatively impacted by the number of trematode metacercariae lodged in gill tissue for both host species regardless of reproductive strategy. No effects of parasites were detected in the summer sample despite significantly higher number of parasites. In addition, sexually reproducing mollies harbored a significantly larger number of gill parasites in the spring sample when compared to the parthenogenetic relatives. The Red Queen Hypothesis is therefore not supported by our data.

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DESCRIPTION OF THE SPERMATOPHORE OF THE BLOOD-FEEDING LEECH *HAEMENTERIA OFFICINALIS* AND ITS PREVALENCE, ABUNDANCE AND INTENSITY IN A WILD POPULATION FROM GUANAJUATO, MEXICO

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Fertilization through hypodermic implantation of spermatophores (ampulla or mass containing spermatozoa that is transferred in their entirety to other individual during copulation) has been recorded in at least three groups of leeches: Glossiphoniidae, Piscicolidae and Erpobdellidae. During mating, the male gonopore of the sperm donor leech becomes into intimate contact with the body of another leech and spermatophores are subsequently ejaculated. In *Piscicola respirans* (Piscicolidae), vector tissue connecting a specific part of the body wall to the ovaries has been described explaining the non-random attachment placement of the spermatophores. In glossiphoniid leeches, such as *Haementeria officinalis*, spermatophores are implanted in any part of the recipient leech without apparent preferences regarding the region of the body. In order to determine if a specific region of the recipient leech is selected by their mates for spermatophore attachment, we sampled 81 specimens of *H. officinalis* from a natural pond close to Coroneo, Guanajuato, Mexico and quantify the number and location of spermatophores *per* individual. In addition, we describe the spermatophores using optical and scanning electron microscopy. Of the 81 leeches examined, 26 (32%) were found to possess at least one spermatophore with a range of 1-8, mean intensity of  $1.80 \pm 1.64$  and mean abundance of  $0.58 \pm 1.25$ . Of the 47 spermatophores recorded, only one was found attached to the ventral surface, 46 to the dorsal surface and none on the suckers. On the dorsal surface, most spermatophores were concentrated on the longitudinal median line from somites XVI to XXX. The analysis of the data presented here suggests that the placement for spermatophore attachment is not randomly selected. This might suggest the presence of some sort of vector tissue in this species and its presence should be investigated in further studies. However, alternative explanations of the apparently restricted attachment place can be proposed such as the mechanical characteristics of the copulation. These results represent the beginning of a long-term study of the reproductive strategies of wild populations of *H. officinalis* from Central Mexico.

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## SPECIALIZED PARASITE IS NOT RESTRICTED TO USE OF CLOSELY RELATED HOSTS

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Ecological theory predicts a trade-off between niche width (i.e. specialization) and the number of suitable niches. We investigated the relationship between the number and phylogenetic distance of suitable hosts and host exploitation in *Euhaplorchis* sp., a parasite known to migrate to the brain to manipulate the behavior of Longnose Killifish, *Fundulus similis*. We hypothesized that the specific migration pattern in the host and manipulative ability of *Euhaplorchis* sp. on host behavior involve a high degree of specialization. Therefore, the parasite should be restricted to using very few and closely related host species. We examined three fish species that are ecologically similar to *F. similis* but that vary in the phylogenetic distance from the confirmed host *F. similis*; Gulf Killifish (*Fundulus grandis*), Rainwater Killifish (*Lucania Parva*) and the Sailfin Molly (*Poecilia latipinna*). To confirm whether or not they serve as suitable hosts, they were experimentally infected with *Euhaplorchis* sp., and the number of behaviors that could increase transmission of *Euhaplorchis* sp. to the definitive host (a wading bird) were measured in both infected and control (uninfected) fish. Our results demonstrate that *Euhaplorchis* sp. was able to infect and change the behavior of two of the four fish species examined. One of them, *F. grandis* is closely related to the known host *F. similis*. Interestingly, *P. latipinna* a species distantly related to *F. similis* also served as a suitable host suggesting that host behavior manipulation does not necessarily restrict the specificity of suitable hosts. Previous research suggests that behavior modification results from alteration of host production of neuromodulators (e.g. serotonin and dopamine). We are currently conducting Lowry assays to assess the existence of a dose-dependent relationship between the number of parasites and the amount of protein present in brain tissue. Expression of specific proteins will be evaluated using vertical gel electrophoresis to elucidate a plausible mechanism for host manipulation of *Euhaplorchis* sp.

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## AMINO ACID MUTATION IN *PLASMODIUM VIVAX* DHFR AND DHPS GENES IN THE BORDER OF SISTAN AND BALUCHESTAN PROVINCE, IRAN

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Molecular markers are a useful approach for recognition of mutations in *P. vivax*. The aim of this study was the genetic analysis of the dihydrofolate reductase-thymidylate synthase and Dihydropteroate synthetase genes in *P. vivax* at the border of Sistan and Baluchestan provinces for recognition of mutation at codons 33, 57, 58, 117, 173 and 382, 383, 512, 553, 585 related to antifolate drug resistance. Clinical isolates of *P. vivax* were collected from malaria endemic areas at the border of Sistan and Baluchestan province in Iran from June 2008 - November 2010. All 40 isolates were analyzed for the *pvdhfr* and *pvdhps* genes using semi-nested PCR and sequencing methods. The mutant *pvdhfr* alleles were seen in 26 (65%) samples in three positions. Mutations were found in 14 (35%), 25 (62.50%) and 33 (7.50%) isolates at 58, 117 and 33 codons respectively. No mutations were observed at codons 57 and 173. Among 26 mutant isolates, double mutations in the form of S58R-S117N (30%) and P33L-S117N (2.5%) were seen in 13 (32.5%) isolates. Triple mutations in codons 33, 58 and 117 were observed in 1 (2.5%) of the isolate and two novel mutation were found at codons 50 and 196. Mutation in the *pvdhps* gene at codon 383 in 7

(17.50%) out of 40 *P. vivax* isolates was seen. Two of the mutant isolates showed mutations in codons 383 and 459. Therefore, of the 40 isolates, 5 isolates (12.50%) were single mutant and 2 (5%) were double mutant. In spite of this fact that the antifolate drugs are not prescribed for *P. vivax* malaria, observed mutant alleles in *pvdhfr* and *pvdhps* gene of *P. vivax* is probably due to exposure of *P. vivax* to the fansidar drug.

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PCR DETECTION OF WATERBORNE PROTOZOA IN ENVIRONMENTAL WATER

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The infection of water-borne protozoa results in the severe gastrointestinal troubles such as diarrhea and dehydration. Among water-borne protozoa, *Cryptosporidium parvum* can be transmitted to human by contaminated food and water, and sometimes, resulted in large outbreaks. The major source of *C. parvum* infection is animal feces which are disseminated in the small stream of cattle breeding areas. Recently, climate change often gives rise the rainfall and river flooding. Especially, farms located in rural area do not have a good sewage treatment plant for cattle feces. Therefore, it is easy to contaminate near small stream. To examine the contamination of *C. parvum* in the small stream, cattle feces were examined by MAF staining, and environmental water samples from the small stream in the endemic area of *C. parvum* were also examined. Water samples were filtrated using 160, 56, and 25 um meshes and then glass wool filter. All mass were evaluated on the contamination of *C. parvum* using Cry-15 and Cry-9 primers. *C. parvum* oocysts were used for positive control of DNA. In the results, 43.75% (50% - 33.3%) of cattle was infected with *C. parvum* in the village, but not in upstream of village (no cattle). The PCR results showed the *C. parvum* contamination in the stream (midstream and downstream). The PCR band (downstream) is thicker than it in midstream. These results suggest that *C. parvum* in cattle feces was disseminated in a near stream or river, and pollute the river. In this study, PCR detection using Cry-15 and Cry-9 primers successfully detected *C. parvum* in the small stream despite a small amount of DNA.

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MICRORNAS IN *LEISHMANIA BRAZILIENSIS*

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MicroRNAs have been described in most organisms from worms to human and more recently in protozoans. MicroRNAs are a group of small RNAs that regulate gene expression post-transcriptionally in a complex process of binding to mRNA in a perfect complement or almost perfect complement that cleave mRNAs or inhibit their translation. Gene expression in *Leishmania* is not well understood, however, it is known to be post-transcriptionally regulated. Argonaute-like and Dicer-like protein, the machinery needed for the processing of miRNAs have been shown to exist computationally in *Leishmania braziliensis*. Our hypothesis is that microRNAs may regulate gene expression in *L. braziliensis*. Here we show our results of computational data analysis showing potential microRNAs in *L. braziliensis*.

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## CHARACTERIZATION OF LB-MIR-1 IN *LEISHMANIA BRAZILIENSIS*

**B. Hannible** and **J.M. Porter-Kelley**, Winston Salem State University

MicroRNAs have been described in most organisms from worms to human and more recently in protozoans. MicroRNAs are a group of small RNAs that regulate gene expression post-transcriptionally in a complex process of binding to mRNA in a perfect complement or almost perfect complement that cleave mRNAs or inhibit their translation. Gene expression in *Leishmania* is not well understood, however, it is known to be post-transcriptionally regulated. Argonaute-like and Dicer-like protein, the machinery needed for the processing of miRNAs have been shown to exist computationally in *Leishmania braziliensis*. Our hypothesis is that microRNAs may regulate gene expression in *L. braziliensis*. Here we show our initial work on the characterization of the first microRNA in *Leishmania*.

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## CALCIUM BINDING PROTEINS WITH EF-HAND DOMAINS IN *GIARDIA INTESTINALIS*

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Calcium plays a fundamental role as a second messenger in eukaryotic cells. Many different signals raise cytosolic calcium concentration in the cell, which is sensed by calcium-binding proteins. Even though a number of proteins are able to decipher calcium signals, the EF-hand proteins are the most important ones. This type of protein contains calcium binding EF-hand motif, which is commonly found in pairs. *Giardia intestinalis* is recognized as a valuable model for gaining basic insights of fundamental cellular processes. In order to identify all EF-hand-containing proteins in *G. intestinalis*, we analyzed data from its completed genome at GiardiaDB. We used Interpro Domain on table of GiardiaDB for isolate WB. Results were 18 possible EF-hand proteins, among which only 2 have been reported in literature. Each protein sequence was then analyzed for the presence of an EF-hand motif and other domain(s) by using Prosite at expasy.org. We found that *G. intestinalis* has a reduced repertoire of EF-hand proteins compared with similar analysis on *Trichomonas vaginalis* (120 sequences) or *Trypanosoma cruzi* (71 sequences). This result can be hypothetically explained by the compact genome or highly divergent sequences that are not identifiable using a typical profile for search. It is important to note that there are a large number of proteins with an odd number of EF-hand motifs (1 or 3). We also found different types of proteins. Some of them are subunits of phosphatases; others are involved in motility, while others correspond to hypothetic proteins. This bioinformatic analysis was validated to verify calcium-binding activity of ORF\_2933 (Programmed cell death protein-like protein). This gene was amplified by PCR and cloned into Pinpoint vector and expressed in bacteria. Dye Stains-all was used to demonstrate the calcium-binding properties of recombinant protein.

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## PATHOLOGY CAUSED BY *LEPTORHYNCHOIDES THECATUS* (ACANTHOCEPHALA) IN *MICROPTERUS DOLOMIEU* (SMALLMOUTH BASS)

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The pathological effects of *Leptorhynchoides thecatus* (Phylum Acanthocephala) on the intestine and pyloric caecae of *Micropterus dolomieu* (Smallmouth bass) were examined. Fish were collected using hook



and line or seine from Otsego Lake (Cooperstown, New York) during the 2011 summer months. Intestines and pyloric cecae of *M. dolomieu* were opened with a single longitudinal incision and preserved in the 10% neutral buffered formalin. Plugs of tissue with attached *L. thecatus* were removed and prepared for embedding in paraplast using conventional methods. The embedded specimens were sectioned at 10 µm intervals with an Olympus CUT 4060 retracting rotary microtome. Sections were mounted with 2.5% sodium silicate and stained with Delafield's hematoxylin and Eosin. The histological sections allowed assessment of the pathology associated with individual worms at the cellular and tissue level. Damage of the tissues included tearing of the epithelial and lamina propria layers in both the intestine and pyloric cecae due to embedding of the proboscis. The damage observed in this study is of concern because of the frequency of *L. thecatus* in *M. dolomieu* and the importance of that fish host in fisheries.

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**EFFECTS OF THE PARASITIC NEMATODE, *PHILOMETROIDES PARALICHTHYDIS*, ON THE SWIMMING AND BURYING PERFORMANCE OF THE SOUTHERN FLOUNDER, *PARALICHTHYS LETHOSTIGMA***

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**E.J. McElroy, W.A. Roumillat**

**I. de Buron**, College of Charleston

The southern flounder (*Paralichthys lethostigma*) is commonly parasitized by the philometrid, *Philometroides paralichthydis*. These nematodes embed themselves in place of the inclinator muscles of the dorsal and anal fin elements. We hypothesized that infection by these parasites impairs the fish use of these fins and we tested whether the swimming and burying performance of the infected fish is negatively impacted. Two groups of individuals (14 parasitized and 16 non-parasitized) ranging from 124 to 272 mm in total length were captured in the Charleston (South Carolina, USA) estuarine system. After acclimating in captivity for 24 hours, the fish were individually filmed with high speed video cameras to determine swimming velocity and acceleration as a measurement of swimming performance as well as the time to bury and percentage of body exposed as a measurement of burying performance. Fish were then euthanized and dissected to document the number, location, and stage of maturation of the worms. Tests showed that the swimming acceleration and both measures of burying performance did not differ between parasitized and non-parasitized fish whereas the swimming velocity of parasitized fish was significantly lower than that of non-parasitized fish. However this difference was not constant across the range of body size; smaller infected fish swam with significantly slower speeds than smaller non-infected fish whereas there was no difference in speed when comparing larger fish. Neither the position nor the number of worms had an effect on either swimming or burying performance. The decrease in swimming velocity in smaller infected fish could be sufficient in rendering them more vulnerable to predation. This result could provide the mechanism (i.e. mortality due to decreased swimming ability) that may explain a previous observation that larger fish (>300 mm) are rarely infected by this parasitic nematode.

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**SEATROUT HEART INFECTION BY *CARDICOLA* SP.: ARE SMALL FISH IN MORE TROUBLE?**

**B.J. Fazzone, P.J. Cosmann**

**I. de Buron**, College of Charleston

**W.A. Roumillat**, College of Charleston

**V.A. Connors**, University of South Carolina Upstate

Spotted seatrout, *Cynoscion nebulosus* (Cuvier, 1830), are important game fish in South Carolina estuaries and are thought to be negatively affected by parasites. In particular, seatrout in South Carolina are heavily infected with *Cardicola* sp., an aporocotyloid trematode whose eggs often penetrate the heart ventricle and become encapsulated in granulomas that are thought to potentially lead to heart dysfunction. Because of high prevalence and parasite burden in adult fish, we hypothesized that infection in smaller fish would lead to a greater proportion of tissue damaged than in larger fish. Histological sections of spotted seatrout ventricle were taken from each specimen and three sections from each ventricle were chosen randomly and inspected for the presence of granulomas. All granulomas in a given field of view were counted in each section and the average calculated. The 10 largest [ $> 375$  mm total length (TL)] and 10 smallest ( $< 325$  mm TL) most infected fish were used for comparison of relative tissue damage. Two of the three sections of ventricle tissue were subsequently examined and six pictures were obtained at 400X magnification from each examined section. ImageJ software was used to analyze percent of granulomatous tissue area per section as a measure of heart tissue damage. Preliminary analysis indicates that a higher percent of heart tissue is granulomatous in smaller infected fish than in larger infected fish.

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#### PREVALENCE OF THE PARASITIC ISOPOD *PROBOPYRUS PANDALICOLA* IN DAGGERBLADE GRASS SHRIMP *PALAEEMONETES PUGIO* IN FOUR MARSH CREEKS NEAR SAVANNAH, GEORGIA

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The daggerblade grass shrimp *Palaemonetes pugio* is one of the most prevalent macroinvertebrates along the East and Gulf coasts of the United States and is an integral part of the estuarine food web. *Probopyrus pandalicola* is a bopyrid isopod that parasitizes *P. pugio* and feeds on its hemolymph, thereby decreasing the daily energy intake of the shrimp by 6-10%. The parasite also causes both male and female shrimp to be sexually castrated. The purpose of this study was to determine parasite prevalence in *P. pugio* in four marsh creeks on the coast of Georgia between 2008 and 2011. Shrimp were collected near Savannah, GA, and examined for the presence of the bopyrid parasite. Based on preliminary results, average monthly shrimp densities were highest during the summer ( $143.2 \pm 33.0$  shrimp  $m^{-2}$ ). Monthly parasite prevalence ranged from 0 to 3.1% for all locations. The maximum prevalence (3.1%) of the bopyrid was seen during the summer at the most saline sampling site (32.2-33.4 psu). Grass shrimp typically spawn through the summer until late October. The increased parasite prevalence during summer months may have a negative effect on the reproductive output of *P. pugio*. Additional sampling is currently being conducted to determine how parasite prevalence varies over the course of a year.

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#### MITES OF NORTH AMERICAN STRIGIFORM BIRDS

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Parasitic mites of owls include those which feed on blood, feather oils, feather tissue, skin, and tissue fluid. Host relationships range from monoxenous to polyxenous, and mite geographic distribution ranges from endemic to cosmopolitan. Of 43 species of North American owls, mites are known from 18 species, but records from Holarctic owls are mainly from the Palearctic region. The mite fauna of *Asio otus* is most well known, 16 species, but only 2 species are known from North American Long-eared Owls. The North American fauna of *Bubo virginianus*, the Great Horned Owl, is the best known, 11 species, followed by



that of *Athene cunicularia*, the Burrowing Owl, with 9 species, *Strix varia*, the Barred Owl, with 5 species, and *Megascops asio*, the Screech Owl, with 4 species.

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BEHAVIORAL ANALYSIS OF A DIGENETIC TREMATODE CERCARIA (*MICROPHALLUS TURGIDUS*) IN RELATION TO THE MICROHABITAT OF GRASS SHRIMP (*PALAEMONETES* SPP.)

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The behavior of *Microphallus turgidus* was examined in relation to microhabitat selection of the second intermediate host *Palaemonetes pugio*. A behavioral ethogram was established for cercariae for comparison with known host behavior. Cercariae were tested for phototactic, geotactic and chemical responses. Phototaxis trials were performed using a half-covered Petri dish, and geotaxis trials used a graduated cylinder. Both phototaxis and geotaxis trials used lighted conditions as the experimental treatment and unlighted conditions as the control. The chemical response trials used water from a container which had housed grass shrimp for 72 hr as the experimental treatment and unconditioned water for the control. The majority of *M. turgidus* cercariae swam horizontally towards the covered side of the Petri dish in both lit and unlit trials, however the mean percentage of cercariae in the uncovered side of the Petri dish was significantly lower in the dishes exposed to light than in those kept in the dark suggesting that light may negatively affect the horizontal distribution of cercariae. *Microphallus turgidus* also preferred the bottom of the water column in the lit and unlit geotaxis trials. The behavior of the cercariae was not affected by shrimp-conditioned water. The results show that the behavior of *M. turgidus* cercariae corresponds to the demersal behavior of *P. pugio*. A host congener, *P. vulgaris*, differs in microhabitat selection and prefers to live near structures, such as pilings. This variation in behavior may explain the difference in metacercarial abundance between these two closely related host species. In the chemical response study the cercariae did not show altered behavior in response to host odors. The results suggest an innate search pattern based on physical taxes that allows *M. turgidus* cercariae to find areas where the probability of encountering the primary host is highest.

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AVIAN MALARIA IN CALIFORNIA: HOST-VECTOR LINKAGES AND DISEASE DYNAMICS IN A SONGBIRD COMMUNITY

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Although avian malaria has been shown to affect the health and fitness of birds worldwide, very little information is available on the prevalence and distribution of these blood parasites in California. In addition, the mosquito species that transmit avian malaria are largely unknown. In order to address the spread of vector-borne disease in the face of global climate change, we must begin to understand the degree of susceptibility mosquito vectors have to malaria parasites, vector host-feeding preferences, and the mechanisms governing susceptibility and pathology in avian hosts. Here we describe the results from the first year of an ongoing study of the transmission patterns of avian malaria in a riparian songbird community at China Creek County Park in California's Central Valley. The ongoing study targets hatch-year migrants, nestlings, resident birds, and mosquitoes. Using both molecular and microscopy methods to screen for avian haemosporidian parasites, we have identified the linkages among hosts, vectors and parasites transmitted at China Creek, examining how seasonality and host-vector characteristics influence

avian malaria transmission, spread and maintenance. Results from this study confirm high diversity of malaria parasites at China Creek. We found nine distinct lineages of *Plasmodium* species in 57 of 1,934 mosquitoes (2.9% overall prevalence) and eight distinct lineages in 70 of 206 bird blood samples (34% overall prevalence) collected during the summer and fall of 2011. Moreover, we found four identical *Plasmodium* lineages common to both mosquitoes and birds, which enabled us to identify these *Plasmodium* lineages to species level with blood smears from the birds. Half of recaptured birds presented changes in their infection status over the course of weeks to months. To our knowledge, this is the first study that uses molecular techniques to identify the interrelationships among birds, mosquitoes and parasites in a complex natural ecosystem over several seasons.

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**TRANSPOSABLE ELEMENT DYNAMICS IN SCHISTOSOMA MANSONI STRAINS**

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Transposable elements (TEs) are mobile DNA sequences with an intrinsic ability to move within and among genomes. The process of transposition increases copy number of TEs, at the cost of the host genome and is known to be triggered by environmental challenges. Such proliferations tend to decrease fitness of the host by the mutagenic effects of insertions, metabolic costs of transcription and translation, and chromosomal damage due to ectopic recombination among dispersed copies of TEs. Purifying selection eliminates excessive proliferation of TEs. Also in host genomes, epigenetic mechanisms have evolved as a defense system against bursts of TEs. Therefore, the TE landscape of a population is determined by the arms race between TEs and host genomes. When a large population is subdivided into small subpopulations, each subpopulation could inherit some of the active TEs. If these subpopulations remained separated over a long time, they are expected to accumulate unique sets of transposable elements by local fixation. These differences could affect the genetic composition of sub populations, eventually leading to reproductive isolation. We attempted to identify the differential activity of transposable elements in two isolated strains of the trematode parasite, *Schistosoma mansoni*. PR-1 and NMRI strains were originally collected from Puerto Rico and maintained in the laboratory for over 50 years. Relaxed selection in laboratory strains of *S. mansoni* strains could result in excessive proliferation of TEs by genetic drift, thus differentiating isolated populations. We selected six transposable elements of *S. mansoni*, Merlin, SmTRC1, Perere-1, Saci-1, Saci-2 and Saci-3 for our study. Our preliminary PCR analysis indicated a disparity of TE copy number between PR-1 and NMRI strains. Quantitative PCR analysis of gDNA and cDNA in adults, miracidia, and cercarial stages of the parasite provides further evidence for the variation of copy number and activity of TE in *S. mansoni* strains. Quantification of multiple families of TEs enabled us to estimate their differential proliferation ability against host defense. Differential TE activity in PR and NMRI strains implies genetic structure differences, which could explain the differences in infectivity between the two strains.

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**PREVALENCE OF ENCYSTED APICOMPLEXAN PARASITES IN MUSCLE OF RAPTORS FROM NORTH CAROLINA**

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**M. Griffin, R. Jones, K. Stanford** and **S. Barnes**, Johnson C. Smith University  
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**A.C. Rosypal**, Johnson C. Smith University  
**D.S. Lindsay**, Virginia Tech

Protozoal encephalitis is increasingly being reported in raptors from the United States. We examined the prevalence of encysted protozoan parasites in the muscles of raptors submitted to the North Carolina Raptor Rehabilitation Center, Huntersville, NC for treatment and rehabilitation. Birds that died or were humanely euthanasia due to poor clinical prognosis were used in the present study. Portions of heart and breast muscle were examined using PCR primers for *Toxoplasma gondii*, *Neospora caninum*, *Sarcocystis neurona*/*S. falcatula*, and *Sarcocystis* species. Hematoxylin and eosin (H&E) stained tissue sections of heart and breast muscle were also examined microscopically for parasites. Our PCR studies are still being conducted. *Toxoplasma gondii* and *N. caninum* were not observed in H&E stained sections. Sarcocysts were seen in heart and breast muscle. Sarcocysts were microscopic. The genotypes of *T. gondii* present in the samples are currently being determined and the relationships of *Sarcocystis* species present in various raptors is being investigated using molecular methods. Supported in part by a Historically Black Universities and Colleges-Undergraduate Program (HBCU-UP) and Smith Institute for Applied Research grant to ACR and student training grants from the Virginia-North Carolina Alliance for Participation Program at Virginia Tech to DSL.

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PREVALENCE OF APICOMPLEXAN PARASITES IN THE MUSCLES OF HOUSE FINCHES  
(*CARPODACUS MEXICANUS*)

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Little is known about prevalence of protozoan parasites in the muscles of house finches (*Carpodacus mexicanus*). The muscles from 18 (heart and breast from 15 and breast only from 3) house finches were examined for the DNA of *Toxoplasma gondii*, *Neospora caninum*, *Sarcocystis neurona*/*S. falcatula* and *Sarcocystis* species using PCR. Eight were female and 10 were males. The birds were part of a research project on the effects of infection with the naturally occurring bacterium *Mycoplasma gallisepticum* in house finches. Birds were collected in the wild then housed at the aviary of the Biology Department Virginia Tech. Birds that died or were euthanized due to poor health were submitted for necropsy at the Center for Molecular Medicine and Infectious Diseases, Virginia Tech where DNA isolations and PCR was conducted. Thirteen (72%) of the birds were positive for *T. gondii*. Heart and breast tissue were both always positive for *T. gondii* in the same bird. Three (16%) of the finches were positive for *N. caninum*. The distribution of *N. caninum* DNA was more variable in the muscles of house finches and was found in the heart only of 1, heart and breast muscle of 1, and the breast muscle only of 1 finch. No birds were positive for *Sarcocystis* species DNA in their muscles. The genotypes of the *T. gondii* isolates are presently being determined to investigate the role of house finches in the epidemiology of pathogenic genotypes of *T. gondii*. The high prevalence of *T. gondii* in house finches and their predation on by cats suggests that they may play an unrecognized role in maintaining environmental contamination with *T. gondii* oocysts by cats. The contribution of DH was supported in part by NSF IOS-1054675 and EF-0622705. The contribution of M. Mudasser Nazir was supported by a grant from the Higher Education Commission of Pakistan to DSL.

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CHRONIC INFECTION OF *TOXOPLASMA GONDII* IN THE BRAIN INDUCES M2 MICROGLIA  
PHENOTYPE BY REDUCING INDUCIBLE NITRIC OXIDE SYNTHASE

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Chronic infection of *Toxoplasma gondii* is mainly dependent on the concentration of IFN- $\gamma$  in the CNS. IFN- $\gamma$  polarizes microglia toward the M1 phenotype. Microglia activated with IFN- $\gamma$  is involved in parasitism control and in tissue pathologies. M2 microglia (CD163+) has an important role in tissue remodeling during a chronic infection of *T. gondii*. The present study investigated the polarization of microglia in the brain after *T. gondii* infection. A chronic strain of *T. gondii* (ME49) was infected to C57BL/6 mice. After the infection with 10 ME49 cysts, cytokine levels and NO production in the brain were determined using ELISA. In addition, cytokines in the primary cells and BV-2 microglia were also examined using qPCR and ELISA. Results in the brain and primary microglia showed that anti-inflammatory cytokine levels were increased and NO production was decreased after *T. gondii* infection or antigen treatment. In this study, we suggest that NO production of IFN- $\gamma$ -activated microglia is inhibited during a chronic infection of *T. gondii*, and the decreased IFN- $\gamma$  and the increased anti-inflammatory cytokines (IL-10 and TGF- $\beta$ ) may contribute to neuron viability in the brain after *T. gondii* infection. In the early phase of *T. gondii* infection, microglia shows M1 phenotype mainly depending on the IFN- $\gamma$  and NO production in the CNS. However, during the chronic infection, microglia shows M2 polarization by secreting anti-inflammatory cytokines and low NO production. This study also suggests that the plasticity of microglia during a chronic infection of *T. gondii* may be toward a neuronal protection. Therefore, *T. gondii* is considered as a well-adapted parasite to avoid host immune defense system.

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IMMUNE CHARACTERISTICS IN TUMOR-BEARING BALB/C AND BALB/C NU/NU MICE AFTER THE TREATMENT OF *TOXOPLASMA GONDII* LYSATE ANTIGEN

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Anti-tumorigenic effects of a protozoan parasite infection have been studied in *T. gondii* (RH)-infected mouse model although the mechanism remains unknown. The present study in order to examine the anti-tumorigenic mechanism was performed by mouse infection as well as *T. gondii* lysate antigen (TLA) treatment (100 $\mu$ g/mouse). S-180 cells or CT-26 cells, colon cancer (Luc+, GFP+) cell lines, with plain matrigel was inoculated into BALB/c and BALB/c nu/nu mice to produce tumors. Both the intraperitoneal infection of *T. gondii* tachyzoites and TLA treatment into tumors induced the decrease of the size and weight of tumors in both mice ( $p < 0.05$ ). In order to examine the relationship of immune response, cytokine profiling was examined in serum and tumor mass. In addition, splenocytes were analyzed for the kinetics of immune cell population. Our result showed that IL-12, chemokines (MCP-1, Leptin, PF-4), colony stimulating factors (GM-CSF, M-CSF), and cytotoxic T (Tc) cells were dominantly increased after *T. gondii* infection in BALB/c mice. Interestingly, IL-12 and NK cells were increased in BALB/c nu/nu mice. In our study, *T. gondii* infection as well as TLA treatment induced Th1 cytokine profiling (IL-12, IFN- $\gamma$ ) and decreased Th2 cytokines (IL-10, IL-4, IL-5). Taken together, the present study suggests that the increase of IL-12 may induce preferentially cytotoxic cells against tumors (Tc cells and NK), and the increased cytotoxic cells may have a role for anti-tumorigenesis.

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RESISTANCE TO *SCHISTOSOMA MANSONI* IS CORRELATED WITH THE NUMBERS OF SPREADING GRANULOCYTES IN *BIOMPHALARIA GLABRATA*

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Molluscan internal defenses rely heavily on circulating hemocytes. In most cases, encounters with large foreign bodies result in recognition by hemocytes followed by spreading of these defense cells over the object's surface. The resulting encapsulation concentrates the force of the hemocytes' assault on the foreign object. *B. glabrata* snail lines obtained by self-fertilization of isolated 13-16-R1 [Oregon] individuals have yielded multiple inbred families in which genes are fixed at ~91% of the loci. Among the phenotypic traits that we have measured in 20 of these families are susceptibilities of snails to the PR1 [Oregon] strain of *Schistosoma mansoni*, and hematocrits of quickly spreading granulocytes present in the hemolymph. Higher numbers of these cells predict a snail phenotype that is resistant to *S. mansoni* infection. Both resistant and susceptible snails are found in families with intermediate hematocrits. We infer that within the parental 13-16-R1 population hemocyte numbers are varied. When sufficiently numerous, a snail's hemocytes can generally prevent parasitic infection. At lower hematocrits, a more complex set of variables interact to determine the outcome of an infection. Support: NIH grant AIO16137.

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### OCCURRENCE OF *MECISTOBOTHRUM BREVISPINE* METACESTODES IN BIVALVES

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Eighteen species of bivalves were collected from the northern Gulf of Mexico and examined for the presence of metacestodes. DNA was extracted from the cestodes found after they were photographed. Small subunit, large subunit (LSU), and internal transcribed spacer regions of the ribosomal RNA genes were amplified and sequenced. In addition to genera and species previously reported from bivalves in this geographic area (*Acanthobothrium* spp., *Duplicibothrium* spp., and "*Tylocephalum*" spp.), metacestodes having an LSU sequence identical to that reported for *Mecistobothrium brevispine* were found. One of twelve specimens of *Donax variabilis* collected in Venice, Florida contained two larvae. They were not found in *Donax variabilis* collected from Horn Island (Mississippi) or Dauphin Island (Alabama). One of two specimens of *Spisula raveneli* collected from Panacea, Florida contained five larvae. Cownose rays (*Rhinoptera bonasus*), the adult hosts of *M. brevispine*, are known to feed on these species of molluscs.

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### PREVALENCE AND ASSOCIATED RISK FACTORS OF INTESTINAL HELMINTH INFECTIONS AMONG 5-14 YEAR OLDS IN ANAMBRA STATE, NIGERIA

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A significant portion of the population in Nigeria consists of indigenous people. Epidemiological data of the health status of these groups including intestinal helminthiasis are very limited. Provision of such data will be of great importance in the formulation of policy on control and prevention of diseases in this group. The objective of the study was to determine the prevalence and associated risk factors of intestinal helminth infections among school-aged children. A cross-sectional study, involving 200 school-aged children was conducted between April and July 2011. Structured questionnaires were used to identify potential risk factors. Stool specimens were examined using both direct saline method and concentration technique. All analyses were done using SPSS v16 statistical software. Four species of intestinal helminthes were indentified with overall prevalence of 46% (92 of the 200 children). The predominant parasites involved were *Ascaris lumbricoides* (21%), *Trichuris trichiura* (11.5%), *Strongyloides stercoralis* (8.5%), Hookworm (5%). Male samples recorded a prevalence of 54.3% whereas female samples had a prevalence of 36.8%. The following factors all showed significant difference ( $p < 0.05$ ) as predisposing factors to intestinal helminth infections: water treatment, toilet facilities, latrine use,



sanitary habits, refuse disposal, parental occupation, consuming fruits and vegetables without washing, and consumption of *suya*. However, poor water source and being barefoot did not show significant difference ( $p>0.05$ ) with the prevalence on intestinal helminthes. Results from this study signify the need to pay more attention to indigenous communities, especially children who are at a higher risk of morbidity due to helminth infections. Access to quality health services, which may include mass drug administration (MDA) and health education, should be ensured. However, further studies are required to explore more potential risk factors contributing to the high prevalence recorded in this study.

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EFFECT OF TEMPERATURE ON THE EMBRYONATION OF *ASCARIS SUUM* EGGS IN ENVIRONMENTAL CHAMBER

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Recent climate change affects to ecosystem in the earth and furthermore, it is expected to have a large impact on the interactions between parasites and their hosts. Changes in temperature bring a change in humidity on the ground, alter the development rates of soil-transmitted parasites, shift their geographical distribution, and alter transmission dynamics. Helminth distribution is especially affected by the environmental changes. Among them, the temperature is very important factor for the development of parasite eggs. Accordingly, this study investigated on the relationship between changes in temperature and development of parasite eggs. To collect *A. suum* eggs, adult worms were harvested from the intestines of naturally infected pigs at the slaughterhouse located to Pocheon-si, Gyeonggi-do, Korea. They were kept in PBS for 24 h at 25°C. The fluid containing *A. suum* eggs was collected and stored at 4°C for further use. To provide the experimental environment such as in soil, this study designed a conditioned soil using sand. The sand, collected from aquarium, was washed thoroughly with water and passed through a 1-mm sieve in order to remove large pebbles and debris. Then, the sand was autoclaved for 1h to kill other pathogens and divided by 30 g in petri-dishes. Eggs of *A. suum* were incubated on sand media under 5°C, 25°C, and 35°C with a humidity of 50%. We counted 50 eggs and examined the embryonation of eggs. This study shows that changes in temperature affect to the developmental time to 8-cell-stage of eggs. The temperature condition at 25°C and 35°C takes 19 days and 17 days for the development to embryonated eggs, respectively. Furthermore, the development to 8-cell-stage of egg takes 6 days and 5 days, respectively. The temperature condition at 5°C did not affected to the development of eggs. They remained a 1-cell-stage. Our results show that parasite eggs in soil are embryonated more quickly at high temperature. Our results also suggest that the global warming may result in the increase of the soil-transmitted helminth infection.

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(205)

DETECTION OF ANTIBODIES TO LEISHMANIA DONOVANI IN ANIMALS IN A KALA-AZAR ENDEMIC REGION IN EASTERN SUDAN: A PRELIMINARY REPORT

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The prevalence of antibodies against *Leishmania donovani* in selected domestic and wild animal species in 2 villages in Sudan with active *L. donovani* transmission in humans was investigated. Screening of domestic animals (donkeys, cows, sheep, goats, camels and dogs) with the direct agglutination test (DAT) detected reaction rates above the cut-off titres in donkeys (68.7%), cows (21.4%) and goats (8.5%), and which were also found in wild rats (5.5%). Sera of sheep, camels and dogs had a weak agglutination reaction below the cut-off titre. Testing of the same sera by enzyme-linked immunosorbent assay (ELISA), against a lysate of *L. donovani* promastigotes, showed reaction rates above the cut-off optical density in cows (47.6%), goats (13.6%), and in rats (4.1%). No *Leishmania* parasite was isolated from spleen, liver, bone-marrow or spleen of Nile rats.

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## (206)

### OCCURRENCE OF PARASITIC CO-INFECTION IN DOGS FROM A RURAL SETTLEMENT

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The present study aimed to analyze the rate of parasitic co-infection by, *Leishmania infantum*, *Ehrlichia canis*, *Babesia canis*, *Toxoplasma gondii* and *Neospora caninum* in serum samples of 93 dogs from a rural settlement in Ilha Solteira municipality, SP, Brazil using five indirect fluorescent antibody tests (IFAT) with each one targeting one of the five parasite species. The occurrence rates of dogs with anti-*L. infantum*, anti-*E. canis*, anti-*B. canis*, anti-*T. gondii* and anti-*N. caninum* antibodies were 37.6% (35/93), 75.3% (70/93), 72% (67/93), 47.3% (44/93) and 6.4% (06/93), respectively. Dogs were co-infected with two to five parasites as follow: 17.2% were serum positive for a single parasite, 29% for two, 33% for three, 16.1% for four, 1.1% for five and 4.3% were serum negative for all five parasites. The presence of antibodies of these five parasitic agents in dogs confirmed the exposure of dogs to these parasites and due to the potential zoonotic risk of these diseases, particularly leishmaniasis, ehrlichiosis and toxoplasmosis, special attention must be given in the diagnosis and the control programs.

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## (207)

### TWO NEW AFRICAN SPECIES OF THE GENUS *CHORDODES* (GORDIIDAE: NEMATOMORPHA)

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The genus *Chordodes*, with more than 100 species described so far, has a worldwide distribution inhabiting mainly tropical and subtropical areas. In Africa, 34 species are known, 22 of which are well characterized and 12 need to be reinvestigated. Here, we describe two new species based on 5 indeterminate specimens belonging to the collections of the Museum National d'Histoire Naturelle, Paris (MNHN). Sections of the mid-body cuticle and posterior end of these worms were cut, washed, critically point dried and mounted. All pieces were observed using scanning electron microscopy. We identified 2 new species clearly distinct from previously described species. The first of these new species (2 males and 2 females), are 78-175 mm long in males and 224-249 mm long in females. The cuticle of both sexes has simple, tubercle and crowned areoles, with dimorphism of this last in females. The simple areoles have smooth surfaces with some pores and bristles usually forked, the tubercle areoles are similar to the simple ones but, have a blunt tubercle, the crowned areoles appear in pairs or in groups of 3 areoles. The

intraspecific variations will be discussed. The second new species (1 female) is 282mm long. The posterior end is rounded. The cuticle has 6 types of areoles. The simple areoles have smooth surfaces with few fine bristles; the tubercle, bulging, thorn and crowned areoles are isolated. The bulging areoles are smooth with minute tubercles like granules.

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(208)

SYSTEMATICS AND GENOME SIZE OF *INFIDUM SIMILIS* TRAVASSOS, 1916 (DIGENEA)

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*Infidum similis* (Dicrocoeliidae) a parasite of colubrids in Middle and South America was found in the gall bladder of a parrot snake (Colubridae: *Leptophis* sp.) in south Mexico. A phylogenetic analysis based on partial sequences of the 28S ribosomal DNA gene was carried out to investigate the systematics of *I. similis* and its placement in Gorgoderioidea. Two methods were used to inferring the phylogeny, maximum parsimony (MP) and maximum likelihood (ML) analyses. Phylogenetic trees with both methods indicate that *I. similis* is placed within the Plagiorchoidea rather than Dicrocoeliidae (Gorgoderioidea) where the genus is currently classified. Additionally, we presented data about the estimation of its haploid genome size using Feulgen image-analysis densitometry (FIAD) of sperm nuclei. This is the first genome size estimated for a member of Plagiorchiida, providing a new source of knowledge on helminth diversity and evolutionary studies.

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OXYURID NEMATODES FROM COCKROACHES (BLATTARIA) IN SOUTHERN FLORIDA WITH REVISED MORPHOLOGICAL CHARACTERS FOR *EURYCONEMA PARADISA* AND *PROTRELLOIDES PARADOXA*

**J. Koltek, R. Carreno, D. Ordosch and D. Hamill**, Ohio Wesleyan University

Cockroaches (Insecta: Blattaria) house diverse species of oxyurid nematodes. However, ecological, geographical, and taxonomic data on many of these species are lacking, and relatively few wild hosts have been sampled. In this study, 5 species of thelastomatoid nematodes from 5 genera were collected from cockroaches in southern Florida and the Florida Keys. The morphology of *Euryconema paradisa* and *Protrelloides paradoxa* Chitwood, 1932 was re-examined using scanning electron and light microscopy. Observed female cephalic morphology of *E. paradisa* and the male caudal morphology of *P. paradoxa* differed from original descriptions on papillary form and arrangement. Other species collected were *Leidynema appendiculata*, *Hammerschmidtella diesingi*, and a *Thelastoma* sp. This study provides new morphological data for *E. paradisa* and *P. paradoxa* and extends the known range of these species.

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INNOVATIVE SERUM-FREE MEDIUM FOR IN VITRO CULTIVATION OF PROMASTIGOTE FORMS OF *LEISHMANIA* SPECIES

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**E.A. Khalil**  
**S.A. Omer**, Tropical Medicine Research Institute, National Centre for Research

We described a comparatively simple medium formula (CML) using common, available and reasonably priced ingredients that could be used in place of medium that requires calf serum enhancement for cultivation of *Leishmania* promastigote forms. This medium equivalently supported the growth of parasites at rates comparable with those obtained with serum supplemented RPMI-1640 medium. *Leishmania* promastigotes reproduced in CML exhibited moderate to high infectivity capacities when tested against J774 macrophage cell line. No significant difference was noted between *Leishmania* strains cultivated in the newly modified medium and those grown in RPMI-1640 medium in their cells infectivity and replication potentials. The use of new CML can easily take the place of other biphasic or liquid media because of its easy preparation and instantaneous use, reasonable price, availability of ingredients, and its long shelf life, which is 30–45 days. The fact that this medium is similar to other culture media as far as durability and quantity of produced parasites might give it an advantage over the other currently used media. © 2007 Elsevier Ireland Ltd. All rights reserved.

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## (211)

### TETRAPHYLLIDEAN TAPEWORMS OF ELECTRIC RAYS (TORPEDINIFORMES) OFF THE PACIFIC COAST OF COSTA RICA

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Data on the tetraphyllidean tapeworms of elasmobranchs of the Pacific coast of Costa Rica are scant. Only 10 species of tetraphyllideans have been reported from the approximately 68 species of elasmobranchs known to occur in this region. Off the coast of Costa Rica, electric rays are represented by 4 species: *Narcine entemedor*, *N. vermiculatus*, *Torpedo tremens*, and *Diplobatis ommata*. During a survey of tapeworms of elasmobranchs caught by the deepwater shrimp fisheries of Pacific Costa Rica, specimens of all of these electric ray species, except *N. vermiculatus*, were collected and examined for parasites. While no previous parasite records exist for *T. tremens*, tetraphyllidean tapeworms have been described from *N. entemedor* off the Pacific Coast of Costa Rica and from *D. ommata* in the Gulf of California. In this study, 5 specimens of *N. entemedor*, 6 of *T. tremens*, and 4 of *D. ommata* were examined for tapeworms. Specimens were collected and fixed in 4% formalin buffered seawater, stored in 70% ethanol, and prepared for light and scanning electron microscopy using standard techniques. A total of 9 species of tetraphyllidean tapeworms belonging to 2 genera were found to parasitize these hosts; at least 6 of these are new to science. *Narcine entemedor* hosted 4 species of *Acanthobothrium*: 2 large species (> 1.5 cm) preliminarily identified as *A. cf. inbitorium* and *A. cf. franus*, and 2 small (< 1.5 cm) as of yet undescribed species. *Torpedo tremens* also hosted 4 tetraphyllidean species new to science: 2 large species of *Calyptrobothrium*, and two small species of *Acanthobothrium*. This appears to be the first record of *Calyptrobothrium* from the eastern Pacific Ocean. *Acanthobothrium maryanskii*, originally described from *D. ommata* in the Gulf of California, was the only species found to parasitize *D. ommata* off the coast of Costa Rica. This extends the distribution of this tapeworm species southward. Whether specimens of *N. entemedor* from Costa Rica are host to the same tetraphyllidean species as those in the Gulf of California remains to be determined.

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## (212)

### SCHISTOSOME SHARING: THE ELEPHANT SCHISTOSOME *BIVITELLOBIKHARZIA NAIRI* ALSO INFECTS THE GREATER ONE-HORNED RHINOCEROS (*RHINOCEROS UNICORNIS*) IN CHITWAN NATIONAL PARK, NEPAL

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The digenetic trematode fauna of Nepal is poorly known and this represents our first report of the diversity of schistosomes we have found in the Terai region of southern Nepal, including regions in and around Chitwan National Park (CNP). Both domestic and wild Indian elephants (*Elaphus maximus*) are present, and we found positive one of two samples of dung from wild elephants and one of 22 (4.5%) dung samples from domestic elephants to be positive for schistosome eggs. The morphology of the eggs and both CO1 and 28S sequences derived from eggs were consistent with *Bivitellobilharzia nairi*, the schistosome reported from Indian elephants from two other Asia countries, and here for the first time from Nepal. We also acquired 14 fecal samples from the Greater One-Horned Rhinoceros (*Rhinoceros unicornis*), of which 7 (50%) contained viable eggs indistinguishable from those of *B. nairi*. This identification was confirmed by comparison with both CO1 and 28S sequences from *B. nairi* from Nepalese and Sri Lankan elephants. This represents the first definitive identification of the occurrence of the “elephant schistosome” *B. nairi* in rhinos. A previous report of a similarly-sized schistosome egg from the Javan, or Lesser On-Horned Rhinoceros (*Rhinoceros sondaicus*) is also likely to be *B. nairi* as well. Our work suggests elephants and rhinos share this schistosome species in CNP, even though these members of the “charismatic megafauna” belong to unrelated mammalian families. Their shared life style of extensive contact with freshwater habitats likely plays a role, though the snail intermediate hosts for *B. nairi* has yet to be identified by us or others, despite extensive searching. In addition to providing the first sequence data for a schistosome from any rhinoceros species, this report also supports *Bivitellobilharzia* as a monophyletic group and its status as a distinct genus within the Schistosomatidae.

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### (213)

#### A NEW SPECIES OF CESTODE FROM THE *HIMANTURA WALGA* (DWARF WHIPRAY) OF BORNEO

**A. Daigler and F. Reyda**, State University of New York College at Oneonta

This study is an extension of a large-scale survey of parasites (which include cestodes) found in freshwater elasmobranchs of Borneo. Each of these cestodes is thought to be, or found to be, new to science. In this project data from cestode specimens of two individual *Himantura walga* (Dwarf Whipray) were recorded for various lengths, measurements and counts. The data was recorded through use of light microscope examination of whole mounted specimens. The length measurements include the morphological features and organs such as bothridia, overall size, testes, stalk length, germinative zones, proglottids, loculi, Mehlis glands, ovaries and cirrus sacs. Count measurements included loculi, proglottids, testes, mature proglottids, and proglottids which are wider than long. The above data on cestode specimens from 2 *H. walga* hosts, and the comparison of morphological features to other known cestode species, suggests that these specimens represent genus and species that are new to science.

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### (214)

## INTRODUCING A NEW MUSEUM FOR PARASITES – THE PARASITE DIVISION OF THE MUSEUM OF SOUTHWESTERN BIOLOGY AT THE UNIVERSITY OF NEW MEXICO IN ALBUQUERQUE

**E.S. Loker** and **S.V. Brant**, Museum of Southwestern Biology, Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico

The Division of Parasitology is the newest addition to the Museum of Southwestern Biology at the University of New Mexico in Albuquerque. The Division, officially established in January 2011, is a research; training and education facility dedicated to the concept of 'integrated' research collections. In general, the Division is keen to use the parasite collection to play greater roles in understanding the ecology and evolution of infectious diseases, the impact of control programs on parasite evolution, and to promote the conservation of biodiversity, particularly of parasites. We will emphasize the study of parasites from the southwest of North America but collections from the world over will be accepted. The collection will contain necropsy facilities; both wet and dry processing areas specimen storage areas. The new space is slated for completion in late 2012. Additionally, the Division has genomic quality storage for frozen specimens. Using the MSB database Arctos (a multi-institutional, multi-collection database), information pertaining to parasites deposited in the Division will be integrated with information from their hosts, enabling more comprehensive studies of epidemiology, pathology, ecology and co-evolution of the parasites. For example, specimen data are mappable on Google Earth maps and specimens cited in publications are linked to those publications and specimens vouchering molecular sequence data are linked to the GenBank database. At present, the collection consists primarily of the Rausch Helminthological Collection (RHC), which is the personal research collection of Robert L. and Virginia R. Rausch. It represents over 50 years of continuous survey and inventory of vertebrate hosts and their parasites in biologically unique and sensitive regions throughout the world, with the primary focus on high latitudes in North America and eastern Siberia. The RHC, in excess of 60,000 lots of specimens, is unparalleled in scope and depth particularly for helminths of mammals, and is among the largest collections in the world. We look forward to working with you and encourage you to learn more how we can work together.

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### (215)

#### RECONSTRUCTION OF THE COCCIDIA OF THE WORLD WEBSITE TO ENHANCE ACCESSIBILITY USABILITY, AND UTILITY

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**Z. Roehrs**, Laramie County Community College

The Coccidia of the World website (COW) (<http://biology.unm.edu/biology/coccidia/home.html>) was established at the University of New Mexico in 1998 as part of an NSF *Program to Enhance Expertise in Taxonomy* (PEET). The project has served as an online resource of coccidian taxonomy, biology, methods of study, and directory for coccidiologists worldwide. Today, while still an extremely useful resource, advances in web-based data management, database connectivity/linking, and online information availability have made the COW website difficult to update, unconnected with other related web biodiversity databases, and limited in utility. We currently are in the process of extracting information from the COW into a modern database driven platform that will address these issues well into the future. Once completed, coccidian taxonomists will be able to assist in keeping the COW website up-to-date by entering new species descriptions as they are accepted for publication and updating host and geographic ranges for named species as hosts are studied. Non-specialist users will have access to information on the biology of the coccidia, methods for studying coccidian taxonomy, an up-to-date directory of coccidiologists, and the taxonomy database that will provide links to taxonomic papers as pdf files within

the website (older out of copyright literature) as well as recent literature in PubMed and other public access literature databases. The database structure (i.e. Global Biological Information Facility/ GBIF) also will allow web crawling by other biodiversity databases including the Biodiversity Heritage Library and the Encyclopedia of Life so non-parasitologists can access information on this biodiverse, economically important and fascinating parasite group.

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**(216)**

**EVALUATION OF CHANGES IN NUMBER OF *ANOPHELES SUPERPICTUS* LARVA AT MARGINS OF IZEH CITY MIANGRAN LAKE DURING 20 YEARS, FROM 1970 TO 1990**

**R. Valipour Nouroozi**, Faculty of Medicine Sciences, Tarbiat Modares University, Iran

*Anopheles superpictus* is the most important vector of malaria in Iran. The aim of this study was to evaluate the changes in number of *Anopheles superpictus* larva in margins of Izeh city Miangran lake across a 20 year period, from the year 1970 to the year 1990 and to study the impact of rice farming, in fields around margins of this lake in the years after 1976, on the population of *Anopheles superpictus* larva. Mosquito larva collection was carried out monthly, from 1970 to 1990. The collected larva were sent to parasitology laboratory at Izeh Shohda Hospital where *Anopheles superpictus* larva were identified and counted. Sampling conducted from accumulated centers of larva. Differences between the number of larva in samples collected before 1976 and in years after showed a significant difference. This study proved that population of *Anopheles superpictus* larva in the years after the year 1976 increased. Control strategies should be applied to decrease the number of *Anopheles superpictus* larva in this region. Furthermore, this study showed that artificial geographic changes resulting from farming around this lake might have serious potential threats to human life in this city.

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**(217)**

**HENRY BALDWIN WARD MEDAL LECTURE**

**MY HUMBLE EXPERIENCE WITH PARASITES**

**L.X. XIAO**, Centers for Disease Control and Prevention

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**(218)**

**CLARK P. READ MENTOR AWARD LECTURE**

**MENTORING THEN AND NOW**

**W.F. Font**, Professor Emeritus and Scholar-in-Residence, South Eastern Louisiana University

Mentoring "then" involved me making numerous mistakes, first as an undergraduate, then as a graduate student. Fortunately, I had great mentors who came to my rescue and showed me how to do things the right way. Then, as a new Assistant Professor, I had opportunities to observe my department head, other faculty members in my department, and members of the American Society of Parasitologists who I thought had great talents for directing students. I have stolen shamelessly their best ideas. Now, I use what I have learned from my past mentors to attempt to help my students succeed in attaining their goals. My mentoring "philosophy" is guided by the caption of a cartoon that I saw on a colleague's door. The cartoon showed a scientist in his laboratory saying, "if we knew what we were doing, we wouldn't call it research." Since I really did not know what I was doing, I have tried not to be too dogmatic in mentoring



my students. I have had the good fortune to have great students in my laboratory and their intelligence and self motivation have been the keys to their success. The fact that the American Society of Parasitologist values the importance of mentors is, in my opinion, one of its greatest strengths, and I thank the members of this society for this recognition.

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# ASP Meeting History

1925 Kansas City MO	1957 Philadelphia PA *	1989 Vancouver, BC, Canada
1925 Philadelphia PA	1958 Bloomington IN †	1990 East Lansing MI
1927 Nashville TN	1959 University Park PA †	1991 Madison WI
1928 New York NY	1960 Los Angeles CA *	1992 Philadelphia PA
1928 Des Moines IA	1961 Lafayette IN †	1993 Atlanta GA *
1930 Cleveland OH *	1962 Washington DC ‡	1994 Ft. Collins CO
1931 New Orleans LA	1963 Chicago IL *	1995 Pittsburgh PA **
1932 Atlantic City NJ	1964 Boulder CO †	1996 Tucson AZ ††
1933 Boston MA	1965 Atlanta GA	1997 Nashville TN
1934 Pittsburgh PA	1966 San Juan PR *	1998 Kona HI
1935 St Louis MO	1967 Tucson AZ §	1999 Monterey CA ‡‡
1936 Atlantic City NJ	1968 Madison WI †	2000 San Juan PR ††
1937 Indianapolis IN	1969 Washington DC *	2001 Albuquerque NM
1938 Richmond VA	1970 Washington DC ¶	2002 Vancouver, BC, Canada ¶§§
1939 Columbus OH	1971 Los Angeles CA	2003 Halifax, NS, Canada
1940 Philadelphia PA	1972 Miami Beach FL *	2004 Philadelphia PA **
1941 Dallas TX	1973 Toronto, ON, Canada	2005 Mobile AL
1942 No meeting	1974 Kansas City MO	2006 Glasgow, Scotland ¶
1943 No meeting	1975 New Orleans LA *	2007 Merida, Yucatan, Mexico §§¶¶
1944 Cleveland OH	1976 San Antonio TX	2008 Arlington TX
1945 St. Louis MO	1977 Las Vegas NV	2009 Knoxville TN
1946 Boston MA	1978 Chicago IL *	2010 Colorado Springs, CO
1947 Chicago IL	1979 Minneapolis MN	2011 Anchorage, AK
1948 New Orleans LA *	1980 Berkeley CA	2012 Richmond, VA
1949 New York NY	1981 Montreal, QB, Canada	2013 Quebec City, Quebec, Canada
1950 Cleveland OH	1982 Toronto, ON, Canada ¶	
1951 Chicago IL *	1983 San Antonio TX *	
1952 Ithaca NY †	1984 Snowbird UT	
1953 Madison WI †	1985 Athens GA	
1954 Memphis TN *	1986 Denver CO *	
1955 Atlanta GA	1987 Lincoln NE #	
1956 Storrs CT †	1988 Winston-Salem NC	

\* With American Society of Tropical Medicine; since 1952, American Society of Tropical Medicine and Hygiene

† With American Institute of Biological Sciences

‡ With Helminthological Society of Washington

§ With American Microscopical Society

¶ With the International Congress of Parasitology; 1970 (ICOPA-II), 1982 (ICOPA-V), 2002 (ICOPA-X), 2006 (ICOPA-XI)

# With Wildlife Disease Association

\*\* With American Association of Veterinary Parasitologists

†† With Society of Protozoologists

‡‡ With Society of Nematologists

§§ With Sociedad Mexicana de Parasitología

¶¶ With Parasitology Section, Canadian Society of Zoologists