The 89th Annual Meeting of the American Society of Parasitologists

J.W. Marriott New Orleans

Program & Abstracts

Thanks to Everyone Who Helped Make this Meeting Possible …

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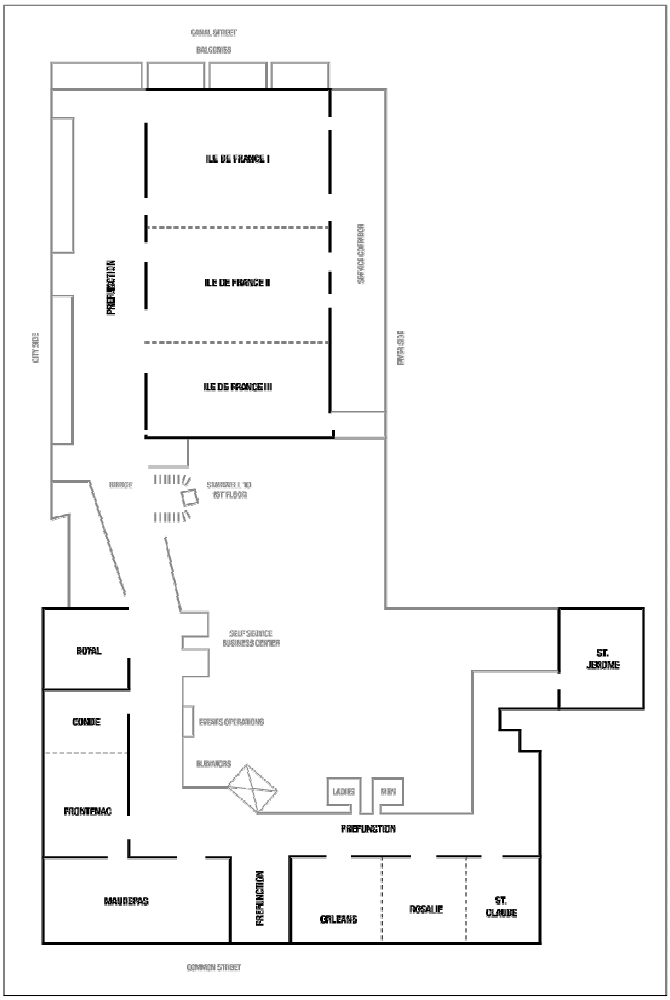
The AMERICAN SOCIETY of PARASITOLOGISTS
ESTABLISHED 1924

Welcome

We would like to welcome you to the 89th annual meeting of the American Society of Parasitologists (ASP). The ASP is a diverse group of over 1500 scientists from industry, government, and academia who are interested in the study and teaching of parasitology. Founded in 1924, ASP members have contributed not only to the development of parasitology as a discipline, but also to primary research in systematics, medicine, molecular biology, immunology, physiology, ecology, biochemistry, behavior, and more.

Herman Eure and Kelli Sapp, Scientific Program Officers

Floor Plan, JW Marriot New Orleans



Day/Times	Activity/Function	Room/Space
July 24 (Thursday)		
8:00 a.m.-Noon	ASP Council	Rex Room (8th floor)
1:00-3:00 p.m.	Ecology I	Ile de France III
1:00-4:30 p.m.	Life Cycles and Epidemiology	Conde
3:15-5:15 p.m.	Immunology, Biochemistry & Physio.	Ile de France III
3:15-5:30 p.m.	Centennial Symposium I	Maurepas
3:00-3:15 p.m.	Coffee Break	Ile de France Foyer
7:00-10:00 p.m.	Welcome Reception	Ile de France I & II
July 25 (Friday)		
8:30-11:00 a.m.	Centennial Symposium II	Maurepas
8:00-11:00 a.m.	Malaria Symposium	Conde
9:30-10 :00 a.m.	Coffee Break	Ile de France Foyer
11:00-Noon	Eminent Parasitologist Lecture	Ile de France II & III
Noon-1:00 p.m.	Editorial Board Luncheon	Rex Room (8th floor)
1:00-3:00 p.m.	Host Parasite Interactions I	Conde
1:00-3:00 p.m.	Ecology II	Maurepas
3:00-3:30 p.m.	Coffee Break	Ile de France Foyer
3:30-5:30 p.m.	ASP Students' Symposium	Maurepas
5:30-6:30 p.m.	ASP Student Social	Ile de France I
3:00-6:00 p.m.	Auction Set Up	Ile de France II & III
6:00-7:00 p.m.	Auction Preview	Ile de France II & III
7:00-9:00 p.m.	24th Annual ASP Student Auction	Ile de France II & III
July 26 (Saturday)		
8:00-Noon	Ecology III	Maurepas
8:00-11:45 a.m.	Taxonomy, Systematics, Phylogeny I	Conde
8:45-11:15 a.m.	Chemotherapy, Drug Resistance & Vector Biology	Ile de France III
9:45-10:15 a.m.	Coffee Break	Ile de France Foyer
Noon-1:00	U.S. National Parasite Collection	Conde
1:00-2:00 p.m.	ASP President's Address	Ile de France II & III
2:15-6:00 p.m.	Host Parasite Interactions II	Conde
2:30-5:00 p.m.	Genetics and Molecular Biology I	Maurepas
3:45-4:00 p.m.	Coffee Break	Ile de France Foyer
5:00-6:00 p.m.	Authors may set up posters	Ile de France Foyer
6:30-9:30 p.m.	Jazz & Dinner Cruise: Steamboat Natchez	
July 27 (Sunday)		
8:00-Noon	Ecology IV	Maurepas
8:00-11:45 a.m.	Taxonomy, Systematics, Phylogeny II	Conde
8:30-11:15 a.m.	Genetics and Molecular Biology II	Ile de France III
9:45-10:15 a.m.	Coffee Break	Ile de France Foyer
8:30-10:30 a.m.	Authors complete poster set up	Ile de France Foyer
12:00-1:30 p.m.	Poster Session, coffee, snacks	Ile de France Foyer
1:45-2:45 p.m.	H.B. Ward Lecture	Ile de France II & III
2:45-4:30 p.m.	ASP Awards and Business Meeting	Ile de France II & III

Thursday Morning, 2014-07-24

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

Presiding: **J. Janovy Jr.**, University of Nebraska Lincoln

Thursday Afternoon, 2014-07-24

1:00-3:00 pm Ecology I

Location: Ile de France III

Presiding: **B. Chobotar**, Andrews University

Time (Abstract No.)

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

1:00 (1)† **D.N. Morton**. USING THE LITERATURE TO DETERMINE THE PARASITIC COMPONENT OF BIODIVERSITY: A CASE STUDY IN THE KELP FOREST.

1:15 (2)† **K.E. Luth**, M.R. Zimmermann, G.W. Esch. DISTRIBUTION AND INFECTION PATTERNS OF *PROTEOCEPHALUS AMBLOPLITIS* AND OTHER CENTRARCHID PARASITES IN 30 STATES ACROSS THE UNITED STATES OF AMERICA.

1:30 (3)† **K.M. Miedema**, G.J. Sandland. THE INFLUENCE OF MACROPHYTES ON THE SPATIAL DISTRIBUTION OF AN INVASIVE SNAIL, *BITHYNIA TENTACULATA*, AND ITS PARASITES IN THE UPPER MISSISSIPPI RIVER.

1:45 (4)† **A.T. Claxton**, R. Heard, R. Overstreet. PARASITE ASSEMBLAGE VARIATION IN SAILFIN MOLLY (*POECILIA LATIPINNA*) AMONG HABITAT TYPES OF COASTAL MISSISSIPPI, U.S.A.

2:00 (5)† **A.M. Gleichsner**, K. Reinhart, D. Minchella. DOES INTRASPECIFIC COMPETITION AMONG PARASITES INFLUENCE HOST AND PARASITE LIFE HISTORY PARAMETERS?

2:15 (6)† **S. Weinstein**. SEARCHING FOR EVIDENCE OF CROWDING IN THE RACCOON ROUNDWORM.

2:30 (7)† **K. Gustafson**, J. Belden, M. Bolek. WHO GETS SICKER, THE HOSTS OR THE PARASITE? THE HERBICIDE ATRAZINE AFFECTS TREMATODE DEVELOPMENT AND TRANSMISSION THROUGH IMPACTS ON INTERMEDIATE HOSTS.

2:45 (8)† **E. Warburton**, M. Vonhof. ENVIRONMENTAL DISTANCE SIGNIFICANTLY IMPACTS PATTERNS OF HELMINTH COMMUNITY DISSIMILARITY IN *EPTESICUS FUSCUS* (MAMMALIA: CHIROPTERA).

3:00-3:15 pm **COFFEE BREAK**

1:00-4:30 pm Life Cycles and Epidemiology

Location: Conde

Presiding: **V. Tkach**, University of North Dakota
E. Villegas, US Environmental Protection Agency

Time (Abstract No.)

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

1:00 (9)† **L. Lu**, S. Zhang, E.T. Gendron, M. Mutuku, C. Dweni, G.M. Mkoji, E.S. Loker. STUDIES OF THE NEMATODE *DAUBAYLIA POTOMACA*, INCLUDING ITS INFECTIVITY TO SCHISTOSOME-TRANSMITTING SNAILS AND EFFECTS ON *SCHISTOSOMA MANSONI* IN *BIOMPHALARIA GLABRATA*.

1:15 (10) **F.O. Akinbo**, B.I. Osanyinbi, R. Omoregie, A.B. Ande. ASYMPTOMATIC MALARIA AMONG PREGNANT WOMEN IN EDO STATE, NIGERIA.

1:30 (11) **J. Dubey**, R. Calero-Bernal, S. Oliveira, S. Kumar, B. Rosenthal. *SARCOCYSTIS* SPP. INFECTIONS IN FERAL PIGS IN THE USA.

1:45 (12) **J. Dubey**, S. Kumar, S. Casey, A. Zajac, S. Wildeus, D. Lindsay, C. Su. GENETIC CHARACTERIZATION OF *TOXOPLASMA GONDII* FROM ALPACA (*VICUGNA PACOS*) AND SHEEP (*OVIS ARIES*) GRAZED ON PASTURE IN VIRGINIA.

2:00 (13) **C. Pierce**, R. Shannon, H.A. Stigge, B. Hanelt, M. Bolek. USING SNAIL "JERKY" TO UNTANGLE THE LIFE CYCLE STRATEGIES OF GORDIIDS (NEMATOMORPHA).

2:15 (14) **G.J. Langford**, J.A. Andrews, J.N. Childress, T.J. Iakovidis. LIFE CYCLE, HOST SPECIFICITY, AND SEASONAL OCCURRENCE OF *DERO HYLAE* (ANNELIDA: NAIDIDAE) A RARELY ENCOUNTERED PARASITE OF TREE FROGS.

2:30 (15) **M. Pickering**, J.N. Caira. GLOBAL COLLECTIONS OF PHYLLOBOTHRIIDEAN CESTODES OF SHARKS OFFER CLUES TO LIFE CYCLES, AND REVEAL LESS HOST SPECIFICITY THAN EXPECTED.

2:45 (16) **R. Fayer**. MICROSPORIDIA, *GIARDIA* AND *CRYPTOSPORIDIUM* IN WHITE-TAILED DEER.

3:00-3:15 pm **COFFEE BREAK**

3:15 (17)† **E.A. Zieman**, M. Schwarzinger, C.K. Nielsen, F.A. Jimenez. THE DISTRIBUTION OF *CYTAUXZOON FELIS* (APICOMPLEXA: THEILERIIDAE) IN BOBCATS AND TICKS IN ILLINOIS.

3:30 (18) **C.M. Adema**, S. Zhang, J. Schultz, J.J. Pena. DETECTION OF CERCARIAE FOR TRACKING TRANSMISSION OF SCHISTOSOMIASIS.

3:45 (19) **O.O. Ikpeze**, C.I. Eneanya, U.C. Ngenegbo. TICKS KNOWN TO TRANSMIT TICK-BORNE INFECTIOUS DISEASES TO HUMANS IDENTIFIED FROM A UNIVERSITY PREMISES IN NIGERIA.

4:00 (20) **U.C. Ngenegbo**, O.O. Ikpeze. GEOPHAGY AND ITS POTENTIAL RISK OF TRANSMISSION OF GEOHELMINTHS AMONG PRE-ADOLESCENTS IN NIGERIA.

4:15 (21) **U.C. Ngenegbo**, O.l. Onyali, O.O. Ikpeze. ASSOCIATION OF *PLASMODIUM* SPECIES WITH LOCATION, GENDER, AGE AND BLOOD PROFILES OF RESIDENTS SAMPLED IN NIGERIA.

3:15-5:15 pm Immunology, Biochemistry and Physiology

Location: Ile de France III

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

Time (Abstract No.)

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

3:15 (22) **M.K. Saifullah**, G. Ahmad, S.M. Abidi. A COMPARATIVE ACCOUNT OF BIOMOLECULES AND POLYPEPTIDES DURING THE DEVELOPMENTAL STAGES OF *GASTROTHYLAX CRUMENIFER* (TREMATODA: DIGENEA).

3:30 (23)† **K.A. Gallagher**, J. Caira, M. Cantino. DESCRIPTION OF TISSUE STRUCTURE AND FUNCTION OF AN ENIGMATIC TAPEWORM.

3:45 (24) **G. Ahmad**, A.A. Siddiqui, R.T. Damian, R.F. Wolf. VACCINE MADE AGAINST INTESTINAL SCHISTOSOMIASIS CAN PROTECT HAMSTERS AND BABOONS INFECTED WITH *SCHISTOSOMA HAEMATOBIUM*.

4:00 (25) **S. Arumugam**, B. Zhan, J. Wei, D. Ward, D. Abraham, S. Lustigman, T.R. Klei. TWO *BRUGIA MALAYI* RECOMBINANT PROTEINS (BM-103 AND BM-RAL-2) CONFER SIGNIFICANT PROTECTION AS A VACCINE AGAINST *B. MALAYI* INFECTION IN MONGOLIAN GERBILS.

4:15 (26)† **S. Roy**, D. Mukhopadhyay, S. Mukherjee, B. Saha, N.K. Das, M. Chatterjee. MODULATION OF IRON ACQUISITION PATHWAYS OF MONOCYTES-MACROPHAGES IN INDIAN POST KALA-AZAR DERMAL LEISHMANIASIS.

4:30 (27) **L. Mortimer**, F. Moreau, K. Chadee. GAL-LECTIN DEPENDENT CONTACT ACTIVATES THE INFLAMMASOME BY INVASIVE *ENTAMOEBA HISTOLYTICA*.

4:45 (28)† **M.A. HasbySaad**. *S. MANSONI* THERAPEUTIC EFFECT ON DSS-INDUCED COLITIS THROUGH TH1/TH2 PARADIGM AND FOXP3+ TREGS.

5:00 (29) **H.M. Elgawadi**. SEROLOGICAL AND MOLECULAR STUDIES ON *TOXOPLASMA GONDII* INFECTION IN SHEEP AND GOATS IN ISMAILIA PROVINCE.

3:15-5:30 pm *Centennial Symposium I: Celebrating One-hundred Years of the Journal of Parasitology*

Location: Maurepas

Presiding: **G.W. Esch**, Wake Forest University
J. Janovy Jr., University of Nebraska Lincoln

3:15 **J. Janovy Jr.** OPENING OF CENTENNIAL SYMPOSIUM.

3:30 (30) **R.E. Clopton**. THE SCIENTIFIC LESSONS OF INTELLECTUAL ELEGANCE IN PARASITIC PROTOZOOLOGY.

3:50 (31) **J. Dubey**. TRANSMISSION OF *TOXOPLASMA GONDII* - FROM LAND TO SEA- A PERSONAL PERSPECTIVE.

4:10 (32) **V.M. Vidal-Martinez**, M.L. Aguirre-Macedo. A CENTURY (1914-2014) OF STUDIES ON MARINE FISH PARASITES IN THE JOURNAL OF PARASITOLOGY.

4:30 (33) **J.N. Caira**, K. Jensen. THE EVOLUTION OF THE STUDY OF THE EVOLUTION OF ELASMOBRANCH CESTODES.

4:50 (34) **M. Bolek**, H.A. Stigge, K. Gustafson. THE IRON WHEEL OF PARASITE LIFE CYCLES: THEN AND NOW!

5:10 (35) **O.M. Amin**. BIOLOGY AND VARIABILITY OF ACANTHOCEPHALANS.

Thursday Evening, 2014-07-24

07:00 - 10:00 pm *WELCOME RECEPTION*

Location: Ile de France I & II

Friday Morning, 2014-07-25

8:30-11:00 pm *Centennial Symposium II: Celebrating One-hundred Years of the Journal of Parasitology*

Location: Maurepas

Presiding: **G.W. Esch**, Wake Forest University
J. Janovy Jr., University of Nebraska Lincoln

8:30 (36) **T.K. Anderson**, M.V. Sukhdeo. THE WORM'S EYE VIEW OF COMMUNITY ECOLOGY.

8:50 (37) **C.D. Criscione**. HISTORY OF MICROEVOLUTIONARY THOUGHT IN PARASITOLOGY: THE INTEGRATION OF MOLECULAR POPULATION GENETICS.

9:10 (38) **E.L. Jarroll**, T.A. Paget. *GIARDIA* METABOLISM AND REGULATION.

9:30-10:00 am **COFFEE BREAK**

10:00 (39) **R.E. Kuhn**. A HISTORY OF IMMUNOPARASITOLOGY IN THE U.S.

10:20 (40) **W.C. Campbell**. CHEMOTHERAPY OF HELMINTH INFECTIONS: HISTORICAL PERSPECTIVE.

10:40 (41) **G.W. Esch**, S. Desser, B. Nickol. CLOSING OF CENTENNIAL SYMPOSIUM.

8:00-11:00 pm *Malaria Symposium*

Location: Conde

Presiding: **S.L. Perkins**, American Museum of Natural History
R.N. Sehgal, San Francisco State University

Theme: RECENT ADVANCES IN THE STUDY OF MALARIAL PARASITES OF WILDLIFE

8:00 **S.L. Perkins**, Introduction.

8:10 (42) **O. Hellgren**. ADVANCES IN HAEMOSPORIDIAN GENOMICS.

8:30 (43) **R.E. Ricklefs**. SPECIES CONCEPTS, POPULATIONS AND GENERATION TIMES OF MALARIA PARASITES.

8:50 (44) **R. Fleischer**, L. Sackett, K. McClure, T. Callicrate. *PLASMODIUM RELICTUM*: A TALE OF HOST, PARASITE AND VECTOR INTERACTIONS.

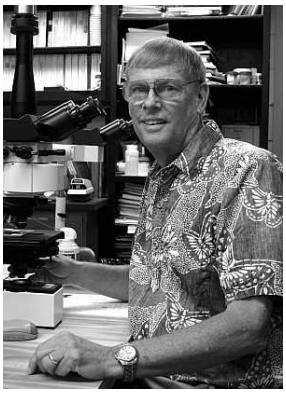
9:10 (45) **G. Valkiunas**. COMPLETING THE CYCLE: STUDIES OF SEXUAL STAGES OF HAEMOSPORIDIANS.

9:30-10:00 am **COFFEE BREAK**

10:00 (46) **R.N. Sehgal**. MANIFOLD HABITAT EFFECTS ON THE PREVALENCE AND DIVERSITY OF AVIAN HEMATOZOA.

10:20 (47) **S.L. Perkins**. THE TAXONOMY OF MALARIA PARASITES: IMPLEMENTING 21ST CENTURY TOOLS.

10:40 **R.N. Sehgal**, Closing Remarks and Questions.



Dr. Robin Overstreet
Eminent Parasitologist Award

11:00 am-NOON Eminent Parasitologist Lecture

Location: Ile de France II & III

Presiding: **L.A. Durden**, Georgia Southern University

11:00 Introduction of 2014 Eminent Parasitologist Lecturer
S.A. Bullard, Auburn University

11:10 (48) **R.M. Overstreet,** MARINE AND COASTAL ZOONOTIC HELMINTH INFECTIONS.

Friday Afternoon, 2014-07-25

12:00 – 1:00 pm Editorial Board Luncheon, Rex Room

1:00-3:00 pm Host Parasite Interactions I

Location: Conde

Presiding: **Q. Han**, Hainan University

Time (Abstract No.)

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

1:00 (49) **N. du Toit**, B. Jansen van Vuuren, S. Matthee, C.A. Matthee. BIOGEOGRAPHY AND HOST-RELATED FACTORS LIMIT GENEALOGICAL CONGRUENCE AMONG SPECIFIC ECTOPARASITIC LICE AND THEIR RODENT HOSTS.

1:15 (50)† **P.M. Ravindran**, B. Hanelt. CHANGES IN BACTERIAL RESISTANCE AND LONGEVITY OF CRICKETS INFECTED WITH GORDIAN WORMS (NEMATOMORPHA).

1:30 (51)† **S.K. Buddenborg**, M. Misra, S. Zhang, G. Mkoji, E.S. Loker. RNA-SEQ ANALYSIS OF FIELD-DERIVED *BIOMPHALARIA PFEIFFERI* INFECTED WITH *SCHISTOSOMA MANSONI* FROM WESTERN KENYA.

1:45 (52) **S. Leclaire**, C. Faulkner. ENDOPARASITIC INFECTION IN A WILD POPULATION OF MEERKATS (*SURICATA SURICATTA*).

2:00 (53)† **J.V. Hopper**, N. Mills, W. Huang. INTERACTIONS BETWEEN A MICROSPORIDIAN PARASITE, *NOSEMA FUMIFERANAE*-LIKE ISOLATE, AND ITS UNEXPECTED HOST, THE INVASIVE LIGHT BROWN APPLE MOTH.

2:15 (54) **N. Lodh**, D.M. Rizzo, B.L. Kerans, S. McGinnis, N. Fytilis, L. Stevens. ASSESSMENT OF SPATIAL, COMMUNITY AND GENETIC STRUCTURE OF STREAM DWELLING TUBIFICID WORMS IN MONTANA, USA.

2:30 (55) **J.L. Sanders**, A.G. Jaramillo, K.D. Lafferty, M.L. Kent. TWO NOVEL MYXOZOANS FROM THE URINARY TRACT OF TOPSMELT, *ATHERINOPS AFFINIS*.

2:45 (56)† **C. Williams**. FEAST AND FAMINE: THE NUTRITIONAL ECOLOGY OF A HAIRWORM (*PARAGORDIUS VARIUS*) AND ITS CRICKET HOST (*ACHETA DOMESTICUS*).

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

1:00-3:00 pm Ecology II

Location: Maurepas

Presiding: **R.N. Sehgal**, San Francisco State University

Time (Abstract No.)

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

1:00 (57)† **H.A. Stigge**, M.G. Bolek. EVALUATING THE ROLE OF PARATENIC HOSTS IN THE EVOLUTION OF COMPLEX LIFE CYCLES: ECOLOGICAL BRIDGES OR EVOLUTIONARY STEPPING STONES?

1:15 (58)† **K. Gustafson**, B. Kensinger, B. Luttbeg, M. Bolek. IS YOUR SNAIL HOST WHO YOU THINK IT IS? ENVIRONMENTAL EFFECTS ON SNAIL SHELL SHAPE AND IMPLICATIONS FOR INTERMEDIATE HOST IDENTIFICATION.

1:30 (59)† **L.A. Gilbert**, N.J. Negovetich. HELMINTHS OF *GAMBUSIA AFFINIS* (CYPRINODONTIFORMES: POECILIIDAE) IN WEST TEXAS.

1:45 (60)† **M.R. Zimmermann**, K.E. Luth, G.W. Esch. THE DILUTION EFFECT IN *ECHINOSTOMA* SPP.: EXAMPLES FROM FIELD COLLECTED DATA.

2:00 (61)† **E.F. Bauer**, C.M. Whipps. BASS PARASITES OF ONEIDA LAKE, EIGHTY YEARS LATER.

2:15 (62)† **V.M. Frankel**, M.E. Torchin. HOST SPECIFICITY OF AN INTRODUCED PARASITE TO A NON-NATIVE FISH IN THE PANAMA CANAL.

2:30 (63)† **O.N. Choi**, N. Nerwin, K. Sgouros, E. Vasquez, J. Morrissey, J. Kawaguchi, S. Orlofske. GASTROINTESTINAL HELMINTH COINFECTION PATTERNS IN EUROPEAN STARLINGS (*STURNUS VULGARIS*).

2:45 (64)† **H. Dutton**, M. Barger. DOES THE BIG THICKET NATIONAL PRESERVE PROTECT AQUATIC COMMUNITIES? A TEST CASE USING PARASITES AS PROXIES FOR BIODIVERSITY.

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

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

Location: Maurepas

Presiding: **H. Robinson-Stigge**, Oklahoma State University

Time (Abstract No.)

3:30 **H. Robinson-Stigge**, Introduction.

3:40 (65) **B. Hanelt**. A REPORT FROM THE FRONT LINES OF AN ACADEMIC JOB SEARCH: CURRENT TRENDS, WHAT THE FUTURE MAY HOLD, AND WORKING ON A VIABLE BACKUP PLAN.

4:00 (66) **S. Little**. THE WONDERFUL WORLD OF TICKS – RESEARCH, MENTORING, AND OUTREACH.

4:20 (67) **M. Siddall**. PUBLISH OR PERISH, GRANT OR GROVEL. DARE THEM ALL TO TAKE YOU SERIOUSLY.

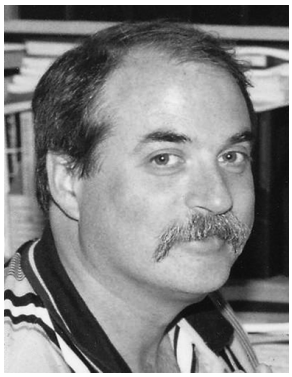
4:40 (68) **D.W. Duszynski**. THE FINAL FRONTIER: MENTORING AND INVOLVING STUDENTS.

5:00 **H. Robinson-Stigge**, Questions and Closing Remarks.

5:30-6:30 pm *The Steve Upton Party for ASP Students*
(sponsored by Sierra Upton)

Location: Ile de France I

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

Friday Evening, 2014-07-25

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

7:00-9:00 pm **24th ANNUAL ASP STUDENT AUCTION**

Location: Ile de France II & III

Saturday Morning, 2014-07-26

8:00-NOON Ecology III

Location: Maurepas

Presiding: **K. Lafferty**, University of California, Santa Barbara; USGS
M. Sukhdeo, Rutgers University

Time (Abstract No.)

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

8:00 (69)† **J.T. Mendez**, S.B. Weinstein. RACCOON LATRINES: HUMAN DISEASE RISK IN SANTA BARBARA COUNTY.

8:15 (70)† **A.E. Garcia-Vedrenne**, A. Quintana, A.M. Kuris, R.F. Hechinger. SOCIALITY IN TREMATODE FLATWORMS – HOW COMMON IS IT?

8:30 (71)† **E.T. Gendron**, E.S. Loker, V. Tkach, N.E. Davis, S.V. Brant. THE ROLE OF HOST MOVEMENTS AND ECOLOGY ON EVOLUTION AND DISTRIBUTION OF *TRICHOBILHARZIA* SPECIES.

8:45 (72)† **R.L. Grunberg**, M.V. Sukhdeo. STARVED AMPHIPODS (*GAMMARUS FASCIATUS*) LIVE LONGER WHEN INFECTED WITH LARVAL ACANTHOCEPHALANS.

9:00 (73)† **A.G. Howard**, M. Lipman, A. Patel, N. de la Sancha, P. Pérez-Estigarribia, S. Boyle, L.E. Luque. FOREST FRAGMENTATION'S EFFECTS ON HEMOPARASITES IN SMALL MAMMALIAN POPULATIONS FROM PARAGUAY.

9:15 (74) **C.D. Criscione**, J.T. Detwiler, I.C. Caballero. ROLE OF PARASITE TRANSMISSION IN PROMOTING INBREEDING. I. IMPACT ON THE PRIMARY MATING SYSTEM.

9:30 (75) **C.D. Criscione**, J.T. Detwiler. ROLE OF PARASITE TRANSMISSION IN PROMOTING INBREEDING. II. IMPACT ON SIB-MATING.

9:45-10:15 am **COFFEE BREAK**

10:15 (76) **L.T. Luong**, D.A. Grear, E.G. Chapman, P.J. Hudson. TRANSMISSION OF TROPHICALLY EMBEDDED PARASITES ARE LINKED TO HOST FORAGING ECOLOGY.

10:30 (77) **J.P. McLaughlin**, A. Jaramillo, C. Wood, J. Shaw, V. Vidal Martinez, L. Aguirre-Macedo, A. James, S. Weinstein, J. Caselle, R. Hechinger, A. Kuris, K. Lafferty. A NOVEL FOOD WEB, INCLUDING PARASITES FOR THE INTERTIDAL SAND FLATS OF PALMYRA ATOLL, CENTRAL PACIFIC.

10:45 (78) **N. Chodkowski**. THE NATURAL HISTORY OF THE PARASITIC TREMATODE *PLEUROGONIUS MALACLEMYS* (TREMATODA: DIGENEA).

11:00 (79) **C. Lagrue**, R. Poulin. HOST POPULATION STABILITY AS A DRIVER OF PARASITE ABUNDANCE.

11:15 (80) **J. Koprivnikar**, L. Penalva. THREATS OF PREDATION AND PARASITISM ON TADPOLE FORAGING BEHAVIOR: WHICH ENEMY TO AVOID?

11:30 (81) **A. Bruno**, A.M. Fedynich, D. Rollins. SURVEY AND ASSESSMENT OF PARASITIC INFECTIONS IN NORTHERN BOBWHITES FROM THE ROLLING PLAINS ECOREGION, TEXAS.

11:45 (82) **K.K. Herrmann**, R. Poulin, D.B. Keeney, I. Blasco-Costa. GENETIC STRUCTURE IN A PROGENETIC TREMATODE: SIGNS OF CRYPTIC SPECIES WITH CONTRASTING REPRODUCTIVE STRATEGIES.

8:00-11:45 pm Taxonomy, Systematics and Phylogeny I

Location: Conde

Presiding: **O. Amin**, Parasitology Center, Inc.
F.A. Jimenez-Ruiz, Southern Illinois University

Time (Abstract No.)

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

8:00 (83)† **C.M. Pinto**, S.L. Perkins. EVOLUTION OF MAMMAL-TRYPANOSOME ASSOCIATIONS AND THE ORIGINS OF CHAGAS DISEASE.

8:15 (84)† **M.E. Ingle**, S.G. Dunbar, K.M. Kohl, C.T. Griffin. *BAYLISASCARIS PROCYONIS*: DOES PARASITE PREVALENCE ACCOUNT FOR SOME PHYLOGENETIC DIFFERENCES BETWEEN SUBPOPULATIONS OF RACCOONS (*PROCYON LOTOR*)?

8:30 (85)† **B. Stenger**, M. Clark, M. Kvac, N. Dyer, J. Schultz, C. Giddings, J. McEvoy. HIGHLY DIVERGENT SMALL SUBUNIT RIBOSOMAL RNA GENES IN A *CRYPTOSPORIDIUM* GENOTYPE FROM EASTERN CHIPMUNKS (*TAMIAS STRIATUS*).

8:45 (86)† **M.J. Andres**, R.M. Overstreet. PHYLOGENETIC AFFINITIES OF TWO OPECOELID (TREMATODA) GENERA CONTAINING MEMBERS WITH FILMENTED EGGS.

9:00 (87)† **J. Foox**, M. Siddall. PHYLOGENOMICS OF MYXOZOA.

9:15 (88)† **M.R. Womble**, R. Orélis-Ribeiro, S.A. Bullard. THE LURE OF PROTEROMETRA: TAXONOMIC DIVERSITY, LIFE CYCLES, AND HOST-PARASITE RELATIONSHIPS WITHIN AN INTRIGUING GENUS OF FRESHWATER TREMATODES.

9:30 (89) **L.E. Camp**, S.A. Nadler. PHYLOGENETIC ANALYSIS OF *BAYLISASCARIS*.

9:45-10:15 am **COFFEE BREAK**

10:15 (90) **A. Sakla**, J.T. Detwiler, I.C. Caballero, C.D. Criscione. IDENTIFICATION AND MORPHOLOGICAL VARIATION OF AN INVASIVE PARASITE IN INTRODUCED AND NATIVE LIZARDS.

10:30 (91)† **S. Rios**, S.V. Brant, V.V. Tkach. DIVERSITY AND DISTRIBUTION OF AVIAN SCHISTOSOMATIDS IN NORTH DAKOTA.

10:45 (92)† **J.P. Bernot**, J.N. Caira, M. Pickering. *CALLIOBOTHRIUM* (CESTODA: TETRAPHYLLIDEA) IN *MUSTELUS* (CARCHARHINIFORMES: TRIAKIDAE) OF THE ATLANTIC OCEAN.

11:00 (93)† **R. Orélis Ribeiro**, M.R. Womble, C.R. Arias, K.M. Halanych, T.H. Cribb, S.A. Bullard. DIVERSITY AND ANCESTRY OF FLATWORMS (DIGENEA: SCHISTOSOMATOIDEA) INFECTING BLOOD OF CRANIATES.

11:15 (94)† **V.M. Bueno**, J. Caira. SPECIATION IN A GONDWANIAN HOST-PARASITE SYSTEM.

11:30 (95)† **E.L. Kasl**, C.T. McAllister, H.W. Robinson, M.B. Connior, W.F. Font, C.D. Criscione. THE CURIOUS CASE OF *ALLOGLOSSIDIUM PROGENETICUM* (DIGENEA: MACRODEROIDIDAE): GEOGRAPHIC VARIATION IN PRECOCIOUS DEVELOPMENT WITHOUT NEUTRAL GENETIC DIVERGENCE.

8:45-11:15 pm *Chemotherapy, Drug Resistance and Vector Biology*

Location: Ile de France III

Presiding: **J. Hillyer**, Vanderbilt University
P.T. LoVerde, University of Texas Health Sciences Center San Antonio

Time (Abstract No.)

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

8:45 (96) **Y. Alemán Crespo**, M.R. Jacob, M.W. Lomas, J.A. Fernández-Robledo. IDENTIFICATION OF INHIBITORS OF *PERKINSUS MARINUS* PROLIFERATION USING AN ATP-BASED BIOLUMINESCENCE ASSAY.

9:00 (97) **P.A. Audu**, A.I. Muhammad. RAPID EPIDEMIOLOGICAL ASSESSMENT (R.E.A.) OF ONCHOCERCIASIS AT THE COMMUNITY LEVEL IN KUDARU, KADUNA STATE, NIGERIA.

9:15 (98) S.R. Stahl, F. Chevalier, A.B. Taylor, X. Cao, S.P. Halloway, P. Hart, T.J. Anderson, **P.T. LoVerde**. WHY DOES OXAMNIQUINE KILL *SCHISTOSOMA MANSONI* BUT NOT *S. HAEMATOBIUM* OR *S. JAPONICUM*?

9:30 (99) **M. Eraifej**, S. Saeed, F. Akinbo, J. Porter-Kelley, G. Mayer. INTERACTIONS BETWEEN ANTIMALARIAL AND ANTIRETROVIRAL DRUGS IN *PLASMODIUM FALCIPARUM*.

9:45-10:15 am **COFFEE BREAK**

10:15 (100) **J. Rodriguez**, A. Castellanos, L. Auckland, J. Light, S. Hamer. TICK-BORNE PATHOGENS IN A RODENT COMMUNITY IN EAST-CENTRAL TEXAS.

10:30 (101)† **S.E. Greiman**, V.V. Tkach, J.A. Vaughan, E. Pulis, T.J. Fayton, S. Curran, A.I. Khalil. LARGE SCALE SCREENING OF DIGENEANS FOR *NEORICKETTSIA* ENDOSYMBIONTS USING REAL-TIME PCR EXPANDS KNOWLEDGE OF DIVERSITY, GEOGRAPHY AND HOST ASSOCIATIONS OF *NEORICKETTSIA*.

10:45 (102) **J.F. Hillyer**, S. Boppana. HEMOLYMPH PROPULSION THROUGH THE MOSQUITO ANTENNAE.

11:00 (103)† **J.S. Carlson**, E. Walther, R. Trout-Fryxell, S. Staley, L.A. Tell, R. Sehgal, A.J. Cornel. HETEROGENEITIES IN THE TRANSMISSION OF AVIAN MALARIA PARASITES: IMPLICATIONS FOR THE ROLE OF MOSQUITOES AS SUPERSPREADERS.

Saturday Afternoon, 2014-07-26

11:00-12:00 *US National Parasite Collection*

Location: Conde

Presiding: **J. Caira**, University of Connecticut
E.S. Loker, University of New Mexico
A.J. Phillips, The Smithsonian Institution

11:00 Update: USNPC relocation to the Smithsonian Institution

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

Location: Ile de France II & III

Presiding: **M. Bolek**, Oklahoma State University

1:00 Introduction of **J. Janovy Jr**.
M. Bolek, Oklahoma State University

Dr. John Janovy, Jr.
ASP President

1:10 (104) **J. Janovy Jr**. WHY AMERICAN HIGHER EDUCATION NEEDS PARASITOLOGISTS.

2:15-6:00 pm Host Parasite Interactions II

Location: Conde

Presiding: **R. Kuhn**, Wake Forest University
U. Ngenegbo, Nnamdi Azikiwe University

Time (Abstract No.)

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

2:15 (105) C.A. Taylor, **A.W. Shostak**. FLOUR BEETLE BEHAVIOR SUPPORTS A TRADE-OFF BETWEEN FOOD, SHELTER AND THE RISK OF PARASITISM.

2:30 (106) **X. Li**, Q. Liu, R. Liu, E. Lewis. THE ACTIVITY CHANGES OF FOUR DETOXIFYING ENZYMES IN *TENEBRIO MOLITOR* LARVAE INFECTED BY ENTOMOPATHOGENIC NEMATODE *HETERORHABDITIS BEICHERRIANA*.

2:45 (107)† **B.A. Brinton**, M.C. Curran. THE EFFECT OF TEMPERATURE ON SYNCHRONIZATION BETWEEN REPRODUCTION OF THE BOPYRID ISOPOD PARASITE *PROBOPYRUS PANDALICOLA* AND MOLTING OF ITS GRASS SHRIMP HOST.

3:00 (108) **B. Jean-Christophe**. GENETIC EVALUATION OF GASTROINTESTINAL NEMATODE RESISTANCE IN GOATS: IMPACT OF THE POST-WEANING PARASITISM LEVEL.

3:15 (109) **D. Deheyn**. SHEDDING NEW LIGHT ON HOST-PARASITE INTERACTIONS WHEN USING ORGANISMS WITH THE ABILITY TO PRODUCE BIOLUMINESCENCE.

3:30 (110)† **M.A. Gordy**. SCREENING SNAIL-TREMATODE RELATIONSHIPS FOR COMMON COMPATIBILITY DETERMINANTS.

3:45 – 4:00 pm **COFFEE BREAK**

4:00 (111) **A.C. Wunderlich**, R.J. Silva, E.O. Zica, M.F. Rabelo, T.E. Parente, V.M. Vidal-Martínez. CAN PARASITES AND DIFFERENCES IN REPRODUCTIVE STATUS INFLUENCE EROD ACTIVITY IN FRESHWATER FISH?

4:15 (112)† **K. O'Dwyer**, R. Poulin, D. Thieltges. DISENTANGLING PHYLOGENETIC CONSTRAINTS FROM ECOLOGICAL DRIVERS OF TREMATODE RICHNESS IN GASTROPOD HOSTS.

4:30 (113)† **L.E. Reid**, S.Y. Sisneros, J. Janovy Jr. GREGARINE PARASITES OF TENERAL AND LARVAL DAMSELFLIES, *ISCHNURA VERTICALIS* (ODONATA: ZYGOPTERA): A COMPARISON.

4:45 (114) **A.J. Phillips**, M. Tessler. ENDOPARASITIC LEECHES FROM FROGS (ANURA: HYLIDAE, RANIDAE) IN PAPUA NEW GUINEA.

5:00 (115) **B. Jean-Christophe**. EFFECT OF ENERGY AND PROTEIN SUPPLEMENTATION IN LAMBS AND KIDS ON THE RESPONSE TO *HAEMONCHUS CONTORTUS*.

5:15 (116) **M. Kent**, T.S. Sharpton, C.B. Schreck. PROGRESSION OF INFECTION OF *CERATOMYXA SHASTA* AND *PARVICAPSULA MINIBICORNIS* IN ADULT CHINOOK SALMON.

5:30 (117)† **M.R. Laidemitt**, M.W. Mutuku, G.M. Mkoji, E.S. Loker. AMPHISTOMES AS NATURAL ENEMIES OF LARVAL SCHISTOSOMES IN KENYA.

5:45 (118) **J.S. Mantilla**, N.E. Matta, A.Y. Sánchez, L.I. Moncada. PATHOLOGY OF *PLASMODIUM (NOVYELLA) UNALIS* AND *PLASMODIUM (HAEMAMOEBA) LUTZI* ON NATURAL AND EXPERIMENTALLY INFECTED BIRDS.

2:30-5:00 pm Genetics and Molecular Biology I

Location: Maurepas

Presiding: **A. Iqbal**, Health Canada, Bureau of Microbial Hazards
T. Yoshino, University of Wisconsin Madison

Time (Abstract No.)

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

2:30 (119) **C. Nessner**. POPULATION GENETIC ANALYSES OF THE CHEWING LOUSE *GEOMYDOECUS EWINGI*.

2:45 (120) **N. Lodh**, J.M. Naples, K.M. Bosompem, J. Quartey, C.J. Shiff. POINT OF CARE DIAGNOSIS FOR SCHISTOSOMIASIS: MULTI PARASITE DNA DETECTION IN SINGLE URINE SAMPLE.

3:00 (121)† **J.J. Peña**, C.M. Adema. HEMOCYANIN-LIKE SEQUENCES IN *BIOMPHALARIA GLABRATA*, SNAIL INTERMEDIATE HOST FOR *SCHISTOSOMA MANSONI*.

3:15 (122)† **B.K. Wijayawardena**, A. DeWoody, D. Minchella. TRANSPOSABLE ELEMENT DYNAMICS IN *SCHISTOSOMA MANSONI* STRAINS: NEW WORLD VS. OLD WORLD.

3:30 (123) **J.M. Porter-Kelley**, L. Dixon, O. Seshie, D.G. Mayer, K. Abernathy, M. Eraifej. MICRORNAS IN *LEISHMANIA BRAZILIENSIS* USING BIOINFORMATICS.

3:45 – 4:00 pm **COFFEE BREAK**

4:00 (124) **A. Da'dara**, R. Bhardwaj, Y.M. Ali, P. Skelly. SCHISTOSOME TEGUMENTAL NUCLEOTIDE METABOLIZING ECTO-ENZYMES.

4:15 (125)† **E. Ideozu**, G. Hide. DETECTION OF TRYPANOSOMES IN BRITISH BADGERS.

4:30 (126)† **M. Jansing**. EFFECTS OF HYDROGEN PEROXIDE AND UV IRRADIATION ON THE VIABILITY OF *ASCARIS SUUM*.

4:45 (127) **Y. Guo**, Y. Feng, T. Kevin, M. Frace, Y. Ortega, M.A. Arrowood, D.M. Roellig, S. Sammons, L. Xiao. DEVELOPMENT OF A MULTILOCUS SEQUENCE TYPING TOOL FOR CHARACTERIZING *CYCLOSPORA CAYETANENSIS*.

5:00-6:00 pm Poster Display Boards delivered

Location: Ile de France Foyer

Authors may set up posters during this time.

Saturday Evening, 2014-07-26

6:30 – 9:30 pm *Jazz & Dinner Cruise: Steamboat Natchez*

6:30, Boarding
7:00, Departure from dock

Sunday Morning, 2014-07-27

8:00-NOON *Ecology IV*

Location: Maurepas

Presiding: **A. Shostak**, University of Alberta
M. Zimmermann, Wake Forest University

Time (Abstract No.)

8:00 (128) **A.A. Castellanos**, S.A. Hamer, L. Auckland, G.L. Hamer, M.E. Morrow, P.D. Teel, J.E. Light. INVASIVE ANTS AS DRIVERS OF TICK-BORNE DISEASE SYSTEMS.

8:15 (129) **C.B. Hubbell**, N.J. Negovetich. FISH ECTOPARASITES OF THE BURRO-BURRO AND ESSEQUIBO RIVERS IN GUYANA, SOUTH AMERICA.

8:30 (130) **L.P. Renoux**, C.A. Cook, N.J. Smit, A.J. Davies, P.C. Sikkel. BLOOD PARASITES OF REEF ASSOCIATED FISHES OF THE EASTERN CARIBBEAN.

8:45 (131) **I.C. Caballero**, A.J. Sakla, J.T. Detwiler, M. Le Gall, S.T. Behmer, C.D. Criscione. IMPACT OF NATURAL PENTASTOME INFECTIONS ON THE RESPIRATION OF STRESSED MEDITERRANEAN GECKOS.

9:00 (132) **S.A. Zemmer**, J.T. Detwiler, J.G. Da Silva Neto, E.F. Benfield, L.K. Belden. TREMATODE COMMUNITY DIVERSITY IN APPALACHIAN STREAM SNAILS.

9:15 (133) **V. Brashear**, T. Cook, A. Smith-Herron. EUGREGARINE INFECTION PATTERNS OF DAMSELFLY NAIADS IN THE SOUTHWESTERN PINEY WOODS, TEXAS.

9:30 (134) **K. Simmons**, D. Kerstetter, C. Blanar. PARASITES OF THE LIONFISH COMPLEX (*PTERIOS VOLITANS* AND *P. MILES*) IN THE WESTERN NORTH ATLANTIC, GULF OF MEXICO, AND CARIBBEAN SEA: EVIDENCE OF THE ENEMY RELEASE HYPOTHESIS?

9:45-10:15 am **COFFEE BREAK**

10:15 (135) **T. Sparkes**. ACANTHOCEPHALAN-RELATED MODIFICATION OF HOST MATING BEHAVIOR: FIELD- AND LAB-BASED EVIDENCE OF CONTEXT-DEPENDENT EFFECTS.

10:30 (136) M. Drake, U. Zieger, R. Pinckney, M. Sterner, **R.A. Cole**. SURVEY OF HELMINTHS, ECTOPARASITES AND CHYTRID FUNGUS OF AN INTRODUCED POPULATION OF CANE TOADS, *RHINELLA MARINA* (ANURA: BUFONIDAE), FROM GRENADA.

10:45 (137) **R.E. Paseka**, M.V. Sukhdeo. PARASITE BIOMASS IN STREAMS OF THE NEW JERSEY PINE BARRENS.

11:00 (138) **D. Benesh**. EXPERIMENTAL EVOLUTION OF LARVAL PERFORMANCE IN A TAPEWORM.

11:15 (139) **M.L. Aguirre-Macedo**, A.L. May-Tec, V.M. Vidal-Martínez. LONG-TERM INFECTION DYNAMICS OF *OLIGOGONOTYLUS MANTERI* IN ITS INTERMEDIATE AND DEFINITIVE HOSTS FROM CELESTUN, YUCATÁN, MÉXICO.

11:30 (140) **K.L. Weinersmith**, C. Warinner, V. Tan, D.J. Harris, A. Mora, A.M. Kuris, K.D. Lafferty, R.F. Hechinger. A LACK OF CROWDING? DENSITY DOES NOT NEGATIVELY AFFECT PARASITE BODY SIZE FOR TWO TROPHICALLY TRANSMITTED TREMATODES OF CALIFORNIA KILLIFISH, *FUNDULUS PARVIPINNIS*.

11:45 (141) **F. Farhang**, K. Lafferty, G. Cardenas, D. Deheyn. LEVELS OF METALS IN TWO LIFE STAGES OF THE TREMATODE *EUHAPLORCHIS CALIFORNIENSIS* AND IN THEIR RESPECTIVE HOSTS, NAMELY THE CALIFORNIA HORN SNAIL AND THE KILLIFISH.

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

Location: Conde

Presiding: **J. Bernot**, University of Connecticut
S. Seville, University of Wyoming-Casper

Time (Abstract No.)

8:00 (142) **M.L. Campbell**, G.H. Jarrell, S.V. Brant, J.A. Cook, E.P. Hoberg, E.S. Loker. A LEGACY FOR THE FUTURE: THE RAUSCH HELMINTHOLOGICAL COLLECTION.

8:15 (143) **S. Brant**, E. Gendron, N. Davis, E.S. Loker. HOW DID WE GET SO MANY SPECIES OF *TRICHOBILHARZIA*, A GLOBALLY DISTRIBUTED SCHISTOSOME?

8:30 (144) **T. Ruhnke**, J. Caira, A. Cox. RHINEBOTHRIIDEA NO LONGER FAMILYLESS: A MOLECULAR PHYLOGENETIC INVESTIGATION OF THE CESTODE ORDER WITH ERECTION OF TWO NEW FAMILIES AND DESCRIPTION OF EIGHT NEW SPECIES.

8:45 (145) **A. Haslach**, F. Reyda, T. Ruhnke. PROBING NEWLY DISCOVERED SPECIES DIVERSITY WITHIN THE RHINEBOTHRIIDEA: A MOLECULAR SYSTEMATIC SURVEY OF KNOWN AND UNDESCRIBED SPECIES OF A NEW RHINEBOTHRIIDEAN GENUS.

9:00 (146) **B. Hanelt**, M.G. Bolek, A. Schmidt-Rhaesa. CROWDSOURCING HELPS REVEAL CRYPTIC SPECIATION OF A NEW WORLD HAIRWORM *GORDIUS ROBUSTUS* USING MOLECULAR DATA.

9:15 (147) **F. Reyda**, M. Rodrigues, F. Marques. *RHINEBOTHRIUM* SPECIES (CESTODA: RHINEBOTHRIIDEA) IN NEOTROPICAL FRESHWATER STINGRAYS: INSIGHTS FROM RECENT COLLECTIONS IN VENEZUELA.

9:30 (148) **D. Sinnott**, R. Carreno, H. Herrera. DISTRIBUTION OF THELASTOMATOID NEMATODES (OXYURIDA: THELASTOMATOIDEA) IN ENDEMIC AND INTRODUCED COCKROACHES FROM THE GALÁPAGOS ISLANDS, ECUADOR.

9:45-10:15 am **COFFEE BREAK**

10:15 (149) **J.E. Light**. PHYLOGENETIC RELATIONSHIPS AND HOST-ASSOCIATIONS OF LICE (INSECTA: PHTHIRAPTERA).

10:30 (150) **K. Herzog**, R. Russell, F. Reyda. AN EXAMINATION OF HOST SPECIFICITY WITHIN A NEW GENUS OF CESTODE OF ELASMOBRANCHS (CESTODA: RHINEBOTHRIIDEA).

10:45 (151) **E.R. Hannon**, D.M. Calhoun, J.M. Kinsella, P.T. Johnson. PARASITE DIVERSITY FROM AVIAN HOSTS IN NORTHERN CALIFORNIA.

11:00 (152) **F.A. Jimenez**. RELEVANCE OF HOST-SWITCHING IN THE SUCCESS OF WORMS IN SIMPSON'S SPLENDID ISOLATION.

11:15 (153) **H. Le**, T. Nguyen, D. Roan, V. Tien, N. Khue, N. De, T. Agatsuma, D. McManus, D. Blair. UPDATED PHYLOGENETIC SCHEME BASED ON THE COMPLETE MITOCHONDRIAL PROTEIN-CODING SEQUENCE FOR COMMON PARASITIC TREMATODES.

11:30 (154) **K.F. Patitucci**, J. Bates, V.V. Tkach. SURVEY OF SOUTHERN AMAZONIAN BIRD HELMINTHS.

8:30-11:15 am Genetics and Molecular Biology II

Location: Ile de France III

Presiding: **G. Mayer**, Manhattan College
J.M. Porter-Kelley, Winston-Salem State University

Time (Abstract No.)

8:30 (155) **V. Ricardo da Silva Fiuza**, F. Carlos Rodrigues de Oliveira, M. Santin, R. Fayer. IDENTIFICATION OF 17 NOVEL *ENTEROCYTOZOON BIENEUSI* GENOTYPES IN PIGS.

8:45 (156) **S. Han**, M. Gardner, V. Gelmedin, K. Goggin, J. Hawdon. CLONING AND CHARACTERIZATION OF *ANCYLOSTOMA CANINUM* HELIX-LOOP-HELIX 13 TRANSCRIPTION FACTOR, A NOVEL TARGET OF DAF-16.

9:00 (157) **R.B. Gagne**, C.G. Sorehn, J.D. Hogan, R.P. Walter, M.J. Blum. RECONSTRUCTING POPULATION STRUCTURE OF A NON-NATIVE PARASITE AND A NATIVE STREAM FISH HOST IN HAWAII.

9:15 (158) **C. Lagrue**, L. Bollache. ARE CRYPTIC SPECIES ALSO CRYPTIC TO PARASITES?

9:30 (159) **A.F. Oceguera-Figureroa**, A. Manzano-Marín, A. Latorre, A. Moya. GENOMIC COMPOSITION OF A BACTERIAL ENDOSYMBIONT OF THE MEXICAN MEDICINAL LEECH *HAEMENTERIA OFFICINALIS* (CLITELLATA: GLOSSIPHONIIDAE).

9:45-10:15 am **COFFEE BREAK**

10:15 (160) **A. Iqbal**, K. Stevens, L. Measures, B. Dixon. MOLECULAR TYPING OF *TOXOPLASMA GONDII* IN BELUGA (*DELPHINAPTERUS LEUCAS*) FROM THE ST. LAWRENCE ESTUARY, CANADA.

10:30 (161) **J. Kvicerova**, A. Macova, N. Dvorakova, P. Siroky, V. Hypsa. DIFFERENT PATTERNS OF GENETIC VARIABILITY IN TWO APICOMPLEXAN GROUPS.

10:45 (162) **E. Villegas**. USING BIVALVES AS BIOSENTINELS TO DETECT *CRYPTOSPORIDIUM* SPP. AND *TOXOPLASMA GONDII* CONTAMINATION IN AQUATIC ENVIRONMENTS.

11:00 (163) **H.H. Mejía Madrid**. MOLECULAR CHARACTERIZATION OF 3 SPECIES OF RHIGONEMATID NEMATODES AND A PRELIMINARY PHYLOGENY OF RHIGONEMATIFORMES.

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

Sunday Afternoon, 2014-07-27

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

Location: Ile de France Foyer

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

CELL BIOLOGY

(164) **N.A. Radwan**. CYSTICERCUS PISIFORMIS: ULTRASTRUCTURAL TRANSFORMATION OF TEGUMENT DURING DEVELOPMENT FROM ONCOSPHERE TO CYSTICERCUS.

CHEMOTHERAPY AND DRUG RESISTANCE

(165) **F. Benavides**. IN VIVO AND IN VITRO EFFECTS OF HYDROGEN PEROXIDE AND METRIFONATE ON *LIGICTALURIDUS FLORIDANUS* (ANCYROCEPHALIDAE) ON THE GILLS.

ECOLOGY

(166) **A.E. Garcia-Vedrenne**, A.C. Quintana, A. Kuris, R. Hechinger. REPRODUCTIVE DIVISION OF LABOR IN CLASS TREMATODA.

(167) **N. Nerwin**, K. Sgouros, E. Vasquez, J. Morrissey, J. Kawaguchi, O. Choi, S. Orlofske. ENDOPARASITE DIVERSITY AS A POTENTIAL INDICATOR OF ECOSYSTEM HEALTH.

(168) **A. Fedynich**, A. Bruno, A. Olsen, D. Rollins. GEOGRAPHIC VARIATION IN *OXYSPIRURA PETROWI* INFECTIONS IN TEXAS NORTHERN BOBWHITES.

(169) **G.S. Sanches**, M.R. André, G.H. Bechara, M.I. Camargo-Mathias. OOCYTES MATURATION OF THE SLOTH´S GIANT TICK *AMBLYOMMA VARIUM* (ACARI: IXODIDAE) IN AN ECOLOGICAL CONTEXT.

(170) **D. Benesh**. LIFETIME INBREEDING DEPRESSION, PURGING, AND MATING SYSTEM EVOLUTION IN *SCHISTOCEPHALUS SOLIDUS*.

(171) **M. Horther**, T. Sparkes. EGG MORPHOLOGY IN THE ACANTHOCEPHALAN ACANTHOCEPHALUS DIRUS: DO EGGS RESEMBLE THE FOOD SOURCE OF TARGET HOSTS?

(172) **B.Y. Kim**, D.G. Buth. AGE COHORTS IN THE MARINE LEECH, *HEPTACYCLUS BUTHI*.

(173) **K. Reinhart**, A.M. Gleichsner, D.J. Minchella. KIN SELECTION AND VIRULENCE: WHAT IS THE ROLE OF RELATEDNESS IN COINFECTION?

(174) **E. Darpino**, R. Russell, F. Reyda. GASTROPODS AND FISH AS HOSTS OF DIGENETIC TREMATODES IN OTSEGO LAKE AND NEARBY WATERS.

(175) **M. Joseph**, Z. Faulkes. SPECIFICITY OF NEMATODE INFECTION IN TWO SAND CRABS SPECIES.

(176) **R. Bernot**, M. Bernot. HOW MUCH ENERGY FLOWS THROUGH PARASITES IN A STREAM ECOSYSTEM?

GENETICS AND MOLECULAR BIOLOGY

(177) **J. Munoz**, G. Mayer. SURVEY OF INTESTINAL CANINE PARASITES IN NEW YORK CITY PARKS.

(178) **T. Jaleta**, F. Schär, A. Streit, P. Odermatt. MOLECULAR DIFFERENTIATION AND GENOTYPING OF *STRONGYLOIDES STERCORALIS* ISOLATED FROM HUMANS AND DOGS IN CAMBODIA, SOUTH EAST ASIA.

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Dr. Kirsten Jensen
H. B. Ward Medal

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

Location: Ile de France II & III

Presiding: **J. Sakanari**, University of California San Francisco

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T. Ruhnke, West Virginia State University

1:55 (210) **K. Jensen**, ARRIVING DEAD CENTER OF A TARGET I DIDN'T KNOW I WAS AIMING FOR.

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

Location: Ile de France II & III

Dr. Gerardo Pérez Ponce de León
C.P. Read Mentor Award

ASP AWARDS

CLARK P. READ MENTOR AWARD LECTURE

Presiding: **A. Jimenez**, Southern Illinois University

Time (Abstract No.)

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Dr. Sarah Orlokske
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ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: G.J. Sandland, University of Wisconsin La Crosse

The recipient of the 2012 New Investigator Award is **Sarah Orlofske**, Northeastern Illinois University.

WILLIS A. REID JR., STUDENT RESEARCH GRANT AWARDS

Presiding: **M.G. Bolek**, Oklahoma State University

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: **K.K. Herrmann**, Tarleton State University

ASP BUSINESS MEETING

Presiding: **J. Janovy Jr.**, University of Nebraska Lincoln

Thank you for attending this year's ASP meeting and have a safe trip home.
*See you **June 25-28, 2015** at our next meeting in **OMAHA, NEBRASKA***

Abstract Listings

(1)

USING THE LITERATURE TO DETERMINE THE PARASITIC COMPONENT OF BIODIVERSITY: A CASE STUDY IN THE KELP FOREST

D.N. Morton, UC Santa Barbara

The parasitic component of biodiversity has only been quantified in a handful of ecosystems, and in those systems, parasites impact energy flow, food web stability, and connectance. I hypothesized that parasites comprise a large, unquantified component of kelp forest diversity. As a preliminary investigation, I used a published food web of the Santa Barbara Channel kelp forests and conducted systematic database searches to assess potential parasite diversity. The majority of parasite records were for commercially exploited fishes, with sparse data for most fishes and invertebrates. Fishes are the most resolved taxon, with 50 species in the food web. For those 50 hosts, 266 parasites have been reported in the literature. Simply adding these fish parasites would more than double the size of the kelp forest web. Parasite diversity was not evenly distributed among fishes, with 4 fish species accounting for 46% of parasite diversity. The number of recorded parasites per host species increased with the number of publications for that host, with many understudied hosts. However, the type of study had a greater impact on parasite diversity than the number of studies. Species accumulation curves suggest that a targeted study can capture a large fraction of the true parasite biodiversity, and demonstrate that studies vary greatly in their contribution to the parasite diversity captured.

(2)

DISTRIBUTION AND INFECTION PATTERNS OF *PROTEOCEPHALUS AMBLOPLITIS* AND OTHER CENTRARCHID PARASITES IN 30 STATES ACROSS THE UNITED STATES OF AMERICA

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

Proteocephalus ambloplitis, the bass tapeworm, is an autogenic parasite which infects copepods, and both planctivorous fishes and piscivorous fishes, primarily from the family, Centrarchidae. True basses in *Micropterus* serve as the primary definitive host, and infection occurs via internal autoinfection following the migration of a plerocercoid from the mesenteries or viscera into the gut. The current study was focused on developing a better understanding the geographic distribution of the parasite, as well as resolving patterns of infection among host species, particularly in terms of prevalence, intensity, and infection site specificity. A total of 2,354 fish were collected from 225 lakes and ponds in 30 states across the United States, including every state between WY and NM in the west, NM and GA in the south, GA and PA in the east, and PA and WY in the north. Plerocercoids of *P. ambloplitis* were found in every one of the sampled states, with prevalence ranging from 3.0-83.9% (with 47% of states having a prevalence between 20-40%), a rather amazing pattern for an autogenic parasite. Furthermore, clear trends were observed for prevalence and intensity based on host species, as well as, infection site specificity based on host species. Finally, in addition to collecting data on *P. ambloplitis*, all other helminths infecting parenteric and enteric sites were identified and enumerated. The current study was able to identify infection patterns—both geographically and based on various host parameters, e.g., host species, sex, age, mass, etc.—of numerous centrarchid parasites, both autogenic and allogenic. To our knowledge, this is the first study to cover such a large geographic

area (30 states) and to maintain such a high sampling frequency (225 ponds) for any single centrarchid parasite—or suite of parasites.

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(3)

THE INFLUENCE OF MACROPHYTES ON THE SPATIAL DISTRIBUTION OF AN INVASIVE SNAIL, *BITHYNIA TENTACULATA*, AND ITS PARASITES IN THE UPPER MISSISSIPPI RIVER

K.M. Miedema and **G.J. Sandland**, University of Wisconsin - La Crosse

Invasive species threaten local biodiversity in ecosystems worldwide; however, the role that invasive species play in disease emergence and persistence in native habitats remains poorly understood. *Bithynia tentaculata* is an invasive aquatic snail that was first discovered in the Upper Mississippi River (UMR) in 2002. Since that time, this snail has been associated with more than 70,000 waterfowl deaths through its transmission of trematode parasites to migrating birds. Although *B. tentaculata* is influencing native biota in the UMR, little is known about the factors underlying snail and parasite distribution in this region. In this study, we used field data to investigate whether aquatic macrophytes are important in the distribution patterns of *B. tentaculata* and its parasites. Macrophytes were collected from three sites along a rocky breakwater in Pool 8 of the UMR in July of 2013. All *B. tentaculata* were counted and subsequently necropsied to determine levels of parasitic infection. Results from this work indicate that *B. tentaculata* tends to occur at higher densities on particular macrophyte species whereas snail infection levels tend to be consistent across plant species. Results from this research suggest that macrophytes may be important for the distribution of this invasive species (and therefore its parasites) in the UMR. Better understanding these associations may help in the development of control strategies aimed at reducing waterfowl mortality in the region.

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(4)

PARASITE ASSEMBLAGE VARIATION IN SAILFIN MOLLY (*POECILIA LATIPINNA*) AMONG HABITAT TYPES OF COASTAL MISSISSIPPI, U.S.A.

A.T. Claxton, **R. Heard** and **R. Overstreet**, University of Southern Mississippi-GCRL

The sailfin molly (*Poecilia latipinna*) is a euryhaline fish widely distributed among coastal habitats in the Northern Gulf of Mexico. Previously, metacercariae of the trematode *Ascocotyle pachycystis* have been shown to affect physiological performance of sheepshead minnow potentially increasing predation risk. The objective of this study is to determine prevalence and mean intensity of metacercariae of *Ascocotyle leighi* within the bulbus arteriosus of sailfin molly as well as those of *Echinochasmus* sp. and *Phagicola* sp. encysted in gill filaments from several different habitat types. Overall prevalences of *A. leighi*, *Echinochasmus* sp., and *Phagicola* sp. are 100, 83.3, and 94.4% respectively. Initial results from one brackish and one oligohaline bayou (n = 18) suggest that molly from the oligohaline bayou have lower total parasite abundance. Mean intensities of all three parasites are higher in molly collected from the brackish water bayou. These initial results suggest that molly infection with parasites which could affect predation-susceptibility varies based upon habitat selection and associated first intermediate hydrobiid snail and definitive hosts. In addition, prevalence of the intestinal trematode *Saccocoeloides* sp. was higher in the brackish marsh than in the freshwater marsh, suggesting potential changes in food web structure between habitat types.

(5)

DOES INTRASPECIFIC COMPETITION AMONG PARASITES INFLUENCE HOST AND PARASITE LIFE HISTORY PARAMETERS?

A.M. Gleichsner, **K. Reinhart** and **D. Minchella**, Purdue University

Understanding factors that influence parasite virulence (the damage a parasite does to its host) is important for disease control efforts. Parasite competition is one variable that has been shown to alter virulence, but previous studies were of short duration and did not validate co-infections. By conducting a long-term study and using molecular tools to validate infection status we tested whether parasite responses to conspecifics ultimately influence host life history or their own development and transmission. The goal of this study was to examine how co-infections between related and unrelated parasites influence host (mortality, growth, and reproduction) and parasite (time to patency and reproduction) life history parameters throughout the course of infection. To do this we infected *Biomphalaria glabrata* snails with a single miracidia from one, two, or three strains of *Schistosoma mansoni*, a trematode parasite that causes schistosomiasis in humans. We then measured host life history and parasite transmission parameters weekly until host death. We used quantitative polymerase chain reaction (SYBR Green qPCR) to validate co-infections and to measure the relative abundance of different parasite strains within an infection over each snail's lifespan; gaining insight into the competitive dynamics of schistosomes over time. Our findings suggest that 1) the majority of co-exposed snails are only infected with a single parasite strain, indicating that studies must validate treatment groups for accurate inference, 2) parasite reproductive output (cercariae) abundance rises and falls at approximately 4 weeks, a finding previously undocumented by past short-term studies 3) co-infected snails do not always shed both strains at the same time, and snails that shed a single strain at the beginning of patency may shed a different strain at later time points, and 4) parasite strain development and transmission patterns differ when they are in a competitive scenario than when they are by themselves. These findings suggest that genetic diversity in a parasite infection can result in different disease and transmission profiles, which has implications for disease control efforts.

(6)

SEARCHING FOR EVIDENCE OF CROWDING IN THE RACCOON ROUNDWORM

S. Weinstein, University of California, Santa Barbara

The raccoon roundworm, *Baylisascaris procyonis*, is a large parasitic nematode capable of producing many thousands of eggs. These eggs pass into the environment and can cause severe disease if consumed by humans or other wildlife. To reduce risk of disease it is necessary to understand the factors that regulate parasite transmission in its natural host population. Although parasites can be regulated through parasite induced host mortality, models of *B. procyonis* suggest that raccoon mortality due to this roundworm is not sufficient to maintain the worms at the observed intensity and prevalence. Instead, host immune responses or competitive interactions between worms might regulate parasite populations if establishment, reproduction, survival decline with intensity. To address these hypotheses, I have been studying a wild population of raccoons and their worms. Worm intensity and size vary among raccoons and with host age class. In worms, mature female length can range between 10 and 20 centimeters and length correlates with egg production. Data on size and fecundity will be combined with information on host age and infection intensity to explore the factors that regulate the establishment and reproduction of the raccoon roundworm.

(7)

WHO GETS SICKER, THE HOSTS OR THE PARASITE? THE HERBICIDE ATRAZINE AFFECTS TREMATODE DEVELOPMENT AND TRANSMISSION THROUGH IMPACTS ON INTERMEDIATE HOSTS

K. Gustafson, **J. Belden** and **M. Bolek**, Oklahoma State University

Trematodes are ubiquitous members of aquatic ecosystems and are known to cause diseases in humans, livestock, and wild animals. Studies of aquatic ecosystem energetics suggest that the biomass of trematodes is greater than those of birds, fish, and other top predators. Despite the fact that trematodes are a major source of energy, food, and disease, we do not understand how transmission of these parasites changes in contaminated environments. For example, field studies indicate that parasite diversity decreases dramatically in contaminated sites compared to control sites. However, the mechanism for this loss of diversity is currently unknown. Here, we test the effects of environmentally-relevant concentrations of atrazine (an herbicide primarily applied to corn) on the establishment and development of a trematode (*Halipegus eccentricus*) in its first-intermediate snail host (*Physa acuta*) and in its second-intermediate ostracod host (*Cypridopsis* sp.). Additionally, we test the interactive effects of pesticide and parasite exposures on snail and ostracod life-history characteristics. Our results indicate that atrazine negatively affects trematode establishment and development within both snail and ostracod hosts. Although atrazine did not affect the survival of uninfected snails alone, atrazine led to the early death of infected snails. Combined, these effects significantly reduced the number of cercariae produced in snail first intermediate hosts. In contrast to the interactive effects of atrazine and trematodes on snails, atrazine significantly reduced uninfected ostracod survival and reproduction. However, when ostracods were also infected with trematodes, the negative effects of atrazine were significantly reduced. These results demonstrate the complex nature of pesticide effects on trematode infections and indicate that trematodes can affect their first- and second-intermediate hosts in dramatically different ways under different pesticide concentrations. Our work has broad implications for disease transmission and aquatic ecosystem energetics, and provides a testable mechanism for the loss of parasites in contaminated wetlands.

(8)

ENVIRONMENTAL DISTANCE SIGNIFICANTLY IMPACTS PATTERNS OF HELMINTH COMMUNITY DISSIMILARITY IN *EPTESICUS FUSCUS* (MAMMALIA: CHIROPTERA)

E. Warburton, Western Michigan University
M. Vonhof, Department of Biological Sciences and Department of Environmental & Sustainability Studies

Distance decay of community similarity, where geographically close communities are more similar to one another than to communities that are geographically distant, has been described for a wide variety of organisms and understanding its underlying causes is key to understanding of mechanisms driving patterns of biodiversity. Parasites represent a unique opportunity in which to study distance decay, because their life cycle requires intimate interactions with other species, and rate of distance decay may therefore depend not only on the parasites' environmental requirements and dispersal capability, but also those of their hosts. We used big brown bats (*Eptesicus fuscus*) and their intestinal helminths to investigate: 1) independent contributions of geographic and environmental distances on dissimilarity of intestinal helminth component communities between populations of big brown bats; 2) which environmental variables best explained variation in community dissimilarity; and 3) whether similar patterns of decay with geographic or environmental distance were observed for within host population and within

individual host parasite communities. We used both compositional and taxonomic measures of community similarity for robust examination of how parasite communities change with distance and changing environmental conditions. We found that parasite compositional dissimilarity (both within host populations and within individual hosts) as well at taxonomic dissimilarity within individual hosts was significantly associated with land cover categories influenced by anthropogenic disturbance. Component community compositional dissimilarity was significantly impacted by the amount of developed open spaces ($F_{2,10} = 6.1895$, $p = 0.003$) and highly developed land ($F_{2,10} = 5.1701$, $p = 0.0031$) within maximum host foraging distance. Infracommunity compositional dissimilarity was significantly by the amount influenced by shrub/scrub ($F_{8,207} = 5.4962$, $p = 0.001$), barren land ($F_{8,207} = 6.8972$, $p = 0.001$), moderately developed land ($F_{8,207} = 4.6708$, $p = 0.001$), open water ($F_{8,207} = 4.4755$, $p = 0.002$), highly developed land ($F_{8,207} = 3.5149$, $p = 0.002$), and evergreen forest ($F_{8,207} = 3.2122$, $p = 0.005$). Component community taxonomic dissimilarity was not significantly tied to any landcover type; however, infracommunity taxonomic dissimilarity was significantly influenced by amount of emergent herbaceous wetland ($F_{2,152} = 7.152$, $p = 0.0004$) and highly developed spaces ($F_{2,152} = 6.043$, $p = 0.0017$). These results indicate that human land use is driving significant patterns of parasite community dissimilarity, most likely by changing the presence or abundance of intermediate hosts in an area. Given that urbanization can change disease vector populations and alter parasite transmission by changing hosts' exposure to infective propagules, we must continue to examine anthropogenic impact on the external environment experienced by hosts and the role of internal host environment experienced by parasites in order to fully understand patterns of community dissimilarity in host-parasite systems.

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(9)

STUDIES OF THE NEMATODE *DAUBAYLIA POTOMACA*, INCLUDING ITS INFECTIVITY TO SCHISTOSOME-TRANSMITTING SNAILS AND EFFECTS ON *SCHISTOSOMA MANSONI* IN *BIOMPHALARIA GLABRATA*

L. Lu, **S. Zhang** and **E.T. Gendron**, Center of Evolutionary and Theoretical Immunology (CETI), Museum of Southwestern Biology, Department of Biology, University of New Mexico, NM
M. Mutuku, **C. Dweni** and **G.M. Mkoji**, Centre for Biotechnology Research and Development, Kenya Medical Research Institute, Nairobi, Kenya
E.S. Loker, Center of Evolutionary and Theoretical Immunology (CETI), Museum of Southwestern Biology, Department of Biology, University of New Mexico, NM

The nematode *Daubaylia potomaca* was found in *Helisoma trivolvis* from both New Mexico and California. Dissections of hundreds of planorbid snails representing eight species from Kenya did not reveal similar nematodes to be present. *Biomphalaria glabrata, B. pfeifferi* and *B. sudanica,* as well as *Bulinus truncatus, Bul. globosus and Bul. ugandae* were all susceptible to the NM isolate of *D. potomaca*, but physid and lymnaeid snails were not. We exposed lab-reared *B. glabrata* (6-9mm) to infections of *D. potomaca* and/or *S. mansoni* to assess the potential of the nematode to interfere with schistosome development. Preliminary results suggest that in comparison to uninfected control snails, snails exposed to *D. potomaca* were subject to higher mortality. At least some snails exposed to *D. potomaca* infection one week before, simultaneous with, or one week after exposure to *S. mansoni* subsequently shed cercariae, suggesting the nematode cannot prevent successful schistosome infections from developing under these exposure conditions. Snails infected with nematodes seven days prior to exposure to *S. mansoni* eventually shed fewer cercariae than snails exposed only to *S. mansoni*, or to *D. potomaca* at the same time or 7 days after *S. mansoni* exposure. Histological sections of co-infected snails revealed the nematodes to occupy different parts of the snail than schistosome sporocysts, and that large areas of digestive gland were occupied by seemingly normal, cercaria-producing daughter sporocysts. The potential of *D. potomaca* to interfere with survivorship of schistosome-transmitting species of snails, with or without schistosome sporocysts being present, deserves further study. Supported by NIH RO1 grant A1101438.

(10)

ASYMPTOMATIC MALARIA AMONG PREGNANT WOMEN IN EDO STATE, NIGERIA

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R. Omoregie, School of Medical Laboratory Sciences, University of Benin Teaching Hospital, Benin City, Nigeria
A.B. Ande, University of Benin Teaching Hospital, Department of Obstetrics and Gynecology, Benin City, Nigeria

Malaria is a serious public health problem in tropical and subtropical regions of the world with far reaching medical, social and economic consequences. Malaria during pregnancy is a major cause of fetal and maternal morbidity and mortality. This study was conducted to determine the prevalence of asymptomatic malaria in pregnant women as well as the risk factors in acquiring asymptomatic malaria in Benin City, Nigeria. A total of 539 patients were recruited for this study. They consisted of 439 pregnant women attending clinics and 100 non-pregnant apparently healthy women served as controls. The age of the study participants ranged from 21years to 45 years. Blood specimen was collected from each participant to detect malaria parasite and to determine haemoglobin concentration using standard techniques. Pregnancy was significantly associated with asymptomatic malaria (OR=2.442 95%; CI= 1.496, 3.987; P=0.0004). Multiparous pregnant women and those who use only insecticide as malaria preventive measures had significantly higher prevalence of asymptomatic malaria (P<0.0001 and P=0.0092, respectively). Age, gestational age, level of education, marital status, occupation, use of antimalarial, type of antimalarial and source of insecticide-treated bed nets had no significant effect on the prevalence of asymptomatic malaria among pregnant women (P>0.05). Pregnant women have a 1 to 4-fold increased risk of developing anaemia than non-pregnant women. Anaemia was associated with asymptomatic malaria among pregnant women (OR=2.268; 95%; CI=1.414, 3.637; P=0.0009). The prevalence of asymptomatic malaria among pregnant women was 44.87% with multiparous women and those that use only insecticide as preventive measure having higher prevalence of asymptomatic malaria. Measures to reduce asymptomatic malaria among pregnant women are advocated.

(11)

SARCOCYSTIS SPP. INFECTIONS IN FERAL PIGS IN THE USA

J. Dubey, **R. Calero-Bernal** and **S. Oliveira**, USDA
S. Kumar and **B. Rosenthal**

Inter transmissions of pathogen between domestic and wild life animals play important role in epidemiology. Feral pig populations are increasing in the USA and may constitute a risk to non-biosecure domestic pig facilities by serving as reservoirs for pathogens. We surveyed hearts of feral pigs trapped or hunted in 27 states during the Comprehensive Feral Swine Disease Surveillance Program of the USDA's Animal and Plant Health Inspection Service, Wildlife Services unit (APHIS-WS) during 2012-2014 for *Sarcocystis* infection. Sarcocysts were detected by histopathology in the 20.9% (193/921) of myocardium with an average parasitic load of 3.48 cysts/section (1.5x0.7 cm), and higher prevalence of myositis in severe infections. Microscopic examination of pepsin digests of 143 hearts revealed a higher prevalence (48.2%, 69/143) of *Sarcocystis* bradyzoites than detected by histology. A specific18S rRNA gene sequence of *Sarcocystis* spp was amplified using primer pairs 2L/3H and amplicon were digested with restriction enzyme *Ssp*I. After PCR-RFLP of 42 positive samples, the pattern of restriction

digestion obtained was consistent with *S. miescheriana* in all the samples. Our results show only *S. miescheriana* infection and not *S. suihominis* infection in feral pigs in the USA.

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(12)

GENETIC CHARACTERIZATION OF *TOXOPLASMA GONDII* FROM ALPACA (*VICUGNA PACOS*) AND SHEEP (*OVIS ARIES*) GRAZED ON PASTURE IN VIRGINIA

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Recent studies from South America have revealed that *Toxoplasma gondii* has a greater genetic diversity than considered previously. In the present study *T. gondii* was isolated and genetically characterized from alpacas for the first time. Alpacas (n=16) and rams (n=12) pastured on a farm in Virginia, USA were examined at necropsy. Antibodies to *T. gondii* were determined by the modified agglutination test (MAT, 1:25) and found in six of 16 alpacas with titers of 1:100 or higher. Tissues of 6 alpacas and 3 rams were bioassayed in mice. Viable *T. gondii* was isolated from tissues of two of six seropositive alpacas by bioassay in mice. Viable T. gondii was isolated from 3 of 3 seropositive sheep bioassayed in mice. All 5 isolates of *T. gondii* were avirulent to Swiss Webster outbred mice. Genotyping using cell cultured tachyzoites revealed four genotypes, including one for ToxoDB PCR-RFLP genotype #2 (Type III), one for genotype #3 (Type II variant), one for genotype #170, and two for a new genotype designated as #230. Our results add to the evidence that *T. gondii* isolates in USA are genetically diverse.

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(13)

USING SNAIL "JERKY" TO UNTANGLE THE LIFE CYCLE STRATEGIES OF GORDIIDS (NEMATOMORPHA)

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A number of gordiid life cycles have been domesticated in the laboratory. Studies on these domesticated hairworms indicate that juvenile gordiids are obligatory parasites of terrestrial definitive arthropods, whereas a variety of aquatic animals serve as paratenic hosts for the cyst stage. Some of these paratenic hosts (such as aquatic insect larvae) carry cysts to land after metamorphosis. However, it is not fully understood, how omnivorous hosts, such as crickets come in contact with gordiid cysts which infect flying insects such as midges and mayflies. One idea is that crickets scavenge on dead and dry paratenic hosts which contain viable cysts. Therefore, we tested the viability of cysts of the domesticated hairworm *Paragordius varius* by exposing crickets to cysts which were dried for 29 days and control (not dried) cysts. Of the 40 crickets exposed to dried cysts, 23% became infected with adult worms with a mean abundance of 0.7 + 1.7 and mean intensity of 3 + 2.3 (range 1-6); whereas of the 25 crickets exposed to control cysts 20% became infected with adult worms with a mean abundance of 0.24 + 0.5 and a mean intensity of 1.2 + 0.4 (1-2). No significant differences were found in prevalence, mean abundance, or mean intensity among cricket groups exposed to dried or control cysts. Our work indicates that gordiid cysts have the ability to survive drying for relatively long periods of time and provides the first mechanism of how omnivorous arthropods such as crickets become infected with gordiids in

nature. More importantly, our work provides a novel tool for maintaining gordiid life cycle stages in a suspended state which will allow nematomorph researchers to establish other gordiid life cycles in the laboratory and help discover the hidden diversity of these worms from around the world.

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(14)

LIFE CYCLE, HOST SPECIFICITY, AND SEASONAL OCCURRENCE OF *DERO HYLAE* (ANNELIDA: NAIDIDAE) A RARELY ENCOUNTERED PARASITE OF TREE FROGS

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The annelid *Dero* (*Allodero*) *hylae* is a rarely encountered asexual parasite that resides in the ureters of tree frogs (Hylidae). The life cycle of *D. hylae* has not been elucidated. Further, no experimental infections have been conducted on this worm to establish its host specificity. Therefore, we conducted experimental infections (in laboratory and semi-natural conditions) to fully elucidate the life cycle of *D. hylae* and determine the ability of the worm to establish infections in sympatric anurans from Polk County, Florida. To establish seasonal occurrence, we collected worms from Cuban tree frogs on the campus of Florida Southern College from 2012-13. In addition, free-living worms were cultured and morphological changes were described. Finally, worms were placed in standard chemotaxis experiments to determine their ability to locate potential anuran hosts. Our experimental infection experiments suggest *D. hylae* used a direct route of transmission via the cloaca, likely occurring in aquatic microhabitats, e.g. bromeliad tanks. Worms infecting Cuban tree frogs displayed no strong seasonal trends in prevalence or abundance. Interestingly, free-living worms transformed morphologically when kept in fresh water over a several day period. Our host specificity and chemotaxis experiments suggest *D. hylae* are attracted to and primarily infect tree frogs, although toads (Bufonidae) were occasionally infected.

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(15)

GLOBAL COLLECTIONS OF PHYLLOBOTHRIIDEAN CESTODES OF SHARKS OFFER CLUES TO LIFE CYCLES, AND REVEAL LESS HOST SPECIFICITY THAN EXPECTED

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Elucidating complex life cycles of cestodes parasitizing sharks is of great interest, as it will provide insight to transmission dynamics in a marine environment. Connecting larval stages, which are morphologically difficult, if not impossible, to identify, with adult specimens is essential for piecing together these life cycles, and can be done using molecular techniques. This study was prompted by the collection of deeper water shark genera from the Azores (*Deania*, *Centroscyllium*, and *Centroselachus*) that revealed several larval phyllobothriids of unknown identity. Available collections of a diversity of squaliform, hexanchiform, and scyliorhinid shark taxa from around the world (off the coasts of Taiwan, Chile, the Solomon Islands, Korea, the UK, South Africa, the eastern U.S.A., and the western U.S.A.) provided a diversity of adult specimens for comparison. Both larval and adult specimens were examined using light microscopy, scanning electron microscopy, and molecular methods (sequencing ~1300bp of partial 28S nuclear gene). This detailed examination provided interesting information regarding 2 cestode genera: *Clistobothrium* and *Phyllobothrium*. The comparison of our larval and adult sequences along with those in GenBank revealed that larvae found in our Azorean sharks belonged to the genus *Clistobothrium*. Our data also indicate that *C. montaukensis*, which parasitizes the shortfin mako, is more widely distributed than previously believed—we found specimens ranging from off the

eastern U.S.A. to Taiwan. *Phyllobothrium squali* was molecularly identified in hosts spanning 2 phylogenetically distant taxa (the dogfish and the catsharks), unusual for a phyllobothriidean cestode, however both host groups are typically found at greater depths; supporting the notion that there may be lower host specificity in deep-water taxa. This study illustrates how broad host sampling (both geographically and taxonomically) may expose patterns of infection that might otherwise be missed.

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(16)

MICROSPORIDIA, *GIARDIA* AND *CRYPTOSPORIDIUM* IN WHITE-TAILED DEER

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White-tailed deer (WTD) (*Odocoileus virginianus)* are the most widespread and abundant member of the deer family and one of the most recognized large mammals in North America. In the last decade the WTD population increased dramatically throughout the United States as abandoned farm fields reverted to forest, human population shifts created habitat preferred by deer, and landowners made many areas off limits to hunters, resulting in a deer population of approximately 32 million in 2008. Conservative annual estimates of deer damage exceed $2 billion nationwide from damage to vehicles, timber, agricultural crops and landscape plants. Human health has been impacted by Lyme disease, babesiosis and ehrlichiosis. The present study was undertaken to determine the presence of other potential human protist pathogens in culled deer in central Maryland. Feces from 80 deer, from fawns to adults, were examined by molecular methods. The prevalence of *Cryptosporidium* spp., *Giardia duodenalis* and *Enterocytozoon bieneusi* was determined by PCR. All PCR-positive specimens were sequenced to determine the species and genotype(s). Ten (12.5%) specimens contained the *Cryptosporidium* deer genotype, one (1.25%) contained *G. duodenalis* Assemblage A, and 26 (32.5%) contained 17 genotypes of *E. bieneusi*. Four genotypes were previously reported (I, J, WL4, LW1) and 13 novel genotypes were named DeerEb1-DeerEb13). WL4 is the only one of these genotypes known to infect humans.

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(17)

THE DISTRIBUTION OF *CYTAUXZOON FELIS* (APICOMPLEXA: THEILERIIDAE) IN BOBCATS AND TICKS IN ILLINOIS

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Cytauxzoon felis is an apicomplexan able to infect mononuclear phagocytes of felines. Infection in domestic cats (*Felis catus*) causes cytauxzoonosis, which is often fatal even with treatment. This disease results in the mortality of 40% of treated and 97% untreated cats exhibiting symptoms. Bobcats (*Lynx rufus*) are the natural host and show no apparent pathology associated with infection by *C. felis*. The vector of *C. felis* is the lone star tick (*Amblyomma americanum*), although the American dog tick (*Dermacentor variabilis*) is a competent vector under laboratory conditions. In this study we aimed to determine the prevalence of *C. felis* in bobcats and *A. americanum* and *D. variabilis* in the southern-forested region of Illinois. Both vector species and bobcats are highly abundant in the area. We screened tissues of 67 bobcats and ticks for the presence of *C. felis* using polymerase chain reaction (PCR) with specific primers. DNA from positive PCR's was sequenced to confirm the presence of *C. felis*. Bobcats from Illinois showed a prevalence of 70% (47 bobcats). The parasite has been documented from Illinois on one occasion.

Our results suggest that many cases are unreported or undiagnosed. The determination of the presence of *C. felis* in free ranging domestic cats is necessary, because in combination with our results, data could be used to construct a comprehensive risk map for cytauxzoonosis. This map could enable veterinarians to recommend risk-based preventative care.

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(18)

DETECTION OF CERCARIAE FOR TRACKING TRANSMISSION OF SCHISTOSOMIASIS

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Schistosoma mansoni, a causative digenean parasite of human schistosomiasis, continues to heavily impact human health. The World Health Organization (WHO) seeks elimination of schistosomiasis as a global health problem by 2025. Control efforts employ mass drug administration (MDA) of praziquantel, an efficacious drug that cures human infections but that does not protect against reinfection. Long-term effective control needs to also interrupt parasite transmission by aquatic intermediate host snails of *S. mansoni* that release waterborne cercariae that are infectious for humans. Low prevalence of patently infected snails in the field and a non-continuous release of cercariae hamper both the identification of transmission sites as targets for control and the tracking of altered transmission risk due to control efforts. Cercarial abundance provides a more direct parameter for local transmission risk. Detection of microscopic cercariae is challenging: large volumes of surface water must be filtered to obtain cercariae for molecular identification, sentinel mice can be examined for adult worms only weeks after exposure. This study reports on efforts to combine previous insights into the biology of *S. mansoni* to attract and detect cercariae in real time. Agarose plugs containing various combinations of chemicals (originally characterized from human skin) that stimulate the attraction, attachment, exploration, penetration phases of parasite infection and chromogenic substrates for Sm-elastase (protease released for skin penetration) were placed in petri dishes containing water with *S. mansoni* cercariae. Results will be presented regarding the monitoring of interactions of cercariae with these targets over time.

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(19)

TICKS KNOWN TO TRANSMIT TICK-BORNE INFECTIOUS DISEASES TO HUMANS IDENTIFIED FROM A UNIVERSITY PREMISES IN NIGERIA

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Important consequence of recent incursion of cattle in Nnamdi Azikiwe University (UNIZIK) premises at Awka was the introduction of ticks in that environment. Public health hazard of infectious tick-bites is their potential for transmission of tick-borne infectious diseases in humans. Eighty nomadic cattle and twenty 40m2 quadrats in pasture were conventionally sampled for ticks in UNIZIK in 2012. Ticks identified from cattle were *Amblyomma* ssp., 115(19%), *Boophilus* spp., 127(20.8%), *Hyalomma* spp., 219(36%), and *Rhipicephalus* spp., 147(24.21%). The determined average tick burdens were 77.2 ticks/head (Wet season) and 44.4 ticks/head (Dry season); while adult sex ratios (female: male) were 1:1.68 (Wet season) and 1: 1.66 (Dry season). Differences in sex ratios among genera of ticks were not significant ($p>0.05$) although sexual dimorphism was observed in all genera, with the males being smaller than female ticks. Mean abundance of ticks per 20 square meter pasture were 42.5 (Wet season) and 29.5 (Dry season). Larvae of *Boophilus*, as well 1-host tick, *Hyalomma* as 2-host tick and *Amblyomma* & *Rhipicephalus* species as 3-host ticks. This paper inferred that cattle incursion had introduced these ticks into UNIZIK environment. Since the identified genera are well-known vectors of disease pathogens in sub-Saharan Africa, the result will increase public health awareness on the

hazards associated with ticks and tick-bites, as well as serve a useful purpose in the formulation of evidence-based decision on control of vectors and movement of cattle in that area.

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(20)

GEOPHAGY AND ITS POTENTIAL RISK OF TRANSMISSION OF GEOHELMINTHS AMONG PRE-ADOLESCENTS IN NIGERIA

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Geophagy-eating of earthly or soil-types such as clay and chalk-and its potential risk of transmission of geohelminths among pre-adolescents at Anaku in Anambra State of Nigeria was studied. Anaku is a farming community on the Anambra River flood plains, rich in clayey soil which is commonly utilized by the people for house building, flooring, moulding of kitchen utensils as well as for eating by pregnant women and children. Geophagy was observed to be an age long cultural practice, with no differences in earth-eating behavior of the people concerned. Anaku was usually flooded during the wet season but its clayey soil became caked-up with intense sunshine in the dry season. Absence of proper toilet in the area has encouraged indiscriminate defecation by humans, in addition by stray dogs which may contaminate the environment with ova of parasitic heminths. Between January and December 2012 and with informed consent of parents, 300 pre-adolescents aged 4 to 10 years were recruited for this study. Fifty subjects were randomly selected from each of the six primary schools in the area. All the subjects admitted that they eat clay and red earth soil regularly both at home and school. Stool samples from the subjects, as well as 25 from locations where clay soil was generally obtained, were routinely examined at Ennembo Biomedical Laboratories Onitsha for ova of intestinal helminths. Ova of five species of parasitic helminths were regularly identified from both subjects and soil samples. They included *Ascaris lumbricoides* (40%), *Schistosoma mansoni* (27.2%), *Trichuris trichiuria* (15.5%), Hookworm species (10.5%), and *Toxocara canis* (6.8%). The overall prevalence of parasitic infection among the subjects was 93% and it was statistically highly significant ($p<0.01$). However, no significant difference was observed in age- and location- specific prevalence of infection in the area ($p<0.05$). Since helminthosis is well knoen to impart negatively on nutritional health of pre-adolescents, this paper inferred that the practice of geophagy posed a high risk of transmission of intestinal parasites, especially geohelminths among its practicing pre-adolescents at Anaku. There is need for sensitization awareness of the potential public health hazard of geophagy in Anaku and similar places in order to assist the Global Health Donor Agencies' in their fight against child and maternal mortality. The result of this paper will also serve as a useful guide for evidence based policy, decision to either provide or enforce the use of adequate toilet facility such as the WHO recommended Improved Ventilated Pit (VIP) Latrines and as well as carry out strategic de-worming of children in resource poor environments like Anaku.

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(21)

ASSOCIATION OF *PLASMODIUM* SPECIES WITH LOCATION, GENDER, AGE AND BLOOD PROFILES OF RESIDENTS SAMPLED IN NIGERIA

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Rapid urbanization going-on in Awka Capital Territory and Greater Onitsha Metropolis is known to have created more breeding sites for mosquito vectors, thereby exposing residents including visitors, travelers, entrepreneurs and rural-urban migrants in these areas to a high-level risk of

malaria infection. This study determined *Plasmodium* species prevalent in blood of subjects examined between June 2012 and October 2013 at Awka (North & South) and Onitsha (North & South) Local Government Areas (LGAs) in Anambra State of Nigeria. Microscopy and Rapid Test Items Diagnostic tools were employed in diagnosing malaria among the 800 consenting individuals whose blood profiles were determined by standard laboratory procedures. Each of the 4 LGAs contributed 200 subjects (100 males and 100 females) to the total sample population, which admitted having been previously bitten by mosquitoes in the study area. The sample population was stratified according to LGA, Gender, Age-group, ABO blood groups, Genotypes, Erythrocyte sedimentation rate (ESR), Haemoglobin count (HB) and Packed cell volume (PCV) which helped to establish their association with 4 *Plasmodium* species identified from positive blood samples. The overall prevalence of malaria among the 800 subjects examined was 436 (54.5%). The parasitaemia was associated with *Plasmodium falciparum* 290 (36.25%), *P. malariae* 79 (9.87%), *P. ovale* 65 (8.13%), and *P. vivax* 2 (0.25%) which was highly significantly different ($p<0.01$). Generally there were no significant differences ($p>0.05$) in the 4 LGA's location-prevalence of malaria (Mean prevalence = 13.62±0.94), and in Gender-prevalence of malaria (Mean prevalence = 27.25±2.25). However, there were significant differences ($p<0.05$) in malaria prevalence among Age-groups (Mean prevalence = 13.62±3.99), ABO blood-groups (Mean prevalence = 13.62±4.99), Genotype (Mean prevalence = 18.16±12.58), and between ESR counts (Mean prevalence = 27.25±10.62), HB counts (Mean prevalence = 27.25±6.62), and PCV counts (Mean prevalence = 27.25±12.25). Subjects under 10 years of age and those with Blood-groups O and A, as well as genotype 'AA' were observed to be highly susceptible to *Plasmodium falciparum* malaria which was found to be the most prevalent species in the study area. Public health implications of these findings, including anemia associated with depressed HB and elevated ESR values during malaria, were discussed. Further work is however needed to unravel the mystery behind the apparent infection of Duffy-negative individuals characteristic of the study area by *P. vivax* demonstrated in this study. The result of this paper will also serve as a useful guide for evidence-based policy decision to equip all health facilities in Nigeria and the sub-West African Region with Rapid Diagnostic Test items that will detect almost all the *Plasmodium* species known to cause human malaria.

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(22)

A COMPARATIVE ACCOUNT OF BIOMOLECULES AND POLYPEPTIDES DURING THE DEVELOPMENTAL STAGES OF *GASTROTHYLAX CRUMENIFER* (TREMATODA:DIGENEA)

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Paramphistomes are one of the most common groups of digenetic trematodes causing the disease 'paramphistomosis' in livestock in tropical and sub-tropical countries. Adult parasites infecting rumen generally render low pathogenecity while the migrating immature flukes are responsible for severe pathological damages including hemorrhagic inflammation in the alimentary tract, oedema and anaemia. Paramphistomes pass through a succession of environments i.e. free living to tissues of intermediate and definitive hosts undergoing multiplication for genome amplification during their life cycle. Inside definitive host, parasites navigate diversified micro-environments by regulating a sequence of metabolic switches. Thus any change in organic state of the habitat or its physico-chemical condition is reciprocated by the parasites through its metabolic features. Most of the basic studies are confined to adult parasites while other developmental stages are almost neglected. In the present study we have investigated biochemical alterations during the larval stages of *Gastrothylax crumenifer* (a rumen infecting paramphistome) which revealed marked differences during the miracidial development as well as in the intra-molluscan larval stages. We observed that the protein, glycogen and lipid of freshly laid eggs were utilized during the development. Concentration of protein, glycogen and lipid contents significantly elevated in the cercariae as compared to the non-feeding metacercarial

stage, indicating an adaptation of the parasite to build up the nutrients for the metacercariae which is a dormant stage. Very little amount of lipid was detected in the fresh eggs (E0) which further decreased in the eggs containing mature miracidia (Em) and then increased sharply in the cercarial and metacercarial stages indicating the substantial build up of lipid reserves. Nucleic acid contents decreased from E0 to the subsequent developmental stages. Such changes could be of intrinsic significance for the cellular differentiation and organogenesis in larval paramphistomes. Further, we analysed polypeptide profile of developmental stages which revealed heterogenous mixture of polypeptides. A total of 27, 15, 14, 15, 14 and 34 polypeptides in E0, Em, cercariae, metacercariae, immature and adult *G. crumenifer,* respectively were resolved. Eight and nine characteristic polypeptides (17-90 kDa) were observed in E0 and adult respectively.

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(23)

DESCRIPTION OF TISSUE STRUCTURE AND FUNCTION OF AN ENIGMATIC TAPEWORM

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This study focuses on clarifying our understanding of an enigmatic species of tapeworm parasitizing pelagic thresher sharks in Taiwan and Mexico. Although molecular data strongly support its place in the genus *Litobothrium*, morphologically the cestode is unlike all other species in the genus. It bears a dome shaped scolex proper and extremely elongate cephalic penduncle rather than a series of cruciform pseudosegments. Furthermore the strobila appears to consist of a series of minute (~20 µm) proglottids and it is believed to be hyperapoltic for mature proglottids have never been observed. Light microscopy of the scolex revealed the presence of a series of unusual tissue types. The first tissue type was PAS positive and thus possibly functions in producing a muccopolysaccharide associated with attachment; the functions of the other tissues were unknown. This cestode also exhibited two lateral pairs of ducts with unusually thick cell walls, their function was unknown. The goal of this project was to examine this cestode using transmission electron microscopy (TEM) in order to investigate its internal anatomy in more detail. Specimens were fixed in 1% osmium tetroxide and embedded in epoxy resin. Semi-thin and ultra-thin cross and longitudinal sections were prepared from the anterior and posterior regions of the cephalic peduncle. Ultra-thin sections were stained using 2% uranyl acetate and Sato's lead citrate and then examined using TEM. Tissue 1, in the anterior most region of the scolex, has a large cytoplasm to nucleus ratio with nuclei that are 2 µm in diameter. The cells of this tissue also contain numerous large, electron dense inclusions. This is consistent with the function originally attributed to this tissue. Tissue 2, found in the anterior half of the cephalic peduncle, has nuclei that are 2 µm in diameter and each cell contains numerous electron lucent inclusions. Tissue 3, which is found more posteriorly, consisted of cells with a small cytoplasm to nucleus ratio and nuclei that are 3-4 µm in diameter. These cells also included electron dense inclusions, but they were much fewer in number than seen in the cells of Tissue 1. Although, the function of the paired ducts were unclear based on light microscopy TEM suggests that they may be excretory. Dense concentrations of flame cells were seen surrounding the ducts and some evidence of small collecting ducts extending between the protonephirdia and main ducts were seen. TEM has been very useful for the exploration of this cestode and it will continue to be used in order to identify the structures and functions of other tissues in the tapeworm.

(24)

VACCINE MADE AGAINST INTESTINAL SCHISTOSOMIASIS, CAN PROTECT HAMSTERS AND BABOONS INFECTED WITH *SCHISTOSOMA HAEMATOBIUM*

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Over a billion people are at risk of being impacted by the negative health-related manifestations of schistosomiasis in 74 countries; at present an estimated 200 to 400 million people are infected and an additional 779 million individuals are at a potential risk of contracting the infection. In the present study, we have explored the potential of Sm-p80 for its prophylactic efficacy against *S. haematobium* in hamsters and in a pilot study using baboons. Pronounced reduction in worm burden (47.66%) and in tissue load (64.03%) was observed in hamsters vaccinated with recombinant Sm-p80 admixed with Glucopyranosyl Lipid Adjuvant-Stable Emulsion (GLA-SE). Similarly, in baboons, Sm-p80-GLA-SE vaccine produced 25.27% reduction in *S. haematobium* adult worms and 63.69% decrease in egg load in the urinary bladder. A 39.93% and 52.91% reduction in fecal and urine egg output, respectively, was observed in vaccinated baboons. A tortuously synchronized pro-inflammatory (Th17 and Th1) and anti-inflammatory (Th2) type of response was generated in response to the Sm-p80 vaccine which appears indicative of an augmented prophylactic efficacy. A schistosome vaccine that protects against the three major species of schistosomes thus providing relief from the clinical manifestations associated with both the intestinal and the urinary schistosomiasis will be greatly beneficial in reducing the overall burden of the disease. These data on cross-species protection coupled with the prophylactic, therapeutic and antifecundity efficacy reinforces the potential of Sm-p80 as a viable vaccine candidate which is currently being slated for GMP-manufacture and for further pre-clinical development leading to human clinical trials. Sm-p80 vaccine is expected to provide relief for both the intestinal and the urinary schistosomiasis and thus will be greatly beneficial in reducing the overall burden of the disease.

(25)

TWO *BRUGIA MALAYI* RECOMBINANT PROTEINS (BM-103 AND BM-RAL-2) CONFER SIGNIFICANT PROTECTION AS A VACCINE AGAINST *B. MALAYI* INFECTION IN MONGOLIAN GERBILS

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Two *Brugia malayi* proteins, *Bm*-103 and *Bm*-RAL-2, are orthologous proteins of confirmed vaccine candidates of *Onchocerca volvulus*. The Ov-103 was identified first as a microfilariae surface associated protein, but later was found to be also expressed in the cuticle, hypodermis and mutivesicular bodies of infective stage larvae of both filarial parasites. *Ov*-RAL-2 and *Bm*-RAL-2

are immunodominant proteins expressed in the hypodermis of all stages. *Bm*-103 was cloned and expressed in *Pichia pastoris* and *Bm*-RAL-2 was cloned and expressed in *Escherichia coli*. These recombinant proteins were tested for their efficacy as a vaccine in the *B. malayi* – Mongolian gerbil animal model of lymphatic filariasis. Alum and Alum- *Glucopyranosyl Lipid Adjuvant (*GLA) were used as adjuvants. Vaccination was via 3 intraperitoneal injections separated by 2 week intervals. Animals were challenged subcutaneously with 100 infective larvae third stage larvae (L3) and worm recovery was performed 42 or 90 days post infection. Vaccination with *Bm*-103 administered with alum showed 40% worm reduction in comparison to alum controls. Vaccination with *Bm*-RAL-2 administered with either alum or alum-GLA showed 43% and 62% worm reduction in comparison to controls, respectively. A fusion protein of *Bm*-103 and *Bm*-RAL-2 was created, cloned and expressed in *E. coli*. Vaccination of gerbils with the *Bm*-103-*Bm*-RAL-2 fusion protein induced a 51% worm reduction in comparison to controls. Vaccination of gerbils with the two antigens, *Bm*-103 and *Bm*-RAL-2, each formulated with alum but injected separately resulted in worm reduction of 69%. In all vaccination experiments, a strong antigen-specific IgG response was detected by ELISA to the recombinant proteins. Moreover, *in vitro* killing assays using peritoneal exudates cells (PEC) in the presence of gerbil anti-serum against *Bm*-103 and *Bm*-RAL-2 showed active killing of L3 larvae in comparison to L3 larvae cultured with appropriate controls sera suggesting that an antibody dependent cell mediated cytotoxicity (ADCC) maybe a potential mechanism of protection. The results suggested that further experiments using these proteins alone or in combination are warranted.

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(26)

MODULATION OF IRON ACQUISITION PATHWAYS OF MONOCYTES-MACROPHAGES IN INDIAN POST KALA-AZAR DERMAL LEISHMANIASIS

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Iron, an essential micronutrient for living cells has diverse functions ranging from being a cofactor of metabolic and antioxidant enzymes to immune surveillance. As pathogen survival hinges upon the availability of iron, host and pathogen both compete for the iron pool making iron a critical factor for influencing disease progression. *Leishmania donovani*, the causative organism of Post kala-azar dermal Leishmaniasis (PKDL) deviously modulates monocyte/macrophages to ensure its survival. However, studies regarding iron, an important micronutrient for both parasite survival and macrophage function, remains ill defined. Accordingly, our study aimed to trace the status of iron within monocytes/macrophages in Indian PKDL. The intramonocytic labile iron pool and frequency of CD71 (transferrin receptor) on $CD14^+$ monocytes from peripheral blood mononuclear cells (PBMC) was measured by flow cytometry, plasma levels of iron, ferritin and transferrin and soluble CD163 (Hemoglobin-Haptoglobin scavenger receptor) by spectrophotometry along with mRNA expression of CD163, heme oxygenase (HO-1), transferrin, transferrin receptor and ferritin in PBMCs and dermal lesions. In PKDL, plasma iron was decreased whereas intramonocytic iron was increased implicating that iron storage is enhanced in monocytes. Furthermore, a decrease in plasma levels of iron-storage protein, Ferritin along with its increased expression in PBMCs corroborated that iron storage was raised in monocytes. A raised plasma transferrin level along with an increased frequency of $CD14^+CD71^+$ monocytes indicated that iron was indeed being imported into monocytes via the transferrin receptor. Another pathway for importing iron by monocytes is the hemoglobin-haptoglobin transport via their receptor CD163, whose mRNA level in PBMC was unaltered in PKDL. However, soluble CD163 was significantly raised in PKDL and was accompanied by raised mRNA expression of HO-1 in PBMCs as also an increase in IL-10, a critical factor for HO-1. At the lesional site, the mRNA expression of transferrin, transferrin receptor, ferritin, CD163 and HO-1 were increased as compared to healthy controls, collective

evidence that at the disease site, modulation of iron transport possibly facilitates parasite survival. Taken together, in PBMCs and dermal lesions, the transferrin-transferrin receptor mediated iron acquisition pathway is upregulated by the parasite for its survival and therefore, modulation of iron transport could be considered as a potential immunomodulatory target in PKDL.

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(27)

GAL-LECTIN DEPENDENT CONTACT ACTIVATES THE INFLAMMASOME BY INVASIVE *ENTAMOEBA HISTOLYTICA*

L. Mortimer, **F. Moreau** and **K. Chadee**, University of Calgary

Entamoeba histolytica (*Eh*) is an extracellular protozoan parasite of the human colon, which occasionally breaches the intestinal barrier. Eradicating ameba that invades is essential for host survival. A defining but uncharacterized feature of amebic invasion is direct contact between ameba and host cells. This event corresponds with a massive pro-inflammatory response. To date, pathogen recognition receptors (PRR) that are activated by contact with viable *Eh* are unknown. In this study we have unravelled that the innate immune system responds in a qualitatively different way to contact with viable *Eh* versus soluble ligands produced by viable or dead ameba. This unique *Eh* Gal-lectin contact-dependent response in macrophages was mediated by activation of the inflammasome. Soluble native Gal-lectin did not induce inflammasome activation, but was sufficient for transcriptional priming of the inflammasome and non-inflammasome-dependent pro-inflammatory cytokine release. We conclude the inflammasome is a pathogenicity sensor for invasive *Eh* and identify for the first time a PRR that specifically responds to contact with intact parasites in a manner that accords with scale immune response to parasite invasion.

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(28)

S. MANSONI THERAPEUTIC EFFECT ON DSS-INDUCED COLITIS THROUGH TH1/TH2 PARADIGM AND FOXP3+ TREGS

M.A. HasbySaad, Egyptian Parasitologists United, Egypt (EPU)

Schistosoma mansoni manipulates the host's immune response during the sequential phases of infection by shifting between the two main arms of T helper cells and stimulation of the lately discovered $FoxP3^+$ T_{regs}. At the same time, Th cell dysregulation is the backbone of inflammatory bowel diseases pathological features, which are very troubling immune diseases with unknown cause, risk of colonic carcinoma and need surgical interference or aggressive drugs to decrease the flare ups only without total cure. The rising evidence of the prevalence of IBDs in people less exposed to parasitic infections drew the attention to the idea of helminthic therapy, as the immune system may become poorly developed if exposed to less challenges especially during childhood. However, the idea of using a living parasite to induce active infection in IBD patients to subsequently regulate their immune system is still widely troublesome. Investigating the impact of schistosomiasis *mansoni* phases on the course of DSS-induced colitis in mice, as an experimental model for IBDs, and the impact of antigenic material driven from the two main long standing stages of the parasite in the human body " adult worms & eggs" to determine which immune strategy is the back-bone in modulation of colitis; Th1/Th2 paradigm or $FoxP3^+$ T_{regs}. Mice were exposed to 5% DSS in drinking water ad libitum, for 7 days after 6 weeks (acute schistosomiasis), 14 weeks (chronic schistosomiasis) post infection (Groups I-a & I-b) or after subcutaneous *S. mansoni* worm homogenate (SmWh) injection and killed *S. mansoni* eggs

intraperitoneal injection in healthy mice (Groups II-a & II-b). Control mice were divided into healthy, drug and schistosomiasis (acute/chronic) controls. Clinical disease activity index was determined, serum Th1/Th2 cytokines (IFN-γ, IL-2, IL-4 & IL-10) were measured, inflammatory scores including; macroscopic inflammatory, MPO activity and microscopic inflammatory scores were measured. Immunohistochemical study of $FoxP3^+$ T_{regs} in colon. A significant less DAI and macroscopic inflammatory score in groups with chronic infection or received either antigenic material. MPO showed the least activity after killed eggs. After acute schistosomiasis colon sections showed less severe mucosal inflammation & goblet cell depletion while chronic schistosomiasis much milder cryptitis. After homogenate; moderate cryptitis, but after killed eggs remarkable improvement of colitis. The Th2 anti-inflammatory cytokine "IL-4" showed the least level after killed eggs. A significant positive correlation between IL-4 and IL-10 was seen in groups with schistosomiasis. There was a significant positive correlation between $FoxP3^+$ T_{regs} and IL-10, while a highly significant negative correlation between IL-10 and IL-4 in group received eggs. $FoxP3^+$ T_{regs} showed a significant infiltration with *S. mansoni* element, the highest after either chronic infection or killed eggs with no significant difference. *S. mansoni* succeeded as prophylactic helminthic therapy against colitis mainly after chronic infection or killed eggs. Th1/Th2 paradigm is still the core of helminthic therapy. Shifting to T_{regs} regulation with killed eggs.

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(29)

SEROLOGICAL AND MOLECULAR STUDIES ON *TOXOPLASMA GONDII* INFECTION IN SHEEP AND GOATS IN ISMAILIA PROVINCE

H.M. Elgawadi, Suez Canal University, Ismailia, Egypt

Blood serum samples from 100 sheep and 100 goats were collected and examined for *Toxoplasma gondi* antibodies by Enzyme Linked Immunosorbent Assay and Modified Agglutination Test. The seroprevalences of *Toxoplasma gondi* in sheep were 34% and 33% and in goats were 32% and 31% by ELISA and MAT respectively. The prevalence in the females of sheep and goats were higher than males. The seroprevalences were higher in adult animals than youngs in both sheep and goats. Using the MAT as a reference test, the sensitivity and specificity of the ELISA test were 100% and 98.5% respectively. Diagnosis of *Toxoplasma gondi* in 20 brain samples (10 from sheep and 10 from goats)using nested PCR techniques by amplification of the *T. gondi* B1 gene revealed that six sheep" s brain samples were positive (60%) and six goats" s brain samples were positive (60%).Bioassay was done by inoculation of *T. gondi* positive PCR samples into healthy mice. Histopathological examination of the experimental mice brains, declared pathological lesions with demonstration of pseudocysts containing bradyzoites within the host cell cytoplasm in the mice killed 30th day and 35th day post- inoculation.

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(30)

THE SCIENTIFIC LESSONS OF INTELLECTUAL ELEGANCE IN PARASITIC PROTOZOOLOGY

R.E. Clopton, Peru State College

The lesson of a century of parasitic protozoology is the importance of intellectual elegance in choosing and manipulating experimental models. From the first century of the Journal of Parasitology, I present vignettes of 7 parasitologists demonstrating 7 critical aspects of a productive research model: diversity, suitability, malleability, feasibility, comparability, and scalability. Minnie Watson demonstrated the importance of choosing diverse but underworked

systems when she published the first protozoology paper in volume 2 of the Journal of Parasitology, describing 17 new species of North American gregarines (ca. 25% of all known New World gregarine species at the time). G. Robert Coatney developed chloroquine to treat malaria, an accomplishment made possible years before at Peru State College when he chose to search for and discover a suitable avian-plasmodium model for the primate malarias. Other protozoologists who made significant contributions to malarial research through the intellectual elegance of their protistan models include Robert Hegner, who revealed that host specificity is variable and manipulation of the host can alter its suitability to a parasite; and William Trager, who's intellectual insight was to culture the red blood cell and let it sustain *Plasmodium* rather than trying to culture the parasite directly. Leslie Stauber revolutionized the way in which we study variation and envision species concepts with comparative studies of rodent model hosts for *Leishmania*. Using host-parasite systems, especially models of anuran hosts and their opalinid protists, Maynard Metcalf confidently outlined methods for inferring host and parasite coevolution, phylogeny, and biogeography only 17 years after Alfred Wegener proposed his theory of continental drift. Most recently, John Janovy Jr's work elegantly capitalizes on the diversity, specificity, and scalability of gregarines systems as models for generalized ecological parasite phenomena. The intellectual elegance and ingenuity of these scientists should inspire our development of new model systems.

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TRANSMISSION OF *TOXOPLASMA GONDII* - FROM LAND TO SEA- A PERSONAL PERSPECTIVE

J. Dubey, USDA

More than 100 years have passed since the discovery of *Toxoplasma gondii in 1908*. However, its full life cycle was not discovered until 1970, when it was found to be a coccidian parasite which utilizes cats as the definitive host and any warm-blooded animal (including humans) as its intermediate host. The discovery of the environmentally resistant stage of the parasite, the oocyst, made it possible to explain its worldwide prevalence. Transmission of *T. gondii* will be summarized and events leading to the discovery of the life cycle of the parasite will be recalled and discussed.

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(32)

A CENTURY (1914-2014) OF STUDIES ON MARINE FISH PARASITES IN THE JOURNAL OF PARASITOLOGY

V.M. VIDAL-MARTINEZ and **M.L. AGUIRRE-MACEDO**
Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional.

Science does not typically advance jumping from one big concept to another, but usually builds incrementally on the knowledge developed by many scientists throughout time. This trend is evident in the studies on marine fish parasites published in The Journal of Parasitology (JP) during the last 100 years. Our aim was to compile and analyze a database including all marine fish parasite papers published in JP from 1914 to 2014. The database was built searching JSTOR from 1914-1949 and the Web of Science from 1950-2014. A total of 365 papers were recovered, published by authors from 33 countries, with 72% of the papers in systematics, 11% in ecology and 17% in biology, with a total of 3258 citations. During the first 80 years period (1914 to 1994), 133 papers were published by 14 countries, producing 1452 citations. However, in the subsequent 20 years (1995 to 2014), 232 papers were published by 27 countries producing 1806 citations. Where do we go from here? The publication trends on marine fish parasitology in JP suggest a steady

increase in studies on morphological and molecular systematics and phylogeny, as well as in climatic, anthropogenic factors affecting parasite communities and populations in space and time. There was also an increase in studies examining deleterious effects of parasites on both cultured and wild marine fishes. Hence, the publication trend in JP in this field represents globalization with a faster publication rate, higher citation levels, and an expansion in the range of issues considered.

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(33)

THE EVOLUTION OF THE STUDY OF THE EVOLUTION OF ELASMOBRANCH CESTODES

J.N. Caira, University of Connecticut
K. Jensen, University of Kansas

Linton's 1916 paper describing two new tapeworms from the spotted eagleray, *Aetobatis* [sic] *narinari*, collected at the Carnegie Institution's Dry Tortugas Laboratory off Florida ushered North American elasmobranch tapeworm taxonomy and systematics out of the obscurity of government publications into the limelight of a soon to be mainstream parasitological journal. His detailed descriptions epitomize the taxonomic standards employed at that time. But, they also illustrate the scientific challenges presented by a less-connected world. The global outlook on parasite biodiversity that has emerged over the last century, in combination with methodological, technological, and analytical advancements, have changed the face of taxonomy and systematics, in all groups, forever. Starting in 1961 with the first International Code of Zoological Nomenclature, a formalized set of rules for the naming of species was mandated; as of 1999, the designation and deposition of type material is required. Scanning electron microscopy and molecular sequence data are often employed to augment light microscopical characterizations of new taxa. The repertoire of genetic loci from which these sequence data are generated is expanding rapidly. A diversity of formalized methods for conducting phylogenetic analyses are available and routinely used to assess species and higher taxon boundaries. These analyses take into account issues associated with gene trees, species trees, and the evolutionary history of organelles. The circumscription of monophyletic taxa at all categories of classification is no longer merely an aspiration, it is a realizable goal. Taxonomic work is now routinely conducted in an evolutionary framework. As host and parasite identifications become more robust so do determinations of host specificity and assessments of geographical distribution. Many parasites and their hosts have been shown to be much more locally distributed than previously thought; estimates of parasite biodiversity globally continue to rise. The issue of host identity has emerged as a serious concern. The high degree of host-specificity exhibited by many groups is associated with unexpectedly little coevolutionary signal. We are rapidly approaching the point at which the phylogenetic patterns in some host/parasite systems are fully characterized and efforts can now be focused on understanding the processes that shape and maintain these associations. Cestodes and their elasmobranchs are one such system.

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(34)

THE IRON WHEEL OF PARASITE LIFE CYCLES: THEN AND NOW!

M. Bolek, **H.A. Stigge** and **K. Gustafson**, Oklahoma State University

The year is 1915, and the first paper on a life cycle of a parasite titled "The Life History of *Gongylonema scutatum*" is published in the *JOURNAL OF PARASITOLOGY*. This work sets the stage in the *JOURNAL* for the many other original and fascinating papers on parasite life cycles to follow. Each of these papers describe original ideas and illustrate the many "A-ha" moments that

are all wrapped up into fascinating stories. One can argue that our current understanding of parasite community structure, life cycle evolution, and the spread of diseases through populations has been shaped by these historical studies. However, over the years the study of life cycles has been looked upon by many as being too risky of an undertaking for graduate research problems. The difficulty in studying parasite life cycles can be summarized in a statement made 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, in recent years 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 my students and collaborators have attempted to disassemble this common misperception of the iron wheel of parasite life cycles. This endeavor has been an evolving experience supported by many fascinating lessons that are all available for free at most university libraries in the 100 volumes of the *JOURNAL OF PARASITOLOGY*. In this presentation, I will share the many lessons that my students, collaborators, and I have learned from the *JOURNAL*; all to better understand the selective pressures that have resulted in the evolution of these highly improbable events we all know as parasite life cycles.

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(35)

BIOLOGY AND VARIABILITY OF ACANTHOCEPHALANS

O.M. Amin, Institute of Parasitic Diseases

Unique and unusual features in the many species of acanthocephalans described and/or studied by Amin from fish, amphibians, reptiles, birds, and mammals, in various parts of the world including South America, Vietnam, Japan, the United States, the Middle East, and North and East Africa, are described. The presentation is in five parts. (1) An introductory section dealing with the classification, general morphology, ecology, and life cycles of the Acanthocephala. (2) Unusual anatomical features of taxonomic or of questionable taxonomic importance addressing variations in the proboscis, proboscis hooks, male and female reproductive organs, and lemnisci. Newly described structures including (a) Para-receptacle structure (PRS) and hoods in certain species as well as a new order of Acanthocephala from Vietnamese birds, are also featured. (3) Structural and functional relationships explaining the relationship between the metamorphosis of the giant nuclei in Eoacanthocephala and worm reproductive cycle. (4) Host-parasite relationships elucidating the relationships between worm anatomy and biology during worm growth. (5) Curiosities in reviews and revisions highlighting taxonomically based zoo-geographical patterns and trends in the genera *Neoechinorhynchus*, *Polymorphus*, and *Pallisentis*. A comprehensive treatment of the acanthocephalans of South America and those marine forms off the Eastern United States is also included here. A look at the September, 2013 classification scheme of the Acanthocephala is included covering 4 classes, 26 families, 157 genera, and 1298 species are included.

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THE WORM'S EYE VIEW OF COMMUNITY ECOLOGY

T.K. Anderson, Georgia Southern University
M.V. Sukhdeo, Rutgers University

Parasitology and community ecology, despite different historical origins and foci, are now coming together to provide important contributions to our understanding of ecosystem functioning. Recent studies have demonstrated that parasites may be a substantial component of community

biomass and energetic flow, and they have significant impacts on community biodiversity and metrics describing food web structure. However, there are no universal laws in parasite community ecology, whereas mainstream community ecology has leapt ahead with phenomenological laws that generate testable predictions. We contend that the central issue that has stymied the progress of parasite community ecology is the absence of synthetic work that considers regional and local processes. Traditional parasitological approaches tend to focus on local characteristics detailing how a complex of factors, some biotic and others abiotic, may impact upon the parasite community. Mainstream community ecology has explicitly considered regional and local processes, and has developed theoretical frameworks with empirical evidence explaining pattern and process. To compete, parasite community ecology must take advantage of advances from within the field of complex system analysis. This approach suggests that molecules, cells, cells with organelles, multicellular organisms, herds, or other organismal groupings and the interactions between these individual parts, may effectively describe system level behaviors. Critically, this approach relies on the integration of parasites within the system as individuals that interact and affect their hosts. That is, we will have to consider the system from the point of view of the parasites and not the hosts.

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HISTORY OF MICROEVOLUTIONARY THOUGHT IN PARASITOLOGY: THE INTEGRATION OF MOLECULAR POPULATION GENETICS

C.D. Criscione, Texas A&M University

I have been tasked with reflecting on the development of microevolutionary concepts in the field of parasitology over the past 100 years, since the first volume of *The Journal of Parasitology* (*JP*). My goal is not to review or make broad generalizations about parasite microevolution, but rather to recap the history of thought and applications of molecular population genetics in parasitology. We were also asked to pick an early paper from *JP* to highlight its relevance or impact in its respective field. I selected Steven Nadler's (1995) review, "Microevolution and the genetic structure of parasite populations," because I believe that it is one of the most under-recognized papers with regards to parasite microevolution. So, why feature an under-recognized paper and why not choose an earlier paper in *JP*'s history? To answer these questions, we need to step back in time. I will first provide a brief history of population genetics in general and then in parasitology. To show how molecular population genetics has resonated in different aspects of parasite population biology and evolution, I will then recount the history of some specific topics: How many species, Hybridization, Mode of reproduction in parasitic protozoa, Comparative approach to studying population genetic structure, Inference of transmission and epidemiological monitoring, Clonal transmission in trematodes, Effective population size, Hermaphroditic mating systems, and Mode of inheritance and genetic mapping. Molecular population genetics studies have contributed greatly to our understanding of parasite population biology and microevolution. Nonetheless, the application of molecular population genetics to parasites has lagged and continues to lag behind that of studies on free-living species. The negative side of this lag is that there are not yet enough data to determine if broad scale population genetic patterns or generalities are present across parasite life histories. The positive side is that many interesting research questions remain to be addressed.

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GIARDIA METABOLISM AND REGULATION

E.L. Jarroll, Department of Biological Sciences, Lehman College-CUNY
T.A. Paget, Sunderland Schoolof Pharmacy, University of Sunderland

Giardia exhibits minimal biosynthetic capacity lacking de novo lipid, de novo purine, and de novo pyrimidine syntheses. This protozoan has a mitosomes but lacks typical eukaryotic organelles such as mitochondria and typical Golgi. Trophozoites use glycolysis (from glucose only) and arginine dihydrolase pathways to synthesize ATP relying on substrate level phosphorylation for energy production rather than cytochrome-mediated oxidative phosphorylation. Enzymes responsible for end product and energy production in *Giardia* are not found in subcellular organelles but are cytoplasmic. End products of glucose catabolism include acetate, ethanol, alanine, carbon dioxide, and hydrogen. There is an active pentose phosphate pathway for the production of reducing power and ribose. *Giardia's* metabolism is tightly controlled and regulated. When *Giardia* trophozoites encyst, they shift their catabolism of glucose from energy production to the synthesis of the cyst wall specific giardan, a beta- 1, 3 N-acetylgalactosamine homopolymer. During giardan synthesis, a pathway of enzymes is induced including a novel enzyme, cyst wall synthase that synthesizes the polymer. Also, encysting trophozoites increase their catabolism of arginine to offset the ATP lost from slowing glycolysis. Most metabolic, proteomics, and transcriptomics studies have been on a limited number of isolates. Few comparative studies of metabolism and biochemistry of isolates have been reported. However, these few studies do indicate metabolic differences among isolates and comparative metabolic studies of genetically distinct isolates are crucial to understanding how *Giardia* in its environments. Variation in reproduction rates and virulence among isolates may be responsible for these differences.

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(39)

A HISTORY OF IMMUNOPARASITOLOGY IN THE U.S.

R.E. Kuhn, Wake Forest University

In the late 1800s, the Europeans, led by Robert Koch and Louis Pasteur and their students, were leaps and bounds ahead of the Americans on studies on infectious diseases and immunology. In the U.S., Theobald Smith and William Henry Welch, both eminent pathologists, would provide the initial leadership to bring parasitology and immunology to the forefront. Smith fostered the use of experimental animals for research on infectious diseases, thereby establishing the field of comparative pathology. Welch would become dean of the newly formed Johns Hopkins University School of Hygiene and Public Health. The new institution would be dedicated to scholarly endeavors with basic scientists and clinicians interacting to solve problems of public health. Welch established a Department of Medical Zoology and appointed William Hegner as the first director. Hegner recruited a stellar faculty that included William W. Cort (parasitology), Francis Root (medical entomology), William H. Taliaferro (parasitology) and others. In the years to come, all of the faculty members would make huge contributions to immunology and parasitology. Cort attacked hookworm problems in the U.S. and abroad. His research answered many questions about the parasite and the disease. His graduate student, Norman Stoll became renowned for his own work, devising the "Stoll dilution egg-counting technique" and writing his famous paper "This Wormy World." Stoll and Merritt Starles convincingly demonstrated that parasites could induce immune resistance in infected hosts. Taliaferro provided the most impetus to the new field of immunoparasitology, beginning with his 1929 book, *The Immunology of Parasitic Infections*. He published 93 papers on host-parasite interactions, the vast majority of which were produced between 1921 and 1950. He moved more into basic immunology after 1950, recognizing that much information about the immune system was required before immunity to parasitic infections could be better understood. In 1958, Asa Chandler, who had focused his effort on the role of immunity induced by parasite-derived metabolites, organized a special symposium on immunity to parasites at the Rice Institute (later University). Thereafter, the field of immunoparasitology gained in stature with the participation of numerous new investigators. Today, several prominent societies have large sessions at their annual meetings dedicated to presentations on immunoparasitology.

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CHEMOTHERAPY OF HELMINTH INFECTIONS: HISTORICAL PERSPECTIVE

W.C. Campbell, Drew University

Early in the 20th Century, The Journal of Parasitology published an article on the treatment of disease caused by worm parasites. Some sense of the status of the field at that time may be gained by reflecting that interest was then being focused on the improved safety of tetraclorethylene over carbon tetrachloride for the treatment of roundworm infections. The remainder of the century saw the successive introduction of many new anthelmintics — drugs with greater safety, potency and breadth of spectrum. These attributes and advances in pharmaceutical technology, led to transformation of treatment practices. Assay methodology for detecting anthelmintic activity evolved throughout the period. With each successive anthelmintic class came knowledge of its biochemical mode-of-action, opportunity to exploit structure-activity relationships for the development of derivative products, and a new potential for epidemiologically based treatment programs. As readily seen in the pages of the Journal, these advances also brought a need for, and a rapidly expanding research response to, the challenge of drug resistance.

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CLOSING OF CENTENNIAL SYMPOSIUM

G.W. Esch, Department of Biology, Wake Forest University, Winston-Salem, North Carolina
S. Desser, Department of Cell and Systems Biology, University of Toronto, Toronto, Ontario, Canada
B. Nickol, School of Life Sciences, University of Nebraska, Lincoln, Nebraska

The closing of the symposium will include a brief commentary regarding the past 100 years of the *Journal of Parasitology's* publication.

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ADVANCES IN HAEMOSPORIDIAN GENOMICS

O. Hellgren, Molecular Ecology and Evolution Lad, Department of Biology, Lund University

Obtaining genomic data of avian haemosporidian parasites has been notoriously difficult due to the fact that the hosts (i. e., birds) have nucleated erythrocytes and the genome sizes between the host and parasite differ more than 50-fold. However, with the use of NGS techniques together with knowledge drawn from traditional parasitology many of these problems have now been solved. This has been done either by I) manipulate the parasites to undergo exflagellation in-vitro, thus making it possible to separate the parasite from host cells before the DNA is extracted and used for genome sequencing, and II) by sequencing blood transcriptomes of hosts during erythrocytic merogony, i.e., when the parasites undergo asexual reproduction in the blood stream and invade numerous new red blood cells. During this period the genetic activity in the parasites is high, making it possible to utilize mRNA sequencing in order to acquire sequence data of nuclear genes of the parasites. Here we present examples of ongoing genome and transcriptome sequencing projects of avian *Haemoproteus* and *Plasmodium* parasites and highlight how these breakthroughs will lead to a deeper understanding of the epidemiology and evolution of this

species diverse group of parasites. We will also discuss how the merging of the field of haemosporidian research in non-primate hosts with the deep knowledge available for the human malaria will benefit a broad community of malaria researchers.

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SPECIES CONCEPTS, POPULATIONS, AND GENERATION TIMES OF MALARIA PARASITES

R.E. Ricklefs, University of Missouri-St. Louis

The work in my laboratory has focused on the host and geographic distributions of avian malaria parasites (Haemosporida: *Plasmodium, Haemoproteus, Leucocytozoon*) as an approach to understanding parasite diversification and the outcomes of host-parasite coevolutionary interactions in this system. New species appear to form primarily by host-shifting, most likely in allopatry. Contemporary avian malaria parasites appear to have diversified from a common ancestor as recently as 10 Mya, which is remarkable considering that population sizes and generation times probably do not differ substantially between host and parasite. Occurrences of parasite lineages indicate highly dynamic changes in distributions among hosts and locations, reflecting parasite-host and parasite-parasite interactions.

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PLASMODIUM RELICTUM: A TALE OF HOST, PARASITE AND VECTOR INTERACTIONS

R. Fleischer and **L. Sackett**, Smithsonian Conservation Biology Institute
K. McClure, Smithsonian Conservation Biology Institute and University of California, Santa Cruz
T. Callicrate, Smithsonian Conservation Biology Institute and University of Maryland

Only a single species of introduced malaria parasite (*Plasmodium relictum*) is typically found in Hawaii, where it infects many of the native and introduced bird species. MtDNA and other DNA marker analyses have shown that the lineage in Hawaii is GRW4, a lineage found mostly in the Old World, although it is also the most common one found on oceanic islands around the World. The vector in Hawaii, and a primary vector elsewhere, is the introduced *Culex quinquefasciatus*, and both mosquitoes and avian malaria occur at elevations below about 1500 m in the Hawaiian Islands. As a result of malaria, most species of native birds occur only above that elevation. Our experiments suggest that Australo-Pacific, but not New World origin *C. quinquefasciatus*, are able to effectively vector the Hawaiian GRW4 lineage. In addition, although GRW4 is relatively benign in Old World bird species, and in most introduced bird species in Hawaii, it exhibits high virulence and causes high mortality rates in many native Hawaiian birds, especially Hawaiian honeycreepers. Collectively, the patterns of virulence in naïve versus longstanding bird hosts and vectors, and the distribution and abundance of Hawaiian avifauna, suggest that both host and pathogen may be evolving in response to the other. One honeycreeper species, the Hawaii amakihi, shows a mixed response to GRW4 infection, with nearly all low elevation, and about 40% of high elevation birds surviving infection. To assess the potential role of genetics in the amakihi's mixed susceptibility, we conducted outlier and association analyses of genomic DNA sequences from a 45k bait capture approach using taxonomic, altitudinal, geographic (within and among islands), and temporal (e.g., present day versus before introduction of malaria in the 1940s) samples. We also present results from next generation sequencing analyses of *Plasmodium relictum* GRW4 to assess variation within Hawaii that may relate to its level of virulence, and to compare samples of GRW4 and its close relatives from elsewhere in the World to better identify its source and how it may have changed subsequent to its introduction to Hawaii. Our hope is that a better understanding of this

invasive pathogen, its vector, and its interactions with its hosts, will aid mitigation efforts to control its devastating impacts on native Hawaiian birds.

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(45)

COMPLETING THE CYCLE: STUDIES OF SEXUAL STAGES OF HAEMOSPORIDIANS

G. Valkiunas, Nature Research Centre, Vilnius

There is marked increase in publications on biology of haemosporidian parasites (Haemosporida) in wildlife during the past 15 years, indicating high potential of this host-parasite system in biomedical research. However, relatively few studies address the host parasite-interactions during sporogonic development. We designed and carried out several experimental studies addressing patterns of the sporogonic development of widespread species of avian *Haemoproteus* in vitro and in vivo (both in co-evolved and not co-evolved vector-parasite associations). Several lineages of *Haemoproteus* spp. were isolated from naturally infected passerine birds and their ookinete development was initiated in vitro by mixing blood containing mature gametocytes of two different parasites. Additionally, mosquitoes (Culicidae) and biting midges (Ceratopogonidae) were infected by allowing them to take infected blood meals on *Haemoproteus* spp. infected birds. These experiments show that 1) the biting midge *Culicoides impunctatus* is a vector of deadly *Haemoproteus minutus*, which is responsible for mortality in captive parrots; 2) heavy *Haemoproteus* infections kill bird-biting dipteran insects; 3) simultaneous sexual process of two genetically distant lineages of haemosporidian parasites might increase the efficiency of reproductive cells, resulting in the development of a greater number of normal ookinetes, indicating possible beneficiary effects of simultaneous sporogony; 4) PCR-based diagnostics should be carefully used in vector studies of haemosporidians because it detects parasites in insects for several weeks after initial infection, but does not distinguish abortive parasite development. The marriage of molecular and morphological approaches worth more attention in haemosporidian researchers, particularly in wildlife studies, because such approach provides much additional knowledge for better understanding patterns of parasite transmission and virulence. That requires close collaboration between researchers from different fields with a common interest.

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MANIFOLD HABITAT EFFECTS ON THE PREVALENCE AND DIVERSITY OF AVIAN HEMATOZOA

R.N. SEHGAL, San Francisco State University

The effects of rapid global environmental changes on parasite distributions are diverse and despite potential consequences to ecosystem health, large-scale studies involving wildlife have been scarce. Here we present data of the effects of deforestation and global climate change on the prevalence and diversity of blood parasites in birds ranging from the tropics to the arctic. Using complementary techniques of blood smear analysis and molecular biology, samples are assayed for species of *Plasmodium*, *Haemoproteus*, *Leucocytozoon* and *Trypanosoma*. We have obtained results regarding the host-specificity, prevalence and lineage diversity of these parasites in several communities of birds from Africa, Central and South America, California and Alaska. We find that habitat degradation leads to altered patterns of parasite prevalence and disruptions in parasite species dominance. We also present data on how habitat and climatic conditions may affect the evolution of specialist vs. generalist strategies in avian malaria. Our work incorporates satellite imagery and bioclimatic data to quantify differences among the collection sites, and

predict how habitat changes may affect the spread of infections. We have also initiated studies on genes involved in host specificity, with the characterization of erythrocyte invasion genes from the chicken parasite *P. gallinaceum*. With our long-term agenda to discern the interplay between habitat, vector ecology, and genetics on the host-specificity of parasites, we emphasize that influences of land use changes on parasite prevalence are complex, and will require the detailed study of the vector ecology, and the further quantification of fine-scale habitat effects. Through time, our multidisciplinary approach will aid in predicting how habitat changes will influence future scenarios of host-parasite interactions.

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THE TAXONOMY OF MALARIA PARASITES: IMPLEMENTING 21ST CENTURY TOOLS

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The taxonomy of haemosporidians has had a tumultuous history with numerous changes at every level over the past century of their research. Vertebrate hosts, insect vectors, life history characteristics, and parasite morphological differences have been utilized to classify the parasites as species, genera, and, at times, families and additional organizing levels such as subgenera have been implemented as well. The advent of molecular phylogenetics has challenged many classifications and some revisionary work has used these data. Molecular sequences can also be utilized for delimiting species and I will present results of these analyses from various groups of haemosporidians. I will also discuss some of the challenges and precautions in moving forward.

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(48)

MARINE AND COASTAL ZOONOTIC HELMINTH INFECTIONS
(Eminent Parasitoloigst Lecture)

R.M. Overstreet, The University of Southern Mississippi

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BIOGEOGRAPHY AND HOST-RELATED FACTORS LIMIT GENEALOGICAL CONGRUENCE AMONG SPECIFIC ECTOPARASITIC LICE AND THEIR RODENT HOSTS

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Parasites and hosts interact across both micro- and macroevolutionary scales where congruence among their phylogeographic and phylogenetic structures may be observed. Within southern Africa, the four-striped mouse genus, *Rhabdomys*, is parasitized by the ectoparasitic sucking louse, *Polyplax arvicanthis*. Molecular data recently suggested the presence of two cryptic species within *P. arvicanthis* that are sympatrically distributed across the distributions of four putative *Rhabdomys* species. We tested the hypotheses of phylogeographic congruence and co-phylogeny among the two parasite lineages and the four host taxa, utilizing mitochondrial and nuclear sequence data. Despite the documented host-specificity of *P. arvicanthis,* limited phylogeographic correspondence and non-significant co-phylogeny was observed. Instead, the

parasite-host evolutionary history is characterized by limited co-divergence and several duplication, sorting, and host-switching events. Despite the elevated mutational rates found for *P. arvicanthis,* the spatial genetic structure was not more pronounced in the parasite lineages compared to the hosts. These findings may be partly attributed to larger effective population sizes of the parasite lineages, the vagility and social behaviour of *Rhabdomys*, and the lack of host-specificity observed in areas of host sympatry. Further, the patterns of genetic divergence within parasite and host lineages may also be largely attributed to historical biogeographic changes (expansion-contraction cycles). It is thus evident that the association between *P. arvicanthis* and *Rhabdomys* has been shaped by the synergistic effects of parasite traits, host-related factors, and biogeography over evolutionary time.

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CHANGES IN BACTERIAL RESISTANCE AND LONGEVITY OF CRICKETS INFECTED WITH GORDIAN WORMS (NEMATOMORPHA)

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The stress of harboring parasites alters a host's physiological state as it induces an acute stress response. In many animals, the acute stress response correlates with immunosuppression. Thus, theory predicts that when these animals are subjected to parasite infection, they also become more susceptible to bacterial and viral infections. This eco-immunological trade-off has been well studied in arthropods including crickets. The parasite *Paragordius varius* (Gordian worm) relies on its cricket host, *Acheta domesticus*, for the resources to grow from a 30µm larva to a 25cm adult; upon parasite maturation, the parasite's mass often exceeds that of the host's. At the end of the host-parasite association, the parasite relies on a physiologically-capable host for transport and release into aquatic environments, where *P. varius* reproduces. Therefore, the need for a healthy, immune-competent host and the immunosuppression caused by enormous stress of hairworm infection appears to pose a conflict within the energy balance of the host-parasite unit. To begin teasing this conflict apart, we tested 1) the resistance of the host-parasite unit to tertiary bacterial threats and 2) the long-term survival of the host-parasite unit. Adult female crickets were exposed to 10-50 *P. varius* cysts. Controls were sham exposed. At 21 days post exposure (DPE), crickets were injected with an LD_{50} dose of the bacterial insect pathogen *Serratia marcescens*. Mortality in both groups was observed until 31 DPE at which time crickets (alive and dead) in the experimental group were dissected to ensure infection with *P. varius*; uninfected individuals were removed from further analysis. In the second experiment, survival rates of *P. varius*-infected crickets were compared with those of uninfected controls. Surprisingly, we found that the experimental group, also infected with *P. varius*, had greater survival success to LD_{50} doses of *S. marcescens* than uninfected control crickets. Furthermore, survival curves showed greater short-term and long-term survival of *P. varius* infected crickets compared to control crickets. The results of these experiments suggest that Gordian worm infections may boost immune activity of host-parasite units, fundamentally allowing for greater disease resistance and increased longevity compared to uninfected control animals. Although the particular mechanisms leading to these results have yet to be determined, several alternative explanations will be discussed.

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RNA-SEQ ANALYSIS OF FIELD-DERIVED *BIOMPHALARIA PFEIFFERI* INFECTED WITH *SCHISTOSOMA MANSONI* FROM WESTERN KENYA

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G.M. Mkoji, Centre for Biotechnology Research and Development, Kenya Medical Research Institute
E.S. Loker, University of New Mexico Center for Evolutionary and Theoretical Immunology Museum of Southwestern Biology, Division of Parasitology

Over 90% of the world's 240 million cases of schistosomiasis occur in sub-Saharan Africa, with the trematode *Schistosoma mansoni* responsible for causing nearly half of these cases. The Neotropical snail *Biomphalaria glabrata* has been an important model host for *S. mansoni* but it is essential that we understand how this parasite interacts with its most widespread African snail host, *Biomphalaria pfeifferi*, the host in which this parasite likely evolved and is today most extensively transmitted. Our previous 454 transcriptome studies of a field-derived uninfected and a *S. mansoni*-infected *B. pfeifferi* have provided us with insight into these interactions, showing a pattern of down-regulation of immune genes, like FREPs and heat shock proteins, in response to *S. mansoni* infection. Microsporidians are among the symbionts found within the infected snail using the 454 transcriptome data. The promise of replicated data sets featuring more in-depth coverage than available with 454 methodology has led us to undertake Illumina HiSeq transcriptomics sequencing of the following additional samples in triplicate, all featuring snails taken directly from a natural transmission focus in western Kenya: uninfected *B. pfeifferi*, *B. pfeifferi* with patent *S. mansoni* infections, and *B. pfeifferi* exposed to *S. mansoni* for 1- or 3-days. Raw reads (over 30 million paired-end reads for each replicate) were screened and trimmed followed by a hybrid transcriptome generation using *de novo* assembly of Illumina reads informed by 454 transcripts. Transcript assembly of samples with *S. mansoni* exposures was performed using the published *S. mansoni* transcriptome. Differential expression was evaluated in order to identify specific immune gene responses and gene pathways of interest. In addition, eukaryotic symbionts have been identified that may play a role in modulating transmission. We will report on general gene response trends between the exposures, specific immune responses, and presence of symbionts, all of which provide insight into the many interactions taking place in a natural transmission focus. Supported by R01 grant AI101438.

(52)

ENDOPARASITIC INFECTION IN A WILD POPULATION OF MEERKATS (*SURICATA SURICATTA*)

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The meerkat (*Suricata suricatta*) is one of the most endearing South African wildlife celebrities and highly studied social mammals. Parasitic infection is widely acknowledged as an important regulatory factor in host populations. However, basic knowledge on the parasitic infections of meerkat populations is lacking. Fecal samples from wild meerkats (n=100) were analyzed by centrifugal flotation for the presence of endoparasitic infection. Endoparasitic taxa identified by the presence of eggs or oocysts included *Toxocara suricattae*, *Oxynema suricattae*, *Pseudandrya*

suricattae, *Cystoisospora* sp. and *Eimeria* sp.. Non-specific diagnoses were made for parasites in the Order Strongylida, Order Spirurida and Family Eimeriidae based on the morphology and size of the eggs and oocysts. The prevalence of infection with *T. suricattae* and the strongylate species increased with host age. The prevalence of coccidian infections and intensity of infection by the strongylate species (estimated by fecal egg count) increased with decreasing group size, suggesting that stress associated with living in smaller group may increase susceptibility to parasitism. Parasite infracommunities were more similar between individuals from the same group than between individuals from different groups, suggesting an important role of the residential environment in parasite transmission. This study represents the first detailed report of gastrointestinal parasitism in a population of wild meerkats, and a benchmark for future studies of host –parasite interactions in the life history of this species.

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(53)

INTERACTIONS BETWEEN A MICROSPORIDIAN PARASITE, *NOSEMA FUMIFERANAE*-LIKE ISOLATE, AND ITS UNEXPECTED HOST, THE INVASIVE LIGHT BROWN APPLE MOTH

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In contrast to most invasive species, after its discovery in California in 2007 and initial spread along the coastal region, the invasive Light Brown Apple Moth, *Epiphyas postvittana,* has been in decline. More typically, invasive species are released from natural enemies allowing their populations to grow more extensively in their new regions. In California *E. postvittana* has experienced biotic resistance from several parasitoid wasps and local predators, as well as from a microsporidian parasite. Partial sequencing of the SSU gene for this microsporidian, suggested a *Nosema fumiferanae*-like isolate. We have conducted laboratory experiments to determine the effects of parasite infection on the life history performance of its novel host when stressed. We altered relative humidity (40% versus 70%) and provided different food sources for the host ranging from artificial diet to foliage from five plant species differing in defensive chemistry. We inoculated third instar *E. postvittana* larvae with 10^3 spores of *N. fumiferanae* and subsequently fed them on the different food sources in both low and high humidity conditions to determine the timing of parasite replication, and the development time, survivorship, pupal weight, and adult longevity and fecundity of infected hosts compared to uninfected control hosts. Overall, uninfected larvae had shorter development times, greater survivorship, larger pupal weight, and increased longevity and fecundity compared to infected larvae. Similarly, larvae reared on artificial diet or in high humidity conditions showed improved performance traits compared to larvae reared on plant foliage or in low humidity, regardless of infection status. The effects of this microsporidian parasite in its host is likely highly dependent on the current conditions in the field. Parasitism by the microsporidian parasite in conjunction with mortality from resident parasitoid wasps may help to explain the declining abundance of this exotic moth species in coastal California.

(54)

ASSESSMENT OF SPATIAL, COMMUNITY AND GENETIC STRUCTURE OF STREAM DWELLING TUBIFICID WORMS IN MONTANA, USA

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Genetic studies are recognized increasingly as playing important roles in understanding naturally occurring disease dynamics, from predicting host genetic diversity and co-evolutionary processes to identifying species composition in ecological communities. This is especially true for parasites with a two-host life cycle, as both hosts will contribute to spatial disease patterns. *Tubifex tubifex*, the definitive oligochaete host of whirling disease parasite *Myxobolus cerebralis,* is now viewed as central to the severity and eventual management of whirling disease for certain trout populations. In this study, we examine the distribution and abundance of *Tubifex* spp.*, Ilyodrilus* spp. and *Rhyacodrilus* spp. in four watersheds in Montana, USA, while simultaneously assessing their spatial genetic variability and relationship to fish disease using 16S ribosomal DNA (16S rDNA). We assessed183 tubificid worms for genetic variability from locations classified as positive or negative for whirling disease based on 5 – 8 years of monitoring by the Montana Department of Fish, Wildlife and Parks. Within genera, we found two groups of *T. tubifex* (lineages I and III), two groups of *Rhyacodrilus* spp. and four groups of *Ilyodrilus* spp. The genetic variability within taxa was relatively high (~10% sequence divergence) for all three taxa. The community composition was non-randomly distributed over the landscape with more similarity among locations within the same watershed than locations from different watersheds that had similar whirling disease classification. In conclusion, the results of this study show the distribution and abundance of these taxa to be spatially related and highlight the importance of watershed features on host-parasite interactions.

(55)

TWO NOVEL MYXOZOANS FROM THE URINARY TRACT OF TOPSMELT, *ATHERINOPS AFFINIS*

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Two myxozoan infections were observed in the kidney of topsmelt, *Atherinops affinis,* during a survey of parasites of estuarine fishes in the Carpinteria Salt Marsh Reserve, California. Fish were collected at three separate time points and examined histologically using hemotoxylin and eosin and Giemsa stains in 2012 and 2013. Large, plasmodia were observed in the renal interstitium of several fish from the first two collections (5/8, 11/20, respectively) , and in some fish these plasmodia replaced over 80% of the kidney. These plasmodia were consistent with

extrasporogonic forms described in several myxozoan species. In addition, presporogonic and polysporogonic stages were observed in the lumen of the renal tubules, collecting ducts and ureters. The latter contained subspherical spores with up to four polar capsules, consistent with the genus *Chloromyxum*. For the third collection (15 May 2013, n=30), kidneys were portioned for examination by histology, wet mount, and DNA extraction for small subunit ribosomal DNA gene amplification and sequencing. Histology showed the large plasmodia in the kidney interstitium of 3 fish, and 2 other fish with subspherical myxospores in the lumen of the renal tubules with smooth valves and two spherical polar capsules consistent with the genus *Sphaerospora*. *Chloromyxum*-type myxospores were observed in the renal tubules of one fish by wet mount. DNA amplification and sequencing of the kidney tissue from this fish yielded a partial SSU rDNA sequence of 1769 bp. BLAST analysis and phylogenetic reconstruction using PHYML suggested this organism to be a novel species of *Chloromyxum,* most similar to *Chloromyxum careni* (84% similarity). In addition, subspherical myxospores with smooth valves and two spherical polar capsules consistent with the genus *Sphaerospora* were observed in 2 other fish. DNA amplification and sequencing of the kidney tissue from 1 fish yielded a partial SSU rDNA sequence of 1937 bp. BLAST analysis and phylogenetic reconstruction using PHYML suggests this organism to be a novel species of *Sphaerospora* most closely related to *Sphaerospora epinepheli* (93%). We conclude that these organisms represent novel species of the genera *Chloromyxum* and *Sphaerospora* based on host, location, and SSU rDNA sequence. We further conclude that the formation of large, histozoic plasmodia in the renal interstitium represent extrasporogonic stages of the *Chloromyxum* species for the following reasons: 1. Large plasmodial stages were only observed in fish that also had *Chloromyxum*-type spores developing within the renal tubules, 2. DNA sequence consistent with the *Chloromyxum* sp. was only detected in fish with the large plasmodial stages and 3. Large extrasporogonic stages have been described for other species in the genus *Chloromyxum* but never in a *Sphaerospora* species.

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(56)

FEAST AND FAMINE: THE NUTRITIONAL ECOLOGY OF A HAIRWORM (*PARAGORDIUS VARIUS*) AND ITS CRICKET HOST (*ACHETA DOMESTICUS*)

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Life-history trait alteration is an example of a host compensatory response when infected with a parasite. For example, if parasites reduce nutrient availability to their hosts, this might cause a reduction in fat storage, leading to increased food consumption by a host to alleviate the cost of parasitism. As a parasitic juvenile, hairworms feed on the fat bodies and tissues of their cricket host. Upon maturation, hairworms begin manipulating the cricket host to enter water. This behavior enables a hairworm to complete the final stage of its life cycle as a free-living adult in water. In this study, we investigate the effects of diet on cricket fat body production and host morphology during infection with hairworms. Additionally, we examined the effect of host diet and choice on parasite growth and fecundity. Female crickets, *Acheta domesticus* were exposed to cysts of the hairworm, *Paragordius varius*. Crickets were subjected to three treatments including a high protein to carbohydrate (3:1) diet, high carbohydrate to protein (3:1) diet, and a third group that provided a choice between the high protein and high carbohydrate diets. Food and water were provided ad libitum. Effects of diet were measured on crickets host morphology during and post hairworm emergence across all diets. All measurements of crickets and hairworm fecundity in different diet treatments were compared to controls. Our work indicates that cricket fat body mass increases within the first 10 days of infection but this mass was significantly reduced as juvenile parasites reached maturity. The effects of diet and diet choice on cricket and hairworm development and reproduction will be discussed. This novel investigation is the first study to examine the effect of diet on hairworm growth and reproduction and diet choice in Acheta domesticus when infected with a parasite. Our work reveals that life-history trait alteration can be used to combat and/or facilitate infection and results can be

quantified. However, the underlying mechanisms that drive these behaviors are poorly understood.

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EVALUATING THE ROLE OF PARATENIC HOSTS IN THE EVOLUTION OF COMPLEX LIFE CYCLES: ECOLOGICAL BRIDGES OR EVOLUTIONARY STEPPING STONES?

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The evolution of life cycles is a fundamental concept in parasitology. Previous work has largely focused on the addition of definitive and/or intermediate hosts while ignoring the role of paratenic hosts in the evolution of complex life cycles. The trematode *Halipegus eccentricus* (Hemiuridae) is a unique system to examine the potential benefits associated with paratenic hosts because this is one of the few species that both utilizes a paratenic host and the entire life cycle can be experimentally manipulated in the laboratory. This study compares the rate of establishment, duration of migration, and time to maturity of metacercariae of *H. eccentricus* that infect anurans via the odonate paratenic hosts and metacercariae of the same age from time-control ostracod 2nd intermediate hosts. To compare these routes of infection, metacercariae from experimentally infected odonates were pipetted into the stomach of toads; whereas control groups of toads were exposed to metacercariae from experimentally infected ostracods. From each group of infections, a subset of toads was dissected 2 DPE to estimate the initial rates of establishment. The mouths of the remaining toads were monitored daily for the presence of worms and if the worms present produced eggs. Our work suggests that *H. eccentricus* from infected odonates are capable of establishing infections at significantly higher rates, and on average, these worms migrate to the mouth and mature nearly twice as fast as those from ostracod 2nd intermediate hosts. All hemiurid trematodes use microcrustaceans as 2nd intermediate hosts, however, this study illustrates that the addition of a paratenic host to the conserved life cycle may benefit parasites by increasing transmission and altering life history traits. Given the presence of paratenic hosts across distinct groups of parasites, it seems likely that paratenic hosts play a major role in the evolution of complex life cycles by serving as a transition from the status of an unsuitable host species to an obligate one. Our work provides the first experimental evidence that supports this hypothesis.

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IS YOUR SNAIL HOST WHO YOU THINK IT IS? ENVIRONMENTAL EFFECTS ON SNAIL SHELL SHAPE AND IMPLICATIONS FOR INTERMEDIATE HOST IDENTIFICATION

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Accurate host identification is critical for any parasitological study. However, for parasitologists, some host groups like the freshwater molluscs have always presented difficulties in accurate species identifications. Historically, snail shell dimensions have been considered informative regarding species identification. However, the ecological conditions of freshwater habitats have been shown to induce plastic changes to shell morphology. Among freshwater gastropods, snails in the family Physidae are morphologically diverse but notoriously difficult to identify. In fact, recent molecular data suggest that morphologically-based species descriptions have overestimated physid species diversity by as much as 50%. Although several studies have demonstrated shell plasticity of physid snails from different environmental conditions, no study has assessed changes in shell plasticity when distinct morphotypes experience the same ecological conditions. In this study, we hypothesize that physid morphotypes, in general, are not distinct genetically, but are plastic responses to their environments. To test this hypothesis, we raised two distinct, but geographically proximate, *Physa acuta* morphotypes under laboratory conditions

and quantified their morphology over two generations. Rapid convergence of shell shape within a single generation among the two *P. acuta* morphotypes suggests that shell shape differences are plastic responses to environmental variation. However, a single-generation lag in size convergence among these two morphotypes suggests there is an epigenetic difference between generations within populations. Future studies will focus on the effects of trematode infections on snail shell shape.

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(59)

HELMINTHS OF *GAMBUSIA AFFINIS* (CYPRINODONTIFORMES: POECILIIDAE) IN WEST TEXAS

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From October 2012 through September 2013, a total of 307 *Gambusia affinis* were collected from a pond on the Red Arroyo, an intermittent waterway in the west-central Texas city of San Angelo, for necropsy and parasitological analysis. Records of fish length, sex, and parasitic infection were kept. The most common parasites found in these fish were *Salsuginus seculus*, *Diplostomum* sp., *Gyrodactylus* sp., *Neoechinorhynchus cylindratus*, and *Eustrongylides* sp. Other parasites found include *Trichodina* sp., *Bothriocephalus acheilognathi*, and an unidentified pentastomid (Sebekidae). The digeneans *Diplostomum* sp., *Clinostomum* sp., and *Posthodiplostomum* sp. were highest in fall and winter, and populations of the monogeneans *S. seculus* and *Gyrodactylus* sp. were highest in spring. Furthermore, *S. seculus* was common throughout the year, whereas *Gyrodactylus* sp. was not. Length frequency was correlated with prevalence and intensity of infection. Sex was also a determining factor of infection such that male fishes exhibited lower mean intensity than females. This difference may be attributed to the strong sexual dimorphism exhibited in this fish species.

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THE DILUTION EFFECT IN *ECHINOSTOMA* SPP.: EXAMPLES FROM FIELD COLLECTED DATA

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Rapid losses of biodiversity due to the changing environmental landscape have spurred increased interest in the role of species diversity and disease risk. A leading hypothesis for the importance of biodiversity in disease reduction is the dilution effect, which suggests that increasing species diversity within a system decreases the risk of disease among the organisms inhabiting it. This hypothesis was investigated using field studies from sites across the U.S. to examine the role of snail diversity in both first and second intermediate larval stages of *Echinostoma* spp. parasites. Neither prevalence of *Echinostoma* spp. miracidia or cercariae infection were affected by increases in snail diversity. However, a significant negative correlation with metacercariae intensity and the number of snail species in a body of water was observed. Additionally, varying effectiveness of the diluting hosts was observed. Species that were incompatible first intermediate hosts were more successful at diluting the echinostome parasites in the focal species than species that can harbor *Echinostoma* spp. first intermediate larval stages. These findings have important implications not only on the role of species diversity reducing disease risk, but the success of the parasites completing their life cycles and maintaining their abundance within an aquatic system.

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BASS PARASITES OF ONEIDA LAKE, EIGHTY YEARS LATER

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A survey of Largemouth (*Micropterus salmoides*) and Smallmouth (*Micropterus dolomieu*) Bass component parasite communities in Oneida Lake was conducted in the summer of 2012 and compared to an earlier survey conducted by Van Cleave and Mueller from 1929 to 1931. The component parasite communities between surveys were 31% similar for Largemouth and 28% for Smallmouth bass. Between species, the component parasite communities were considerably more similar for the present survey (77%) than the survey conducted by Van Cleave and Mueller (47%). Seven species reported by Van Cleave and Mueller were present in this survey and 27 species are new records for the bass of Oneida Lake. Several species of parasites exhibited differences in prevalence and mean abundance between surveys. Two species (*Rhipidocotyle papillosum* and *Crepidostomum. cornutum*) were absent from this survey but were reported as common in the 1929-1931 survey and likely represent extirpations that coincide with the loss of some native freshwater bivalves from Oneida Lake. Other differences in the parasite communities may also be explained by the ecological changes in Oneida Lake in the past 81 years. The changes in bass parasite communities between surveys emphasize the importance of recognizing the historical nature of parasite communities, especially in ecosystems with a history of large-scale changes.

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HOST SPECIFICITY OF AN INTRODUCED PARASITE TO A NON-NATIVE FISH IN THE PANAMA CANAL

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M.E. Torchin, Smithsonian Tropical Research Institute

To establish, persist, and spread, introduced parasites must be either “pre-adapted” to hosts in the new range and/or rapidly adapt to new hosts. Generalist parasites are predicted to be more successful at invading new geographic ranges because they can effectively colonize novel host species compared to specialist parasites. Yet patterns of host range are affected by both ecological and evolutionary factors that could drive a parasite to specialize on a new host species. Here we ask to what extent does the introduced parasite, *Centrocestus formosanus*, specialize on particular hosts when it is introduced to a new environment? We used field comparisons to examine patterns of host use in nature and laboratory infection experiments to determine host specificity (compatibility) and host preference by holding encounter rates constant. In nature, the invasive peacock bass, *Cichla ocellaris*, exhibited higher prevalences and intensities of *C. formosanus* compared to 3 other cichlid species. Laboratory infection experiments demonstrated that while all hosts are susceptible to infection, *C. ocellaris* experiences significantly higher infection rates in both single species trials and mixed species trials compared to other cichlid fish. In contrast to other research findings suggesting that *C. formosanus* is a generalist parasite that can infect a broad array of fish species, our results demonstrate specificity and perhaps specialization on a novel host species. I will discuss the implications of specializing on a novel invasive host species for the success of an introduced parasite and potential evolutionary drivers for this observed pattern. Finally, I will describe an experiment which will test if the observed pattern is the result of rapid adaptation of host-specialization in a human dominated landscape.

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GASTROINTESTINAL HELMINTH COINFECTION PATTERNS IN EUROPEAN STARLINGS (*STURNUS VULGARIS*)

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A growing area of ecological research is the community ecology of parasites within hosts. Because most infected hosts carry multiples species of parasites examining patterns of parasite diversity within hosts is necessary to reflect natural processes. Coinfection can reveal interspecific interactions among parasite species and contribute to understanding mechanisms resulting in host pathology. Factors contributing to coinfection include host exposure, life cycles of the parasite, and host immunity. Coinfecting parasite species may compete through exploitation (both species access the same host resource) or interfere (one species limits of excludes the presence of the other). In this study, we investigated patterns of coinfection by intestinal helminths in a wild population of European Starlings (*Sturnus vulgaris*). European Starlings are a good model for studying coinfection because of their high abundance and previously described parasite diversity. We necropsied 43 juvenile birds donated from O'Hare International Airport, Chicago, Illinois, USA. We used standard parasitological procedures including examination of all internal organs with the aid of a dissecting microscope. Parasites were isolated from host tissue and preserved for either morphological or molecular identification. We isolated one acanthocephalan (prevalence = 37.2%, intensity = 1-23) and one cestode (prevalence = 34.9%, intensity = 1-3). We observed three species of nematodes (sp. 1 prevalence = 5%, intensity 1-5, sp. 2 prevalence = 19.5%, intensity = 1, and sp. 3 prevalence = 9%, intensity = 1). We tested the independence of infection across all three taxa using a log linear model in R (package MASS). We found that 32.6% (14) of all individuals showed coinfection (13 of 14 showing two taxa and one showing all three) but that there was no significant relationship among infection with the different taxa ($p = 0.445$). Variation in the specific life cycles of each parasite could explain the independence of coinfection of the starlings. Although the population of birds shows concurrent infections of multiple species, the birds were likely exposed to each species at different locations, contributing to a random pattern of infection. Alternatively, because the birds were juveniles they may not have acquired infections with a high enough intensity to result in competition among the parasite species, further contributing to the lack of interactions detected. Increasing the sample size could improve our ability to detect coinfection amongst the taxa. Identification of the parasites to a lower taxonomic level via morphological or molecular data would reveal the specific life cycles and methods of transmission for each parasite species, information useful to understanding coinfection within starlings, particularly this population. This study contributes to our understanding of patterns of multiple parasite infection and furthers our understanding of community ecology in a wild population.

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DOES THE BIG THICKET NATIONAL PRESERVE PROTECT AQUATIC COMMUNITIES? A TEST CASE USING PARASITES AS PROXIES FOR BIODIVERSITY

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As part of a long term effort to determine if the Big Thicket National Preserve (BTNP) in Texas is effectively protecting aquatic habitats, a study was conducted to determine if parasite diversity in

catfishes is higher inside the BTNP than outside. Channel catfish (*Ictalurus punctatus*) and yellow bullhead (*Ameiurus natalis*) were collected from 7 sites inside the BTNP and 6 sites outside the BTNP from July 2009 to October 2013. Twenty-seven parasite species (9 trematodes; 2 cestodes; 1 monogene; 1 acanthocephalan; 8 nematodes; 1 myxozoan; 4 crustaceans; 1 leech) were recovered from 57 ictalurids (41 *I. punctatus*; 16 *A. natalis*) inside the BTNP, whereas only 14 parasite species (6 trematodes; 2 cestodes; 1 monogene; 3 nematodes; 2 crustaceans) were recovered from 38 ictalurids (28 *I. punctatus*; 10 *A. natalis*) outside the BTNP. Rarefaction analyses suggest that overall parasite species richness is higher inside the BTNP than outside when all hosts are combined, when *I. punctatus* is considered alone, but not when *A. natalis* is considered alone. Parasite communities inside the BTNP tend to: 1) include more autogenic, adult helminth species; 2) more nematodes and trematodes utilizing other fishes as definitive hosts; and 3) higher abundances of parasites with complex life cycles. These results suggest higher diversity and abundances in both fish and invertebrate communities within the BTNP, and therefore that this conservation unit has some positive effects on the aquatic communities it was intended to preserve.

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A REPORT FROM THE FRONT LINES OF AN ACADEMIC JOB SEARCH: CURRENT TRENDS, WHAT THE FUTURE MAY HOLD, AND WORKING ON A VIABLE BACKUP PLAN

B. Hanelt, University of New Mexico

Many of us have gotten sage advice during our graduate school careers about how to land a tenure track position: 1) Work for a big-name and highly recognized PI, 2) publish in the best journals, and 3) make sure you get a set of glowing recommendation letters from famous scientists who are familiar with you and your work. By simply following this template you will join your colleagues who await you in the ivory tower. Yeah right. Even young scientists who followed this advice are entering one of the toughest job markets in recent times. Between 2005 and 2009, more than 100,000 doctoral degrees were awarded in the United States. In the same period there were just 16,000 new tenure track positions. This gluttony of fresh PhD students and increasingly amassing post-docs, Research Professors, Visiting Professors, and temporary lecturers has led to increased competition for the few available academic jobs. Receiving 400-600 applications for an R1 position and 100-200 applications for a small liberal arts college position has become commonplace. Landing a job with these odds seem insurmountable, but there are things candidates, especially those who did not follow the advice above, can do to land on the top rather than the bottom of the rankings pile. I will discuss the application packet, how to ensure that your packet is not immediately passed over, and how committees go about 'processing' hundreds of packets. I will briefly talk about the ins and outs of a phone interview, campus interview, research seminar, teaching demonstration, and the often dreaded "chalk talk". Finally, I will consider the idea that careers can exist outside of academia. Graduate students who prepare early during their careers for this eventuality will find that the transition between academia and the outside world leads to less anxiety and disappointment.

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THE WONDERFUL WORLD OF TICKS – RESEARCH, MENTORING, AND OUTREACH

S. Little, Oklahoma State University

Ixodid ticks of the genera *Amblyomma*, *Dermacentor*, *Ixodes*, and *Rhipicephalus* transmit several critically important infections to people and pets in North America, serving as an active

conduit moving pathogens between sylvatic and domestic environs. Nonetheless, much remains unknown about ixodid biology and life history, including phenology shifts influenced by widespread biogeographical alterations and climate change. Models for understanding disease transmission, to be of value, must be founded on accurate and deep awareness of the physiology and behavior of these key vectors. Natural history studies focusing on tick systems improve understanding of basic tick biology, feeding patterns, development cycles, distribution, and reproduction in the face of evolving biotic and abiotic conditions. Novel tick-borne pathogens and previously unrecognized tick-pathogen systems continue to be described, with new ixodid-associated viral, bacterial, protozoal, and helminth agents routinely discovered. Ticks are familiar and accessible, and generate strong reactions of both fascination and disgust from scientists and the general public alike. As such, ticks provide an ideal system for encouraging research interest in young scientists, allowing pursuit of independent research projects that result in truly novel discoveries. The notoriety of ticks also facilitates teaching science to the general public, who are often delighted to learn more about the biology of these interesting creatures. For those researchers inherently interested in acarology and vector-borne infections, tick systems provide a wealth of intriguing questions as well as an opportunity to better understand disease ecology responses to a changing environment.

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PUBLISH OR PERISH, GRANT OR GROVEL. DARE THEM ALL TO TAKE YOU SERIOUSLY

M. Siddall, American Museum of Natural History

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THE FINAL FRONTIER: MENTORING AND INVOLVING STUDENTS

D.W. Duszynski, University of New Mexico

Mentoring is a life-long process. You do it as a child and throughout elementary and secondary schools with siblings or friends, but you don't think about it. As an undergraduate, we've all helped (mentored) someone with something (sports, classes, how to use a computer application). In graduate school, lab mates and students in other labs all mentor each other in some way. When ready to face the "real world" you are mentored, or help mentor others, in going through the application and interview process; hopefully, you finally land the academic position you've always desired. Once you've found your niche, both in your research and in networking with departmental (other disciplines) and professional colleagues in parasitology at other institutions, your time has begun to dare journal editors and panels of granting agencies to take you and your ideas seriously. This is the time to recognize that students are a central part of all your future endeavors. Thus, you must set the example and create the opportunities to attract students to your discipline and your laboratory and, in the process, learn to become their mentor. I hope to draw on examples from my own experience and from those of other colleagues in biology to outline ideas for, and methods of, successful mentoring.

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RACCOON LATRINES: HUMAN DISEASE RISK IN SANTA BARBARA COUNTY

J.T. Mendez and **S.B. Weinstein**, University of California, Santa Barbara

Over 80% of the raccoons in Santa Barbara County, California carry the parasitic roundworm *Baylisascaris procyonis*. *B. procyonis* eggs are defecated by raccoons at their communal latrines. Raccoon latrines in residential areas pose a risk to human health because infection with larval worms, though rare, can cause ocular and neurological diseases. In fact, Baylisacariasis resulted in a recent fatality near our study area. Reducing future human exposure to *B. procyonis* eggs requires identifying and removing latrines from areas humans frequent. To generate maps of human disease risk, we are using a combination of latrine mapping, egg quantification, and human and raccoon observations.

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SOCIALITY IN TREMATODE FLATWORMS – HOW COMMON IS IT?

A.E. Garcia-Vedrenne, **A. Quintana**, **A.M. Kuris** and **R.F. Hechinger**, UCSB

The phenomena of behavioral specialization, polymorphism and caste formation is best known for organisms such as the social insects and naked mole rats. Recent findings extend such complex sociality to a new class - Trematoda. A reproductive division of labor involving a caste of non-reproducing soldiers has already been documented for five species of trematodes from different geographic regions and host species, suggesting that this phenomenon is widespread. Here we present the extent of our evidence for trematode social organization. First, we examine the nature of sociality for an additional 14 trematode species that infect the California horn snail, *Cerithidea californica*. Half of these species appear to have a division of labor involving a soldier caste, while the other half provide information on colony structure when soldiers are lacking. We then demonstrate that not all species within a given Family have caste formation by showing that there are Echinostomatidae that lack caste formation. Finally, we search the literature for evidence of sociality in various trematode families. Descriptions of the life history of several species confirm that this phenomenon is widespread. Since there are roughly 18,000 species of digenean trematodes and many may have such a social organization, trematodes may exhibit the most substantial radiation of sociality other than among the social insects.

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THE ROLE OF HOST MOVEMENTS AND ECOLOGY ON EVOLUTION AND DISTRIBUTION OF *TRICHOBILHARZIA* SPECIES

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V. Tkach, The University of North Dakota, Grand Forks
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To further our understanding of how heteroxenous parasites persist across time and geography, we investigated two species within the globally distributed genus *Trichobilharzia* (Digenea: Schistosomatidae), *T. querquedulae* and *T. physellae,* which show discordant microevolutionary patterns. Both species infect migratory ducks as well as the snail intermediate host *Physa*. Previous studies suggest substantial differences in the genetic diversity and evolutionary potential between these species, which appear to be associated with duck ecology. *Trichobilharzia querquedulae* infects a group of dabbling ducks known as the "blue wing" group, which are ecologically distinct from the diving ducks that transmit *T. physellae*. Our data suggests that ecological differences between dabblers and divers contribute to these differences in microevolutionary patterns. Field collections and DNA sequencing confirms the cosmopolitan distribution of *T. querquedulae*; until now no species of *Trichobilharzia* has been reported as globally distributed. What factors have led to the global colonization of *T. querquedulae* and not *T. physellae*? Duck host ecology may again play an important role. We find the "blue wing" group, on average has a more diverse trematode community, and additionally they harbor more cosmopolitan parasites, relative to diving ducks. Migratory ducks likely mediate large-scale movements of *Trichobilharzia* species; however, the snail intermediate host maintains lifecycles. Unlike most *Trichobilharzia* species, *T. querquedulae* and *T. physellae* utilize *Physa* species as intermediate hosts, conferring interest in the potential contribution of this snail in the global distribution of *T. querquedulae*. We have collected and sequenced the CO1 mitochondrial gene region of both parasite and intermediate hosts collected from four different continents in order to compare phylogeographic and population genetic patterns. We find that both host and parasite lack phylogeographic and population genetic structure across large geographic scales, indicating well mixed populations that maintain high amounts of genetic diversity. In summary, several factors likely act in concert to contribute to the global success of *T. querquedulae,* specifically the ecology of the "blue wing" group as well as the global availability of the intermediate host *Physa acuta*. It is likely that host ecology and distribution are both important in determining a parasites distribution and their persistence across geography.

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STARVED AMPHIPODS (*GAMMARUS FASCIATUS*) LIVE LONGER WHEN INFECTED WITH LARVAL ACANTHOCEPHALANS

R.L. Grunberg and **M.V. Sukhdeo**, Rutgers University

In this study we investigate a potential temporary mutualism between a parasite and its host. Larval acanthocephalan infections were monitored over 2 years at North Branch Park in Bridgewater, NJ. Amphipod infection was seasonal starting in July and ending in January both

years. Prevalence of acanthocephalan infections was low with a peak of 6.49%. Out of 3,850 amphipods collected, only 34 were infected. We report positive interactions between an acanthocephalan parasite and its host, a freshwater amphipod (*Gammarus fasciatus*). In this study amphipods were starved for 48 hours in individual well plates. Pre- and post- weights along with mortality rate of the amphipods were recorded. After the starvation period, all amphipods were necropsied for parasites. Uninfected amphipods (n=48) had a survival rate of 0% after the starvation period. Amphipods infected with only gregarines had a survival of 84. 94% (n=93) and decreased in weight (-0.0010 ± 0.00035 g). In contrast, 100% of all amphipods infected with acanthocephalans (n=10) survived the starvation period, and also increased in weight (0.0010 ± 0.00035 g). Histological sections of starved, infected amphipods are being done to investigate host-parasite interactions at the cellular level. Our preliminary results suggest that under certain ecological conditions it may be adaptive for larval acanthocephalans to lower natural mortality of the host, resulting in an apparent temporary mutualism.

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FOREST FRAGMENTATION'S EFFECTS ON HEMOPARASITES IN SMALL MAMMALIAN POPULATIONS FROM PARAGUAY

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S. Boyle and **L.E. Luque**, Rhodes College

Ongoing deforestation in Paraguay's understudied Interior Atlantic Forest (IAF) threatens this region's biodiversity. Deforestation and forest fragmentation can negatively impact the health of mammalian populations through elevated stress, immunosuppression, and increased rate of infection, though the disease-inducing variables are still poorly understood. The goal of this study was to examine the extent to which small mammals living in forest fragments were infected with hemoparasites. We surveyed six forest fragments that ranged in area from 2 ha to 1200 ha in the Tapytá Private Reserve, located in the Department of Caazapá, Paraguay. Each forest fragment was sampled for small mammals using a grid system of arboreal and terrestrial snap and Sherman live traps, as well as pitfall traps. We collected blood from the sampled animals, following protocols approved by the Institutional Animal Care and Use Committee (IACUC) at Rhodes College. Samples were taken retro-orbitally or from the heart and liver tissue of terrestrial and arboreal Sigmodontine rodents and Didelphid marsupials found in each fragment. Blood smears were analyzed using standard histological techniques. Parasite infections were first characterized based on morphology and PCR. We collected blood samples from 134 individuals representing the genera *Oligoryzomys* (63.2 % of all small mammals sampled), *Akodon* (28.6 % of individuals sampled), *Gracilinanus* (6.0 % of individuals sampled), and *Marmosa* (2.2 % of individuals sampled). The majority of the small mammals (82.1 % of sampled individuals) were captured terrestrially. To date, 90 % of the sampled mammals show hemoparasitic infections, with representing parasites in the Phyla Helminth and *Babesia* spp., along with bacterial infections from *Yersinia* spp. and *Bartonella* spp. Infected small mammals were not limited to the smallest forest fragments, as infected individuals were also from the largest 1200-ha fragment. Additional analyses will allow for the quantification of parasitic loads for each individual vector. Our findings indicate that many of the small mammals in these forest fragments are infected with a diverse array of hemoparasites. Findings from this study will help clarify the relationships between hemoparasite infection and forest fragmentation in small mammals, and allow for more-directed conservation management plans.

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ROLE OF PARASITE TRANSMISSION IN PROMOTING INBREEDING. I. IMPACT ON THE PRIMARY MATING SYSTEM

C.D. Criscione, Texas A&M University
J.T. Detwiler, University of Manitoba
I.C. Caballero, Texas A&M University

Because inbreeding (mating between kin) magnifies genetic drift and affects the efficacy of selection, it plays a key role in the evolution of populations by impacting the distribution of genetic variation within and among populations. Indeed, inbreeding may be a major driver of parasite evolution by affecting diversification, host-parasite coevolution, and the selection efficacy for drug resistance. However, our understanding of these evolutionary dynamics in parasites is incomplete as it is largely unknown what parasite traits influence inbreeding in natural populations. For example, in hermaphroditic organisms self-mating is the most extreme form of inbreeding, but there is not a single direct estimate of the primary mating system (i.e., the selfing-rate) for any species of parasitic flatworm in nature. It has been proposed that the transmission process can affect inbreeding by impacting the number and relatedness of potential mates. In this first talk, we test how the intensity of infection alone might impact selfing-rates of parasitic flatworms. By taking advantage of the fact that hosts represent closed mating systems for endoparasites and by using parent-offspring genotype data, we were able to use nature-generated crosses of a cyclophyllidean tapeworm to estimate selfing-rates of field-collected individuals; a first for any parasite. We tested the null-hypothesis that the selfing-rate is determined by random mating within a host (e.g., selfing-rate would be 50% with an intensity of 2, 33% with 3 and so on). We found that our species self-mates more often than expected given the infection intensity, but that there might still be a decline in selfing as infection intensity increases. We propose possible explanations and discuss future avenues to determine what leads to the higher than expected selfing. The primary mating system is not the only determinant of population levels of inbreeding. In our next talk, we discuss how the life cycle of our study tapeworm also promotes bi-parental inbreeding (i.e., sib-mating).

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ROLE OF PARASITE TRANSMISSION IN PROMOTING INBREEDING. II. IMPACT ON SIB-MATING

C.D. Criscione, Texas A&M University
J.T. Detwiler, University of Manitoba

In addition to the number of worms in a host, the transmission process can also influence inbreeding in parasites by affecting the relatedness of potential mates in a host. If transmission leads to a large mixing of parasite offspring before infection of definitive hosts, potential mates will be unrelated. However, if offspring are transmitted as a clump, sibling parasites will end up in the same host. Clumped transmission is a form of non-random transmission and thus, can be detected via tests of genetic differentiation among infrapopulations. To date, studies on flatworm parasites with aquatic life cycles have shown panmixia among hosts whereas semi-terrestrial species have shown low levels of genetic differentiation among hosts. Among-host structure has not been examined in flatworm parasites with terrestrial life cycles. We predicted that the terrestrial life cycle of the tapeworm *Oochoristica javaensis* would promote co-transmission of sibs and consequently, bi-parental inbreeding. First, gravid proglottids are released intact with

host feces. Thus, an intermediate host is likely to consume full/half sibs. In turn, a gecko that eats an infected intermediate host will simultaneously consume those sibling parasites (i.e., clumped transmission). We genotyped over 800 adult worms from 5 subpopulations and in each location, found high levels of genetic differentiation among individual hosts (average Fst=0.359). Kinship coefficients indicated worms within infrapopulations were on the order of full sibs. Subpopulation Fis had negative correlations to mean intensity and prevalence, supporting the hypothesis that the number of potential mates affects inbreeding. Nonetheless, the average inbreeding coefficient was high (Fis=0.549) and could not be fully accounted for by the primary mating system alone. Assuming inbreeding equilibrium, we estimated that 25% of the matings were between full/half sibs. Collectively with the studies on aquatic systems, our results emphasize how life cycles can shape parasite evolution by determining the potential for inbreeding.

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TRANSMISSION OF TROPHICALLY EMBEDDED PARASITES ARE LINKED TO HOST FORAGING ECOLOGY

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Many complex life cycle parasites rely on predator-prey interactions for transmission, whereby definitive hosts become infected via the consumption of an infected intermediate host. As such, these trophic parasites are embedded in the larger community food web. We postulated that exposure to infection and, hence, parasite transmission are inherently linked to host foraging ecology, and that perturbation to the host-resource dynamic will impact parasite transmission dynamics. Here, we combined epidemiological data and molecular analyses (polymerase chain reaction) of the definitive host, the white-footed mouse (*Peromyscus leucopus*) diet to investigate temporal and individual heterogeneities in exposure to infection. We found that individual heterogeneities in consumption of cricket intermediate hosts accounted for much of the variation in infection. In a separate, but similar rodent-parasite system, we employed a large-scale manipulation experiment in which natural populations of the eastern chipmunk were provisioned with a readily available food resource, in clumped or uniform spatial distributions. Using replicated longitudinal capture-mark-recapture techniques, replicated supplemented and un-supplemented control sites were monitored before and after treatment for changes in infection levels of three gastro-intestinal helminth parasites. We predicted that definitive hosts subject to food supplementation would experience lower rates of exposure to infective intermediate hosts, presumably because they shifted their diet away from the intermediate host towards the more readily available resource (sunflower seeds). As predicted, prevalence of infection by the trophically transmitted parasite decreased in response to supplemental food treatment, but no such change in infection prevalence was detected for the two directly transmitted parasites in the system. The fact that food supplementation only had an impact on the transmission of the trophically transmitted parasite, and not the directly transmitted parasites, supports our hypothesis that host foraging ecology (i.e., host diet) directly affects exposure to parasites that rely on the ingestion of intermediate hosts for transmission. Moreover, the outcome does appear to be due to lower parasite establishment or changes to host condition/susceptibility. We conclude that the relative availability of different food resources has important consequences for the transmission of parasites and more specifically parasites that are embedded in the food web. Furthermore, heterogeneities in host diet play a significant in generating variation in the rate of infection.

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A NOVEL FOOD WEB, INCLUDING PARASITES, FOR THE INTERTIDAL SAND FLATS OF PALMYRA ATOLL, CENTRAL PACIFIC

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C. Wood, University of Colorado Boulder
J. Shaw, University of California, Santa Barbara
V. Vidal Martinez and **L. Aguirre-Macedo**, CINVESTAV-IPN, Unidad Mérida
A. James, **S. Weinstein**, **J. Caselle**, **R. Hechinger** and **A. Kuris**, UCSB
K. Lafferty, US Geological Survey

Of the more than 200 published food webs only nine include parasites in a systematic and standardized fashion. This neglect of parasites reduces food web resolution and constrains our understanding of the complex systems that food webs describe. Here, we present a food web for the soft sediment intertidal flats bordering the lagoon of a tropical Pacific atoll, Palmyra. The food web also includes information on the biomass, body sizes and life-stages for all organisms, free-living and parasitic in this remote and trophically intact system. Parasites contribute substantially to system diversity, with digenetic trematodes dominating parasite biomass. Parasites also significantly affect the structure and complexity of the topological food web.

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THE NATURAL HISTORY OF THE PARASITIC TREMATODE *PLEUROGONIUS MALACLEMYS* (TREMATODA: DIGENEA)

N. Chodkowski, Ball State University

Pleurogonius malaclemys is a parasitic intestinal trematode of diamondback terrapins (*Malaclemys terrapin*). Terrapins are found in brackish marshes of the eastern and southern coasts of the United States. Eastern mudsnails (*Ilyanassa obsoleta*) are the intermediate host for *P. malaclemys* and can be an important part of terrapin diets. This study examined the biology and ecology of *P. malaclemys* in its hosts. *Pleurogonius malaclemys* infection was found further north than previously reported. The trematode cysts infect snails year round, but snail infection frequencies vary dramatically by season. Cysts prevalence increased during the summer months and reached maximum levels of ~70% in November. Overall, nearly 58% of Jamaica Bay, NY eastern mudsnails were infected with *P. malaclemys* cysts; mean intensities were 2.63 cysts/snail. Although cysts prevalence was high, only 11 snails (0.28%) were found to have the internal redial stages of *P. malaclemys*. In addition to snails, laboratory experiments revealed that *P. malaclemys* could encyst on other biological substrates, including other common terrapin prey species. The majority of wild adult terrapins from Stone Harbor, NJ were infected with the *P. malaclemys* adult stage (80.30%, $\bar{x}$ = 36.36, n = 66). Juvenile terrapins were experimentally infected with *P. malaclemys*, and on average 22.5% of the consumed cysts successfully developed into adult trematodes in terrapin intestines. Studies on the life cycle of *P. malaclemys* are important because previous research has shown that the frequency of *P. malaclemys* cysts on mud snails can be used as an indirect measure of terrapin abundance. Understanding the factors that contribute trematode abundance, particularly metacercarial encystment on snail hosts, can reduce biases when estimating terrapin population size.

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HOST POPULATION STABILITY AS A DRIVER OF PARASITE ABUNDANCE

C. Lagrue and **R. Poulin**, Department of Zoology University of Otago

Resource stability is a key factor determining species abundance and diversity in natural ecosystems. Through a bottom-up process, the stability of local basal resources should facilitate the maintenance and growth of consumer populations. In host-parasite associations, we would therefore expect parasites to achieve higher abundances where their host populations (resources) are stable, i.e. experience little spatiotemporal variation in local density. Also, we would expect that within localities parasites achieve higher abundances in host species with demographically stable populations than in hosts showing marked spatial and/or seasonal variations in local densities. We tested these predictions using an extensive dataset obtained by sampling all fish and invertebrate hosts and their metazoan parasites across multiple sites and seasons in four New Zealand lake ecosystems. Host stability was computed for each species as the coefficient of variation in density values across all samples from a given lake. Its effect on parasite abundance was tested across all host-parasite species combinations in all four lakes using generalized linear mixed models, to account for other potentially influential factors. Our results provide the first quantitative test of the extent to which resource stability matters for parasite populations, and how much this varies among parasite taxa. These findings also have implications for the geographic distribution of parasite diversity, as more parasite species may persist in host populations or localities characterized by stability.

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THREATS OF PREDATION AND PARASITISM ON TADPOLE FORAGING BEHAVIOR: WHICH ENEMY TO AVOID?

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L. Penalva, Brazil

Predators are known to affect the activities of many animals, including that of larval amphibians. The indirect effects of predation on prey behavior, including changes in foraging and space use, have implications for individuals but can also scale up to affect populations and communities. While it is increasingly evident that this “ecology of fear” is important to understand, the influence of other natural threats such as parasites on behavioral choices is relatively unknown. We examined foraging behavior in tadpoles when cues relating to predator (larval odonate) or parasite (the trematode *Echinostoma trivolvis*) threats were present. Tadpoles spent about three times longer in the arm of the choice arena that had only food as compared to the arm containing food and predator scent cues, indicating that tadpoles prefer foraging in relatively safe habitats if given the choice. Similarly, tadpoles also spent about three times more foraging in the arm only containing food compared to the one with both food and parasite cues. Our results show that tadpoles avoided foraging in habitats where they perceived a threat from predators or parasites; however, they did not treat them as equal hazards. When both threats were simultaneously present, tadpoles strongly preferred to forage in the arm with parasite cues and food compared to the arm with predators and food. Our results indicate that spatial avoidance is likely an important anti-parasite behavior in larval amphibians, and also that parasites can affect foraging behaviors similar to predators, warranting greater study of their indirect effects.

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SURVEY AND ASSESSMENT OF PARASITIC INFECTIONS IN NORTHERN BOBWHITES FROM THE ROLLING PLAINS ECOREGION, TEXAS

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D. Rollins, Rolling Plains Quail Research Foundation

Recent research on the parasitic infections found in Texas northern bobwhites (*Colinus virginianus*) has sparked new interest in the bobwhite-parasite relationship. In an attempt to gain new information on the role parasitic infections play in bobwhite ecology, a 3-year helminth and disease survey was conducted throughout the Rolling Plains ecoregion, Texas. The objectives of this study are to survey for the presence of *Trichomonas gallinae,* assess helminth infection, and identify potential pathological responses caused by the eyeworm *Oxyspirura petrowi*. Northern bobwhites were trapped and euthanized in August and October of 2011, 2012, and 2013 (n = 167) and examined for helminths. Eye tissue from infected and uninfected bobwhites was collected for pathological analyses. Samples for *T. gallinae* were taken from 381 live bobwhites during trapping. *Trichomonas gallinae* infections were not found. Eleven species of helminths were found of which *Aulonocephalus pennula, O. petrowi,* and *Tetrameres pattersoni* were the most frequently occurring species. Statistical analyses will compare the most frequently occurring parasites' prevalence and abundance to host age, host sex, month, year, location, and their interactions. Preliminary results from histological analyses of the eyeball and intraorbital gland tissue infected with *O. petrowi* will also be discussed. The present study will advance our understanding of the helminth parasites that occur in bobwhites across the Rolling Plains and their potential impact on individuals.

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GENETIC STRUCTURE IN A PROGENETIC TREMATODE: SIGNS OF CRYPTIC SPECIES WITH CONTRASTING REPRODUCTIVE STRATEGIES

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R. Poulin, **D.B. Keeney**, **I. Blasco-Costa**

Complexes of cryptic species are rapidly being discovered in many parasite taxa, including trematodes. However, after they are found, cryptic species are rarely distinguished from each other with respect to key ecological or life history traits. In this study, we applied an integrative taxonomic approach to the discovery of cryptic species within *Stegodexamene anguillae*, a facultatively progenetic trematode common throughout New Zealand. The presence of cryptic species was determined by the genetic divergence found in the mitochondrial cytochrome *c* oxidase I (COI) gene, the 16S rRNA gene and the nuclear 28S gene, warranting recognition of two distinct species and indicating a possible third species. Speciation was not associated with geographic distribution or microhabitat within the second intermediate host; however frequency of the progenetic reproductive strategy (and the truncated life cycle associated with it) was significantly greater in one of the lineages. Therefore, two lines of evidence, molecular and ecological, support the distinction between these two species and suggest scenarios for their divergence.

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EVOLUTION OF MAMMAL-TRYPANOSOME ASSOCIATIONS AND THE ORIGINS OF CHAGAS DISEASE

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Chagas disease is caused by the protozoan parasite *Trypanosoma cruzi*. Despite the public health importance of Chagas disease, there are still doubts on the evolution and biogeography of *T. cruzi* and its relatives, which form the *T. cruzi* clade. This clade has a cosmopolitan distribution, and is composed by several species of parasites of mammals —mostly bats. Here, I analyze genetic data from multiple loci of previously known as well as newly found trypanosomes from the New and Old Worlds. I used phylogenetic model based methods, performed species delimitation, ancestral reconstruction and historical biogeography analyses to follow the association of the parasites and their mammalian hosts. These analyses support bats as the original hosts of both —the clade and Chagas disease, also a southern super-continent (New World/Africa/Australia) biogeographic origin for the clade. In addition, the current distribution of the group is better explained as a result of long distance dispersal. Lastly, cryptic diversity is recognized within this clade. These results indicate a long evolutionary relationship between bats and their trypanosomes, suggesting a scenario where bats were key players for a radiation of trypanosomes, triggered by bat-mediated long distance dispersal of parasites and sporadic host switches to non-volant mammals, then Chagas disease appeared in humans recently (<15,000 years) with the colonization of the Americas.

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BAYLISASCARIS PROCYONIS: DOES PARASITE PREVALENCE ACCOUNT FOR SOME PHYLOGENETIC DIFFERENCES BETWEEN SUBPOPULATIONS OF RACCOONS (*PROCYON LOTOR*)?

M.E. Ingle, Loma Linda University, Cedarville University
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K.M. Kohl and **C.T. Griffin**, Cedarville University

Baylisascaris procyonis is an intestinal roundworm that parasitizes raccoons (*Procyon lotor*) as a final host. *B. procyonis* often develops using an indirect life cycle, requiring an intermediate host. Several vertebrate species, including humans, can serve as intermediate hosts for *B. procyonis*. Infection by *B. procyonis* causes visceral larva migrans in intermediate hosts, and is one of the leading causes of larva migrans encephalopathy in humans, a potentially deadly neurological disease. Parasites reduce relative fitness and exert selective pressures on host individuals and populations of hosts. In this study, we aimed to determine how *B. procyonis* affects the genetic structuring of raccoon subpopulations. We removed the alimentary canal from 226 raccoons from Clark and Greene Counties, Ohio that we obtained from fur trappers. We obtained prevalence data for raccoons from nine townships within these counties. We isolated DNA from the greater omentum, and amplified a portion of exon 2 from MHC II and the mitochondrial gene for NADH5 using real-time PCR. We sent the amplified DNA to Ohio State University to have the loci sequenced. We calculated heterozygosity for the nuclear locus, and used this to determine the amount of genetic structuring in the raccoons from Clark and Greene Counties. Townships of these counties were treated as subpopulations, and differences in *B. procyonis* prevalence between these subpopulations were noted. Heterozygosity for exon 2 of MHC II differed among raccoons from these counties, and raccoons from subpopulations with *B. procyonis* prevalence

above 0.60 had significantly lower heterozygosity than raccoons from subpopulations with prevalence below 0.60 (Chi-squared = 39.01, $p < 0.001$). Phylogenetic trees using NADH5 showed genetic structuring as well, with raccoons from the same subpopulation grouping closer to raccoons from the same subpopulation than other raccoons. Our data suggest that at least some of the genetic structuring in raccoons may be explained by difference in *B. procyonis* prevalence among raccoons from these counties.

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(85)

HIGHLY DIVERGENT SMALL SUBUNIT RIBOSOMAL RNA GENES IN A *CRYPTOSPORIDIUM* GENOTYPE FROM EASTERN CHIPMUNKS (*TAMIAS STRIATUS*)

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The multiple copy small subunit (SSU) rRNA gene is a popular target in phylogenetic studies of eukaryotes. Sequence homogeneity among SSU copies, which is necessary for the accurate inference of organismal relationships, is generally maintained by concerted evolution. However, SSU genes in some apicomplexans, including Plasmodium and Cryptosporidium, evolve by an alternative birth-and-death model, which can result in divergence among copies (paralogs). In the present study, we identified two Cryptosporidium SSU types, A and B, in eastern chipmunks (Tamias striatus). Types A and B had a sister group relationship but shared less than 93% sequence identity. Type A clustered with a sequence previously identified as Cryptosporidium chipmunk genotype II. Using type-specific PCR assays, both types were found to co-occur in 26 out of 28 Cryptosporidium positive chipmunks. To determine whether Types A and B are separate Cryptosporidium taxa or divergent paralogs from a single taxon, we amplified and sequenced fragments ofthe single-copy actin and HSP70 genes. Sequences from both actin and HSP70 were found to be monomorphic, supporting the conclusion that Types A and B are divergent paralogs in Cryptosporidium chipmunk genotype II. The extent of divergence between Types A and B is far greater than previously found in Cryptosporidium, and is similar to that found in Plasmodium spp. In Plasmodium, divergent SSU copies are expressed during differentlife cycle stages; therefore, a critical next step in this research will be to determine the functional significance of the divergent SSU copies in Cryptosporidium chipmunk genotype II. This study shows that Cryptosporidium phylogenies based on SSU alone may be unreliable.

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(86)

PHYLOGENETIC AFFINITIES OF TWO OPECOELID (TREMATODA) GENERA CONTAINING MEMBERS WITH FILMENTED EGGS

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The Opecoelidae is one of the largest trematode families restricted primarily to fishes. It occurs in freshwater, brackish, and marine fishes, including some from the deep-sea (≥200m). Understanding the systematics of the group is difficult because of the relatively unspecialized features of its members, the acceptance of several poorly defined genera, and the great species diversity within the family. The plagioporine *Helicometra* and *Helicometrina* both have eggs with a unipolar filament and parasitize marine fishes but are distinguished by the number of testes (2 compared with 3 to 9, respectively). A recent molecular phylogeny demonstrated the paraphyly of

the Plagioporinae, with some 'plagioporine' opecoelids from shallow-water marine fishes forming a clade separate from deep-sea and freshwater plagioporines. We use Bayesian inference analysis of the partial 28S rDNA gene of 2 species of *Helicometra*, 1 species of *Helicometrina*, 15 other species of Plagioporinae, 5 species of Opecoelinae, and 2 species of *Paragonimus* as outgroups. Our estimated phylogeny shows a close affiliation of *Helicometra* and *Helicometrina*, strengthened the paraphyly of the Plagioporinae, and demonstrated the paraphyly of the Opecoelinae.

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(87)

PHYLOGENOMICS OF MYXOZOA

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A bizarre assemblage of obligate, microscopic, oligocellular parasites, Myxozoa has been in a state of phylogenetic flux since its first formal description in the 1880s. Myxozoans have been variously categorized as protists, nematodes, triploblasts, basal bilaterians, and cnidarians. Beyond myriad descriptions of individual host-parasite interactions, the group has been rarely studied in a wide phylogenetic context, despite its destructive, pathogenic impact on marine fish aquaculture worldwide. In recent years, the advent of high-throughput, next-generation sequencing has enabled the acquisition of molecular sequence data for wide swaths of non-model organismal diversity. Such data include complete mitochondrial genomes, orthologized expressed sequence tags (ESTs) from transcriptomes, and reduced shotgun nuclear genomes. These next-generation efforts are now being implemented for Myxozoa. These data are used for robust phylogenetic placement of this group, with multiple lines of molecular evidence. Moreover beyond phylogeny, these data allow us to characterize critical proteins including venom and filament production, as well as to elucidate the pathogenesis and life histories of these parasites.

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(88)

THE LURE OF *PROTEROMETRA*: TAXONOMIC DIVERSITY, LIFE CYCLES, AND HOST-PARASITE RELATIONSHIPS WITHIN AN INTRIGUING GENUS OF FRESHWATER TREMATODES

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Proterometra comprises 9 species of trematodes that reportedly infect 25 species of primary division freshwater fishes (Actinopterygii: Teleostei) and 12 species of freshwater prosobranch snails (Cerithioidea: Pleuroceridae) in North America. Species of *Proterometra* are of interest because little is known about their biodiversity, life cycles, and the identities of their hosts in the southeastern United States. We collected fishes of Centrarchidae (species of *Lepomis* and *Micropterus*) and snails of *Elimia* from Terrapin Creek, Coosa River, Alabama, and adjacent watersheds. Naturally shed cercariae were collected from aquaria containing isolated snails, and trematodes were collected from the epithelial surfaces of the buccal cavity of fishes. Specimens for morphology were heat killed, stained, permanently mounted, studied with light microscopy, and compared with published descriptions of congeners and type materials of *P. albacauda*. Specimens for molecular biology were fixed directly in RNALater or 95% EtOH and processed for sequencing. Morphological studies indicated that our specimens represent a putative new species and that understudied features of the adults are likely taxonomically valuable. No species level molecular data exists in GenBank for *Proterometra*; however, our ITS2 rDNA sequence data

indicated conspecificity of our cercarial and adult specimens. Those data also indicated that other putatively unnamed species of *Proterometra* infecting centrarchids and *Elimia* spp. range in the southeastern US. This study represented (i) the first taxonomic study of a species of *Proterometra* from Alabama since 1936, including novel taxonomic information pertaining to the adults, specifically regarding the male and female reproductive systems, (ii) the first demonstrated life cycle from Alabama, and (iii) the first use of molecular methods to elucidate a life cycle for a species of *Proterometra*. Additionally, the taxon detailed herein is likely an unnamed species, and *Micropterus punctulatus* and *Elimia* cf. *modesta* are previously undocumented hosts for *Proterometra* spp.

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(89)

PHYLOGENETIC ANALYSIS OF *BAYLISASCARIS*

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Nematodes in the genus *Baylisascaris* are difficult to distinguish based on morphological characters. *Baylisascaris procyonis* and *B. columnaris* in particular have few to no morphological differences between them at all life cycle stages. Traditionally, these species are differentiated using behavioral disparities evident in experimental infections of intermediate hosts. These species appear to be reproductively isolated based on preliminary molecular work, but sampling is currently inadequate in terms of the number of individuals included in analyses. I intend to use phylogenetic and population genetic methods to investigate whether *B. procyonis* and *B. columnaris* are supported as separate species. Preliminary phylogenetic analysis included sequence data from four *Baylisascaris* spp. and was based on five markers (two nuclear and three mitochondrial). *Baylisascaris procyonis* and *B. columnaris* were supported as separate lineages, but the pairwise differences between them were minimal (or non-existent) for all genes. This study presents analyses based on additional markers, and includes sequence data from additional individuals of *B. procyonis* and *B. columnaris* as well as all *Baylisascaris* species except *B. laevis*. Population genetic analyses have not been performed for any *Baylisascaris* spp., but microsatellite markers developed in *B. procyonis* will also be used to determine if there are fixed differences for *B. procyonis* and *B. columnaris* that are diagnostic for each species.

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(90)

IDENTIFICATION AND MORPHOLOGICAL VARIATION OF AN INVASIVE PARASITE IN INTRODUCED AND NATIVE LIZARDS

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Exotic species can threaten biodiversity by introducing parasites to native hosts. Thus, it is critical to identify if the same parasite species is infecting both native and exotic hosts. Developmental, plastic, or heritable variation in morphology, however, may complicate identification. Geckos are one of the most successful invasive families of vertebrates and are known to host lung parasites, pentastomids of the genus *Raillietiella*. Raillietiellids have a cosmopolitan distribution, which in part, may have been facilitated by the introductions of their hosts. Indeed, *Raillietiella frenatus*, a Southeast Asian parasite, has been reported in TX from the exotic Mediterranean gecko *Hemidactylus turcicus*. Here we report on the recent introduction (between 1998 and 2008) of a *Raillietiella* sp. into an established population of *H. turcicus* in LA. More critically, we found infections in native green anoles, a new host record for pentastomes. Upon sequencing 600 bp of

the pentastome's CO1-mtDNA gene, we observed identical sequences from parasites of anoles and geckos. In fact, there was no sequence variation to published sequences of *R. frenatus* from geckos and cane toads in Australia (Kelehear et al. 2011. PLOS One 6:e24935). Interestingly, Kelehear et al. found that traditional taxonomic analyses based on hook dimensions would have led to the false conclusion of two pentastome species. We repeated their analyses on our specimens and also observed 2 apparent species within *H. turcicus*. But, as in Kelehear et al., when pentatstome body size is accounted for distinction between the 2 groups disappears. These results along with prior molting studies on *R. frenatus* suggest hook size varies ontogenetically. Nonetheless, even after accounting for pentastome body size, hook dimensions differ significantly between host species. This result suggests these traits may be plastic as a result of host environment, but quantitative genetic experiments will be needed to disentangle phenotypic plasticity from genetic variation.

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(91)

DIVERSITY AND DISTRIBUTION OF AVIAN SCHISTOSOMATIDS IN NORTH DAKOTA

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Avian schistosomatids inhabit the blood circulatory system of birds. Their life cycles include snails as intermediate hosts and birds as definitive hosts. They are found in representatives of several bird orders but are most prevalent in waterfowl. North Dakota has a large number of wetlands which provide important breeding sites for many aquatic birds and serve as stopover sites for migratory birds. The abundance and diversity of bird species that congregate in these wetlands ensures optimal conditions for schistosomatid transmission. However, data on schistosomatids in North Dakota were lacking. We have undertaken a state wide survey of the diversity and host associations of avian schistosomatids in North Dakota with emphasis on schistosomatid larval stages in snails. Between May and September of 2013 nearly 18,000 snails belonging to the genera *Lymnaea, Stagnicola, Physa, Helisoma, Promenetus,* and *Aplexa* were collected from 106 sites throughout North Dakota and examined for the presence of schistosomatid larvae. Adult schistosomatids collected from a variety of birds in the region between 2008-2014 were used for morphological identification and as a source of reference sequences in cercarial screening, along with data available in GenBank. Adult specimens were studied morphologically on total mounts. Sequences of the nuclear ribosomal RNA (mostly 28s) and mitochondrial cox1 genes were obtained from all samples of adult worms and cercariae. Cercariae were identified by matching their DNA sequences with those of adult worms. As a result, members of the genera *Trichobilharzia, Gigantobilharzia, Dendritobilharzia, Allobilharzia* and *Austrobilharzia* have been found in the state, some of them (e.g. *Austrobilharzia* that has a marine life cycle) found only in birds. Distribution and prevalence of schistosomatid cercariae in different water bodies and mollusk groups are discussed. Phylogenetic affinities of avian schistosomatid taxa found in North Dakota have been studied by inclusion of newly obtained sequences into a previously available broader dataset. This study was supported by the grant DEB 1021431 from the National Science Foundation.

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CALLIOBOTHRIUM (CESTODA: TETRAPHYLLIDEA) IN *MUSTELUS* (CARCHARHINIFORMES: TRIAKIDAE) OF THE ATLANTIC OCEAN

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This study aims to resolve several issues with tapeworms of the genus *Calliobothrium* van Beneden, 1850. Confusion exists regarding the host identities of the first species of *Calliobothrium* described, including the type, *C. verticillatum* (Rudolphi, 1819) van Beneden, 1850, and also *C. eschrichti* (van Beneden, 1849) van Beneden, 1850, and *C. leuckarti* van Beneden, 1850, all 3 of which were collected in the northeast Atlantic Ocean. Unfortunately, the descriptions are brief and type material of all 3 species is lacking. Furthermore, since shark taxonomy was poorly understood at that time, the identities of the hosts of all 3 species are also unclear given that 3 species of smoothhound shark are now considered to occur in the northeast Atlantic: *Mustelus asterias*, *Mustelus mustelus*, and *Mustelus punctulatus*. Also confusing, given the typically high degree of host specificity in the genus, are reports of *C. verticillatum* from the western Atlantic endemic *Mustelus canis*. For this study 29 specimens of *M. asterias* were collected off Lowestoft, England and 86 specimens of *M. canis* were collected off Connecticut and Massachusetts. *Mustelus asterias* was found to host 2 species of *Calliobothrium* that are consistent with the original descriptions of *C. leuckarti* and *C. verticillatum*, but no specimens of *C. eschrichti*. This suggests that the type host of the latter species may in reality be one of the 2 other *Mustelus* species occurring in the Northeast Atlantic. *Mustelus canis* was found to host a new species of *Calliobothrium,* suggesting that specimens identified as *C. verticillatum* from *M. canis* by Linton (1890), Euzet (1959), and Cislo and Caira (1993) were misidentified. Not only do they possess a unique configuration of proglottid laciniations for the genus, but they were also found to be distinct from the other laciniate species of the genus, (i.e., *C. australis* and *C. verticillatum*) based on *lsu* rDNA (D1-D3) sequence data. Thus, after almost 200 years, both the identity of the host of *C. leuckarti* and *C. verticillatum* and the distribution of the latter species are clear!

(93)

DIVERSITY AND ANCESTRY OF FLATWORMS (DIGENEA: SCHISTOSOMATOIDEA) INFECTING BLOOD OF CRANIATES

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We analyzed new and all available sequence data for the partial D1–D2 domains of 28S rDNA from 83 blood flukes to test monophyly of fish blood flukes (Aporocotylidae) and their interrelationships with tetrapod blood flukes (i.e., Schistosomatidae and “Spirorchiidae”). We also tested monophyly of the blood flukes infecting gastropods compared with those of bivalves plus polychaetes. Based on this analysis, the blood flukes infecting marine bony fishes (Euteleostei) are monophyletic. The clade comprising a chondrichthyan blood fluke plus all marine euteleost blood flukes is the sister group to all tetrapod blood flukes (= spirorchiids and schistosomes). Several innominate blood fluke cercariae from freshwater gastropods were monophyletic and sister to the clade comprising spirorchiids and schistosomes but low nodal support indicated that they may represent a distinct blood fluke lineage with phylogenetic

affinities also to fish blood flukes. Blood flukes that utilize gastropod intermediate hosts were monophyletic (= unidentified gastropod cercariae + tetrapod blood flukes) and those utilizing bivalves and polychaetes were monophyletic (= marine fish blood flukes). Low or no taxon sampling among blood flukes of basal fish lineages and primary division freshwater fish lineages are significant data gaps needing closure. We also note that no record of a blood fluke infection exists in a hagfish (Myxiniformes), lamprey (Petromyzontiformes), or non-tetrapod sarcopterygiian, i.e., coelacanths (Coelacanthomorpha) or lungfishes (Dipnoi). The present phylogenetic analysis reiterated support for monophyly of Schistosomatidae and paraphyly of Spirorchiidae, with the blood flukes of freshwater turtles basal to those of marine turtles plus schistosomes.

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(94)

SPECIATION IN A GONDWANIAN HOST-PARASITE SYSTEM

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The recently resurrected skate genus *Zearaja* has been considered to include 3 species: *Z. nasuta* from New Zealand, *Z. maugeana* from Tasmania, and *Z. chilensis* reported from localities in the Southeastern Pacific Ocean such as Chile and Southwestern Atlantic Ocean such as the Falkland Islands. However, the most recent molecular phylogenetic analyses of elasmobranchs, which included specimens of *Z. nasuta* and also *Z. chilensis* from both Pacific and Atlantic localities, questioned the conspecificity of *Z. chilensis*. Unexpectedly, specimens of *Z. chilensis* from Chile grouped more closely with those of *Z. nasuta* than they did with their conspecifics from the Falkland Islands. The goal of this study was to explore these findings using parasitological data. In total, 44 specimens of *Z. chilensis* were collected in Chile and 36 specimens were obtained from the Falkland Islands. A subset of those had their spiral intestines examined and specimens of cestodes belonging to the order Rhinebothriidea were selected for molecular analyses. Sequence data were generated for partial 28S rDNA (D1-D3) for at least 10 rhinebothriideans from each locality. Interestingly, some of the samples were found to be identical in sequence between the two localities. Phylogenetic analyses using a variety of methods consistently produced trees in which specimens formed two distinct clades, each of which included samples from both Chile and the Falkland Islands. These findings may suggest that speciation in these cestodes is lagging behind that of their hosts. The genus *Zearaja* is thought to be a Gondwanian lineage, possibly dating back to the Cretaceous, when New Zealand and South America were still part of that southern super-continent. The geological history shared by these two modern continents may help explain the phylogenetic relationships observed among *Zearaja* species. Future work will focus on specimens of *Z. nasuta,* which are key to understanding the patterns of cestode speciation in this system. The phylogenetic relationship of *Z. maugeana* among *Zearaja* species should also be explored as should its parasite fauna.

(95)

THE CURIOUS CASE OF *ALLOGLOSSIDIUM PROGENETICUM* (DIGENEA: MACRODEROIDIDAE): GEOGRAPHIC VARIATION IN PRECOCIOUS DEVELOPMENT WITHOUT NEUTRAL GENETIC DIVERGENCE

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The digenean genus *Alloglossidium* is notable for a high amount of interspecific variation in life cycle complexity (number and host species needed to complete development). Like many digeneans, species of *Alloglossidium* with a 3-host life cycle sexually reproduce in a vertebrate final host; however, 70% of the species exhibit a 2-host pattern where precocious development leads to sexual maturation in what is typically considered the second intermediate host. However, of the 17 species, only *Alloglossidium progeneticum* is known to have facultative precocious development. Reported from a single site in Georgia, previous work found gravid individuals both encysted in crayfish second hosts as well as unencysted in the intestines of bullhead catfish. Our recent survey work across the southern U.S., however, has expanded both host and geographic ranges for *A. progeneticum*. In our talk, we present the life cycle, morphological, and molecular variation associated with these new records. Sequence data (mtDNA and nuclear rDNA) were used to confirm species identifications and multivariate analyses were used to compare morphological traits. Results showed that, although molecularly indistinguishable, specimens from separate locations can be morphometrically different. Intriguingly, we found that the facultative precocious life cycle appears to be restricted to sites within Georgia. We have yet to find encysted gravid worms in crayfish from sites in Louisiana, Texas, Oklahoma, and Arkansas suggesting an obligate 3-host life cycle in this part of the range. We further highlight potential links between this intraspecific variation in life cycle pattern and morphological differences. We will also discuss future plans to use *A. progeneticum* as a model to investigate the impact of changes in life cycle complexity on parasite evolution (i.e., the effect of precociousness on inbreeding).

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IDENTIFICATION OF INHIBITORS OF *PERKINSUS MARINUS* PROLIFERATION USING AN ATP-BASED BIOLUMINESCENCE ASSAY

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"Dermo" disease caused by the protozoan parasite *Perkinsus marinus* (Perkinsozoa) is one of the main hurdles for the restoration of oyster populations in the USA and a concern worldwide (Dermo is currently under surveillance by the OIE). The approaches for intervention against the disease, including the drugs available, are very limited. Based on the phylogenetic affinity between the Perkinsozoa and Apicomplexa (both are constituted exclusively by parasites), we exposed *Perkinsus* trophozoites to a compound library constituted by 400 drug-like and probe-

like compounds highly active against *Plasmodium falciparum* erythrocyte stage and evaluated the effect on Perkinsus proliferation using a bioluminescence assay. We found that 46% the compounds active against *Plasmodium* were also active against *Perkinsus* at day 4 after exposure. For the best compounds tested, we used the IC_{50} to compare seven *Perkinsus marinus* isolates. Here, we have expanded the range of compounds available for inhibiting *Perkinsus* proliferation and characterize *Perkinsus* phenotypes on base to the resistance to the compounds and we discuss the implications for host-parasite interaction, ecology, and oyster management. We also show that *Perkinsus* and *Plasmodium* species share sensitivity to numerous probe-like/drugs making the simplicity of the *Perkinsus* bioluminescence assay useful not only as a tool for prescreening large compound libraries before testing them against *Plasmodium* but also for dissecting the action mechanism of compounds of interest.

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RAPID EPIDEMIOLOGICAL ASSESSMENT (R.E.A.) OF ONCHOCERCIASIS AT THE COMMUNITY LEVEL IN KUDARU, KADUNA STATE, NIGERIA

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The impact of repeated mass treatment with Ivermectin on the prevalence of onchocerciasis in Kudaru, Kaduna State Nigeria, was assessed. The Rapid Epidemiological Assessment (R.E.A.) method was used to determine the prevalence of clinical manifestation as an alternative to the more invasive skin snipping. From the 1982 pre-control data, the prevalence of the disease was 37.2% in the human population. In 2010, 400 persons were examined by R.E.A. alone, of which 19 (4.75%) showed clinical manifestation of the disease. Of these persons, patients with palpable nodules were 10 (2.50%), blindness 5 (1.25%), depigmentation of skin 4 (1.00%) and no individual had hanging groin. Prevalence reduction 21 years post-Ivermectin mass treatment was significant for the disease. Males had insignificant higher prevalence 9 (5.23%) in the clinical manifestation than females 10 (4.38%). Fishermen showed higher prevalence rate 2 (13.33%) than farmers 11 (8.03%) and others 6 (2.42%) who were neither farmers nor fishermen. By age, individuals between 12 years to less than 18 years, 6 (11.52%) had the highest prevalence, followed by individuals of less than 12 years with 7 (9.46%), then individuals with ages up to 45 and above had 5 (5.65%), 1 (2.70%) was the rate of prevalence that was examined in individuals between 18 to less than 25 years and no prevalence rate was observed in persons of 25 to less than 45 years. Based on the assessment there was no relationship between the disease and sex ($\chi^2 = 3.841$, $\alpha = 0.05$) but a significant relationship did exist between the disease and type of occupation ($\chi^2 = 5.991$, $\alpha = 0.05$). There was a weak negative correlation ($r = -0.49$, $\alpha = 0.05$) in the prevalence of the disease with respect to age indicating a decrease in prevalence rate with the ages of individuals that were examined. The observed significant reduction in the prevalence of onchocerciasis following Ivermectin intervention suggests the efficacy of the drug in curbing the spread of onchocerciasis in the community. Therefore, house to house administration of Ivermectin is advocated as an important approach towards eradicating the disease.

(98)

WHY DOES OXAMNIQUINE KILL *SCHISTOSOMA MANSONI* BUT NOT *S. HAEMATOBIUM* OR *S. JAPONICUM*?

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Oxamniquine (OXA) is a highly efficacious drug against the human blood fluke *Schistosoma mansoni*. It is a prodrug that is activated by a parasite enzyme. Recently, the activating principle was identified as a sulfotransferase (*Sm*SULT, Smp_089320) and this resulted in the elucidation of the mode of action of OXA. The homologs Sha_104171 (*Sh*SULT) in *S. haematobium* and Sjp_FN317462.1 (*Sj*SULT) in *S. japonicum* share >50% homology with Smp089320 and are expressed in adult parasites. With this information we address the question of why OXA can kill *S. mansoni* but not the other human species *S. haematobium* and *S. japonicum*. We first demonstrated that *Sh*SULT and *Sj*SULT can transfer a sulfonate group to an acceptor in a SULT-catalyzed sulfonation reaction. We then performed comparative structural analyses of *Sm*-, *Sh*- and *Sj*SULTs in complex with cofactor (PAP) and OXA to empirically determine proteinŸdrug interactions and to identify differences that underlie the differential abilities of these enzymes to activate OXA. Of the 16 residues that contact OXA, 3 differ in *Sh*SULT and 6 differ in *Sj*SULT from *Sm*SULT. These structural analyses of drugŸprotein interactions suggest testable hypotheses to explain the species-specific drug action of OXA. To experimentally probe the importance of residues involved in drug binding and activation, we used site directed mutagenesis to construct modified proteins that differ at 3 key amino acids for OXA contact between *Sm*SULT and *Sh*SULT. Our preliminary data indicate that when we perform site-directed mutagenesis to make *Sm*SULT look like *Sh*SULT and *Sm*SULT look like *Sh*SULT, the *Sm*SULT mutant where SmF39 has been mutated to Y39 (Y54 in *Sh*SULT), *Sm*SULT L149I, and the double mutant *Sm*SULT F39Y/L149I, the mutated *Sm*SULTs can activate OXA as well as the wildtype *Sm*SULT. However, when *Sh*SULT is mutated from ShY54 to F54 (F39 in *Sm*SULT), the mutated *Sh*SULT shows almost twice the activating potential as the wildtype *Sh*SULT. Further studies are underway to identify the remaining amino acids that may be involved in the mechanism of action of *Sm*SULT and *Sh*SULT.

(99)

INTERACTIONS BETWEEN ANTIMALARIAL AND ANTIRETROVIRAL DRUGS IN *PLASMODIUM FALCIPARUM*

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HIV and malaria are deadly infectious diseases endemic to tropical and subtropical areas of the world. Due to similar geographical distribution, co-infection of *Plasmodium falciparum* and HIV can occur in individuals. Malaria is caused by the protozoan parasite *Plasmodium,* whereas HIV is a retrovirus. Previously, we have shown that individuals infected with HIV and *P. falciparum*

receiving antimalarial and antiretroviral treatment still have the *Plasmodium* parasite in their bloodstream. We have found *P. falciparum* to be the only species in this cohort (region Benin City, Nigeria) and no correlation between $CD4^+$ T-cell counts and parasitemia suggesting that there is no interaction between the parasite and the virus. Thus, we hypothesized that the antiretroviral drugs were inhibiting the antimalarial drugs causing the parasite to remain in the bloodstream. *In vitro* assays were performed using different drug combinations and parasitemia was assessed by microscopy and ^{3}Hypoxanthine assays. Our results show that the parasites are not killed *in vitro* when antimalarials are combined with antiretrovirals. We have identified the antiretroviral drug that interferes with the antimalarials. These studies might suggest new treatment guidelines for individuals co-infected with *Plasmodium* and HIV.

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(100)

TICK-BORNE PATHOGENS IN A RODENT COMMUNITY IN EAST-CENTRAL TEXAS

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Tick-borne diseases are emerging worldwide, causing significant illness and death in human and animal populations. The southern United States is an area of particular concern for tick-borne disease emergence due to high tick species diversity and longer periods of seasonal tick activity. Wild rodent species are important in the ecology of many tick-borne diseases due to their ability to feed ticks and serve as reservoirs for pathogens. Using a longitudinal study design, the temporal dynamics and degree to which wild rodents are involved were explored in tick-borne disease systems at a field site in east-central Texas. For nineteen months, small mammals were live-trapped two consecutive nights and subjected to blood and ear biopsy collections. To survey the vegetation for ticks, drag sampling was performed monthly. All captured mammals were checked for the presence of ticks, which were removed for diagnostic testing. Ear biopsies, blood samples, and ticks were subjected to screening for pathogens in the genera *Borrelia*, *Rickettsia*, and *Ehrlichia* using PCR and DNA-sequencing methods. Preliminary data from 943 captures of small mammals of four species (*Peromyscus leucopus*, *Sigmodon hispidis*, *Reithrodontomys fulvescens*, and *Baiomys taylori*) indicate that tick infestation of rodents was rare; 2.3% of rodents (22 of 943) harbored ticks at the time of capture (96.9% *Amblyomma maculatum*; 3.1% *Ixodes scapularis*). In over 14,000 meters of drag-sampling, no ticks were collected. In an analysis of 787 rodent ear biopsies, we detected *Borrelia miyamotoi* (etiologic agent of relapsing fever in humans) in 22 mammals (2.8%), and *B. lonestari* (putative etiologic agent of southern tick-associated rash illness in humans) in a single mammal (0.1%); no mammals were infected with *B. burgdorferi* (etiologic agent of Lyme disease). No ticks were found to be infected with *Borrelia*. Analyses for *Rickettsia* and *Ehrlichia* pathogens are ongoing. While much is yet to be learned about the ecology of *B. miyamotoi*, our study suggests that at least three rodent species (*P. leucopus*, *S. hispidus*, and *R. fulvescens*) may serve as reservoirs, and our work also extends the geographic distribution of enzootic cycles of *B. miyamotoi* to include Texas. Furthermore, in contrast to previous studies which indicate that *B. miyamotoi* prevalence is typically an order of magnitude lower than *B. burgdorferi* prevalence within ticks, our data indicate that *B. miyamotoi* is established at this field site in rodent hosts in the apparent absence of *B. burgdorferi* and without established *I. scapularis* populations. With recent reports of emerging tick-borne diseases, ecological studies of zoonotic tick-borne pathogens in native fauna remain important tools in assessing the possible health risks of newly-exposed populations.

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LARGE SCALE SCREENING OF DIGENEANS FOR *NEORICKETTSIA* ENDOSYMBIONTS USING REAL-TIME PCR EXPANDS KNOWLEDGE OF DIVERSITY, GEOGRAPHY AND HOST ASSOCIATIONS OF *NEORICKETTSIA*

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Digeneans possess complex life cycles including one or two intermediate hosts and a vertebrate definitive host. Digeneans may harbor intracellular endosymbiotic bacteria *Neorickettsia* (order Rickettsiales, family Anaplasmataceae). Some *Neorickettsia* may invade cells of the digenean's vertebrate host and are known to cause diseases of wildlife and humans. In this study we screened more than 2,000 digenean samples for *Neorickettsia* collected from various vertebrates and invertebrates in terrestrial, freshwater, brackish and marine habitats in the United States, China, Australia, Philippines, Vietnam, Ukraine, Laos, Japan, Peru, Argentina, Costa Rica and Egypt. *Neorickettsia* were detected using a newly designed real-time PCR protocol targeting a 152 bp fragment of the heat shock protein coding gene, GroEL, and verified with nested PCR and sequencing of a 1371 bp long region of 16S rRNA. Twelve isolates of *Neorickettsia* have been obtained. Sequence comparison and phylogenetic analysis demonstrated that 9 of these isolates, provisionally named *Neorickettsia* sp. 1-9 (obtained from allocreadiid *Crepidostomum affine* , haploporids *Saccocoelioides beauforti, Saccocoelioides lizae*, and *Plagioporus* n. sp., faustulid *Bacciger sprenti*, deropegid *Deropegus aspina*, 2 lecithodendriids, and a pleurogenid) represent new genotypes and two were identical to a published sequence of *Neorickettsia* known as SF agent (obtained from *Metagonimoides oregonensis* and *Nanophyetus salmincola*). Members of 3 of the 6 digenean families (Haploporidae, Pleurogenidae, and Faustulidae) are reported for the first time as hosts of *Neorickettsia*. We have detected *Neorickettsia* in digeneans from China, Australia, Egypt (Africa as a whole) and Vietnam for the first time based on PCR and sequencing evidence. Our findings suggest that further surveys from broader geographic regions and wider selection of digenean taxa are likely to reveal new *Neorickettsia* lineages as well as new digenean hosts of these bacteria. This study was supported by the grant R15AI092622 from the National Institutes of Health.

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HEMOLYMPH PROPULSION THROUGH THE MOSQUITO ANTENNAE

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Mosquito antennae are sensory appendages that modulate, among other things, host seeking and oviposition behaviors. Because of their essential role in blood feeding and reproduction, mosquitoes must ensure that molecules are efficiently transported into and out of these sensory appendages. The primary motor that drives hemolymph (insect blood) propulsion throughout the mosquito hemocoel (body cavity) is the abdominal heart. However, the contractile force of the heart is insufficient to propel hemolymph into dead-end appendages such as the antennae. To overcome this limitation, mosquitoes and other insects have evolved antennal accessory pulsatile organs that drive hemolymph into the antennal space. The goal of this study was to characterize the structural mechanics of hemolymph propulsion throughout the antennae of the African malaria mosquito, *Anopheles gambiae*. Using intravital fluorescence imaging we found that antennal APOs contract at approximately 1 Hz, which is about 50% slower than the abdominal heart. Then, by means of histology and intravital video imaging we determined that each

antennal APO propels hemolymph through a narrow vessel that, at the end of the antenna, empties into an antennal cavity. Once in the antennal cavity, hemolymph returns to the head at which point it completes its antennal circulatory cycle. Because a narrow antennal vessel empties into a larger antennal cavity, hemolymph travels up the antenna at velocities approaching 0.2 mm/sec but then reduces its velocity by 75% as it travels back toward the mosquito head. Another implication of using a narrow antennal vessel is that it restricts the size of objects that can enter these appendages, and perhaps for that reason we seldom see hemocytes (immune cells) inside the antennal space. In summary, these data describe circulatory physiology in the mosquito antennae.

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HETEROGENEITIES IN THE TRANSMISSION OF AVIAN MALARIA PARASITES: IMPLICATIONS FOR THE ROLE OF MOSQUITOES AS SUPERSPREADERS

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The role of mosquitoes in the transmission of avian malaria parasites (*Plasmodium* spp.) remains understudied. It is widely accepted that the community composition of avian *Plasmodium* parasites is determined by the avian host immunity, but whether or not mosquitoes can act as a barrier to the distribution of these parasites is unclear. Our group has been particularly interested in addressing this facet of avian malaria research. Here we present two years worth of avian malaria prevalence and diversity data from both avian and mosquito collections at China Creek Park, Fresno County, California. A total of 24 lineages of *Plasmodium* spp. were isolated from both avian hosts (13 lineages) and from mosquitoes (11 lineages). Of these, 7 were shared between the 2 populations. *Culex tarsalis, Culex stigmatosoma,* and *Culex restuans* were implicated as major vectors based on PCR confirmed salivary gland infections. Of these 3 species, *Culex tarsalis* was identified as the competent vector for the most common *Plasmodium* lineage among all tested birds (88 of 400 bird blood samples infected with this lineage). This suggests that *Culex tarsalis* can act as a superspreader for this particular parasite. *Culex stigmatosoma,* on the other hand, was implicated with the ability to transmit 9 of 11 *Plasmodium* lineages found at our field site, which did not include the most common *Plasmodium* lineage. The differences in vector competence between *Culex stigmatosoma* and *Culex tarsalis* suggest that there are heterogeneities in the transmission of avian malaria parasites.

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(104)

WHY AMERICAN HIGHER EDUCATION NEEDS PARASITOLOGISTS (ASP President's Address)

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Immigration, the culture wars, and global changes in information technology, combined with financial pressures on institutions of higher learning in the United States, have created an American educational enterprise in which content delivery, economics, uniformity, and certification are the driving forces. Among the winners in this socio-economic trajectory are publishing companies seeking, if not competing, to supply a very wide diversity of dehumanizing

"aides;" losers are students, especially biology majors, for whom truly meaningful encounters with living, tiny, dumb, and uncooperative organisms—i.e., most of the eukaryotes on Earth—are increasingly rare. Yet it is just such encounters that produce the breadth, confidence, and vision that characterize what I'll call "neoclassical" parasitologists—the teachers who can best deliver human resources with a wonderful and effective repertoire of transferable skills. If the national conversation on scientific issues is any indication, the American system of higher education is desperate for just such teachers in the introductory classrooms. This talk is likely to end up being a call to arms.

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FLOUR BEETLE BEHAVIOR SUPPORTS A TRADE-OFF BETWEEN FOOD, SHELTER AND THE RISK OF PARASITISM

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Trade-off theory predicts that many animal behaviors balance the costs and benefits of particular actions. Animals can place themselves at increased risk of parasitism when seeking superior resources of various kinds, such as food, shelter, and opportunities for reproduction. The flour beetle *Tribolium confusum* is adapted to use flour as a food source. While not completely photophobic, these beetles also prefer dark areas, which may confer protection against predation. Flour beetles are also host for various parasites, including the rat tapeworm *Hymenolepis diminuta*, which they acquire by ingesting eggs passed in the feces of infected rats. This parasite causes behavioral changes, reproductive impairment, and intensity-dependent mortality in beetles, yet despite these costs it is well established that uninfected beetles are attracted to the feces of infected rats. We tested using artificial arenas whether movement pattern and resulting infection of fasted beetles varied when offered shelter, flour and infective rat feces in various spatial configurations that exposed them to different presumed cost-benefit scenarios for predation, nutrition and parasitism risks. Prevalence and intensity of infection were highest when feces were in the dark zone and flour was in the light, and lowest when feces were in the light and flour was in the dark. The presence of flour in the same zone as feces only slightly reduced infection levels. Video recording of beetle movements indicated a correlation between time spent in a zone containing feces and resulting infection levels. Collectively, the results suggest a strong tendency to reduce predation risk even at an increased risk of parasitism. The presence of flour, as a food source with no risk of parasitism, did not substantially override the tendency of beetles to seek shelter or to be attracted to infective rat feces.

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THE ACTIVITY CHANGES OF FOUR DETOXIFYING ENZYMES IN *TENEBRIO MOLITOR* LARVAE INFECTED BY ENTOMOPATHOGENIC NEMATODE *HETERORHABDITIS BEICHERRIANA*

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In order to explore both the resistance mechanism of the insect and the infection mechanism of *Heterorhabditis beicherriana* on insect and the biochemical response of hosts infected by this nematode, the four detoxifying enzymes of tyrosinase (TYR), acetylcholinesterase (AChE), carboxylesterase (CarE) and glutathione s-transferase (GSTs) were analyzed in this study to observe the enzyme activity changes in *Tenebrio molitor* infected by *H. beicherriana*. The results showed that the infection of *H. beicherriana* could increase the activity of four detoxifying

enzymes while the doses of the nematode increased within 20-80 IJs/larva. The activity GST-S increased quickly than the other three enzymes, and CarE had two peak of activity. TYR activity began to increase from the 32 h of infection, which companied with the colors of *T. molitor* corpses darkening gradually with increasing of that time. Moreover, the activities of AChE began to climbed up on 32 h infection then sharply fell down. The results indicated that the increase of these four detoxifying enzymes' activity could enhance *T. molitor* detoxification or resistance on the nematodes and symbiotic bacteria in vivo.

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THE EFFECT OF TEMPERATURE ON SYNCHRONIZATION BETWEEN REPRODUCTION OF THE BOPYRID ISOPOD PARASITE *PROBOPYRUS PANDALICOLA* AND MOLTING OF ITS GRASS SHRIMP HOST

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The bopyrid isopod *Probopyrus pandalicola* is a hematophagous ectoparasite that infects palaemonid shrimp, such as the daggerblade grass shrimp *Palaemonetes pugio*. The reproduction of parasitic isopods is thought to occur synchronously with host molting because the brood would be unsuccessful if molting occurred before the larvae were free swimming and could search for copepod hosts. Temperature affects the length of the molting cycle for shrimp, and therefore may also affect the timing of isopod brood development. The purpose of the present study was to determine the duration of each developmental stage of parasite young as a function of temperature, and to determine fecundity of the parasite. Parasitized shrimp were monitored at 15°C and 23°C within environmental chambers. Development was slower at 15°C than at 23°C, with a significant effect of temperature on the duration of brood incubation (34.6 d and 11.1 d, respectively) and shrimp intermolt period (33.1 d and 12.1 d, respectively). Epicaridium larvae remained in the parasite marsupium for 3.1 times longer at 15°C (8.7 d) than at 23°C (2.7 d) ($p<0.0001$). Epicaridium larvae were released closer to shrimp molting at 23°C than at 15°C, indicating greater synchronization between host and parasite at 23°C. Brood size ranged from 391 to 4,596 young, and was positively correlated with parasite and host size. Brood development progressed more rapidly at 23°C, suggesting that long-term increases in temperature may increase the prevalence of *Probopyrus pandalicola*. The corresponding reduction in the abundance of grass shrimp as a result of sexual sterilization by bopyrids could adversely impact the health of estuarine ecosystems.

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GENETIC EVALUATION OF GASTROINTESTINAL NEMATODE RESISTANCE IN GOATS: IMPACT OF THE POST-WEANING PARASITISM LEVEL

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In the Tropics, kids and lambs are reared mainly at pasture for meat production. Under such conditions, gastrointestinal nematodes (GIN) infections are a major cause of their morbidity and mortality. The chemotherapy alone is no longer an efficient solution because of the spread of anthelmintic resistance in GIN and the increasing public demand of chemical-free animal products. The philosophy of the different research programs is to develop more sustainable alternative control strategies in order to reach a favorable equilibrium for animal production between host and parasites. The selection of genotype resistant to these parasitic infections is a

promising alternative control strategy. Thus, resistance against GIN is an important component of small ruminant breeding schemes, based on phenotypic measurements of resistance in immune mature infected animals. We have showed that naturally infected tropical pastures allow genetic evaluation (*i.e.* estimated breeding values, EBV) of Creole goat resistance to GIN. In this study we evaluated both, the impact of the post-weaning parasitism history on the response to an experimental *Haemonchus contortus* infection of resistant and susceptible Creole kids chosen on the basis of their EBV, and the interaction with the kid's genetic status. Three trials were involved in this study with a total of 169 male kids chosen from 3 successive cohorts. Kids were reared at pasture from 3 months (weaning) until 7 months of age into mixed rotational stocking system with Creole cattle. Kids were allocated in 4 grazing groups according to the stocking rate based on the metabolic live weight ($LW^{0.75}$): 25% (kids 150 kg $LW^{0.75}$ and cattle 450 kg $LW^{0.75}$), 50% (kids 300 kg $LW^{0.75}$ and cattle 300 kg $LW^{0.75}$), 75% (kids 450 kg $LW^{0.75}$ and cattle 150 kg $LW^{0.75}$) and 100% (kids 600 kg $LW^{0.75}$). At 7 months of age, FEC of all kids were determined twice at one-week interval. Thereafter, all kids were drenched, placed indoors and received *ad libitum* parasite-free *Dichanthium* spp. hay. At 11 months of age, all kids were infected with a single dose of 10,000 *H. contortus* L_3. The FEC, packed cell volume (PCV), blood eosinophilia were recorded at 0, 28 and 35 days post-infection. During the post-weaning period at pasture, the level of infection of the kids decreased significantly from 50% of association with cattle. After the experimental infection at 11 months of age, the FEC were significantly lower in the groups showing the highest FEC at pasture. No effect on packed cell volume and blood eosinophilia was observed. This result suggests that a degree of protection against an experimental *H. contortus* infection occurred during the post-weaning period and was dependant on the level of parasitism. Interestingly, no interaction was evidenced between this level of protection and the genetic status. In conclusion, the level of post-weaning natural parasitism history at pasture would not influence the genetic status evaluation. More generally our results suggest that it would be better to expose kids to a high level of gastrointestinal parasitism during the post-weaning period in order to increase the basal level of resistance thereafter.

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SHEDDING NEW LIGHT ON HOST-PARASITE INTERACTIONS WHEN USING ORGANISMS WITH THE ABILITY TO PRODUCE BIOLUMINESCENCE

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Many organisms produce light signals as a tool of visual communication that involves intra- and/or interspecific interactions. This living light phenomenon is called bioluminescence: it is produced with intensity and kinetics that are species specific, and it thus involves elaborated neuro-physiological control mechanisms. Luminous organisms sometimes harvest symbionts to help with their ability of light production, such as the case for luminous squids that selectively culture a strain of luminescent bacteria in their light-producing organ. Other organisms, such as brittlestars for example, have intrinsic light production (thus not originating from symbiosis). Such organism however can also be infested by a variety of parasites, from crustaceans to mesozoans ciliates. Here, I will review some of the fundamental knowledge from the literature where both fields of bioluminescence and parasitism/symbiosis have been considered together. I will describe the fundamental mechanisms by which bioluminescence capacity is affected by symbiosis. The luminous brittlestar *Amphipholis squamata* broods its juveniles, which comes together with an increase of its ability to produce light, presumably (anthropocentrically perhaps) to increase protection of its offspring. A crustacean copepod can be parasitic of the brooding bursae as well, which is lethal to the offsprings, yet triggering similar increase of light production from the brooding parent. Such ability from the parasite to mimic the brooding stage emphasizes the use of change/s in bioluminescence properties of light-producing organisms as a tool to detect neuro-physiological effect of parasites on their hosts. Being able to quantify such effects readily

from the host offers a unique approach to identify the molecular mechanisms by which some parasites are able to carefully manipulate the biology of their host.

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SCREENING SNAIL-TREMATODE RELATIONSHIPS FOR COMMON COMPATIBILITY DETERMINANTS

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Of the over 18,000 known species of digenetic trematode, most undergo larval development within a snail host. Commonly, trematodes display a high degree of specificity for the snail hosts they can infect. This specificity is, at least in part, dictated by immunological interactions that appear to have established over the long co-evolutionary history of these two groups of organisms. Recent evidence has revealed the presence of specific immunological and environmental factors that are determinants of infection susceptibility in snails. However, much remains unknown about the factors that influence compatibility between snails and trematodes, especially within their natural environments. To better understand the driving factors of host and parasite specificity, diversity, and compatibility, we are conducting a field surveillance study of snail and trematode species across different lakes in Alberta. In our first season, we collected 8,910 snails, of which 1,174 had patent trematode infections (5 species of snails from 3 families and ~ 16 trematode species from 6 families). We now have baseline data related to the snail-trematode associations that are commonly found in central Alberta. With this information, we are able to experimentally design compatible and incompatible test challenges in the lab and then measure the impact of environmental and immunological factors on infection success. We have begun to assess the influences of temperature and the circulating lectins, fibrinogen-related proteins (FREPs), on snail-trematode compatibility. Both of these factors have been demonstrated to influence infection outcome when a trematode challenges a naturally resistant snail. Temperature stress, specific FREP repertoires, and lower FREP expression levels are associated with a loss of the resistance phenotype. The conservation of these factors in determining infection outcome is currently being assessed in more depth, with deep sequencing being used to determine whether FREPs remain relevant to infection outcomes across all snail-trematode associations.

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CAN PARASITES AND DIFFERENCES IN REPRODUCTIVE STATUS INFLUENCE EROD ACTIVITY IN FRESHWATER FISH?

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Ethoxyresorufin-O-deethylase (EROD) activity has been considered an important biomarker for aquatic environmental contamination. Although EROD activity has been widely used as a biomarker of exposure to planar aromatic hydrocarbons in fish, in the field its activity can be influenced by parasites, seasonal or host related factors. We therefore compared the hepatic

EROD activity levels in the silver croaker *Plagioscion squamosissimus* to determine if there is a variation in enzyme activity, especially in relation to reproductive status, parasite load, and seasonality. For this purpose, we collected fish among three localities with different pollution levels and on the dry (July to August, 2013) and rainy (November-2013) seasons from Tietê River, Southeast Brazil. Two helminth parasite species were recovered: metacercariae of *Austrodiplostomum* sp. free in eyes (prevalence = 95.3, mean abundance = 34.15 ± 47.8), and *Diplectanum piscinarius* in gills (prevalence = 100, mean abundance = 63.3 ± 31.6). We tested whether parasites had an effect on EROD activity, but no significant statistical association was found. In contrast, we observed a marked effect of seasonality (dry season) in hepatic EROD activity in P. squamosissimus among the localities. Analysis of Covariance (ANCOVA) indicated that sex had a significant positive effect on the seasonal variability of EROD levels in the most polluted locality (near Sao Paulo). A potential explanation for the statistical association between EROD activity and sex is that the reproductive status of females influenced the EROD levels. Further support for this explanation is that the literature suggests suppression of EROD levels in mature females by 17β-estradiol and a decline of this enzyme during the onset of ovulation until spawning. Our results revealed that the reproductive status of females can be a significant confounding factor to determine EROD activity in freshwater ecosystems when compared to males. With respect to parasites, we suggest that there should be a threshold in the number of individuals from which a significant effect in EROD levels should become evident.

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DISENTANGLING PHYLOGENETIC CONSTRAINTS FROM ECOLOGICAL DRIVERS OF TREMATODE RICHNESS IN GASTROPOD HOSTS

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Large-scale determinants of parasite species richness have previously been examined in multiple host and parasite taxa, with most studies controlling for the effect of host phylogeny. However to our knowledge no study has attempted to disentangle ecological from phylogenetic influences, and quantify the effect of the latter on parasite species richness. Here we investigated the host phylogenetic effect on trematode species richness in a comparative analysis of first intermediate gastropod host species. We used taxonomy as a nested random effect and quantified the proportion of variance in parasite richness for which it accounted. For all analyses we controlled for sample size. A number of ecological variables were tested in an attempt to uncover why particular gastropod groups might host a species-rich suite of parasites while others do not. These variables included the host snail size, density, habitat and latitude. We found that taxonomy, included as a nested random effect, accounted for a large proportion of the variation in parasite species richness across snail species, and uncovered several ecological variables which could help to explain this result. Our results provide the first attempt at quantifying the effect of host taxonomy on parasite species richness. From preliminary analyses it appears taxonomy could contribute more to the structure of parasite species richness in snail intermediate hosts than the various ecological variables examined.

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GREGARINE PARASITES OF TENERAL AND LARVAL DAMSELFLIES, *ISCHNURA VERTICALIS* (ODONATA: ZYGOPTERA): A COMPARISON

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Gregarine parasites (Ph. Apicomplexa, O. Eugregarinorida) occur in most invertebrate phyla, but are particularly diverse in insects and annelids. Previous studies have demonstrated host stadium specificity among septate gregarine species in at least one species of coleopteran host (*Tenebrio molitor*, Tenebrionidae), but other work showed that parasite species from tenebrionid larvae (*Triboliuim confusum, Tr. castanaeum*, and *Tr. brevicornis*) could experimentally infect conspecific adults. The question remains whether or not different host life cycle stages represent distinct ecological niches to be colonized by these parasites. A large emergence of *Ischnura verticalis* (Odonata: Zygoptera) allowed comparisons to be made between the gregarine fauna of teneral (newly emerged adult) and larval hosts, all collected at a single site within 24 hr. Three species of gregarines were identified in larval *Ischnura verticalis*: *Steganorhynchus dunwoodii* Percival, Clopton, and Janovy, 1995, *Nubenocephalus nebraskensis* Clopton, Percival and Janovy, 1993, and *Actinocephalus carilynnae* Richardson and Janovy, 1990. Only *S. dunwoodii* and *N. nebraskensis* survived host metamorphosis; prevalence and intensity of parasites were significantly higher in larvae than in tenerals, indicating loss of parasites during metamorphosis. Furthermore, newly emerged adults often either occur sporadically in nature or are not collected in numbers large enough to support statistical analysis of their parasite fauna. Unique weather conditions occurred in late May 2013 in western Nebraska, however, producing a large emergence from a site used for many years by students and faculty studying gregarine parasites in odonates, allowing comparison of larval and teneral parasite prevalence and intensities.

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ENDOPARASITIC LEECHES FROM FROGS (ANURA: HYLIDAE, RANIDAE) IN PAPUA NEW GUINEA

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The majority of blood-feeding leeches feed from the external surface of their hosts, but some blood-feeding leeches will enter the vertebrate host to temporarily feed from inside the host's body. In leeches, endoparasitism is a behavior exhibited most often by members of Praobdellidae on mammalian mucous membranes and by Theromyzon (Glossiphoniidae) in the nares of waterfowl. Members of Hirudinidae or Haemadipsidae have been reported occasionally to inadvertently slip into a host's orifice to feed, but primarily feed from the exterior. Tree frogs collected in Papua New Guinea were found to have live leeches residing inside the dorsal lymph sacs and body cavity that were expelled by the frog through the cloaca upon capture or soon thereafter. Body length of the leeches ranged from 6–60mm. Frogs were infected with 1–4 leeches constituting up to 20% of the total mass of the frog. Morphological examination revealed the leeches to be two species of Haemadipsidae: Leiobdella singularis Richardson, 1975 and an undescribed species of Leiobdella. Leiobdella singularis was redescribed from Litoria angiana and the new species was described from Litoria cf. angiana, both from the Eastern Highlands of Papua New Guinea. DNA sequence data were generated for nuclear 18S rDNA and 28S rDNA and mitochondrial COI and COIII for *L. singularis* and the new species. Pairwise genetic distances of the mitochondrial gene fragments showed the new species to be distinct from L. singularis and

Parsimony and Maximum Likelihood analyses supported the new species as a member of Leiobdella. The endoparasitic behavior of these two leech species posed a unique opportunity for a formal assessment of host specificity of leeches. The new species is only known to parasitize a single host species and by definition is oioxenous (HSS = 0) while *Leiobdella* singularis is known from nine species of two families of frogs (Hylidae and Ranidae) and was found to be euryxenous (HS rank = 375,258, HSS = 5.574). Of the five species that comprise the genus, *L. singularis* and the new species are the only members, and the only species of Haemadipsidae to exhibit endoparasitic behavior. These two species represent a third transition to endoparasitism in the evolution of blood-feeding leeches.

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EFFECT OF ENERGY AND PROTEIN SUPPLEMENTATION IN LAMBS AND KIDS ON THE RESPONSE TO *HAEMONCHUS CONTORTUS*

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Gastrointestinal nematode (GIN) infections have an important negative impact on small ruminant production. The manipulation of host nutrition to improve resistance and/or resilience of small ruminants to GIN infections is a promising strategy and easy to implement at short-term. The objective of this study was to evaluate the effect of the level of supplementation with energy and protein during the post-weaning period on the response to an *Haemonchus contortus* infection by comparing lambs and kids. Forty eight Creole kids and 48 Black Belly lambs at 4 months old were used. They were placed into six groups defined by the combination of 3 protein levels (5; 12 and 20% Dry Matter of crude protein in the diet) and 2 energy levels (1 and 1.6 time the requirement level). The six groups were fed according to their respective diet during 3 months, from 4 to 7 month of age. Thereafter, kids and lambs were drenched and received *ad libitum* parasite-free *Dichanthium* spp and 200g/day of a commercial concentrate until the end of the experiment. After one month on this diet, they were infected with a single dose of 10,000 *H. contortus* L_3 for 35 days. During this period, the average daily gain (ADG), blood eosinophilia, packed cell volume (PCV), faecal egg counts (FEC), serum pepsinogen and total serum protein were monitored weekly. Moderate protein and high energy diet have led to an optimal growth before infection with an ADG of 66 and 147g/day for kids and lambs respectively. Lambs fed with the diet defined above showed the lower FEC (1500 *vs.* 7 000 for lambs fed with low protein diets) ($P<0.05$). No difference in FEC was observed between the different diets in kids. The decreased in PCV was more pronounced in kids ($P<0.001$) and no difference was observed between the groups. The blood eosinophilia response was significantly lower in the groups fed with the lower protein and energy diet ($P<0.05$). No effect of the diet was observed on the level of serum pepsinogen but a higher level was observed in kids compared with lambs (515 *vs.* 238 Units tyrosine respectively, $P<0.001$). In contrast, no difference in total serum protein was observed between kids and lambs but a lower concentration of total serum protein was observed in the groups fed with the lower protein and energy diet ($P<0.001$). Interestingly, in lambs a compensatory growth was observed during the infection in the groups with the lower protein and energy diet (mean ADG =26.3 g/day) when the groups with high or moderate protein and energy diets showed negative ADG (-23.2 g/day). In kids, no difference in ADG was observed between groups. This study comparing a local breed of goats with a more commercial breed of sheep suggest that improved nutrition during the post-weaning period, by increasing both protein and energy in diets, improved the response to *H. contortus* infection in lambs but not in kids. Moreover, our results suggest that the response of lambs is dependent on the level of nutrition before the infection.

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PROGRESSION OF INFECTION OF *CERATOMYXA SHASTA* AND *PARVICAPSULA MINIBICORNIS* IN ADULT CHINOOK SALMON

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Pre-spawning mortality (PSM) is common Pacific salmon after they return to freshwater to spawn. We are investigating causal relationships between pathogens and PSM in Chinook salmon (*Oncorhynchus tschawytscha*). Two myxozoans, *Ceratomyxa shasta* and *Parvicapsula minibicornis* are a common in both PSM fish and those that survive to spawn in the autumn. Both use the freshwater polychaete *Manayunkia speciosa* as their alternate host. We followed infections by these parasites from early summer until spawning for the last 4 summers. *Parvicapsula mininbicornis* was first detected in the kidney glomeruli, where it was often associated with severe glomerular nephritis. Later in the summer and in the autumn, presporogonic stages and spores occurred in the lumen of renal tubules. With *C. shasta*, many fish showed large numbers of prespore stages in the intestine, increasing until spawning. However, spores were rarely observed in live fish, even though they were exposed and presumably infected for months before spawning. In contrast, the parasite sporulates within a few weeks in juvenile salmon. Because salmon are destined to die after spawning in fresh-water by the end of September, we reasoned that *C. shasta* may have evolved to sporulate in their host post-mortem in syncopation with the salmon life cycle. So, we evaluated the ability of *C. shasta* to sporulate following fish death in 23 infected fish. We compared spore intensities in pieces of intestine at time zero (T0) (collected from euthanized adults) and after holding pieces of intestine from the same fish at 17 C for 7 d (T7). A significant increase in spore concentrations was observed in some fish, which ranged from 1.5 to 14.5 fold increase. The fold-increase in spore density was significantly correlated with histopathological severity (Pearson's $R = 0.41$, $p < 0.004$). The most heavily infected fish exhibited about a 4.6 fold increase from 27,841 to 129, 352 spores/cm. This indicates presporogonic forms of *C. shasta* are viable and continue to sporulate after death in some adult salmon.

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AMPHISTOMES AS NATURAL ENEMIES OF LARVAL SCHISTOSOMES IN KENYA

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We are interested in exploring and exploiting the potential of natural enemies, including digenetic trematodes, to interfere with the development of human schistosomes in their snail hosts in Kenya. This could potentially provide a much needed complement to chemotherapy in ongoing attempts to control and eliminate schistosomiasis in tropical Africa. Thus far we have focused on stream environments in western Kenya where *Biomphalaria pfeifferi* transmits the human parasite *Schistosoma mansoni*. Amphistomes (and other trematode species) are also transmitted by *B. pfeifferi* and are of interest because they produce rediae that may prey upon or otherwise interfere with *S. mansoni* sporocyst development. Amphistome infections, which originate from

domestic ruminants, are common in *B. pfeifferi,* and during some of our collections over 20% of snails were infected with amphistomes. We have combined sequence data (ITS2) and anatomical studies and learned that at least ten different species of amphistomes are transmitted in western Kenya with three species being transmitted by *B. pfeifferi.* Interestingly, about four species of amphistomes are also transmitted by *Bulinus* snails. We exposed 80 *B. pfeifferi* snails that were naturally infected with amphistomes to five *S. mansoni* miracidia; only one *B. pfeifferi* subsequently shed a few *S. mansoni* cercariae. In 50 size-matched control snails lacking amphistome infections, 93% became infected upon exposure with *S. mansoni*. This suggests pre-existing amphistome infections can suppress the development of *S. mansoni* in *B. pfeifferi*. We have acquired amphistome eggs in large quantities from adult worms collected at Kenyan local slaughterhouses and from ruminant fecal samples collected on the banks of our study sites. We are in the process of testing the infectivity of these eggs for both *Bulinus* and *Biomphalaria* snails, and will attempt to learn if amphistome infections can be superimposed on, and replace, both naturally occurring and experimental infections of *S. mansoni* in *B. pfeffieri*. This study was supported by R01 AI101438.

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PATHOLOGY OF *PLASMODIUM (NOVYELLA) UNALIS* AND *PLASMODIUM (HAEMAMOEBA) LUTZI* ON NATURAL AND EXPERIMENTALLY INFECTED BIRDS

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Despite that the infections of Plasmodium parasites are rare in high altitudes, the great thrush (*Turdus fuscater*) has been found infected with *P. unalis* and *P. lutzi* with a prevalences of 28 % and 3.7% respectively, at Bogotá city (2,600 m.a.s.l), although 39 avian species were analyzed, the great thrush was the only infected species, for this reason they are an interesting model for the study of the host-parasite relationship. the aim of this study was: evaluate the pathology of these *Plasmodium* species, , first with the relation between parasitemia (the number of parasites by 10,000 erythrocytes on the Blood slide) and hematocrit level on 54 live Great thrush and second examine the macroscopic changes (coloration, size and weight) and histological sections of the internal organs of 10 Great thrush that were found dead in Bogotá. Also in order to establish an experimental model, the susceptibility of *Serinus canaria* (canary) to these plasmodium species was tested by inoculation of 6 canaries with infected blood with *P. lutzi* and *P. unalis*. The results showed a significative difference in the hematrocrit when comparing infected and uninfected birds, specifically when the level of parasitemia was higher than 0,1 % (p-value= 0,01776). The dead infected birds showed darker colorations of the lungs, liver and spleen also splenomegaly . The histological inspection showed the presence of many pigment granules and schizonts mainly on the lungs and less frequently in the liver and spleen. In some of the infected live Great thrushes with P. lutzi, the production wheezing when the bird breathing was noted, this affectation of the lungs is not usual in Plasmodium infections, representing an interesting pathology that should be studied in detail, the presence of schizonts in endothelial cells was higher in Turdus infected with P. lutzi, respect to the infected with P.unalis, also the presence of pulmonary edema and necrotic tissue was observed in the lungs of two great trush infected with P.lutzi, so this specie seems to be more pathogenic to the Host and it may be an explanation of the less prevalence of P.lutzi observed at the study area. We were able to infect canaries with P. lutzi; instead any infection were obtained in canaries when challenge with blood infected with P. unalis, further studies to analize the possible specificity of P.unalis infecting turdidae species are ongoing. Also the positive infection of canaries with P.lutzi, goes against the results previously found for this specie, so our P.lutzi could be a cryptic species, The results of this study show the importance of studies on avian Plasmodium, into the conservations programs, because this infections are not, asymptomatic as previously had been proposed and the absence of Plasmodium infections on the other bird species of the area could be related with a mortality causing for these pathologies to the other birds, however more studies are needed.

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POPULATION GENETIC ANALYSES OF THE CHEWING LOUSE *GEOMYDOECUS EWINGI*

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Studies of parasites offer a multiple of opportunities for investigating evolutionary associations with often distantly related hosts. For example, because parasites often have complex ecological interactions with their hosts, thorough examination of host-parasite associations can yield significant information about evolutionary interactions. *Geomydoecus ewingi* is a relatively well-known chewing louse that parasitizes the pocket gopher *Geomys breviceps* in the rodent family Geomyidae. The flightless and obligate nature of the lice coupled with few opportunities to colonize new hosts has helped to make them model organisms for cospeciation studies. This research aims to determine the microevolutionary processes driving macroevolutionary patterns, such as cospeciation, in gopher-louse assemblages. Through the use microsatellite data, a series of population genetic analyses were conducted on lice parasitizing *G. breviceps* to better understand the population structure of lice among host individuals and across localities. These data will be useful in future studies exploring the population dynamics in host-parasite systems, potentially yielding a better understanding of the processes underlying symbiotic associations.

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POINT OF CARE DIAGNOSIS FOR SCHISTOSOMIASIS: MULTI PARASITE DNA DETECTION IN SINGLE URINE SAMPLE

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Schistosomiasis is one of the most widespread and important of the neglected tropical diseases, however this information is based on analyses using inadequate diagnostic tests that are low in sensitivity. The standard diagnostic tests, including stool examination by Kato-Katz (KK), detection of egg (filtration method) and blood (haematuria) in urine lack accuracy, especially in low endemic settings. Hence true disease prevalence in endemic countries remains unclear, and this is very important in Africa where *Schistosoma haematobium* and *S. mansoni* often occur sympatrically. The need for a single easy to operate diagnostic test with high sensitivity and specificity for both parasites is important as many African countries are implementing Mass Drug Administration (MDA) following recommendations of the World Health Organization (WHO). The presence of species-specific DNA in the host is definitive evidence of a parasite and is important to differentiate between one or more different species. We compared diagnostic efficacy of KK, haematuria and parasite species-specific DNA detection by PCR to detect *S. mansoni* and *S. haematobium* infection from 86 urine sediment specimens obtained through filtration collected in an area of Ghana of low to moderate endemicity. Because low level infections will maintain the reservoir of infection and many infections will still persist following MDA. It is important to have accurate tests of high sensitivity so that it is feasible to detect and treat such infections. Our approach showed promising signs with much higher sensitivity (ranges from 99% – 100%) and specificity (100%) compared to KK and haematuria (sensitivity: 76% and 30%) devoid of any cross amplification. High positive and negative predictive values (90% - 100%) were also indicative of robustness of our approach. The same pattern was observed when stratified for age group and sex specific analysis. In addition 11 individuals found to be infected for both parasites that were considered not infected by either parasite. We have demonstrated a

significantly higher prevalence of both these species than indicated by the classical examination of urine or stool. Our approach of disclosure of multi schistosome infection from urine by PCR is an effective means to detect low intensity infection and would enhance the effectiveness of surveillance and MDA control programs of schistosomiasis.

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HEMOCYANIN-LIKE SEQUENCES IN *BIOMPHALARIA GLABRATA*, SNAIL INTERMEDIATE HOST FOR *SCHISTOSOMA MANSONI*

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Intestinal schistosomiasis is a debilitating human disease caused by the blood fluke *Schistosoma mansoni,* endemic to Africa and Latin America that continues to challenge control efforts. Massive drug administration benefits those infected but does not protect against re-infection. Prior to infecting humans, *S. mansoni* develops in a snail intermediate host, like *Biomphalaria glabrata*. Study of the intermediate host may provide approaches to reduce snail-mediated parasite transmission. *Biomphalaria glabrata* employs red-pigmented hemoglobin, an iron atom-containing molecule as oxygen carrier. However, most mollusks use hemocyanin, a blue-pigmented glycoprotein with copper atoms to transport oxygen. Remarkably, *B. glabrata* also expresses hemocyanin-like sequences but their function remains unknown. Hemocyanin-like sequence-containing clones from a BAC library produced with *B. glabrata* genomic DNA were identified using relevant ESTs. Sequencing of two BACs yielded a 290kbp contig that contained a hemocyanin gene (50kbp). The computationally predicted gene transcript contains three functional units and was named HcABH. Expression was confirmed by reverse transcriptase (RT)-PCR yielding full-length transcripts from two lab strains (BB02 and M line) and two field isolates (VG2 and VG3) of *B. glabrata*. Tissue-specific RT-PCR and immunoblotting with anti-keyhole limpet hemocyanin antiserum (α -KLH) and mass spectrometry showed HcABH expression in the albumen gland and presence in egg masses. Bioinformatics revealed that the *B. glabrata* genome has an additional hemocyanin gene with 6 functional subunits (named Hc6FU) that encodes a hemolymph-circulating protein (immunoblotting with α -KLH). These observations imply different functions for the two hemocyanins. Functional analyses, including tracking responses to infection, will be performed to understand how hemocyanin-like sequences define biological properties of *B. glabrata*, especially in relation to transmission of schistosomiasis.

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TRANSPOSABLE ELEMENT DYNAMICS IN *SCHISTOSOMA MANSONI* STRAINS: NEW WORLD VS. OLD WORLD

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Parasites of the trematode genus *Schistosoma* are the causative agents of schistosomiasis, a widespread tropical disease causing severe morbidity and mortality in infected individuals. The genomes of all three major human infecting schistosomes (*S. japonicum*: in South East Asia, *S. haematobium*: Africa, and *S. mansoni*: South America and Africa) are relatively large and loaded with transposable elements (TEs); approximately 40% -50% of each genome is composed of TEs. Transposable elements are mobile DNA sequences with an intrinsic ability to move within and among genomes. According to “Epi-transposon hypothesis” TE proliferations are associated with “genomic stress”, such as invasion of new habitats and merging of distinct genomes (e.g.

hybridization). The TE-rich nature of schistosome genomes is indicative of massive TE proliferations that occurred in the past as well as the susceptibility of the genome to TE proliferations. Previous studies have suggested that the species *S. mansoni*, carries more transposable elements than its congeneric relatives. Also, unlike other species of schistosomes, *S. mansoni* has a wide distribution, ranging from the old world to the new world. Phylogenetic analysis indicates that ancestors of *S. mansoni* originated in East Africa and then expanded to South America and Caribbean islands through the slave trade, during last 500 years. As invasion of new habitats can lead to increased TE-expression, we hypothesized that the new world strains of *S. mansoni* would have more copies of transposable elements than the old world strains. We quantified the copy number of six transposable elements in new world and old world strains of *S. mansoni* using a SYBR Green qPCR assay with an internal control gene, GAPDH (Glyceraldehyde-3-phosphate dehydrogenase). Our results indicate significant increase in expression of TEs in new world strains of *S. mansoni*, compared to the old world strains. Although TE proliferations are often thought to be detrimental, emerging evidence suggests possible adaptive advantages of such events. In fact, increased TE activity facilitates emergence of new genes, modifies gene expression patterns and promotes chromosomal re-arrangements that can contribute to the evolution of traits that increase adaptability of the lineages, sometimes leading to speciation. New world and old world strains of *S. mansoni* differ in their habitat/host preference. High TE content in new world strains of *S. mansoni* may have facilitated the invasion of new world habitats and hosts through genome dynamism.

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MICRORNAS IN *LEISHMANIA BRAZILIENSIS* USING BIOINFORMATICS

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MicroRNAs have been described in most organisms from worms to human and recently in protozoans. They are a group of small RNAs that regulate gene expression post-transcriptionally in a complex process of binding to mRNA in an imperfect 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 that microRNAs in *L. braziliensis* has high homology to known miRNAs in human and mouse. These results show our discovery of putative microRNA in *L. braziliensis* using bioinformatics.

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SCHISTOSOME TEGUMENTAL NUCLEOTIDE METABOLIZING ECTO-ENZYMES

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Schistosomes are parasitic platyhelminths that can live in the bloodstream of their vertebrate hosts for many years. The tegument (skin) of intravascular schistosomes is a syncytium that is bounded on the exterior by a double lipid bilayer. This surface constitutes a major site of interaction with the host. Proteomic analysis of the *Schistosoma mansoni* tegument has

confirmed earlier biochemical work documenting the existence of a series of three nucleotide metabolizing enzymes at the host/parasite interface. These are alkaline phosphatase (SmAP), phosphodiesterase (SmNPP-5) and ATP diphosphohydrolase (SmATPDase1). These ecto-enzymes may participate in the hydrolysis of extracellular nucleotides like the pro-inflammatory mediator ATP and its pro-thrombotic derivative ADP. To test this hypothesis, we used RNA interference to knock down expression of the genes encoding these enzymes in schistosomula (juvenile) and adult life stages of the parasite. We then compared the abilities of these parasites to degrade exogenously added ATP and ADP relative to control parasites. The results showed that only SmATPDase1-suppressed parasites were significantly impaired in their ability to degrade the added nucleotides. Suppression of the SmAP or SmNPP-5 genes did not appreciably affect the worms' ability to catabolize ATP or ADP. These findings were confirmed by the characterization of an enzymatically active, full-length recombinant SmATPDase1 expressed in CHO-S cells. The enzyme was found to be a true apyrase: SmATPDase1 degraded ATP and ADP in a cation dependent manner. Optimal activity was seen at alkaline pH. The Km of SmATPDase1 for ATP was recorded at 0.4 ±0.02 mM and for ADP at 0.25 ± 0.02 mM. The results confirm the role of tegumental SmATPDase1 in the degradation of the exogenous pro-inflammatory and pro-thrombotic nucleotides ATP and ADP by living intravascular stages of the parasite. By degrading host inflammatory signals like ATP, and pro-thrombotic signals like ADP, these schistosome ecto-enzymes may minimize host immune responses, inhibit blood coagulation and promote parasite survival.

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DETECTION OF TRYPANOSOMES IN BRITISH BADGERS

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The Eurasian Badger (*Meles meles*) is a popular animal in the UK that is statutorily protected. It has been the subject of intense public health concern resulting from its role as a wildlife reservoir for tuberculosis. Trypanosomes are blood parasites that infect a wide range of hosts, including humans, and have the potential to cause disease in mammals such as badgers perhaps resulting in declining populations. The objectives of this study were to detect trypanosomes in UK badgers using novel molecular biological diagnostic tools. A total of 82 badger blood samples were examined by ITS-PCR using a set of nested primers that targeted the ribosomal RNA gene locus. Twenty-nine of the samples were found to be positive for trypanosomes giving a prevalence of 35.4%. Analysis of ITS sequence data suggested that the badger trypanosomes are closely related to *Trypanosoma (Herpetosoma) otospermophili* and phylogenetic analysis from this study supports the belonging of *T. otospermophili* in the *Herpetosoma* subgenus (NJ and ML tree; 100% bootstrap support). These results show that a significant proportion of UK badgers could be infected with trypanosomes indicating they are susceptible to infection with pathogens. Trypanosome infections in badgers are mediated by transfer of blood by fleas and high prevalence indicates this may be happening frequently. The possibility exists that other important pathogenic diseases, such as tuberculosis, could be transmitted in similar ways. This study could give an insight into the general transmission of infectious diseases in this important wildlife reservoir. Future work is aimed at sequencing other ITS regions.

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EFFECTS OF HYDROGEN PEROXIDE AND UV IRRADIATION ON THE VIABILITY OF *ASCARIS SUUM*

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Ascaris lumbricoides is a parasitic intestinal helminth that infects 807 million – 1.22 billion people worldwide. A. *lumbricoides* ova have shown to be resistant to common treatments such as strong acids and bases and disinfectants such as chlorine. Hydrogen peroxide (H_2O_2) and UV irradiation have been proposed to effectively kill bacteria and viruses in drinking and wastewater matrices; although, little research has been done with using this approach to inactivate *Ascaris* ova. This study focuses on evaluating the effects of H_2O_2 and UV irradiation on the viability of *A. suum* (a surrogate for *A. lumbricoides*) ova; specifically to determine the lowest concentrations of UV irradiation and H_2O_2 required to achieve at least a 99% inactivation rate for *Ascaris* ova. Four different concentrations of H_2O_2 and UV on their own as well as in combination were used to treat viable *Ascaris* ova. Using a microscopic examination approach that monitors egg embryonation to measure ova viability, revealed that at least a 99% inactivation rate with UV irradiation at 20 and 100 mJ/cm^2 was achieved. By contrast, treatment H_2O_2 alone was not effective at inactivating *Ascaris* ova at any concentration tested. The combination of H_2O_2 and UV irradiation also did not show any significant synergistic effect. This study reveals that UV irradiation, at relatively low doses is effective at inactivating *Ascaris* ova. Future research will evaluate other advanced oxidation treatment processes that are effective at killing *Ascaris* ova.

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DEVELOPMENT OF A MULTILOCUS SEQUENCE TYPING TOOL FOR CHARACTERIZING *CYCLOSPORA CAYETANENSIS*

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Cyclospora cayetanensis is an important foodborne pathogen, causing numerous outbreaks of cyclosporiasis in North America since the mid-1990s, mostly associated with imported fresh produce. The investigation of cyclosporiasis outbreaks has been hampered by the lack of genotyping tools for *C. cayetanensis*, making case linkage and infection/contamination source tracking impossible. This was exemplified in the most recent multi-state outbreak in the United States in summer 2013. To identify potential markers for the development of a genotyping tool, we sequenced the genome of a *C. cayetanensis* isolate from Henan, China. Altogether, 46.8 Mb of nucleotides in 4,811 assembled contigs (N50=55,741 bp) were obtained by 454 and Illumina sequencing. We screened the data for sequences with simple tandem repeats. Fifteen potential loci were tested by PCR and DNA sequence analysis. Among them, five loci (CYC3, CYC13, CYC15, CYC21 and CYC22) with good amplification efficiency and sequence polymorphism were chosen in the analysis of DNA from 23 *C. cayetanensis* isolates. At each locus, 18 to 22 DNA preparations

were amplified successfully, generating four, four, two, six and four sequence types at CYC3, CYC13, CYC15, CYC21 and CYC22 loci, respectively. As expected, most sequence polymorphism was in the form of insertions and deletions in microsatellite regions. However, single nucleotide substitutions were also common at CYC22. Sixteen specimens had sequence data at all five loci, forming 13 multilocus sequence types. At these loci, isolates from China clustered into one group, except for one isolate at CYC0013. Thus, a multilocus sequence typing tool was developed for characterizing *C. cayetanensis*. This tool should be useful for field investigations of cyclosporiasis outbreaks and population genetic studies of *C. cayetanensis*.

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INVASIVE ANTS AS DRIVERS OF TICK-BORNE DISEASE SYSTEMS

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Ticks are important vectors of pathogens that impact both animal and human health, making them and their ecological interactions an important scientific concern. Rodents serve as both blood feeding hosts for ticks as well as reservoirs for many tick-borne pathogens, and therefore the study of rodent populations can provide information useful for understanding disease ecology and protecting human and animal health. In the southeastern United States, small mammal and tick populations are affected by the prevalence of red imported fire ants (RIFA; *Solenopsis invicta*), an invasive predator that consumes both vertebrate and invertebrate species. Our objective was to elucidate the impact of RIFA on tick-borne disease systems. Two field sites in Texas were assessed for the ecological relationships among small mammals, ticks, tick-borne pathogens, and RIFA. Untreated and treated plots (to suppress RIFA populations) were sampled monthly using Sherman live traps and tick drag sampling to determine mammal and tick density and collect specimens (ticks, ear biopsies, blood samples) for pathogen testing. Field samples were processed in the lab to detect tick-borne pathogens in the genera *Borrelia, Ehrlichia*, and *Rickettsia*. To date, we have captured over 900 mammals of seven species, of which the most abundant was the hispid cotton rat, *Sigmodon hispidus*. The most common tick species encountered was the Gulf Coast tick, *Amblyomma maculatum*. We have detected at least three human tick-borne pathogens at low prevalence within ticks and rodents: *Borrelia burgdorferi* (agent of Lyme disease), *Borrelia miyamotoi* (agent of relapsing fever), and *Rickettsia parkeri* (agent of American tick bite fever). Preliminary data indicate that treatment plots (where RIFA populations are suppressed) have higher densities of small mammals and ticks relative to control plots, suggesting that RIFA may be impacting the ecology of tick-borne disease transmission at these study sites.

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FISH ECTOPARASITES OF THE BURRO-BURRO AND ESSEQUIBO RIVERS IN GUYANA, SOUTH AMERICA

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During the summer of 2013, a research expedition was led on the Burro-Burro and Essequibo rivers in the Iwokrama and Surama forests of Guyana, South America, to survey the fish parasites within these regions. A total of 127 fishes including 35 species and 6 orders were captured and examined for ectoparasites. Ninety-one ectoparasites were recovered from 23 fishes spanning 10

species and 4 orders (Siluriformes, Characiformes, Gymnotiformes, and Rajiformes). Of these fishes, 12 individuals from 2 species of Siluriformid fishes (*Trachycorystes trachycorestes* and *Phractocephalus hemilopterus*) harbored 6 ectoparasitic species, including branchiurans (1 *Argulus* sp. and 2 species of *Dolops),* isopods (1 *Exocorollana* sp. *and* 1 *Braga* sp.), and 1 parasitic catfish (Trichomycteridae). Nine individuals from 6 species of Characiformid fishes (*Pygocentrus nattereri, Serrasalmus rhombeus, Tetragonopterus chalceus, Hoplerythrinus unitaeniatus, Hoplias aimara, and Hydroclycus scomberoides*) were infected with 6 ectoparasitic species, including branchiurans (1 *Argulus* sp. and 2 *Dolops* sp.), an isopod (1 *Asotana* sp.), an unidentified copepod, and a single parasitic catfish (Trichomcteridae). For Gymnotiformes, an unidentified leech species (Hirudinea) was found on the head of a single *Electrophorus electricus*. For Rajiformes, an unidentified isopod was found on the gills of a single freshwater stingray (*Potamotrygon* sp.). In total, the survey found 11 ectoparasitic species including 5 species of branchiurans (1 *Argulus* sp. and 4 *Dolops* sp.), 1 copepod (unidentified), 3 isopods (1 *Asotana* sp., 1 *Braga* sp., and 1 *Exocorollana* sp.), 1 hirudinean (unidentified), and 2 individuals of parasitic catfish (Trichomcteridae).

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BLOOD PARASITES OF REEF ASSOCIATED FISHES OF THE EASTERN CARIBBEAN

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Although Apicomplexans are common parasitic protozoans of the blood of many vertebrates, no systematic surveys of their occurrence in Caribbean fishes have been undertaken since the 1960's. A total of 1513 fishes representing 83 species, 26 families, and 5 orders were collected by divers or obtained from local fishermen from the Northeast Caribbean. Among the samples examined, 60 (6.3%) were infected with blood parasites. Species infected included damselfishes: *Stegastes diencaeus* (12/39), *S. fuscus* (16/32), *S. leucostictus* (8/18), and *S. planifrons* (4/4); parrotfishes: *Scarus taeniopterus* (1/4), and *Nicholsina usta* (3/4); the mugilid mullet, *Mugil curema* (1/2); the clupeid scad *Selar crumenophthalmus* (1/1); blennoid fishes of the families Blenneidae (*Ophioblennius macclurei* 3/5) and Labrisomidae (*Hypleurochilus bermudensis* (1/6), *Malacoctenus triangulatus* (1/2), and *M. macropus* (1/4)); the lutjanid snapper *Ocyurus chrysurus* (6/7); and the pomacanthid angelfish *Pomocanthus arcuatus* (2/8). None of the blood parasites found conformed to the description of any of the previously reported parasites from the Caribbean. Parasites found resembled in morphology typical *Haemogregarina*-like intraerythrocytic parasites as well as *Haemohormidium*-like parasites collected from fishes on the GBR, Australia. In total, eight distinct types of blood parasites were found and future work will include classifying these to species level through molecular analysis. Current focus is on molecular characterization of the parasite in Damselfish, which exhibit higher parasitemias and are common reef inhabitants.

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IMPACT OF NATURAL PENTASTOME INFECTIONS ON THE RESPIRATION OF STRESSED MEDITERRANEAN GECKOS

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Knowledge about the energetic costs that parasites induce on their hosts is limited. Moreover, results contrast among studies in that parasites may increase, decrease, or have no effect on host resting metabolic rate (RMR). Surprisingly, pentastomes, which infect their host's respiratory tract, have not been studied for their effects on host respiration. Here, we tested for a correlation between pentastome infection and gecko respiration. Host metabolic rate, measured as the rate of carbon dioxide emission (VCO2), was assessed from field-collected geckos. We conducted 2 studies: we measured RMR on non-stressed geckos and MR on geckos stressed for 3 minutes. Pentastome lung infections were determined by dissecting geckos after respirometry trials. In the stressed study, we recorded VCO2 from its max until its decline to a stationary phase. We fitted an exponential function with 3 phases (initial, secondary, stationary) to this decline and then tested significance of explanatory variables on the curve-fitted parameters. Variables included infection intensities of 5 metazoan parasite species, including pentastomes, host sex, host mass, sample location, and days-since-capture. In the RMR study, there was no effect of parasites on VCO2. In the stressed study, however, 3 of 6 model parameters showed significance to pentastome intensities. Max VCO2 and secondary phase VCO2 had negative relationships; duration of the secondary phase had a positive relationship. These results suggest pentastomes might mechanically constrain breathing and prolong stress recovery. Geckos are sit-and-wait predators, so parasite-induced energy expenditures may be greatest in predator escape. A prolonged stress recovery could decrease foraging time and thus, reduce fitness. Indeed, Pence and Selcer (Copeia. 1988. 3:565) found that pentasome infected geckos had reduced body fat and fecundity. Nonetheless, an experimental study is warranted to confirm our results and to determine if metabolic energetic cost is the mechanism for reduced fitness or body condition.

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TREMATODE COMMUNITY DIVERSITY IN APPALACHIAN STREAM SNAILS

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Parasites play important roles in ecosystems, but the diversity and ecology of wildlife parasites remains poorly understood. Digenetic trematodes (Phylum: Platyhelminthes, Subclass: Digenea) are parasitic flatworms with complex, multiple host life cycles: they infect vertebrates as definitive hosts and mollusks as first-intermediate hosts. Freshwater trematodes are common parasites in ponds and streams containing aquatic snails. We conducted a large survey of headwater streams in the New River watershed to characterize the regional diversity and prevalence of trematode infection in stream snails (*Elimia* spp.). We screened snails from 25 sites for trematode infection and identified five types of larval trematodes based on morphology. These five types varied in prevalence, with the most prevalent infecting up to 38% of snails at some sites, but there was not strong evidence for dominance by any one particular morphotype across sites. To confirm visual identification we sequenced the 28S rRNA gene in a subset of samples and identified 21 unique haplotypes within the five morphotypes, possibly representing 21 unique species from 8 different families. Given this high level of diversity, we are currently sequencing additional samples of each morphotype from each stream to ensure that we have captured all haplotype diversity. This will provide a high level of resolution for examining community-level patterns of trematode first-intermediate host infection in streams.

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EUGREGARINE INFECTION PATTERNS OF DAMSELFLY NAIADS IN THE SOUTHWESTERN PINEY WOODS, TEXAS

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The environment influences host community assemblages and parasite infections may be predictable based on this pattern. Presence of particular species is sometimes an indicator of environmental conditions but the reverse could also be true, that is the environment could forecast the presence of parasite species. To predict eugregarine (Apicomplexa: Eugregarinida) assemblages based on environmental conditions, damselfly naiad were sampled in two habitat types (managed and unmanaged pond) in the Southwestern Piney Woods, Texas, U.S.A. A total of 1246 damselfly naiads (3 families, 7 genera and 14 species), were collected from May to November 2013. Water quality measurements (temperature, pH, salinity) were taken throughout the study. Host species assemblages differed between ponds, but four host species were found in both habitats. Only 3 host species were distinct in the managed pond and 8 host species were distinct in the unmanaged pond. In the managed pond, temperature, salinity and pH decreased but in the unmanaged pond, temperature and pH increased, while salinity remained stable, during the study. Overall prevalence of eugregarines in both ponds was 15.57%. Prevalence in the managed pond was low (0.04%) but increased mid-season to (0.14%). Prevalence in the unmanaged pond increased slightly as the season progressed (from 0.38% to 0.41%). Infections in the managed pond exhibit an inverse relationship with changes in the environment. Infections in the unmanaged pond appear to remain stable despite changes in the environment.

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PARASITES OF THE LIONFISH COMPLEX (*PTERIOS VOLITANS* AND *P. MILES*) IN THE WESTERN NORTH ATLANTIC, GULF OF MEXICO, AND CARIBBEAN SEA: EVIDENCE OF THE ENEMY RELEASE HYPOTHESIS?

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The establishment of the invasive lionfish complex Pterois volitans and P. milesfrom the Indo-Pacific into the Western Atlantic, Gulf of Mexico, and the Caribbean Sea has had significant negative effects on reef fish biodiversity in these areas. The rapid colonization and high abundance of lionfishes in their expanded range have been attributed to several aspects of their biology and lifehistory, such as a varied diet and high fecundity. Invasive lionfishes may alsobe benefiting from enemy release, experiencing decreased predation and / or parasitism pressure relative to native fishes. However, the parasite fauna ofinvasive lionfishes remain poorly studied; making it difficult to assess thepotential role parasite release may have played in their successful invasion ofthe Greater Caribbean. To address this knowledge gap, endoparasite biodiversity and community structure were assessed in 516 lionfishes from 15 sites in the Western North Atlantic, Gulf of Mexico, and Caribbean Sea. Sites ranged from Bermuda and North Carolina southwards to Trinidad and Tobago, effectively covering much of the hosts' expanded range. The most commonly observed parasite was the digenean Lecithochirum floridense. Eight new parasites were described for the first time in lionfishes: a cymothoid isopod, Rocinela stignata; fournematodes, Raphidascaris sp., Contracaecum sp., Paracuaria adunca and Hysterothylaceum sp.; one digenean: Tergestia sp.; two acanthocephalans, Serracentis sp. and Dollfusentis sp., and two cestodes: Nybelinia sp. and Tentacularia sp. A leech, tentatively identified as Trachelobdella

lubrica, was also noted. Regarding parasite community structure, several patterns emerged. First, the endoparasite fauna of invasive Lionfishes was largely composed of widely-occurring generalist species. Second, endoparasite diversity and abundance were low (1-6 species); we did not observe any parasites in lionfishes from Bonaire, Barbados, or Texas. Thus, our data suggest that lionfishes may be benefiting to some extent from release from parasitism. Third, although there were broad differences among sites in endoparasite community structure, none could be correlated to broad ecological factors such as latitude, although there were slight differences among bioregions (ANOSIM Global-R0.069, p = 0.014). Lastly, lionfishes from the east coast of Florida exhibited the highest endoparasite abundances and diversity in this survey. We regressed endoparasite species diversity against date of first observation of lionfishes at each site, and found a significant (r2 = 0.368 ,DF = 1, F = 7.57, p = 0.017) positive relationship. Previous studies have noted increasing parasite diversity andabundance in introduced species in the years following their establishment; we suggest that a similar process may be at work in Greater Caribbean lionfishes.

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ACANTHOCEPHALAN-RELATED MODIFICATION OF HOST MATING BEHAVIOR: FIELD- AND LAB-BASED EVIDENCE OF CONTEXT-DEPENDENT EFFECTS

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The acanthocephalan *Acanthocephalus dirus* is a trophically transmitted parasite that infects freshwater isopods in streams in the midwestern United States. Infected isopods undergo changes in mating behavior, as well as changes in several other behavioral and physiological traits, that increase conspicuousness to predatory definitive hosts. In the field, infected male isopods are less responsive to females than uninfected males and are less likely to be found in mating pairs than uninfected males. Since mating pairs are typically found in hiding (under rocks) this suppression increases exposure to predators. Here, the potential role of ecological context to variation in male mating response was examined to determine whether modification of host mating was context-dependent. In field-based experiments, it was shown that infected males were generally less responsive to females than uninfected males (occurring in 6 of 7 surveys) and that this effect could be reversed over a relatively short time-period (< 4 hr.). This reversal occurred when the infected isopods were removed from their natural ecological context and placed in artifical conditions. The potential importance of predator exposure to this reversal was then examined using a lab-based experiment in which infected isopods were exposed to either the presence or absence of predators. In the laboratory, the modification of host mating was reversed, as in the field, but this reversal was not associated with the presence of absence of predator cues. Thus, acanthocephalan-related modificatin of host mating was context-dependent but this variation was not associated with predator cues.

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SURVEY OF HELMINTHS, ECTOPARASITES AND CHYTRID FUNGUS OF AN INTRODUCED POPULATION OF CANE TOADS, *RHINELLA MARINA* (ANURA: BUFONIDAE), FROM GRENADA

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One hundred specimens of *Rhinella marina*, (Anura: Bufonidae) collected in St. George's parish, Grenada, from September 2010 to August 2011, were examined for the presence of ectoparasites and helminths. Ninety-five (95%) toads were parasitized by one or more parasite species. Nine

species of parasites were found: 1 digenean, 2 acanthocephalans, 4 nematodes, 1 arthropod, and 1 pentastome. Endoparasites represented 98.9% of the total number of parasite specimens collected, and of all groups identified, Grenada represents a new locality record for *Mesocoelium monas, Raillietiella frenatus*, *Acanthacephalus* sp., *Aplectana* sp., *Physocephalus* sp., Acanthacephala cystacanth, and Physalopteridae larvae. In contrast to previous studies of *R. marina*, where nematodes dominated the parasite infracommunity, in this study, the digenean *M. monas* occurred with the highest prevalence of 82%. Female toads were found to have a significantly higher prevalence of *Amblyomma dissimile* than male toads. Only two parasites exhibited a significant seasonal difference in prevalence, with *Parapharyngodon grenadensis* prevalence highest in the wet season and *A. dissimile* prevalence highest during the dry season. Additionally, *A. dissimile* was significantly more abundant during the dry season. No chytrid fungus was seen on histopathology.

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PARASITE BIOMASS IN STREAMS OF THE NEW JERSEY PINE BARRENS

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Despite the ubiquity of macroparasites in aquatic ecosystems, little is known about the importance of parasitism to ecosystem function. Measuring parasite biomass alongside that of free-living consumers is a necessary first step for understanding the potential roles of parasites in processes such as energy flow or nutrient cycling. In this study, I collected quantitative, seasonal data on all consumers (free-living and parasitic) in two stream ecosystems in the New Jersey Pine Barrens. At each stream, I conducted quarterly sampling across a 100 meter reach divided into five transects. Quantitative sampling of each transect allowed me to measure the biomass of all fish, macroinvertebrates, and associated parasites with a common unit of g/m^2 of streambed. Preliminary data from the first season sampled (Fall 2013) reveal that parasites make up 4-5% of total consumer biomass in these streams. Fish and macroinvertebrates made up 18-26% and 69-78% of consumer biomass, respectively. Just a few miles separate these two streams, but they differ strongly in productivity and nutrient profiles due to differences in surrounding land use. Total biomass of all three consumer groups was 2-3 times higher in the nutrient-rich stream compared to the nutrient-poor stream. Completion of this study will capture the dynamics of parasite biomass in response to seasonality and stream productivity.

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EXPERIMENTAL EVOLUTION OF LARVAL PERFORMANCE IN A TAPEWORM

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For parasites with complex life cycles, the optimal size and age at transmission is thought to be shaped by growth and mortality rates experienced in consecutive hosts. The trophically-transmitted tapeworm *Schistocephalus solidus* experiences higher growth rates and lower mortality rates in its second intermediate host, sticklebacks, compared to its first intermediate host, copepods. In this situation, life history theory predicts the parasite to shift more of its growth and development to fish, as growth is faster and safer in a fish, relative to a copepod. This worm spends approximately two weeks growing in copepods before becoming infective to fish, time that, at least from an optimality perspective, would be more profitably spent in a fish. To examine potential constraints on the larval strategy of *S. solidus*, I experimentally selected worms for faster or slower development in copepods. Significant responses to selection were achieved in both directions, indicating the presence of genetic variation for developmental rate in copepods. Moreover, after four generations of selection, worms from the 'fast' line had higher infection rates in fish. However, selected lines had reduced fecundity relative to controls, and this largely

negated the fitness gains achieved through faster larval development. These results suggest that selection could improve early-life performance in *S. solidus*, but increases in lifetime fitness are limited by the genetic covariances across life cycle stages. A previous cross-species comparative analysis found parasite taxa that have independently evolved a copepod-fish life cycle to spend a similar amount of time growing and developing in their first host, which is suggestive of convergent evolution to a universally adaptive life history strategy. Thus, one explanation for the results is that the selection regime, by moving worms away from an adaptive peak, perturbed a robust genetic system (i.e. decanalization), with negative effects on fecundity.

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LONG-TERM INFECTION DYNAMICS OF *OLIGOGONOTYLUS MANTERI* IN ITS INTERMEDIATE AND DEFINITIVE HOSTS FROM CELESTUN, YUCATáN, MéXICO

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Olygogonotylus manteri, is a digenean using the mayan cichlid fish *Cichlasoma urophthalmus* as definitive and second intermediate host, and the hydrobiid snail *Pyrgophorus coronatus* as first intermediate host. This digenean has been one of the most frequent (adult prevalence 92± 10.1; metacercariae 98±5.9) and abundant (adutl 27± 29; metacercaria 4683±5289.54) parasite species in the mayan cichlid along 10 years of monthly samples at Celestun, Yucatán, México. This digenean has been also a prevalent species in the snail host samplings throughout the last 6 years (1.0±1.2). The aim of this study was to identify temporal patterns of trasmission of *O. manteri* among hosts, and the potential effect of environmental conditions over these patterns through time. Fourier time series analysis was use to identify infection peaks through time and cross correlation between environmental variables and infection parameters. This statistical technique was useful to identify the key time lags in the trasmission of *O. manteri*. Two interesting patterns were found: 1) peaks in mean abundance of adult worms were followed by peaks in prevalence in the first intermediate host and, 2) the peaks of mean abundance of adult and metacercariae followed the same variation pattern over time, but with the former being a lot less abundant than the latter.

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A LACK OF CROWDING? DENSITY DOES NOT NEGATIVELY AFFECT PARASITE BODY SIZE FOR TWO TROPHICALLY TRANSMITTED TREMATODES OF CALIFORNIA KILLIFISH, *FUNDULUS PARVIPINNIS*

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Do trophically transmitted parasites typically experience the iconic negative affect of crowding, where parasites grow to smaller body sizes at higher densities? Whether or not high densities cause crowding for trophically transmitted parasites firstly depends on whether or not they experience substantial resource completion. Whether resources are limiting should depend on several factors: the size of the parasites relative to their hosts, infection intensity, the extent to

which parasites share costs of immune system defense or host manipulation, and the extent to which parasites share transmission goals. Despite theoretical expectations for there being no, or even positive density dependence, most studies on crowding in trophically transmitted parasites document the iconic negative density dependence. However, there has been a lack of study in systems where trophically transmitted parasites likely do not experience resource limitation, as most studies have focused on systems where parasites are large relative to their hosts, despite the fact that systems with relatively small parasites can be common. We looked for signs of crowding in the metacercariae of *Euhaplorchis californiensis* and *Renicola buchanani*, two trematode parasites infecting wild-caught California killifish (*Fundulus parvipinnis*). These parasites are small relative to killifish (suggesting resources are not limiting), and are associated with parasite intensity-dependent changes in host behavior that increase predation rates by the parasites' shared final host (indicating the possibility for cost sharing). In a survey of metacercaria body size in naturally infected fish, we did not observe negative density dependence for body size of either trematode species (indicating a lack of resource limitation). In fact, observed patterns indicate possible mild positive density dependence for each species. Although experimental confirmation is required, our findings indicate that the "jury is still out" concerning whether trophically transmitted parasites typically suffer crowding effects and that they may even benefit by being "crowded" by conspecifics.

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LEVELS OF METALS IN TWO LIFE STAGES OF THE TREMATODE *EUHAPLORCHIS CALIFORNIENSIS* AND IN THEIR RESPECTIVE HOSTS, NAMELY THE CALIFORNIA HORN SNAIL AND THE KILLIFISH

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Pollutants can accumulate through the food chain from prey to predator. Less considered is that parasites might absorb pollutants from a host and then transfer them to the next host in the life cycle. We measured metal pollutants in *Euhaplorchis californiensis*, a trematode species whose complex life cycle involves two aquatic hosts, the California horn snail (*Cerithidea californica*) and the California killifish (*Fundulus parvipinnis*). Snails and killifish were collected from Carpinteria Salt Marsh Reserve (Santa Barbara, CA), a site where we had also mapped contaminants in the sediment. Infected hosts were dissected and host and parasite tissues were analyzed for a suite of metals using the inductively coupled plasma optical emission spectrometry (ICP-OES). In addition to tracing the flow of pollutants among species in an ecosystem, this cross interdisciplinary study can help identify hot spots of chemical contamination in ecological health assessments across host species and environments.

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A LEGACY FOR THE FUTURE: THE RAUSCH HELMINTHOLOGICAL COLLECTION

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The Division of Parasitology at UNM was recently established with the acquisition of 50,000 lots of slide and fluid preserved material donated by Robert and Virginia Rausch. This collection contains specimens from a lifetime of research on parasites of mammals, birds, and other vertebrates in the Beringian arctic and subarctic regions of Alaska, Canada, and Russia. Parasites

and hosts were collected over a period of more than fifty years, beginning in the 1940s, providing vouchers for approximately 280 publications. Since acquiring the collection, we have begun physical conservation of slides and fluid-preserved specimens. We have developed database paradigms and workflows and have trained students in specimen stabilization, data capture, conservation assessment and object tracking (e.g., bar coding). Specimen data and digitized images of Rausch's original data ledgers are being incorporated into the Arctos online database, where several thousand of the Rauschs' host vouchers are already cataloged. This has provided a unique opportunity to develop online relational linkages between parasites and their host vouchers across multiple collections. The Rausch's 5000-page necropsy ledger has been digitally scanned and is available online. We are in the process of linking specimen records with these scanned images. Fully documenting the relationships of Rausch specimens to vouchers in at least five museums and relating them to hundreds of publications will be ongoing. In building this data resource we are providing a foundation for exploring parasite-host biodiversity that will be of increasingly critical importance in a world experiencing accelerating and dynamic environmental change. The collections accumulated over decades of field explorations by Robert and Virginia Rausch are being incorporated into a new museum division tied to biodiversity informatics, providing a critical baseline for understanding long-term patterns in host-parasite dynamics at high latitudes. This work was funded by support from NSF Award# 1057383.

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HOW DID WE GET SO MANY SPECIES OF *TRICHOBILHARZIA*, A GLOBALLY DISTRIBUTED SCHISTOSOME?

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Blood trematodes in the family Schistosomatidae are a noteworthy example of diversification by host switching, especially among the schistosome species inhabiting birds. One genus in particular stands out from the rest of the avian schistosome genera as the most speciose – about 35 species. In fact, other than *Trichobilharzia*, most of the other avian schistosome genera have one to very few species. Here we will summarize what specific features of a host-parasite association that can lead to a diverse assemblage of species. Species of *Trichobilharzia* are globally distributed, but include species that are both widespread as well as endemic. They are parasites of ducks and two families of pulmonate snails (both globally common) and occur in the mesenteric veins and nasal passages in a duck host. There are three characteristics of *Trichobilharzia* that could have contributed to their widespread success: 1) Species of duck hosts – Most species of *Trichobilharzia* occur in one of the most vagile hosts, migratory ducks, mostly species that are abundant and widespread. The ecology of these ducks hosts are distinct enough to create at least some reproductive isolation between species of *Trichobilharzia;* 2) Habitat within the duck host – species of *Trichobilharzia* have been found in intestinal veins as well as in the nasal cavities of their duck hosts. These two different habitats each support several different species of *Trichobilharzia*; and 3) Families of snail hosts – Species of *Trichobilharzia* are found in two families of pulmonate snails, Physidae and Lymnaeidae. Members of both of these families are globally widespread and common (in some cases invasive), especially the species used by *Trichobilharzia*. Each of the above three characteristics will be discussed in detail within a phylogenetic context of both host and parasite. The combination of these three characteristics likely launched the impressive success of *Trichobilharzia*. This study supported by grants NSF DEB 1021427 to SVB and NIH to ESL P20RR18754 and R01 AI101438

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RHINEBOTHRIIDEA NO LONGER FAMILYLESS: A MOLECULAR PHYLOGENETIC INVESTIGATION OF THE CESTODE ORDER WITH ERECTION OF TWO NEW FAMILIES AND DESCRIPTION OF EIGHT NEW SPECIES

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This present study initially concentrated on the taxonomy and molecular systematics of eight new species of *Anthocephalum*, but evolved into building the familial taxonomy of the new order Rhinebothriidea. A total of 29 dasyatid stingray specimens of the genera *Dasyatis* (2 species), *Himantura* (4 species) and *Neotrygon* (2 species), *Taeniura* (1 species), *Urogymnus* (1 species) collected from the coastal regions of Northern Australia, Borneo and Senegal were examined for *Anthoephalum* species for the first time. These hosts yielded 11 new species of *Anthocephalum*, 7 of which are described. An 8th new species, included in previous rhinebothriidean molecular analyses, is also described. Novel partial *lsuDNA* (D1-D3) and the entire *ssuDNA* sequence data were generated for a total of 15 specimens of the 11 new and 4 previously described species of *Anthocephalum*. Ribosomal sequence was also generated for a species of *Escherbothrium* from the urotrygonid species *Urotrygon aspidura* from Costa Rica. These data were combined with GenBank data for 1 to 8 species belonging to 16 of the 19 other genera assigned to the Rhinebothriidea by Healy et al., (2009) and Caira et al. (in review). Likelihood, Bayesian and parsimony analyses were conducted on 45 species. These analyses yielded trees generally consistent in topology that supported the existence of 4 major subgroups of rhinebothriideans that are considered appropriate for establishment of families within the order. The Echeneibothriinae de Beauchamp, 1905 and Rhinebothriinae Euzet, 1953 are proposed for elevation to family status and two others are erected *de novo*. Eleven new species of *Anthocephalum* have been detected via ribosomal DNA analysis, and formal species descriptions have been prepared for eight of them. Analyses of the ribosomal sequence revealed two main clades of *Anthocephalum*: one whose species parasitize species of *Dasyatis* and closely related genera, and one whose species parasitize species of *Himantura*.

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PROBING NEWLY DISCOVERED SPECIES DIVERSITY WITHIN THE RHINEBOTHRIIDEA: A MOLECULAR SYSTEMATIC SURVEY OF KNOWN AND UNDESCRIBED SPECIES OF A NEW RHINEBOTHRIIDEAN GENUS

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Healy et al. (2009) erected the Rhinebothriidea for cestode genera whose species parasitize batoid fishes. Their molecular systematic survey included a number of cestode species of unknown generic assignment. The present study concerns an expansion of the possible species diversity of Healy et al.'s (2009) "New genus 3". Field collections from batoid hosts taken from Senegal, Australia, Borneo and Vietnam yielded a number of specimens consistent with this yet to be named generic entity. Sequencing of the small and large ribosomal is ongoing for these specimens. The molecular phylogenetic survey of Healy et al. (2009) included eight samples of "New genus 3, representing seven distinct OTUs. Work has been completed thus far for partial

large ribosomal subunit DNA for 13 samples. Sequences for these 13 have been aligned to the eight samples of Healy et al. (2009). Analyses of these sequence data preliminarily revealed eleven distinct OTUs. The sequence data are consistent with the morphotypes of "New genus 3" identified by Reyda (unpublished), but those morphotypes appear to represent more than one species in most cases. Samples of these putative species groups correspond to specific host genera, such as *Himantura*, and *Dasyatis*.

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CROWDSOURCING HELPS REVEAL CRYPTIC SPECIATION OF A NEW WORLD HAIRWORM *GORDIUS ROBUSTUS* USING MOLECULAR DATA

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Recognizing cryptic species promotes a better understanding of biodiversity, systematics, evolutionary biology, and biogeography. When cryptic species are disease-causing organisms, such as parasites, their correct recognition has important implications for the study of epidemiology, disease ecology, and host-parasite relationships. Freshwater nematomorphs (Nematomorpha: Gordiida) or hairworms, are a fascinating group of parasites that are known to manipulate host behavior to aid transition from the parasitic phase, within terrestrial insects, to the free-living aquatic stage. Hairworm taxonomy has been hampered by a paucity of informative diagnostic characters and it has long been suspected that this group contains numerous cryptic species. However, study of hairworms over large geographical areas has been difficult due to extremely rare encounters and unreliable methods of collecting adult worms. Here we report that by using crowdsourcing, citizen scientists have collected and submitted samples of *Gordius robustus* from throughout its range in North America making its genetic study possible. Combined with our own local collections, we examined samples from 28 localities. Mitochondrial CO1 genetic distances revealed that specimens grouped into 8 genotypes separated by genetic distances from 8 to 24.3%, suggesting that *G. robustus* is a species complex of 8 species. In addition, molecular evidence from mitochondrial (CO1 and cytB) and nuclear (partial 28S, ITS1, 5.8S and ITS2) DNA suggests that these 8 species are paraphyletic, since the North American species *G. attoni* and the European species *G. aquaticus* and *G. baltius* group among the *G. robustus* lineages. Furthermore, there was a significant correlation between genetic and geographic distance between the 8 *Gordius* species. This study demonstrates the value of involving the general public in biodiversity studies and highlights the feasibility of using the mitochondrial CO1 gene as a taxonomic marker for 'barcoding' and species identification within the phylum Nematomorpha.

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RHINEBOTHRIUM SPECIES (CESTODA: RHINEBOTHRIIDEA) IN NEOTROPICAL FRESHWATER STINGRAYS: INSIGHTS FROM RECENT COLLECTIONS IN VENEZUELA

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Multiple species of the diverse, cosmopolitan, and problematic genus *Rhinebothrium* Linton, 1890 (Cestoda: Rhinebothriidea) have been reported from Neotropical freshwater stingrays (Potamotrygonidae). Previous taxonomic studies of *Rhinebothrium* in potamotrygonids focused on species in the La Plata and Amazon drainage basins. In order to fill a gap in our knowledge of *Rhinebothrium* species in potamotrygonids, survey work was undertaken in Venezuela, at

multiple localities in Maracaibo Lake and in the Orinoco River basin. A total of four species of potamotrygonids were infected with specimens consistent with *Rhinebothrium* during the survey in Venezuela. These specimens were subsequently analyzed using molecular sequence (mitochondrial cytochrome oxidase I) and morphological data. Analysis of a 572 base pair region of CO I for 119 worms, including 47 worms from the Venezuelan survey work and 72 worms from previous studies, served as a framework with which to consider the species boundaries and distribution patterns proposed by Reyda and Marques in 2011. *Rhinebothrium fulbrighti*, previously only known from the lower portion of the Amazon, was found to occur in the lower Orinoco during this study. Intriguingly, *Rhinebothrium paratrygoni* appears to have a discontinuous distribution in South America; it was previously known to occur almost entirely within the southerly La Plata drainage, but was found in the Maracaibo Lake and the Orinoco basin in this study. Finally, the phylogenetic tree suggested that at least one new species of *Rhinebothrium* may be present in Venezuela, represented by 10 sequenced samples from the Apure River in the Orinoco basin. The voucher specimens for those terminals, however, are morphologically consistent with *Rhinebothrium copianullum*, a species with a great amount of size variation that occurs throughout the Amazon Basin. Additional sequence data, at a minimum, are needed before the taxonomy, morphological discontinuity, biogeography, and molecular diversity of this intriguing, albeit puzzling, host parasite system can be reconciled.

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DISTRIBUTION OF THELASTOMATOID NEMATODES (OXYURIDA: THELASTOMATOIDEA) IN ENDEMIC AND INTRODUCED COCKROACHES FROM THE GALÁPAGOS ISLANDS, ECUADOR

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The thelastomatoid pinworm fauna was surveyed from 540 cockroaches collected in the Galápagos Islands between 1966 and 2003. Eight species of nematodes were identified from 5 host species with a total prevalence of parasitism of 26.1%. *Cephalobellus ovumglutinosus* was found in the endemic hosts *Ischnoptera santacruzensis* and *Chorisoneura carpenteri*, as well as in the introduced species *Pycnoscelus surinamensis*, *Periplaneta americana*, and *Symploce pallens*. A *Blatticola* sp. was also found in *I. santacruzensis*. A *Severianoia* sp. was found in the introduced *Periplaneta americana* and *Pycnoscelus surinamensis*. A possible *Blattophila* sp. was recovered from *P. surinamensis*, and from this host, a single female of *Cephalobellus magalhaesi* was found. The hosts *Periplaneta autraliasiae*, *P. americana*, and *P. surinamensis* were infected with *Leidynema appendiculata*. Finally, a protrellid species closely resembling *Napolitana australiasiae* was found in the introduced host, *Symploce pallens*. The island of Santa Cruz had the greatest number of pinworm species and was the island where the most introduced host species were sampled. This survey reveals introduction of pinworms to the Galápagos Islands that have been reported on the South American continent. However, the only previous report of *C. ovumglutinosis* was from *Blatella germanica* in Madagascar. With ongoing sampling of additional endemic and introduced cockroaches in the Galápagos Islands, a clear picture of distribution and infection of endemic species will emerge.

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PHYLOGENETIC RELATIONSHIPS AND HOST-ASSOCIATIONS OF LICE (INSECTA: PHTHIRAPTERA)

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Lice are obligate and permanent ectoparasites of mammals and birds, parasitizing over 3000 host species. All four suborders of lice are wingless insects that often are host specific and morphologically adapted for life on their hosts. The morphological adaptations and high specificity of lice are possibly the result of cospeciaton, with associations beginning with the initial radiations of host taxa. To reconstruct the evolutionary history of host-parasite associations, robust hypotheses of phylogenetic relationships are first necessary. Molecular data is used to hypothesize phylogenetic relationships of louse suborders, families, and genera and dating techniques are used to estimate divergence times. Results will be discussed in reference to louse taxonomy and host evolutionary history.

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AN EXAMINATION OF HOST SPECIFICITY WITHIN A NEW GENUS OF CESTODE OF ELASMOBRANCHS (CESTODA: RHINEBOTHRIIDEA)

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Recent survey work has revealed the presence of a variety of new cestode genera from elasmobranchs. One of these newly discovered taxa is a genus within the order Rhinebothriidea referred to by Healy et al (2009) as “new genus 3”. Species within this genus are distinguishable from other Rhinebothriidean genera by their possession of teardrop-shaped bothridia that posses a posterior row of loculi that are longer than they are wide. Recent efforts have been made to understand and quantify the diversity within “new genus 3”, including several species descriptions of individuals within this genus. Morphological data was obtained through the use of methods such as light microscopy, scanning electron microscopy, and histological sectioning. These characteristics include bothridial features such as the overall number and arrangement of loculi, the number of complete transverse septa in the anterior region and the presence or absence of complete longitudinal septa in the posterior region, as well as terminal proglottid features such as the presence or absence of a seminal vesicle or seminal receptacle and the possession of a vagina that does or does not recurve anteriorly. One the whole, these data suggest that there are multiple (~12) species in this new genus. Using morphological characteristics in combination with host data, it has been determined that the majority of the species of this new genus parasitize more than one elasmobranch host species. Relaxed host specificity is unusual when compared to numerous other studies that have demonstrated strict host specificity.

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PARASITE DIVERSITY FROM AVIAN HOSTS IN NORTHERN CALIFORNIA

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In current the times of increased biodiversity loss, survey studies have become a necessary ecological tool. Parasites, in particular, are a key focal group to examine because they contribute to an estimated 40% of the living organisms worldwide and vastly outnumber the free-living species. Birds are the most relevant wildlife host to survey for parasitic diversity because not only do they serve as the definitive host for most taxa of parasites with complex lifecycles, but also they have extensive migratory ranges. The helminthes of birds have been well studied in most parts of the United States, however, there are no studies that examine birds from the San Francisco Bay area of California and few elsewhere along the Pacific flyway. My study addresses this knowledge gap by assessing the adult parasitic diversity in birds within the flyway. Our previous research of larval stages found in snails, amphibian, fish, and aquatic invertebrates indicate that a high diversity of parasites exist in these ecosystems. We obtained the intestinal tract of 68 birds samples sacrificed from other organizations such as airports, wildlife rescues, and wildlife refuges. Our bird samples represent 22 different species from the following families: Accipitridae, Anatidae, Ardeidae, Charadriidae, Laridae, Podicipedidae, Rallidae, Recurvirostridae, and Tytonidae. Using a stereoscope, we performed dissections, counted and preserved all parasite specimens. We performed morphological analysis using mounted specimens along with a detailed molecular analysis using a combination of the following gene fragments: 28S internal transcribed spacer including 5.8S and COX1 of select specimens. Using this combination analysis, we have discovered a high diversity of parasites, with approximately 50 different identified genera identified. Most of our diversity lies in nematodes followed closely by trematodes with an average parasite species richness of 2.7. We have not identified *Ribeiroia ondatrae* despite finding *R. ondatrae* highly prevalent as larval stages in several different host species including *Helisoma trivolvis*, amphibians, and fish. However, we have found species from the Echinostomatidae, Strigeidae, and Diplostomatidae, which were also previously found as larval stages. We developed a Bayesian tree comparing all parasites identified to demonstrate the phylogenetic relationship and verify cryptic species using the COX1 gene.

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RELEVANCE OF HOST-SWITCHING IN THE SUCCESS OF WORMS IN SIMPSON'S SPLENDID ISOLATION

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The mammal fauna of South America is the mixture of endemic lineages (Stratum 1 of Simpson's Splendid Isolation) and diversification of invaders. These invaders arrived at two notorious and independent events during the Eocene (Stratum 2) and Pliocene (Stratum 3). As a result, some of the endemic elements went extinct, a few South American endemics dispersed northward and several of the invaders underwent rapid radiations. The phylogenetic reconstruction for seven taxa of helminths in mammals allows the identification of host-switching events involving parasites occurring in rapid-radiating mammalian groups. Herein these phylogenies are analyzed for patterns closely associated with the two main events of the Interchange: the westward invasion of caviomorphs and primates (Stratum 2) and the southward invasion of cricetid rats (Stratum 3). The phylogenetic trees of 3 of these taxa (Aspidoderidae, *Rhopalias*, Viannaidae)

suggest an origin in South America independent of the invasions. The marsupial-dwelling pinworms share a common ancestor with pinworms present in primates. Lastly, the relationships among taxa in *Litomosoides*, *Nematomystes* and *Stilestrongylus* are influenced by the invasion and diversification of caviomorph and cricetid rodents. The inclusion of outgroups present in African mammals, as well as the phylogenetic reconstruction of additional parasite groups will allow the determination of the impact of invaders in the parasite diversification of South American mammals.

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UPDATED PHYLOGENETIC SCHEME BASED ON THE COMPLETE MITOCHONDRIAL PROTEIN-CODING SEQUENCE FOR COMMON PARASITIC TREMATODES

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D. Blair, James Cook University (Australia)

The entire mitochondrial genome for nearly 30 species of parasitic trematodes has now been sequenced and fully annotated, including recently obtained Vietnamese, Korean, Japanese, Russian, Chinese samples of neglected tropical parasitic heterophyids (*Echinochasmus japonicus*; *Haplorchis taichui*), paragonimids (*Paragonimus heterotremus; P. ohirai*), opisthorchiids (*Clonorchis sinensis; Opisthorchis viverrini; O. felineus*), fasciolids (*Fasciola gigantica; Fasciolopsis buski*) by our research group. The entire coding portions of these trematodes are now available in common database and in our collection. This has enabled us to prepare an updated phylogenetic scheme for these species using the complete protein-coding sequence. The mitochondrial genome of parasitic trematodes has 12 protein-coding genes (*cox*1-3; *nad*1-6; *nad*4L, *atp*6 and *cob*) and *nad*4L overlaps *nad*4 by 37 or 40 bp. Nucleotide and translated amino acid sequences were used for phylogenetic analyses, revealing unexpected placements for several species. For example, *Opisthorchis felineus* is more closely allied with *Clonorchis sinensis* rather than with its congener, *O. viverrini*, supporting several published opinions that these taxa belong in a single genus. Intra- and inter-specific pairwise difference comparisons indicate that inter-specific divergence is very slight (less than 10%) in the Asian schistosomes. Pairwise differences among the opisthorchiids is about 22%, fasciolids is about 25%, but even higher in many other trematode taxa, but does not exceed 40%. Mitogenomic data are also precious in designing primers for taxonomic identification and analysis of interspecies hybrid formation. Updated mtDNA data for common parasitic trematodes provide rich and valuable sources of genetic markers for species diagnosis/identification, studies in biogeography, phylogeny, genetic variation/ hybridization of genotypes, population genetics and taxonomy/systematics.

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SURVEY OF SOUTHERN AMAZONIAN BIRD HELMINTHS

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There is a substantial amount of published information on parasitic worms of birds in some parts of South America. However, very little is known about the diversity, distribution, and host associations of avian helminths in the southern Amazonia. Majority of avian orders in the region have not been examined so far. At the same time, the expected helminth diversity is high, given

that Amazonian birds are extremely diverse and their fauna is characterized by a high level of endemism. In this work we studied helminth fauna of birds from two sites in the Cordillera Azul, Peru, belonging to the westernmost Southern Amazonian region of endemism, Inambari. Birds were examined and parasites were fixed following standard endoparasite collecting procedures. Specimens were processed in the laboratory for morphological and molecular analyses. Morphology was studied on total permanent (cestodes, digeneans) or temporary (nematodes, acanthocephalans) mounts. When necessary, DNA sequences of nuclear ribosomal and mitochondrial genes were obtained to aid in species differentiation and/or phylogenetic analysis. Two hundred and thirty-three birds belonging to 9 orders were examined for endoparasites during November, 2013. Seventy two birds (31%) belonging to orders Apodiformes, Columbiformes, Coraciiformes, Passeriformes, Pelecaniformes, Galliformes, Galbuliformes and Trogoniformes were infected with helminths. A single examined bird belonging to the Accipitriformes was not infected. Cestodes were the most prevalent among all helminths. They were found in 44 birds (18.9%), followed by digeneans (29; 12.4%), nematodes (14; 6%), and acanthocephalans (4; 1.7%). Helminth taxonomic diversity and distribution among taxonomic and ecological groups of birds is discussed. This study was supported by the Field Museum's Marshall Field Funds, National Science Foundation grants DEB1050525 to VT and DEB-1120055 to JMB, and the Field Museum's Emerging Pathogens Project funded by the Davee Foundation and the Dr. Ralph and Marian Falk Medical Research Trust.

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IDENTIFICATION OF 17 NOVEL *ENTEROCYTOZOON BIENEUSI* GENOTYPES IN PIGS

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Of 14 species of microsporidia known to infect humans, *Enterocytozoon bieneusi* is considered the most important cause of clinical symptoms and has also been largely reported in animals. Currently, 39 *E. bieneusi* genotypes have been described from pigs at locations worldwide with only one report of pig infection in South America, but none in Brazil. Fecal samples were collected from 91 pigs (1- to 12-mo-old) in 10 properties from 2 different locations in the State of Rio de Janeiro, Brazil. A nested polymerase chain reaction (PCR) protocol to amplify an 390-bp fragment of the ITS and portions of the flanking large and small subunits of the rDNA was followed by sequencing all positive PCR samples. Up to four clones from each specimen were sequenced when mixed infections were observed. Fifty four (56%) samples were positive for *E. bieneusi*, being found in all 10 properties. Genotypes O, EbpA, CS-1, H, and 17 novel genotypes not previously described (PigEb1-17) were observed. The most prevalent genotypes were PigEb2 (17/91, 18.7%) and PigEb4 (16/91, 17.6%). The previously known genotypes EbpA and CS-1 were the third most prevalent (7/91 for each; 7.7%), followed by genotypes PigEb1 (5/91, 5.5%), O (3/91, 3.3%), PigEb6 (2/91, 2.2%), and the rest of the genotypes (1/91 for each; 1.1%). Thirteen samples had mixed infections. The high prevalence observed in this study (second highest worldwide) and the description of 17 new genotypes of *E. bieneusi*, represent an important advance in the study of the wide genetic diversity of this organism, emphasizing the importance of such studies, especially where little or no data are available. The zoonotic risks of these novel genotypes and their importance to other animal species and environment contamination are not known. The presence in pig feces of genotypes O and EbpA, previously described in humans, reinforces the need for molecular testing to determine the presence and understand the epidemiology of *E. bieneusi*.

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CLONING AND CHARACTERIZATION OF *ANCYLOSTOMA CANINUM* HELIX-LOOP-HELIX 13 TRANSCRIPTION FACTOR, A NOVEL TARGET OF DAF-16

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Hookworm infection ranks among the most serious diseases worldwide. Infection occurs when a host is exposed to the infective third stage larvae (L3s) in soil. Upon entry into the host, the developmentally arrested L3 encounters host specific signals that re-initiate developmental pathways and maturation to adulthood. However, little is known about the molecular basis of the infection process. The resumption of development during infection is analogous to recovery from the facultative arrested dauer stage in the free-living model nematode *Caenorhabditis elegans*. In *C. elegans,* the insulin and insulin-like growth factor signaling (IIS) regulates entry into and exit of dauer stage by negatively controlling the FOXO transcription factor DAF-16. DAF-16 conducts diverse biological functions, including cell cycle control, apoptosis, stress responses and development, by regulating different subsets of targets. One of the targets involved in *C. elegans* dauer recovery is helix-loop-helix 13 (HLH-13). We hypothesize that HLH-13 is involved in L3 activation and development during hookworm infection. We identified the hookworm *hlh-13* gene by BLAST search of the draft *A. caninum* genome using *Ce*-HLH-13. Primers were designed and used to amplify the *hlh-13* cDNA from L3 first strand cDNA. The full length *Ac-hlh-13* cDNA was 516 base pairs and encoded a 137 amino acid protein. The *A. caninum* HLH-13 is 73% identical to and shares all but one intron/exon boundary with *C. elegans* HLH-13. To determine whether *hlh-13* is a target of *daf-16*, we created transgenic *C. elegans* lines in which a red fluorescent protein (mCherry) is transcriptionally regulated by 1.4 kb of 5' sequence upstream of the *A. caninum hlh-13* start codon. Interestingly, the fluorescence signal was up-regulated in transgenic dauers and arrested L1s of *C. elegans*, suggesting that *Ac-hlh-13* is a functional target of *C. elegans* DAF-16. To further investigate whether *Ac-hlh-13* can respond to its native DAF-16 signaling, we will express the *hlh-13* transcriptional reporter with *A. caninum* DAF-16::GFP in wildtype, *daf-2 (e1370)* or *daf-16(mu86); daf-2 (e1370) C. elegans*. We will also identify the DAF-16 binding site on *hlh-13* promoter region using transcriptional reporters. The results will help us better understand the molecular mechanism of hookworm infection.

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RECONSTRUCTING POPULATION STRUCTURE OF A NON-NATIVE PARASITE AND A NATIVE STREAM FISH HOST IN HAWAII

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Comparisons of population genetic structure of introduced parasites and their hosts can be a powerful approach for inferring the nature of parasite transmission and spread. In stream fishes across the Hawaiian Archipelago, infections by an introduced nematode parasite, *Camallanus cotti*, have become wide spread and occur in remote, relatively pristine watersheds. We have characterized the geographic patterns of genetic variation of *C. cotti* and the native host *Awaous stamineus* to assess likely conduits of introduction, the dispersal potential of the parasite, and the genetic diversity of the parasite and host. The mitochondrial *cytochrome oxidase 1* gene was sequenced from *C. cotti* and mitochondrial *cytochrome b* gene was sequenced for the native host

fish *A. stamineus*. Patterns of genetic variation indicated that *C. cotti* has spread across the archipelago following introductions on two islands, Maui and O'ahu, and that the remote watersheds harboring the highest levels of parasitism lie at the intersection of invasion pathways. Similarly, the distribution of sequence variation and haplotype frequencies indicate that the native *A. stamineus* initially colonized a single island and subsequently dispersed to other islands in the archipelago. In addition, we found low haplotype diversity of *C. cotti* which is consistent with an initial founder effect during parasite introduction with minimal subsequent diversification.

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ARE CRYPTIC SPECIES ALSO CRYPTIC TO PARASITES?

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Generally, diversity is estimated as the number of species present at any one time and has long been based on morphological characters. However, speciation processes do not necessarily imply morphological changes. New genetic techniques have identified numerous cryptic species (i.e. morphologically similar but genetically distinct) in many animal taxa. Recently, several highly divergent genetic units have been detected within the morphological amphipods species *Gammarus pulex* and *Gammarus fossarum*. These amphipods are used as hosts by several species of acanthocephalan parasites. However, whether different genetic units of amphipods are infected indifferently by acanthocephalans or display contrasting vulnerability to these parasites remains unknown. Here we documented acanthocephalan prevalence and abundance among sympatric but genetically divergent cryptic units of *G. pulex* and *G. fossarum* and tested for potential ecological implications of differential infection patterns between cryptic hosts. Results show that acanthocephalan prevalence can greatly vary between sympatric cryptic amphipod hosts. One amphipod host unit often supported most of the parasite population when its sympatric counterpart was almost parasite free. Furthermore, differences in acanthocephalan abundances among sympatric host units were shown to influence well known and accepted ecological patterns like parasite-induced host mortality. Overall, data suggest that cryptic diversity in host species may strongly influence parasite dynamics and since it is becoming obvious that cryptic diversity is a widespread phenomenon, parasitologists should be aware of the potential implications underlined by our results.

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GENOMIC COMPOSITION OF A BACTERIAL ENDOSYMBIONT OF THE MEXICAN MEDICINAL LEECH *HAEMENTERIA OFFICINALIS* (CLITELLATA: GLOSSIPHONIIDAE)

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Three different morphotypes have described for bacteriomes (bacteria bearing organs) within leeches of the family Glossiphoniidae. For the genus *Haementeria*, bacteriomes are present as two pairs of spheroidal organs connected to the esophagus via thin ductules. Previous microscopic and phylogenetic studies have shown that the bacteria inhabiting these organs belong to Gammaproteobacteria, a bacterial class that includes several well-known insect endosymbionts such as *Buchnera aphidicola* and *Wigglesworthia glossinidia*. Using 454 GS-flx technology, tissues from the bacteriomes of *Haementeria officinalis*, the Mexican medicinal leech, was

sequenced and analyzed for genomic composition, G+C content and gene presence. A total of 646,927 reads (DNA fragments) belong unequivocally to the bacterial endosymbiont and these were used as the basis for genome assembly. The reads were assembled into four contigs, the shortest of which was fully 24 Kb. The total length of the four contigs was 843,810 bp. No plasmids were detected, suggesting that these contigs belong to a single circular genome within the endosymbiont. A total G+C content of 22.3% was recovered. The proteins and coding regions account for 85% of the genome and all genes were recovered as single copy representatives, including the ribosomal operon. In total, 33 tRNAs and three rRNAs were recovered. Average gene length was 688 bp; neither insertions nor transposons were detected within the genome. A broad comparison between the newly generated bacterial genome and the genome of *Wigglesworthia glossinidia* (an endosymbiont of another strictly haematophagous organism, the tsetse fly) was conducted and revealed remarkable similarities between the bacterial genomes. One of the most important findings within the newly sequenced genome was the numerous genes related with the synthesis of vitamin B, an essential nutrient that is commonly lacking from the strictly hematophagous diet of this bloodfeeding leech.

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MOLECULAR TYPING OF *TOXOPLASMA GONDII* IN BELUGA (*DELPHINAPTERUS LEUCAS*) FROM THE ST. LAWRENCE ESTUARY, CANADA

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Little is known of the genetic diversity of *Toxoplasma gondii* circulating in the marine environment. In the present study, stranded St. Lawrence Estuary (SLE) belugas (*Delphinapterus leucas*) in Québec, Canada were examined for *T. gondii* infection. A total of 55 samples, including 22 brain and 33 heart tissues, were collected from 2009 to 2012. *T. gondii* was genotyped from the cerebral cortex and heart, for the first time, from this threatened population of beluga. Samples were characterized using nested PCR-restriction fragment length polymorphism (RFLP) analyses. Genomic DNA from brain and heart tissue samples were analysed using a nested PCR targeting the 529bp fragment, 5'- and 3'-SAG2 locus encoding tachyzoite surface antigen p22, and dense granule antigen GRA6 gene. RFLP analyses with Sau3AI, HhaI, and MseI were successfully conducted on PCR-positive samples to group the isolates into one of the three genotypes of *T. gondii*. Of the samples tested to date, 20% are positive for *T. gondii* and all have been identified as type II. Results demonstrated the presence of *T. gondii* infection in SLE beluga and suggest pervasive contamination of their aquatic environment by zoonotic agents. Further work is required to determine the possible sources of contamination of the marine environment either through natural or anthropogenic transmission.

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DIFFERENT PATTERNS OF GENETIC VARIABILITY IN TWO APICOMPLEXAN GROUPS

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Evolutionary relationships within the phylum Apicomplexa are often debated as uncertain due to the lack of molecular data in some groups. Consequently, revised classifications are being released repeatedly. Here we present molecular data and analyses on two different apicomplexan groups, *Hemolivia* (Coccidia: Adeleorina) infecting tortoises of the genus *Testudo*, and *Eimeria* (Coccidia: Eimeriorina) parasitizing field mice of the genus *Apodemus*. Phylogenetic analyses of 113 *Eimeria* samples obtained from three species of field mice (*Apodemus agrarius*, *A. flavicollis* and *A. sylvaticus*) collected in 9 European countries revealed the presence of several distinct lineages (and many haplotypes), independent of geographic distribution, and usually also of the host species. In the phylogenetic trees, the lineages did not form a monophyletic cluster; they were scattered among the eimerians from other rodent genera. Morphologically, the obtained eimerians corresponded to four described species/morphotypes. Some of them (*E. apionodes* morphotype) infected more than one host species and possessed high molecular variability, forming several distant sublineages located at different places in the tree. Others were less variable, and only one lineage/morphotype was strictly specific to a single host species (*E. alorani* morphotype to *A. agrarius*). On the contrary, phylogenetic analyses of 33 samples of *Hemolivia mauritanica* infecting *Testudo graeca* and *T. marginata* tortoises collected in 5 countries revealed considerably low intraspecific variability. Despite the large geographic range of the collections, all *H. mauritanica* samples formed a single monophyletic cluster, with only weak inner differentiation.

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USING BIVALVES AS BIOSENTINELS TO DETECT *CRYPTOSPORIDIUM* SPP. AND *TOXOPLASMA GONDII* CONTAMINATION IN AQUATIC ENVIRONMENTS

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Current methods to monitor microbial water quality involve collecting discrete samples at specific time-points. While informative, this approach only provides a snapshot of the microbial community at the time of sample collection. Conversely, bivalves have the ability to continuously filter large volumes of water and concentrate particulate matter including pathogens over long periods of time. In previous studies, multiple organisms, including viruses, bacteria, and protozoa have been detected in bivalves. The purpose of this study is to investigate the potential for using indigenous bivalves to monitor for the occurrence of *Toxoplasma gondii* and *Cryptosporidium* spp. in water sources. In this study, DNA extraction, end-point PCR, and quantitative real-time PCR methods were developed to detect *Toxoplasma* and *Cryptosporidium* oocysts in the hemolymph, gills, and digestive glands of mussels (*Mytilus edulis*). Results showed that the method developed in this study was able to consistently detect down to 10 oocysts. A survey of indigenous mussels from Point Lobos and Morro Bay, California, areas known to have

high *T. gondii* seroprevalence in sea otters, were indeed positive for *T. gondii* (54% and 33%, respectively). *Cryptosporidium* spp. was also detected in mussels from Point Lobos, California (27%) and sequence analyses identified two distinct *C. parvum*-like isolates. This study demonstrates the potential of using natural filter feeders, like mussels, as biosentinels for assessing water quality in a marine environment. More importantly, using this newly developed method, a high prevalence of *Cryptosporidium* spp. and *T. gondii* oocyst DNA were detected in mussels collected from the California coastline.

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MOLECULAR CHARACTERIZATION OF 3 SPECIES OF RHIGONEMATID NEMATODES AND A PRELIMINARY PHYLOGENY OF RHIGONEMATIFORMES

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Only seven species of rhigonematids, endoparasites of diplopods, have been described from Mexico. In a span of 30 years no other species of rhigonematid has been recorded. The first seven species recorded from Mexico belong to the Rhigonematida and were found in the intestine of 3 families of diplopods: Rhinocricidae, Spirobolidae and Aphelidesmidae. We have recently characterized both morphologically and molecularly 3 new species of specimens that belong to the genus *Heth* Cobb, 1898 from 2 families of spirobolids, Rhinocricidae and Atopehtolidae from the tropical rain forest region of Los Tuxtlas in eastern Mexico and from a deciduous forest from the huasteca region. A preliminary phylogeny of Rhigonematiformes with ribosomal genes 18S and 28S was recovered from the sequences of these 3 species plus 6 sequences from GenBank. The phylogeny reported here recovered from a ML analysis utilizing the GTR+I model indicates that rhigonematids are monophyletic and comprise a sister clade with ascarids.

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CYSTICERCUS PISIFORMIS: ULTRASTRUCTURAL TRANSFORMATION OF TEGUMENT DURING DEVELOPMENT FROM ONCOSPHERE TO CYSTICERCUS

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Cestode tegument is the barrier that separates the parasite from the host allowing it to develop and survive the hostile environment of the host. It is the only site for nutrient intake. The present study was conducted to reveal the fine structural transformation of the tegument of *Taenia pisiformis* cysticerci (*Cysticercus pisiformis*) during development from egg to cysticercus stages**.** The present study records the development of *C. pisiformis* in experimentally infected domestic rabbits, with special emphasis on ultrastructural variations within different stages of larval development using both scanning (SEM) and transmission electron microscopes (TEM). 3-6 days post infection (PI), the early developed scolex appeared as an invaginated thickening in the anterior end of the developed metacestode. The first development of the rostellar hooks and invagination canal was observed 1 wk PI, where the hooks appeared as minute conical bodies. Complete development of the invagination canal and hook crown was observed 2 wk later, synchronizing with the onset of sucker differentiation. Fine structural transformation of the tegument included variations in the structure of microtritches (length, density and shape); distal cytoplasm and parenchymal vesicles and inclusion bodies (size, shape, distribution and electron density); and tegumental and parenchymal muscles (thickness, orientation and distribution). The tegument of different developmental stages of *T. pisiformis* cysticerci have the same basic pattern, with some variations in the subcellular structures, which supports the suggestion that *T. pisiformis* can be used as an experimental model in cysticerci research.

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IN VIVO AND IN VITRO EFFECTS OF HYDROGEN PEROXIDE AND METRIFONATE ON *LIGICTALURIDUS FLORIDANUS* (ANCYROCEPHALIDAE) ON THE GILLS

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In aquaculture, parasites cause significant losses due to subclinical infections, host death, feeding cessation and growth parameters reduction; they cause stress, increasing disease susceptibility by immunosuppression. Monogenean trematodes are commonly found on the skin and gills of aquatic animals. *Ligictaluridus floridanus* (Muller 1936), parasites channel catfish (*Ictalurus punctatus*) gills, whose natural distribution extends from the northeast part of Mexico, to the central and southeast part of the United States. This study was set out to examine the efficacy of hydrogen peroxide (H_2O_2) and metrifonate (Mtf) against *L. floridanus* infections on channel catfish. *In vitro* trials were conducted with excised fish gills infected with more than five *L. floridanus* per gill arch, which were immersed by triplicate on H_2O_2 and Mtf solutions. The efficacy of the treatments was registered by observing under a stereomicroscope the live lasting time of the parasites, i.e. how long it took for them to die. On the other hand, an *in vivo* challenge using thirty-six juvenile channel catfish, clinically healthy, but naturally infected with *L. floridanus*, was performed. One group received immersion baths of 570 mg/L H_2O_2 (3%) for 4 minutes; the Mtf group received 0.5 mg/L Mtf for 10 minutes. Treatments were done on days 3, 7 and 11 of the experiment. Results indicate that baths with of Mtf does not significantly reduce the mean abundance of the parasite per gill arch; whereas hydrogen peroxide baths at 570 mg/L during 4 min were significantly ($p < 0.05$) effective against adult and immature stages of *L. floridanus*. The conclusion of this study suggest that H_2O_2 is may be used in the treatment of this parasite, however further studies are needed to evaluate the particular damage of H_2O_2 over *L. floridanus*, and to establish tissue effects on catfish, before its use in farming conditions.

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REPRODUCTIVE DIVISION OF LABOR IN CLASS TREMATODA

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We present evidence that 7 species infecting the California horn snail have distinct soldier and reproductive castes while 7 other species lack castes. A reproductive division of labor is well known for some organisms, including arthropods (e.g., bees and ants) and naked mole rats. Recently, comparable social organization has been documented for some parasitic trematode flatworms. Trematodes form clonal colonies within their molluscan first intermediate hosts, and these colonies of some species have both reproductive and soldier castes. Reproductives are large and filled with offspring. Soldiers are small, slender, have relatively large pharynxes, and, in some cases, have been shown to attack and kill unrelated trematodes. This reproductive division of labor has previously been documented in five trematode species from different geographic regions and host species. Here we systematically explore the trematode fauna of the California horn snail, *Cerithidea californica*, parasitized by 20 morphologically-distinct trematode species. We report evidence that 8 species show a reproductive division of labor with a soldier caste. We further detail seven species that lack such a division of labor. The wide variation in social organization between trematode species infecting the California horn snail indicates that this system will be a valuable tool for research examining the ecology and evolution of social organization.

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ENDOPARASITE DIVERSITY AS A POTENTIAL INDICATOR OF ECOSYSTEM HEALTH

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Studying the health of an ecosystem is important in order to observe changes over time, determine possible causes, and propose potential management strategies. Ecosystem health can be defined as productivity, stability, or resistance to change. Biodiversity is one potential indicator for health of an ecosystem. Beyond the number of species within a community, their interactions are key to ecosystem structure and function. These relationships are depicted in food webs through the linking of trophic (feeding) levels. Specifically, predator-prey interactions have the ability to depict what types of organisms are involved in this community. However, documenting all the species and their interactions in a community is difficult. Parasites have been proposed as a type of biological indicator of free-living diversity and the trophic connections between species. Here we address the viability of parasites of a European starling (*Sturnus vulgaris*) population as indicators of biodiversity within a community. European starlings are an ideal model system because of their abundance in urban, fragmented habitats and a previously documented diversity of parasites. We hypothesized that starlings would host a wide diversity of parasites with complex life cycles (i.e. multiple hosts required for parasite development and reproduction) providing evidence of biodiversity within the habitat through the required intermediate hosts. We obtained 182 juvenile European starlings from O'Hare International Airport for our study. For a subset of birds (N = 41), we conducted necropsies according to standardized protocols, inspecting external surfaces, and removing internal organs and tissues which were carefully examined under dissecting microscopes. All parasites were preserved for molecular and morphological identification. For each parasite we calculated prevalence (proportion of hosts infected) and mean intensity (mean number of parasites in all infected hosts). We found a wide range of parasite taxa in the gastrointestinal tract and liver. Based on preliminary morphological identification, endoparasite diversity included one species of Acanthocephalan (Thorny-headed worm) and Cestode (Tapeworm), two species of Trematode (Flatworm), and three species of Nematode (Roundworm). Prevalence of Acanthocephalans and Cestodes were 34% and 37%, respectively. More precise identification of the parasite taxa will allow us to determine the parasite life cycles and therefore, predator-prey interactions of the starling hosts, which acquired many of these parasites through their diet. For example, acanthocephalan life cycles depend upon bird consumption of crustacean intermediate hosts, while trematodes depend both upon snails and a wide range of invertebrates depending on the species. By recovering the parasites in the birds, we can infer that the other species required in their life cycles are present in the environment. Limitations to the study include a lack of information on the bird home range size.

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GEOGRAPHIC VARIATION IN *OXYSPIRURA PETROWI* INFECTIONS IN TEXAS NORTHERN BOBWHITES

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Oxyspirura petrowi is an indirect lifecycle nematode found under the nictitating membrane and within the intraorbital glands of various bird species. A recent study documented tissue damage from *O. petrowi* infections in the eyes of the northern bobwhite (*Colinus virginianus*). Historically, much of what is known about *O. petrowi* infections in bobwhites

within Texas comes from the Rolling Plains ecoregion, whereas little is known about this species in bobwhites from South Texas. The bobwhite is an economically and ecologically important game bird in both regions. Considering this worm's potential negative effect, the objective of this study are to compare the prevalence, intensity, and abundance of *O. petrowi* in bobwhites from the Rolling Plains (n=161) and South Texas (n= 125) using hunter-shot and trapped samples collected from August to February 2012–2013. Bobwhites collected in the Rolling Plains, had a mean intensity of 13.3 ± 1.6 (SE) worms (range 1–67). Bobwhites collected in South Texas had a mean intensity of 2.6 ± 0.2 (SE) worms (range 1–7). Prevalence of *O. petrowi* was higher in the Rolling Plains (52%) than in South Texas (8%) (P<0.0001). Abundance of *O. petrowi* was higher in the Rolling Plains (7.0 ± 1.0) than in South Texas (0.2 ± 0.1) (P<0.0001). Based on our results, future studies are needed to explain the discrepancies of *O. petrowi* occurrence between the two regional bobwhite populations.

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OOCYTES MATURATION OF THE SLOTH´S GIANT TICK *AMBLYOMMA VARIUM* (ACARI: IXODIDAE) IN AN ECOLOGICAL CONTEXT

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The sloth´s giant tick *Amblyomma varium* Koch, 1844, a Neotropical species that inhabits tropical rainforests, is considered to be the largest tick reported so far. Its adult stage parasitizes exclusively mammals from Bradypodidae and Magalonychidae families. These hosts are found in the treetops, descending only every three to eight days to defecate. This study aimed to analyze, in an ecological context, the oocytes maturation in this tick species. The ovaries dissected from three fully engorged females collected from *Bradypus variegatus* captured at Serra do Japi Biological Reserve, municipality of Jundiaí, São Paulo, Brazil (23°13'S; 46°53'W) were processed for histological and transmission electron microscopy analysis, according to routine techniques. The analysis show that the ovary of is a long single tubular organ with a large number of oocytes attached to the ovary wall by the pedicel. This tick species probably increases the reproductive capacity producing lots of eggs by increasing of the engorged female body size to compensate the difficult to meet its host. *Amblyomma varium* oocytes were classified into five development stages, and specific characteristics were observed: processes of yolk and chorion deposition starts early from the oocytes stage II; oocytes V with a very thick chorion (responsible for preservation of the egg); and eggs of moderated to large size. These are adaptations that enhance the survival and the reproductive success of this very host-specific tick, which is limited in a particular environment.

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LIFETIME INBREEDING DEPRESSION, PURGING, AND MATING SYSTEM EVOLUTION IN *SCHISTOCEPHALUS SOLIDUS*

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Classical theory on mating system evolution suggests that simultaneous hermaphrodites should either primarily outcross if they have high inbreeding depression or self-fertilize if they have low inbreeding depression. Previous studies showed that the tapeworm *Schistocephalus solidus* has high inbreeding depression, yet self-fertilization nonetheless occurs under some circumstances. This strategy of mixed-mating (some selfing, some outcrossing) is counterintuitive and contradicts mating system theory. The probability for selfing to spread depends on the relative

fitness of selfed offspring, as well as the genetic basis for inbreeding depression and whether it can be effectively purged. We bred *S. solidus* through two consecutive generations of selfing and recorded several fitness-correlates over the whole life cycle. After one round of selfing, inbreeding depression was pronounced, particularly in early-life traits, and the conservatively estimated lifetime fitness of selfed progeny was only 9% that of the outcrossed controls. After a second generation of selfing, inbreeding depression remained high but was significantly reduced in several traits, which is consistent with the purging of deleterious recessive alleles. We suggest that severe inbreeding depression strongly limits the favorability of self-fertilization, and even if the genetic load can be rapidly purged, inbreeding depression likely prevents transitions towards pure selfing in this parasite.

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EGG MORPHOLOGY IN THE ACANTHOCEPHALAN *ACANTHOCEPHALUS DIRUS*: DO EGGS RESEMBLE THE FOOD SOURCE OF TARGET HOSTS?

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The acanthocephalan parasite *Acanthocephalus dirus* infects the stream isopod *Caecidotea intermedius* when its eggs are consumed along with the isopod's typical food source. Infection of juvenile isopods occurs during the summer and negative effects on the isopod host occur as the parasite develops into the cystacanth stage (e.g., castration, increased predator exposure). As a consequence, the ability to detect *A. dirus* eggs within a food source is likely to be favored by selection if the eggs could be distinguished from the other food items in the diet. We examined the relationship between the morphology of *A. dirus* eggs and the phenotype of abundant food sources in nature to determine whether egg morphology resembled the typical food source of the target host, and hence could avoid detection. Using field samples of both the sediment and the water column, we identified the most common food source present in the stream to be pennate diatoms which were highly abundant (50,000 per ml.). We then examined the contents of the intestines of juvenile isopods and found that pennate diatoms were common in the diet. Pennate diatoms and *A. dirus* eggs have a similar fusiform shape. Comparison of the size distributions of *A. dirus* eggs and the diatoms present revealed that the *A. dirus* eggs fit into the size range of the most abundant diatoms. These results are consistent with the interpretation that *A. dirus* eggs are not detected by juvenile *C. intermedius* because they resemble the typical food source of the target hosts.

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AGE COHORTS IN THE MARINE LEECH, *HEPTACYCLUS BUTHI*

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Heptacyclus buthi was harvested from fish hosts in rocky intertidal zones of Sonoma and Marin Counties, California in 2008 (N = 162) and 2010 (N = 51). The size of the leeches was quantified using a method that approximated the sagittal cross-section of each specimen. Size-frequency curves were modeled to estimate the number of size-class cohorts in each year. If *H. buthi* is an annual species like many of its relatives, the single cohort modeled for in 2010 and the comparable "older" cohort in 2008, both with a broad range of sizes, may represent one component of its reproductive life history. A second, younger, more-numerous, less-variable cohort modeled from the 2008 sample may represent a second reproductive bout during that year that was prevented in the subsequent La Niña period of 2010-11.

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KIN SELECTION AND VIRULENCE: WHAT IS THE ROLE OF RELATEDNESS IN COINFECTION?

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Understanding parasite infections from an ecological perspective may potentially aide in the management and reduction of parasitic disease. Different parasites often coexist within a single host, and the interaction between these individuals can affect the intensity of disease, here referred to as virulence. The nature of the interaction can also affect the parasite's survival and reproduction, and thus the transmission of the parasitic disease. Kin selection theory predicts that closely-related parasites will be less competitive, will not exploit host resources as intensely, and will therefore have lower virulence than a population of unrelated parasites. Our experiment focused on the effect of competitive interactions on parasite virulence and transmission for the human parasite *Schistosoma mansoni*. *S. mansoni* has a complex life cycle: humans are the ultimate host, but larval stages live in *Biomphalaria* species snails. To investigate the impact of competition on parasite virulence, we infected 550 *B. glabrata* snails with ten different combinations of three genetically-distinct strains of *S. mansoni*. Each snail was infected by one, two, or three strains, and then monitored for the duration of infection. Snail reproduction, mortality, growth and parasite reproduction were used to measure virulence and transmission. Cercariae samples were also collected and analyzed by quantitative polymerase chain reaction (qPCR) in order to both verify our treatment groups and measure relative strain transmission and virulence in co-infections. This goes beyond previous studies, which have assumed that co-exposed snails became co-infected snails. Significantly, qPCR analysis showed that the majority of cases of co-exposure did not result in co-infection, suggesting that treatment groups must be verified. Our results support kin selection theory, in so far that snails infected with multiple strains had lower reproduction than singly-infected snails, suggesting that multi-strain co-infections were more virulent.

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GASTROPODS AND FISH AS HOSTS OF DIGENETIC TREMATODES IN OTSEGO LAKE AND NEARBY WATERS

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This is a study of digenetic trematodes as part of a survey of the intestinal parasites of fishes of Otsego Lake and its tributaries (Cooperstown, New York) that took place from 2008 to 2014, in which 27 species of fish were examined. Among the fish examined, eight fish species were infected with the adult stage of a digenetic trematode species in the digestive system, whereas the majority of fish species were infected with a larval stage (i.e. metacercaria) in other organs. Once the adult trematodes from fish were identified to species, the scientific literature was reviewed in order to compile information on their life cycles and determine what other organisms in the ecosystem are possibly serving as hosts to the larval stages of the trematodes. Following this, a survey of the snails was undertaken. The survey included six species of snails, three of which were infected with stages of larval trematodes (redia, sporocysts and cercaria). Techniques used to identify redia, sporocysts and cercaria included light microscopy, scanning electron microscopy and DNA sequencing in combination with known life cycle information. Another identification technique that is currently underway is a live-staining technique to identify cercaria. Given that trematode life cycles utilize the food web, this data adds to our growing knowledge of the ecosystem of Otsego Lake as whole.

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SPECIFICITY OF NEMATODE INFECTION IN TWO SAND CRABS SPECIES

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The beaches of South Padre Island, Texas, are home to two digging sand crab species: albuneid sand crabs (*Lepidopa benedicti*) and hippid mole crabs (*Emerita benedicti*). About 87% of *L. benedicti* are infected by a single, as yet unidentified, species of small (~1 mm length), immobile nematode. We examined whether these nematodes also infect *E. benedicti*. Because both species are found in the same homogeneous habitat (intertidal swash zone), and belong to the same superfamily, one possibility is that nematodes infect both crab species. The two crabs have different ways of eating, however: *L. benedicti* is a sediment feeder, while *E. benedicti* is a filter feeder. If the nematodes infect *L. benedicti* through ingestion, they may not be as prevalent in *E. analoga*. Data collected to date indicate that *E. analoga* are not infected by the nematodes that infect *L. benedicti*.

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HOW MUCH ENERGY FLOWS THROUGH PARASITES IN A STREAM ECOSYSTEM?

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M. Bernot

Beyond affecting their hosts, parasites may affect community and ecosystem patterns and processes. To more fully understand how parasite biomass production related to stream energy flow, we compared the production of trematodes to macroinvertebrates in a stream ecosystem. Macroinvertebrates including gastropods were systematically sampled monthly or biweekly from the White River in east central Indiana in 2011. Secondary production was estimated for each taxon as the amount of biomass flux through each animal annually using a cohort method. Ephemeroptera and Coleoptera secondary production dominated energy flow in the White River with Gastropod secondary production being 50% less than these two groups combined. Eleven taxa of trematode were found in five different gastropod species. Trematode secondary production constituted approximately 30% of gastropod biomass during summer sampling periods but much less during other months. Overall, trematodes contributed approximately 1% of overall invertebrate secondary production calculated on an annual basis. However, seasonal differences in host performance and production rates indicate that annual production rates may underestimate parasite production because they exhibit more rapid turnover rates than both their hosts and other macroinvertebrates. Energy flow through parasites continues to be an overlooked aspect of ecosystem ecology, but these results suggest that trematodes may be seasonally important to stream ecosystem function.

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SURVEY OF INTESTINAL CANINE PARASITES IN NEW YORK CITY PARKS

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Dogs have the ability to get infected with a wide range of parasites. Some of the most common types of parasites in dogs are those that infect the gastrointestinal tract. Recent studies have shown that common types of parasites of dogs in the United States (U.S.) are hookworms, roundworms, whipworms, and protozoans of the genus *Cystoisospora* and *Giardia*, respectively.

Some of the common tests used to diagnose dogs with intestinal parasites are fecal flotation, and enzyme-linked immunosorbent assay (ELISA). Polymerase chain reaction (PCR) is a less common method that can be used to identify intestinal parasites in fecal samples. A survey was conducted in which NYC veterinarians were asked to identify which species of intestinal parasites they encountered most often in their practices. Surprisingly, all of the surveys indicate that the veterinarians were not able to identify specific species because the method they use to diagnose dogs with intestinal parasites is not species specific. The current study will determine the prevalence of intestinal parasites in NYC dogs using PCR. Seven species of intestinal parasites were chosen: *Echinococcus granulosus*, *Echinococcus multilocularis*, *Toxocara canis*, *Ancylostoma caninum*, *Giardia duodenali,s Cryptosporidium parvum,* and *Toxoplasma gondii*. Fecal samples were collected from three parks in NYC and DNA was extracted. The samples were then used in PCR reactions in order to detect parasitic DNA.This study will provide insight into which species of intestinal parasites are most common in New York City.

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MOLECULAR DIFFERENTIATION AND GENOTYPING OF *STRONGYLOIDES STERCORALIS* ISOLATED FROM HUMANS AND DOGS IN CAMBODIA, SOUTH EAST ASIA

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Strongyloides stercoralis is a parasitic nematode with complex and unique life cycles consisting of free living and parasitic form. It is the most neglected soil transmitted tropical disease affecting more than 100 million people worldwide. In rural community of Cambodia, South East Asia, peoples share the same premises with domestic animals, the sanitation and hygiene practice is very poor and most people in the village walk barefoot which will allow the iL3 of *S. stercoralis* to penetrate the skin and infect the host. We collected fecal samples from 104 humans and 78 dogs of the same household from two villages in Preah Viher District, Cambodia and isolated *S. stercoralis* using Bearman technique and Koga Agar method to investigate if humans and dogs share the same strains of *S. stercoralis* and if the parasite can be transmitted from humans to dogs and vise versa. We sequenced 18S rDNA covering hyper variable region 1(HVR1) which is variable with in *Strongyloides spp* and HVR4 which is invariable with in *Strongyloides spp*) to differentiate and genotype the *S. stercoralis* isolated from humans (339 worms) and dogs (119 worms). We also sequenced cox1 gene for subset of worms from humans and dogs and construct phylogeny using Maximum Likelihood method. At HVR1 we detected genotypes of 5T+3T, 4T+3T, and 5T +TAT with frequency of 87.6, 8.3 and 4.1 respectively from *S.stercoralis* isolated from humans and isolates from dogs we found genotypes of 5T+3T, 5T+TAT, 4T+3T, 4T+TAT and 3T+3T with frequency of 9.4, 0.86, 81, 0.86 and 7.76 respectively to reference gene AF279916 (5T/4T at position 176 and 3T/TAT at position 458). All the *S. stercoralis* sequences from humans have the same sequence of at HVR4 of 18S rDNA. 10 % of the worms from dogs have the same sequence at HVR4 to human isolates and the rest 90% have different sequences, with two indels and one substitution (A/T). Phylogenetic analysis of partial sequence of both 18S rDNA and cox1 gene showed clear separation of *S.stercoralis* of humans and dogs isolates into two clades with strong nodes. Worms that have the same sequences at HVR4 as those from humans were grouped in clade containing human isolates. In summary, in both hosts *S. stercoralis* form genetically diverse populations. The canine strains of *S. stercoralis* may have been adapted to dogs since the time of domestication, and never come back to humans and formed separate subspecies. Even though the number is low s there is a high probability for *S. stercoralis* to be considered as zoonosis so possible clinical intervention should be taken to minimize the risk of *S. stercoralis* infection from dogs to humans. Molecular analysis of *S. stercoralis* from humans and dogs should be conducted in large scale from different parts of the world in endemic areas to support the current findings.

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EXPERIMENTAL EXPOSURE OF THE MAYAN CICHLID FISH *CICHLASOMA UROPHTHALMUS* TO *APHANOMYCES INVADANS* (FORMERLY KNOWN AS EARLY MORTALITY SYNDROME OR EUS)

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The aim of this study was to determine the susceptibility of the Mayan cichlid *Cichlasoma urophthalmus* to the infection with the fungus *Aphanomyces invadans*. To address this aim, *C. urophthalmus* was exposed to the original strain that caused the first outbrake of the disease in Japan in 1971. To assess the susceptibility of *C. urophthalmus*, experimental infections were undertaken exposing 27 individual fish to *A. invadans*. The experimental design included two treatments: intramuscular injection and passive exposure. Nine fish were infected intramuscularly with 25, 000 zoospores/ml each. In the passive exposure another nine individuals were exposed individually to a suspension of 25,000 zoospores/ml suspended in 6 L aquaria. Nine fish were used as negative controls. To assess the infective capacity of *A. invadans*, three golden barbs *Puntius semifasciolatus* were infected intramuscularly with a concentration of 200,000 zoospores. The experiment lasted 30 days. As a diagnostic technique, the Polymerase Chain Reaction (PCR) test was standardized using two sets of oligonucleotides proposed by the OIE. After 30 days of experimental exposure, all the individual fish were killed and muscle and gills collected. None of the exposed *C. urophthalmus* developed skin lesions related to the infection *by A. invadans*. However, the PCR showed positive cases of infection with *A. invadans*. Results showed that for the intramuscular treatment, there were significant differences between controls and the muscle samples (Fisher's exact test $p < 0.05$). In contrast, there were not significant differences between controls and gill samples ($p > 0.05$). All of the three fish used as positive controls became infected as suggested by PCR, and developed the skin lesions typical of *A. invadans* infection. It was concluded that *C. urophthalmus* became infected with *A. invadans*, but since it did not develop skin lesions it was considered as an asymptomatic carrier.

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CLONING OF P23 GENE FROM *CRYPTOSPORIDIUM PARVUM* IN VECTOR PQE-32, PREPARATION OF RECOMBINANT PROTEIN P23 AND IT ANALYSIS FOR ISOLATION OF PARASITE VIA CHROMATOGRAPHY

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Cryptosporidium parvum is a coccidian protozoan that causes diarrhea in immunocompromised humans and newborn animals. Billions oocysts of *C. parvum* can be released from the infected calves and can contaminate environment. The severity of the disease depends on immunological status of the individual. Oocysts of *Cryptosporidium* are extremely resistance to many environmental stresses and no effective disinfectant and curative agent against this organism is available. In our study, recombinant *C. parvum* p23 was prepared for application in isolation and detection of cryptosporidium oocysts. P23 is a glycoprotein belongs to a family of protein with 23-27 kDa and is believed to be expressed in the different life stages of the parasite. We isolated *Cryptosporidium* oocysts from the naturally infected calves. The oocysts were then purified and characterized as C. parvum by nested PCR. To obtain the recombinant P23 protein, we isolated the mRNA from oocyst of *C. parvum*, and synthesized the cDNA. The cDNA was then amplified using specific primers for P23 gene. Sequencing of PCR product showed 100% homology to the known P23 sequences in GenBank. The double strand P23-cDNA was then cloned in PQE-32 expression vector and P23-recombinant protein was prepared. Western blot analysis of recombinant P23 showed that it could be recognized by the positive *C. parvum* serum. The dot

blot analysis showed that antibody against P23 was detectable at 1:200 to 1:1000 dilutions in serum of immunized rabbit with recombinant P23. The antibody prepared in rabbit against p23 was first analyzed by dot blot analysis and then bound to the sepharose 4B and used for isolation of oocysts. The results showed that the prepared column was able to bind specific only the oocystes. These results showed that it could be possible to design a new method for isolation of *C. parvum* oocysts based on anti P23 antibody.

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USING AN ENGINEERED TROJAN HORSE TO KILL NEMATODES

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Infections due to parasitic nematodes result in nearly 125000 deaths annually. Strikingly, this rate remains nearly unchanged in the past 50 years likely owing to the fact that treatment options are either inefficient or inaccessible. Prior to infecting humans, many parasitic nematodes begin as larvae where they feed nearly exclusively on bacteria. This unique property may offer an opportunity to develop new biological control agents with the use of synthetic biology. In this study, we aim to develop gene circuit components that may be used to engineer Escherichia coli to act as a biological control agent of the model nematode *Caenorhabditis elegans*. We independently characterize two genetic modules: an attraction module and a killing module. The attraction module consists of genes that produce acylhomoserine lactones, which serve as natural attractants of *C. elegans*. The killing module consists of an inducible promoter that drives the expression of a toxin gene, cry5B. We independently characterize the response of *C. elegans* to each of these modules towards the ultimate goal of implementing and optimizing the function of both modules together in a single strain of E. coli. As such, our study establishes a quantitative framework for using these modules, and ultimately engineered bacteria, as a robust biocontrol agent for nematodes.

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MOLECULAR DETECTION OF *LEISHMANIA (LEISHMANIA) CHAGASI* IN EXPERIMENTALLY INFECTED MICE'S SPLEEN TISSUES BY REAL TIME PCR

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Visceral Leishmaniasis (VL) is a zoonotic ilness considered one of the most six important tropical diseases in developing countries. In Brazil, the etiological agent of this disease, *Leishmania chagasi*, is transmitted by *Lutzomyia longipalpis*, that acquires the parasite when accomplishes hematophagism in infected animals. In order to clarify the immunological mechanisms which confer parasite persistence and multiplication within the host, many studies have been performed to assess T cells subpopulations and subclasses of immunoglobulins using a murine model. BALB/c and C57BL/6 mice lineages are used for primary tests due to their susceptibly to the pathogen and immune response similar to those from humans. However, the infectivity of these animals is not always easy, depending on the virulence of the strain, route of inoculation, and amount of inoculated parasites. Since the parasite load in this animal species is frequently low, it is necessary the use of a very sensitive diagnostic test that may detect the presence of amastigotes. We aimed at evaluating the presence and quantification of amastigotes in spleen tissues of BALB/c mice inoculated with *L. chagasi*, by Real Time PCR. In the present study, twelve BALB/c mice (4-6 weeks old) were inoculated with 1×10^7 *L. chagasi* promastigotes (MHOM/DR/73/BH46 strain)/mL by intravenous or subcutaneous route. Three animals

inoculated with saline were used as negative controls. Mice were euthanized 7, 15 and 45 days after inoculation in order to verify the presence of amastigotes in spleen tissues. DNA samples were extracted from spleen tissues using QIAamp Blood and Tissue Kit (Qiagen, Santa Clarita, CA, USA) following manufacturer instructions. DNA samples were submitted to both conventional (MJ Research – PTC 200 machine) and Real Time PCR assays (Bio-Rad – CFX96 machine), using primers previously described targeting a 120 bp of kinetoplastic DNA (MICHALSKY et al., 2002). The reagents concentration of PCR reactions was the same for both techniques but Syto 9 was only used as an intercalating in Real time PCR assays. All animals were positive in real time PCR but negative in conventional PCR assays. We also verify that positive results in Real Time PCR showed low Cqs, suggesting a low parasite load in spleen tissues. Our results demonstrated that Real Time PCR was more sensitive than conventional PCR in detecting *L. chagasi* burden in spleen tissues from experimentally infected mice.

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EFFECTS OF HYPOXIA ON BLOOD GLUCOSE AND MEAN ABUNDANCE OF *LIGICTALURIDUS FLORIDANUS* ON CHANNEL CATFISH

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In Mexico one of the most important fish cultured is the channel catfish, *Ictalurus punctatus*. *Ligictaluridus floridanus* is a monogenean trematode that affects channel catfish gills in farms in Tamaulipas state; this parasite may represent a risk, affecting the fish growth rate. In aquaculture it is very important to understand the stress responses induced by stressors such as low levels of oxygen produced by environmental changes, which can impair the resistance against pathogens and affect the fish growth. The aim of this study was to assess the effect of sub lethal hypoxia in the blood glucose and in the mean abundance of *L. floridanus* in channel catfish. Three groups of fish (Control, Group 1, Group 2) with 3 replicates each were allocated in nine 37 L tanks; 18 fish were randomly assigned to each tank. Group 1 and 2 were infected with *L. floridanus*. Every week, fish from Group 2 only were exposed to sub lethal dissolved oxygen levels. Aeration and water flow were interrupted during 6 hours; after this time, aeration and water flow were resumed. One fish from each tank was taken for blood sampling; this was performed in all groups before hypoxia: 0 h, 6 h after the water flow and aeration was interrupted, and 24 h after aerations and water flow were resumed. The blood sample was taken with a syringe, and a drop of blood was measured with a commercial kit. Dissolved oxygen was measured each hour during the hypoxic conditions. Every two weeks the mean abundance of *L. floridanus* was measured sampling one fish from each tank, which was euthanized with benzocaine; the four brachial arches of the left side were taken and placed onto a clean glass slide for examination and parasite counting. This was run for six weeks. Results suggest that neither blood glucose levels nor the mean abundance of *L. floridanus* were affected by sub lethal hypoxia. We concluded that short periods of hypoxia (6 h) do not affect the levels of stress measured through blood glucose and that it does not have an effect on the mean abundance of the parasite.

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OXYSPIRURA PETROWI IN SCALED QUAIL FROM WEST TEXAS

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Oxyspirura petrowi is an indirect lifecycle nematode found under the nictitating membrane and within the conjunctival sacs, lacrimal canals, and the Harderian glands of gallinaceous birds. Because of this nematode's relatively large size and its occurrence in the eye, *O. petrowi* may impair the vision of quail, thereby decreasing this host's chances of survival. *Oxyspirura petrowi* has been found in scaled quail from Texas, but little is known about this host-parasite relationship. The objective of this study was to determine prevalence, intensity, and abundance of *O. petrowi* in scaled quail from the Rolling Plains and surrounding areas using hunter-shot and trapped samples collected 2011–2014. Prevalence of *O. petrowi* in hunter-shot scaled quail during the 2012–2013 hunting season was 21% (n = 28) and the 2013–2014 season was 88% (n = 42). Prevalence for trapped scaled quail in 2011 was 0% (n = 2), 2012 was 54% (n = 13), and 2013 was 24% (n = 17%). Additional findings are discussed in this presentation. Our research provides the first comparison of *O. petrowi* in scaled quail from two collection methods.

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DOES THE BOPYRID PARASITE *PROBOPYRUS PANDALICOLA* AFFECT THE PREDATION PREFERENCES OF MUMMICHOGS BY ALTERING THE BEHAVIOR AND/OR CAMOUFLAGE OF THE GRASS SHRIMP *PALAEMONETES PUGIO*?

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The bopyrid isopod *Probopyrus pandalicola* is a hematophagous ectoparasite that infects palaemonid shrimp, including the daggerblade grass shrimp *Palaemonetes pugio*. Isopod parasites affect shrimp physiology, and possibly behavior, but may also decrease the transparent camouflage of their grass shrimp hosts. The purpose of this study was to determine if the isopod affected the predation preferences of a visual predator, the mummichog *Fundulus heteroclitus*, by altering the behavior and/or camouflage of its grass shrimp prey. The effects of the parasite were differentiated by camouflage and/or behavior by pairing combinations of parasitized, unparasitized, and marked shrimp. The branchiostegite of marked shrimp was painted to mimic the appearance of the parasite. Two shrimp were presented to two mummichog predators in 23x13x16 cm aquaria (n=106). Mummichog preference and shrimp behavior immediately prior to a predation event were recorded. Both the behavioral and visual effects of the parasite affected predator preference. Parasitized shrimp swam more (P=0.048) and backward thrusted less (P=0.027) than unparasitized shrimp immediately prior to predation. Across all shrimp pairings, mummichogs preferentially selected the more active shrimp (83/84 replicates), and selected the less camouflaged shrimp if there was no difference in shrimp behavior (19/22 replicates). Parasitized shrimp were preferentially consumed (51/85 shrimp) if they were paired with unparasitized shrimp, as they behaved differently and were more poorly camouflaged than unparasitized shrimp. Although the sample size was small, marked shrimp were not preferentially selected over unparasitized shrimp (8 and 4 shrimp, respectively), nor were parasitized shrimp preferentially selected over marked shrimp (6 and 2 shrimp, respectively). The major findings of this study were that *Probopyrus pandalicola* affected the predation preferences of mummichogs through both shrimp behavior and decreased camouflage. Ultimately, a possible unexpected

benefit of the chronically depressed energy stores caused by the isopod parasite may be a decrease in high visibility behaviors of the host that may be observed by predators.

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LOW SUSCEPTIBILITY OF INVASIVE INDO-PACIFIC RED LIONFISH (*PTEROIS VOLITANS*) TO A COMMON CARIBBEAN ECTOPARASITE

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The enemy release hypothesis proposes that introduced species can become invasive by leaving behind natural enemies (predators, competitors and parasites) when they are introduced to a non-native habitat. Since its introduction to the tropical western Atlantic in the 1980s, the Indo-Pacific red lionfish, *Pterois volitans*, has become one of the most devastating species invasions in the marine environment. It remains unclear whether release from parasitism has played a role in its success. The capsalid monogenean *Neobenedenia parguerensis* is a common Caribbean ectoparasite with a broad host range that, in high numbers, can kill hosts. In our previous studies, lionfish collected from the Bahamas, Puerto Rico and the US Virgin Islands have not been found to be parasitized by *N. parguerensis*. Possible reasons for this are that 1) lionfish do not occupy habitat where infective stages are present; and 2) lionfish are not susceptible to this parasite. The goal of this project was to determine the susceptibility of red lionfish to *N. parguerensis*. Experiments were conducted in spring/summer of 2012 and 2013 using the overflow trough of an exhibit at Coral World Marine Park on St. Thomas, US Virgin Islands. The trough contains high levels of Neobenedenia. Lionfish (n = 25) and control blue tang (n = 21) were caught from nearby shallow reefs by divers and transported to Coral World. Prior to placement into the trough, each fish was dipped in fresh water to remove any existing parasites. After a 14 d exposure, all fish were individually processed in the same manner. Fish were removed from the trough and placed in a container of fresh water, and gently rubbed with a small paint brush to dislodge any parasites. The fresh water was then filtered and the contents examined under a microscope. Despite exposure to high concentrations of parasites, only one of 25 lionfish presented with one *Neobenedenia*. All blue tang were infected with an average of 10 parasites per fish. These results suggest that invasive red lionfish are not highly susceptible to *N. parguerensis*.

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RODENT AND PARASITE DIVERSITY AT THE SOLTIS CENTER IN COSTA RICA

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There are over 30 known species of rats and mice found throughout Costa Rica. While most of the basic ecology of these rodent species is known, many more detailed aspects of their biology are not. Specifically, few studies have documented the parasitic infections of Costa Rican rodents (Rodriguez-Ortíz et al. 2004) and the absence of this information highlights a need to further study these mammals to survey the wide diversity of parasitic organisms infecting them. To help fill this gap in our knowledge, I completed a biodiversity survey of both small mammals and their parasite species at Texas A&M University's Soltis Center, located at the base of the Children's Eternal Rainforest in Costa Rica, in 2014. Small mammals were trapped daily for four weeks, and captured mammals were identified to genus or species level, processed for parasites, tagged, and released. During processing, ectoparasites were removed and fecal, blood, and tissue samples were collected for endoparasite discovery. Using standard fecal floatation, sedimentation, and staining techniques, fecal samples were investigated for intestinal parasites. Blood samples were used to created blood smears, which were then stained and checked for blood-borne parasites. Both ectoparasite and tissue samples were returned to Texas A&M University for genus and species level identification and pathogen assessment, respectively. A wide variety of small mammals were captured: multiple genera of Rodentia, including *Reithrodontomys* spp.,

Sigmodon sp., *Peromyscus* sp. were processed, as well as some species of Soricomorpha, including *Cryptotis* spp.. Multiple genera of Protozoa, Nematoda, Cestoda, and Trematoda were found to infect these Costa Rican small mammals. While this study is not exhaustive in its survey of small mammal or parasite diversity in Costa Rica, it does provide some of the first insights into the biodiversity of small mammal and parasite species in this region of Costa Rica.

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ANALYSIS OF LARVAL SCHISTOSOME GLYCANS BINDING *BIOMPHALARIA GLABRATA* PLASMA USING A SPOROCYST N-GLYCAN-SPOTTED MICROARRAY

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Previously comparative proteomic analyses of plasma from *Schistosoma mansoni*-susceptible (NMRI) and–resistant (BS-90) strains of *Biomphalaria glabrata* revealed qualitative and quantitative differences in plasma proteins isolated from larval transformation protein (LTP)-affinity columns. Because affinity-isolated proteins included various lectin-like molecules (e.g., Freps, C-type lectins) as well as other immune-related molecules, we labeled affinity-isolated plasma fractions with Cy3/5 dyes and assayed their reactivities to carbohydrates derived from *in vitro* cultured primary sporocysts using a newly-constructed glycan microarray. Each array was spotted with HPLC-isolated fractions/subfractions of PNGase F (PNGF)-digested *in vitro* transformed *S. mansoni* sporocysts (101 elements) and with isolated eggs fraction (72 elements). Normal phase and reverse-phase HPLC was used in fractionation and subfractionation steps, respectively, and was followed by MALDI-TOF analyses of N-glycan structures. Preliminary results indicate widespread binding of snail plasma proteins to a diversity of PNGF-released sporocyst N-glycans with greatest reactivity to Fractions 1.1 and 8.1 glycans consisting of decahexoses (Hex10-AA*) and a Hex1HexNAc2 (likely consisting of a Man-GalNAc-GlcNAc-AA trisaccharide), respectively. Other plasma-reactive sporocyst fractions included Fr. 3 (Hex3-AA), 6 (Hex4-AA, Fuc1Hex2HexNAc2-AA), 7 (Hex4 & 5, Pen1Fuc1Hex2HexNAc2-AA), 8 (Fuc1Hex3HexNAc2-AA), 9 (Fuc1Hex3HexNAc2-AA) and 11 (Pen1Hex3HexNAc3-AA). In initial trials, plasma of resistant snail (BS-90) exhibited stronger reactivity to most of the test fractions compared to susceptible NMRI snail plasma. Recombinant Freps are currently being prepared to test for their larval glycan binding specificities. *Key to sugar identification: Pen (xylose), Fuc (fucose), Hex (man, gal, glc), HexNAc (galNAc or glcNAc). The number following each sugar = no. of residues.

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MAJOR CYST FLUID ANTIGENS OF *ECHINOCOCCUS GRANULOSUS* IN SHEEP, GOATS AND CAMELS SLAUGHTERED IN KANO ABATTOIR, NORTHERN NIGERIA

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Crude hydatid cyst fluid (HCF) of *Echinococcus granulosus* was purified using the high pressure liquid chromatography(HCF). Antigenic profiles of the purified cyst fluid antigen were determined by sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). Of 21 hydatid cysts obtained from liver and lungs of sheep (6), camel (7) and goats (8) slaughtered in Kano abattoir, northern Nigeria, 19(90.5%) of the cysts were collected from the lungs and 2(9.5%) from the liver. The major antigenic components in the hydatid cyst fluid preparations were protein molecules of 12, 45, 50-66kDa, 118-160kDa, with slight differences among the animals. Camel purified antigen preparations showed prominent bands of 32, 66,118,150 and 160kDa.

Goat purified antigen preparations showed prominent bands of 45-52kDa, 66, 100 and 118kDa while sheep HCF contained the 16, 24, 36-52, 66, 96, 118 and 150kDa bands. The most consistent demonstrable protein in *Echinococcus granulosus* occurred as a complex of 52-62kDa in all the animals. Common antigen bands occur mainly between 30 and 67kDa in the electrophoresed cyst fluid of animals. The use of crude antigen in serodiagnosis of hydatidosis has been found to be unsuitable for effective diagnosis of the disease. Purification and standardization of cyst fluid improves diagnostic sensitivities and specificities of the test.

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RELATION OF M2 MACROPHAGES WITH COMPARTMENTALIZED IMMUNE RESPONSE IN DOGS WITH VISCERAL LEISHMANIASIS

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The immune response of dogs with visceral leishmaniasis (VL) may vary in different compartments, promoting *Leishmania infantum* survival. The M2 macrophage phenotype may influence a pro-tumor immune response in humans. Therefore, **the objective** of this study was to analyze the relationship of M2 macrophages (immunohistochemistry) with parasite load (RT-qPCR) in the skin (muzzle and ear), lymph nodes (popliteal and prescapular), spleen and liver of dogs with VL. We used 17 symptomatic and 12 asymptomatic dogs naturally infected by the parasite and six control dogs from non-endemic area for VL. The number of amastigote forms of the parasite and M2 macrophages in each organ was subjected to non-parametric Kruskal-Wallis and Dunn for comparison between organs in each group. The parasite load in the organs within each group differed in symptomatic dogs ($P<0.0001$). Spleen was the organ that showed the highest number of parasites, whose amastigote counts differed statistically from those found in liver, muzzle and ear ($P<0.001$). On the other hand, the popliteal lymph node differed from those found in muzzle and ear ($P<0.05$) and prescapular lymph node ear ($P<0.05$). Immunostained-M2 macrophage occurred in granulomas with or without parasites. Among symptomatic dogs, we found no statistically significant difference in the number of M2 macrophages between the organs. Asymptomatic dogs showed highest immunostaining in spleen, followed by the popliteal lymph nodes and prescapular. The spleen differed from those found in muzzle ($P<0.0001$), ear ($P<0.0001$) and liver ($P<0.05$). The popliteal lymph node differed from that found in ear ($P<0.05$). The spleen and lymph nodes showed a greater number of M2 macrophages and increased number of amastigote forms of the parasite. So it is suggested that the M2 macrophage phenotype could be favoring the survival of *Leishmania* sp. in these organs, because macrophages have a regulatory activity, inducing a Th2 immune microenvironment, which may have an inhibitory effect on the cellular immunity of the host. Acknowledgement: FAPESP-2013/00763-4.

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MORPHOLOGY OF THE FILARIFORM LARVA OF *ANCYLOSTOMA BRAZILIENSE* DE FARIA, 1910 FROM DOMESTIC DOG EXPERIMENTALLY INFECTED

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For many years the term cutaneous larva migrans has been synonymous with creeping eruption wich is caused by zoonotic hookworms larvae as well as other larvae of nematode species. However, most recently it has been proposed the term "hookworm-related cutaneous larva migrans", just for the disease referred specifically when animal hookworm larvae are involved. Penetration through the skin of infective larvae from varios animal nematodes is a common dermatological problem in people who live in or travel to tropical regions in and out the US., *Ancylostoma braziliense* is the most frequent etiological agent. For this study we obtained filariform larvae from an experimentally infected dog, cultivated with the Harada-Mori technic. Nine parameters are suggested to describe the morphology of the aceto-carmin stained infective larvae using the light microscope (SEM). The nine parameters are: total length, total length inside the sheath, length of oral cavity, length of esophagus, distance of the genital primordium to anterior end, maximum wide at the end of the esophagus, distance of the genital primordium to anterior end, distance of anal pore to the body tip and length from the tip of the body to the tip the sheath (when is present). Lateral cord, transverse striations and fine wrinkles of the cuticle are clearly seen with SEM as well as with differential interference contrast. Twenty larvae were measured; photomicrographs and drawings were obtained from permanent slides. This knowledge will be useful to distinguish these larvae from other animal hookworm larvae, mostly from tropical beaches where dogs and cats defecate freely.

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CALLING BEHAVIOR OF ADULT MALE *ACHETA DOMESTICUS* CRICKETS INFECTED WITH *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA)

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Parasite-induced modification of host behaviors and the adaptive nature of these modifications is of continued interest to evolutionary biologists and parasitologists alike. Parasitoids, which kill their host upon emergence to their free living stage, should alter behaviors of hosts in ways that a) bring the parasitoid to the appropriate habitat for emergence, b) decrease the host's risk of predation, thereby increasing the parasitoid's chance of survival, or c) conserve energy, thus maintaining sufficient resources for the parasitoid development within the host. It is well-established that parasitoids in the phylum Nematomorpha induce suicide behavior of their orthopteran hosts; bringing the host to water where the nematomorphs emerge to mate. It is not well-established however, whether other behavioral alterations occur prior to worm emergence. Previous unpublished studies have shown that male *Acheta domesticus* crickets infected during their penultimate instar failed to call when infected with the nematomorph *Paragrodius varius*. These results are consistent with the hypothesis that this behavioral alteration may conserve energy or reduce predation by auditory predators. However, because these crickets were infected prior to wing development, the question arises whether the absence of calling is an adaptation or a result of compromised wing development due to infection. In order to further evaluate the potential that these parasitoid-induced behavioral modifications are adaptive, we assessed the calling behavior of male *A. domesticus* crickets exposed to *P. varius* encysted larvae two to three days after wings had fully developed. In the first trial, we recorded individual cricket calling over a 12-hour period starting five days post-exposure (DPE) and every five days after until worms emerged or day 25. We found that crickets infected with *P. varius* two-three days after wing development did not fail to call. We also found no significant correlation between worm burden and calling intensity. In the second trial, similar methodology was employed with two exceptions: uninfected control crickets were included and calling behavior was assessed for each cricket one day prior to *P. varius* exposure or sham-exposure (-1 DPE). Preliminary data shows that a) 52% of sham-exposed crickets assessed as non-callers on -1 DPE became callers by 5 DPE compared to 27% of exposed crickets and b) no clear difference in calling intensity between exposed and sham-exposed crickets exists early in infection (5-15 DPE).

Infection status will be determined after 25 DPE at which time any differences in calling intensity between infected and control crickets over time will be assessed. Additional trials are set to compare calling behavior of crickets infected as penultimate instars with those infected as winged adults and with uninfected controls. In addition, a trial to assess wing development of crickets infected as penultimate instars will indicate if indeed wing morphology is altered by infection. By testing multiple hypotheses, we aim to provide appropriate evidence to determine whether this behavioral modification is a parasitoid adaptation.

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TOXOPLASMOSIS SEROPREVALENCE IN WILD SMALL RODENTS, POTENTIALLY PREYS OF OCELOTS IN NORTH-EASTERN MEXICO

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Toxoplasma gondii in wildlife is important due to the increasing interaction between this protozoan parasite and urban populations, and the consequent risks for species conservation and public health. The prevalence of *T. gondii* infection in rodents that coexist with ocelots in North-eastern Mexico is reported in this study. Serum samples from 80 rodents were tested for IgG antibodies to *T. gondii* by indirect in house-ELISA. Molecular detection was performed in a *Liomys irroratus* rodent using *B1* gene real time PCR. Captured rodents belonged to five genera. Prevalence values of 6.8% (3/44) and 33.3% (4/12) were found in *Sigmodon hispidus* and *Liomys irroratus,* respectively, with statistically significant difference ($Chi^2 = 6.06$, $p = 0.013$). All samples rodents of *Baiomys taylori* and *Oligoryzomys fulvescens* were negative for the presence of anti-*T. gondii* IgG antibodies. The samples from *Peromyscus spp* could not be analysed because none of the three conjugates tested recognized their immunoglobulins. Infection was confirmed in one rodent species by qPCR, giving a burden of 146 parasites per mg of muscle tissue. A larger number of other intermediate wild host species is necessary in order to determine their role in the sylvatic cycle of *Toxoplasma gondii* in Mexico.

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LITERATURE REVIEW OF BONE ECHINOCOCCOSIS

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Bone echinococcal infection is rare and very difficult to cure. Besides the consensus for a combined aggressive surgical and medical therapy, there are no much recommendation what to do when confronted with such cases. Recurrences despite several surgical interventions and years-long suppressive antihelminthic therapy are frequent. The migration and the chronicity of the disease, a substantial proportion of physicians and surgeons in tertiary hospitals in rich countries may witness. We perform a literature review 1930-2012 with emphasis on epidemiology, therapy, and outcome. We retrieved 200 publications with 721 different episodes all over the world. Most reports concerned one single case (136/200; 68%). Only 24 papers (12%) resumed the proper experience for 10 episodes or more. Half of the manuscripts were published since 1996.

Since most publications were in surgical journals, the main topic of interest was the surgical approach. Turkey ranked highest with 158 different reported cases (22%), followed by Spain with 78 cases (11%), and Germany with 67 reported cases (11%). Among the 721 different patients, median age was 37 years (22% females). Most infections involved one single bone (602/721; 83%), and among them often the spine (321 cases; 45%; of which 111 cervico-thoracic). Surgical intervention was performed in the most cases (702/721; 97%) with the exception of 19 episodes where a surgical approach was not possible without potential substantial harm to the patient. In 687 episodes (95%), there was only 1 surgical intervention. Complete excision of the lesion, as far as it could be known, was possible only in 117 cases (16%), of which five amputations. The rest was potential incomplete debridements, drainages or laminectomies, arthrodeses or hemipelvectomies. Another option, it was injected hypertonic saline or ethyl alcohol into the cavities. The excised cavities were stabilized with osteosynthesis in 661 episodes (92%), while fractures occurred in 48 cases. Most osteosynthesis were plates or spondylodesis. In five cases of femoral infection, the surgeons performed a total joint arthroplasty. Bone grafting was performed in 30 episodes. Bone echinococcosis is a rare parasitic disease and occurring all over the world with hot spots in southern Mediterranean regions; and a 17% risk of recurrence. Combined surgical and medical approaches are the standard of care, while treatment modalities vary considerably.

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ONCHOCERCIASIS IN IFELOJU L.G.A. OYO STATE, NIGERIA AND THE EFFECT OF SOME ANTHELMINTHIC DRUGS ON THE MICROFILARIAE OF *ONCHOCERCA VOLVULUS* IN VITRO

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A survey and experimental study on *Onchocerca volvulus* infection were carried out in four villages viz., Afefu, Ibele, Oba-Akintaro and Bale-Agbe, both in Ifeloju Local Government Area (L.G.A.) of Oyo state, Nigeria in 1990. Infection was determined by finding characteristic microfilariae from skin snips. A total of 126 people were examined and nodule excisions were done on two people. The overall prevalence was 23.8% (30 of 126). Infection was seen in all the villages sampled. The prevalence in males was 25.7%, while that of female was 20.0%. Various clinical manifestations of the infection were seen in the area. Three anthelminthic drugs-Piperazine hydrate BPC (Antepar), pyrantel pamoate (Combantrin) and Levamisole hydrochloride (Ketrax) and aqueous extracts of three different Nigerian plants viz., *Albizia coriaria* (leaf), *Carica papaya* (seeds) and *Momordica charantia* (leaf) were tested for their micofilaricidal effects against the microfilariae of *O. volvulus*. Ketrax and *M. charantia* were most effective, while *A. coriaria* extract was least effective. All the drugs and plant extracts had microfilaricidal effects at the concentrations of 100µg/ml, 50µg/ml, 10µg/ml, and 1µg/ml, although the periods of their effectiveness differed. Further study through *in vivo* screening may find the application of these drugs and herbal extract in onchocerciasis chemotherapy effective.

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TRYPANORHYNCHS FOUND IN THE RAY *UROBATIS JAMAICENSIS* USE PENAEID SHRIMP AS INTERMEDIATE HOSTS.

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Although only two trypanorhynch species have been described from the yellow-spotted ray *Urobatis jamaicensis* (*Prochristianella thalassia and Parachristianella caribbensis*), trypanorhynchs with five different rRNA genotypes were found in rays collected in the vicinity of Key Largo Florida from 2008 through 2013. All are eutetrarynchids. A survey of shrimp, crabs and bivalves from the same area revealed plerocercoids having three of the same genotypes in the shrimp *Farfantepanaeus duorarum*. None of the same species were found in non-penaeid shrimp, other crustaceans, or bivalves, although these hosts did harbor other trypanorhynch plerocercoids.

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WHERE ARE THE INFECTED SNAILS? SEARCHING FOR AN ALTERNATIVE SENTINEL ORGANISM FOR GORDIAN WORMS (PHYLUM NEMATOMORPHA)

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Horsehair worms (Phylum Nematomorpha) are parasites of terrestrial arthropods, but are free-living in aquatic environments as adults. These parasites modify host behavior, leading the definitive arthropod host to enter water, where the adult worms are released. Studies focused on Gordian worms are limited, even when compared to most other parasitic organisms. Until recently, establishing the presence or absence of Gordian worms in freshwater bodies was difficult due to the ephemeral nature of adult worms, which die quickly after mating and laying eggs. This limitation restricted attempts to discover the biodiversity and natural history held within this phylum on animals. It has been discovered that freshwater snails served as reliable sentinels for nematomorph cysts in Nebraska, providing a relatively easy method to detect the presence or absence of these worms regardless of adult activity. This study aimed to assess the spatial distribution and taxonomic classification of a peculiar Gordian worm from central Florida that utilized aquatic dragonfly naiads as hosts in lieu of the paradigmatic terrestrial insect. Intensive sampling throughout 2013 for gordiids encysted in aquatics snails was unsuccessful; thus, it was concluded that snails are an unreliable sentinel organism in central Florida. Subsequent efforts in 2014 have focused on testing other substrate sampling organisms as potential sentinel hosts for Gordian cysts; specifically the gastrointestinal tract of tadpoles and the common invertebrate *Hyallela*. This project was supported by a Research Opportunity Award (ROA) funded by the National Science Foundation.

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HOST ASSOCIATIONS AND GENETIC DIVERSITY OF AVIAN CHEWING LICE (INSECTA: PHTHIRAPTERA) FROM SOUTH AFRICA

O.M. Takano, **G. Voelker** and **J.E. Light**, Texas A&M University

Despite a relatively well-known host fauna, avian chewing lice are relatively unknown in South Africa. Here we present a study on diversity of chewing lice from birds collected in Limpopo Province in northern South Africa. We obtained lice from previously collected museum skin specimens representing a diversity of avian families. Lice were identified by morphology to genus and species, when possible. The mitochondrial cytochrome c oxidase subunit I and the nuclear elongation factor 1-alpha genes were used to conduct phylogenetic analyses of louse taxa. Phylogenetic analyses also were conducted including African louse lineages represented on GenBank. Host associations new to science will be based on morphological identifications and genetic characterizations. Potential host-parasite coevolution also will be discussed.

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A SURVEY OF *SPINITECTUS* SPECIES (NEMATODA) FROM OTSEGO LAKE, NEW YORK

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

Since 2008, Otsego Lake has been intensely surveyed for species of parasites that infect the various fish host located in the lake. The lake has a range of different parasitic groups within these fish. One group is the genus of nematode, *Spinitectus*. Initial survey work on this lake indicated three species of *Spinitectus* were present in fishes; however, a fourth species that is new to science has been discovered. All the species used in this project were collected from a partial necropsy of several fish species. These include *Spinitectus gracilis* in *Ampbloplites rupestris, Micropterus dolomieui*, and *Lepomis auritus*; *Spinitectus carolini* in *M. dolomieui* and *A. rupestris*; *Spinitectus micracanthus* in *Lepomis macrochirus, Lepomis gibbosus, L. auritus, A. rupestris, Perca flavescens,* and *M. dolomieu*; and *Spinitectus* sp.in *L. auritus, and L. gibbosus*. The most recent descriptions of the three previously known species of *Spinitectus* are approximately forty years old, and lack concise details of certain morphological structures, such as quantitative measurements of spine length. The goal of this project is to describe the new species of *Spinitectus* found on Otsego Lake through the use of light microcopy, scanning election microscopy, and collaboration with a known expert of nematodes.

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SPECIMEN RELATIONSHIPS, DATA CAPTURE, DIGITIZATION, AND OBJECT TRACKING AT THE DIVISION OF PARASITOLOGY, MUSEUM OF SOUTHWESTERN BIOLOGY

M.L. Campbell and **G.H. Jarrell**, Division of Parasitology Museum of Southwestern Biology Albuquerque, NM

A major effort at the Parasite Division of the Museum of Southwestern Biology is the incorporation of 50,000 helminth specimens donated by Robert and Virginia Rausch. The division is integrating data from the Rausch specimen records and other collections into the Arctos online database, which serves as both a collection-management tool and as a public portal for specimen information. Arctos is a relational database hosted by the Texas Advanced Computing Center (UT, Austin), archiving two million specimen records from seventy collections. Specimen data are being entered into Arctos and linked to their digitized data records. This is the first time a collection of parasites has been incorporated into a comprehensive, freely accessible online database capable of linking parasite and host vouchers across multiple collections. The database provides for online queries and linkage to specimen vouchers for taxonomic, phylogenetic, and biogeographic studies of both hosts and parasites. The museum database will be used to demonstrate: (1) Host/parasite voucher relationships across collections and institutions within Arctos and in external databases, including GenBank. (2) Host/parasite relationships archived in a dedicated host catalog, when no host voucher is known. (3) How host and parasite records are individually related to entries in the Rauschs' 5000-page, hand-written necropsy ledger. (4) How data from microscope slides and fluid-preserved specimens are being captured, digitized, and tracked prior to cataloging. This work was funded through support from NSF Award# 1057383.

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A SURVEY OF DIGENETIC TREMATODES OF AMPHIBIANS AT THAYER FARM, SUNY ONEONTA BIOLOGICAL FIELD STATION (COOPERSTOWN, NEW YORK)

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

This study is a preliminary survey of digenetic trematodes that parasitize amphibians (e.g. frogs, toads and salamanders) in Otsego County, New York. SUNY Oneonta students in Parasitology and Invertebrate Zoology classes have repeatedly visited Thayer Farm at the SUNY Oneonta Biological Field Station in recent years to conduct basic biodiversity surveys and exercises. Frogs and salamanders have been obtained as part of this endeavor, and have been subsequently examined for parasitic worms. One group of worms that was especially abundant in these hosts was the digenetic trematodes. For example, the Green frog (*Rana clamitans*), was found to be parasitized by two species of *Haematoloechus* in the lung and one species of *Megalodiscus* in the rectum. Spring Peepers (*Pseudacris crucifer*) were parasitized by a species of *Glypthelmins* in the intestine. The Leopard frog (*Rana pipiens*) was parasitized by a single species of *Haematoloechus* in the lung. The Eastern newt (*Notophtalmus viridescens*) was parasitized by a species of *Manodistomum* in the intestine. At present, there are ongoing efforts to identify to species these and other digenes from their amphibian hosts.

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TRYPANOSOMES IN FRESHWATER TURTLES OF THE GENUS *PELUSIOS* IN TROPICAL AFRICA

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Till now, five *Trypanosoma* species infecting freshwater turtles have been described from Africa. However, it is rather difficult to describe or assign a newly found trypanosome without sufficient amount of molecular data on the previously described taxa. In this study, we examined blood smears from 119 recently imported terrapins belonging to family Pelomedusidae (*Pelomedusa subrufa*, *Pelusios* sp., *P. bechuanicus*, *P. castanoides*, *P. gabonensis*, *P. marani*, *P. nanus*, *P. rhodesianus*, *P. sinuatus*, *P. subniger*, *P. upembae* and *P. williamsi*). The animals were imported from Angola, Central African Republic, Democratic Republic of the Congo, Gabon, Kenya, and Mozambique. By light microscopy of Giemsa-stained blood smears, we detected a presence of two trypanosome morphotypes in 9 *P. upembae* turtles. All samples were also examined by PCR method that revealed a presence of trypanosomes in 22 (18.5 %) of the examined turtles: 14 *P. upembae*, 3 *P. rhodesianus*, 4 *P. subniger* and one unrecognized species of genus *Pelusios*. Partial 18S rDNA sequences of the approximate length of 900 bp were used to infer phylogenies. Analysed trypanosomes formed a monophyletic cluster, most closely related to fish trypanosomes. Highly supported subclades were separated by the genetic distance (p-distance) of 0.031. The obtained subclades did not correlate with host species; each isolated trypanosome can infect turtle-related species of the genus *Pelusios*. This work was supported by grant P506/11/1738 (Czech Science Foundation) and project CEITEC (CZ.1.05/1.1.00/02.0068). Participation of M.A.Q. was supported by project OP VK CZ.1.07/2.3.00/30.0014.

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HELMINTHS OF THE ENDEMIC FROG, *LITHOBATES ZWEIFELI* (AMPHIBIA: RANIDAE), IN TWO STATES FROM MEXICO

A.R. Romero Mayen and **V. Leon Regàgnon**, Universidad Nacional Autonoma de México.

The knowledge of the helminth fauna of amphibians in Mexico is still far from complete, with only the 17.5 % of this group of hosts studied in this aspect, and 136 helminth species reported. Of the genus *Lithobates,* 15 of the 27 Mexican species have be reported with at least one helminth species. The aim of this work is to present new helminth records of the endemic frog *Lithobates zweifeli*, which has been reported as host of three helminth species: *Gorgoderina tarascae, Haematoloechus elongatus* and *Gnathostoma turgidum*. 41 frogs were collected from 5 localities in Morelos (1) and Michoacán (4), Mexico. Frogs were dissected under a microscope, helminths were extracted, fixed and processed (stained and mounted) for identification. We found 274 helmints belonging to 3 Phyla: Trematodes, with 5 genera, Nematodes, with 3 genera and

Cestodes with one species. The frogs in Morelos hosted 3 trematode species (*Haematoloechus* sp., *Langeronia* sp. and *Glypthelmins quieta*) and one nematode (*Foleyellides* sp.). *Langeronia* sp. was exclusive of Morelos and *Gorgoderina* sp., *Megalodiscus americanus*, *Rhabdias* sp. and *Eustrongylides* sp. were only found in Michoacán. Three species were found in both localities: *Haematoloechus* sp.; *G. quieta* and *Foleyellides* sp. Only one nematode was found in larval stage: *Eustrongylides* sp. The trematodes *Glypthelmins quieta*, *Gorgoderina* sp., *Langeronia* sp. *M. americanus* and *Haematoloechus* sp. were found in adult stage as the nematodes *Foleyellides* sp. and *Rhabdias* sp.

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PATTERNS OF DISTRIBUTION OF *PARAGONIMUS* AND THEIR HOSTS IN MéXICO

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V. Leon Regàgnon, Instituto de Biología, UNAM

A wide variety of trematodes may infect humans; this is the case of *Paragonimus* spp. a very speciose group. It has been estimated that 20 million people are infected worldwide, especially in tropical and subtropical areas. The species of this genus present a complex life cycle that includes snails and crustaceans as first and second intermediate hosts respectively, and mammals as definitive hosts, adult worms are generally found in the lungs. *Paragonimus mexicanus* is the causal agent of human paragonimiasis in México and several countries of the Americas. Ecologic niche modeling identify the set of conditions that best predict the geographic distribution of a species, approximating the full range of distribution with environmental data from georeferenced sites of known occurrence. In the present work we modeled species distributions, weight the individual variables contribution, the relationship between environment and host distribution of *P.mexicanus* in Mexico and their intermediate hosts. The models were generated using confirmed dataset of parasite records, 19 climatic layers at 1 km resolution from Worldclim and data layers of topography from Hydro 1k. To determine the possible distribution, two separate approaches to ecological niche modeling were implemented. First, a model only with parasite data and a second with models generated from four of the seven species reported as intermediate hosts *Pseudothelphusa dilatata*, *P.seiferti*, *P. terrestrial* and *Tehuana poglayenorum*. The results indicated a high probability of the presence of the parasite in the states from southern Sinaloa to Chiapas and the southern part of Veracruz. Our results suggest a narrower distribution for *P.mexicanus* when set to that obtained for intermediate hosts. However, the manifestation of strong and complex interactions with environmental variables must be taken into account.

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ATRIASTER LEBEDEV ET PARUCHIN, 1969 (MONOGENEA: MICROCOTYLIDAE) FROM OMANI WATERS: AN OUTLOOK INTO SPECIES COMPOSITION AND DISTRIBUTION ALONG COASTS

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E.V. Dmitrieva, **N.A.M. Al-Mazrooei**

The new genus *Atriaster* Lebedev et Paruchin, 1969 was erected to accommodate a new species of microcotylid monogeneans *Atriaster heterodus* Lebedev et Paruchin, 1969, found on the gills of Sparid fish *Sparus heterodus* (Sparidae) near Walvis Bay (South West Africa). The second species of this genus *Atriaster salpa* (Parona et Perugia, 1890) Ktari,1969 was originally described as *Microcotyle salpa* from *Sarpa salpa* (Sparidae) from the Mediterranean Sea. Later (1975) in the

Arabian Sea off the coast of Oman and Yemen described three species of this genus were described *A. spinifer, A. acanthopagri, A. bifidacanthus* from fish family Sparidae (*Argyrops spinifer, Acanthopargus bifasciatus, Sparus sp.)* (Mamaev et Paruchin, 1975). Additionally, *Microcotyle sargi* Parona et Perugia, 1889 (Mamaev et Paruchin, 1975) parasitizing *Sargus sargus* (Sparidae) in the Mediterranean Sea was assigned to the same genus. Almost simultaneously, this group joined another species *A. seminalis* from the Atlantic Ocean, as a parasite of sparids in French waters (Euzet, Maillard, 1974). From the obtained information, we can conclude that at present the genus *Atriaster* has only 6 species exclusively parasitizing fish belonging to the family Sparidae. The number of published works on this species of monogeneans is less than ten, which gives us enough reason to assume that this an under studied group of monogenean parasite and lead us to further investigate it from Omani waters. As far as we know, comprehensive parasitological investigations are almost non existing in Oman (Paruchin, 1976, 1989) and since 16 sparid species are known inhabit Omani waters (Randal, 1995) we present the results of the species composition and distribution of *Atriaster* along the coast of Oman from its Southwest (Salalah) to the Northeast (Muzandam) coasts. The parasitological parameters of the invasion and host specificity of the genus *Atriaster* monogeneans are presented.

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FIRST REPORT OF NATURAL INFECTION WITH *BAYLISASCARIS* SPP IN THE SOUTH AMERICAN SPECTACLED BEAR (*TREMARCTOS ORNATUS*) FROM VENEZUELA

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J.G. Gauta, professor of Animal Health Department, Unibersidad Politecnica Kleber Ramírez, División Bailadores Mérida

Baylisascaris transfuga has been reported from several species of bears in different countries. This is the first report of natural infection with *Baylisascaris* spp in the South American spectacled bear (*Tremarctos ornatus*) from Venezuela. In November 2010, a spectacled bear was found dead by National guards during a routine patrol in The National Park “India Carú”, (Bailadores Mérida, Venezuelan Andes). Necropsy revealed congestion, hemorrhagy of the lungs, small bowel enlargement. A large amount of big witish nematodes were filling the intestinal lumen. Nematodes were morphologically identified as *Baylisascaris* **spp**, on the basis of host, presence of denticular ridges on internal surface of lips, cervical alae slightly striated, caudal extremity of male showing *area rugosa* near cloaca and equal, stout spicules (0,9mm). Molecular characterization (sequence analysis of the ITS-1 and ITS-2 rDNA regions) positioned the spectacled bear nematode in the *Baylisascaris* genus, however important divergences were noted when compared to homologous sequences from other members of this genus deposited at the GenBank. Indeed, some SNPs were located into the highly conserved 5.8S as compared with *B. transfuga, B. schroederi, B. procyonis and, B. columnaris* and strongly suggest that this specimen constitutes, at least, a new genotype of the *Baylisascaris* genus.

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BOTHRIOCEPHALUS SPECIES (CESTODA: BOTHRIOCEPHALIDEA) FROM FISHES FROM OTSEGO LAKE, NEW YORK AND NEARBY WATER BODIES

I. Delgado, **A. Sendkewitz** and **F. Reyda**, State University of New York College at Oneonta

Recent survey work on the intestinal parasites of fishes in Otsego Lake, New York and nearby water bodies has revealed the presence of two species of *Bothriocephalus* that could serve as the focus of future investigations. The introduced species *Bothriocephalus acheilognathi* was found

in two species of cyprinids. This species has not previously been reported from New York. The species *Bothriocephalus cuspidatus*, was found in the digestive system of three freshwater fish species in Otsego Lake; Bluegill (*Lepomis macrochirus),* Walleye (*Sander vitreus*), and most notably the Yellow perch (*Perca flavescens)*. The scolex and strobilae of the *B. cuspidatus* were studied via scanning electron microscopy (SEM) or light microscopy. Specimens examined, specifically using SEM, were found to possess "small bodies" identified as cytoplasmic protrusions within and on their bothria and scolex (Andersen 1979). Due the lack of fully mature specimens however, variations of the species *B. cuspidatus* were only identified by scolex morphology. To fully complete this study, mature specimens must be collected specifically from Otsego Lake.

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BLACK YEASTS (*EXOPHIALA* SPP.) FROM INLAND AND COASTAL HABITATS IN THE SOUTHEASTERN UNITED STATES

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Using light microscopy, oil flotation isolation, and molecular methods, we enumerate the prevalence, intensity, and biodiversity of black yeasts (Chaetothyriales: Herpotrichiellaceae: *Exophiala*) associated with channel catfish (*Ictalurus punctatus*) from farm ponds in Central Alabama as well as from blue crabs (*Callinectes sapidus*) and associated environmental samples (i.e., sediment and particulate organic matter [POM]) from Mississippi-Alabama Gulf Coast. *Exophiala* spp. have been isolated from environmental samples, including sites contaminated with hydrocarbons, as well as from humans, fishes, amphibian, turtles, and invertebrates. They range in marine and freshwater habitats across a wide span of latitudes. Some *Exophiala* spp. are commercially important: *E. cancerae* causes "Lethargic Crab Disease" in South America, and a 1969 infection in channel catfish, *Ictalurus punctatus*, caused mortality in pond aquaculture. No record of an infected wild-caught or captive fish or invertebrate has been documented in North American since 1985, suggesting these agents largely have been ignored in routine diagnostics activities. In our study, no strain of *Exophiala* spp. was recovered from a channel catfish; however, molecular phylogenetic analyses showed that a strain isolated from the blue crab was similar to *Exophiala lecanii-corni*, which has also been isolated from insects, humans, and gas biofilters. In addition, we isolated two strains from sediment and one from POM samples that grouped with some uncultured and unnamed species putatively of *Exophiala*.

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THE STATUS OF THE LECANICEPHALIDEAN GENUS *ANTEROPORA* (CESTODA) AND A DESCRIPTION OF A NEW SPECIES FROM THE JAPANESE SLEEPER RAY, *NARKE JAPONICA*, OFF TAIWAN

R. Guyer and **K. Jensen**, University of Kansas

The genus *Anteropora* was erected in 1955 by C. K. Subhapradha, who at that time transferred *Discobothrium japonicum* Yamaguti, 1934 to *Anteropora* as its type species. *Anteropora japonica* (Yamaguti, 1934) Subhapradha, 1955 was described from the Japanese sleeper ray, *Narke japonica* (Temminck and Schegel), off Kuki, Japan. To date, a total of nine species of *Anteropora* are considered valid, collectively parasitizing an eclectic suite of hosts: electric rays (Narkidae and Narcinidae), stingrays (Dasyatidae), and one species of shark (Hemiscylliidae), all from the western Pacific from Japan to Indonesian Borneo. The nine species exhibit unusual variation in apical organ morphology (glandular vs. muscular) and reproductive strategy (euapolytic vs. hyperapolytic) compared to species in other lecanicephalidean genera. In October of 2005, a specimen of *N. japonica* caught off Nanfang-ao, Taiwan was found to be parasitized by *Anteropora japonica* and a previously undescribed species of *Anteropora*. Specimens of both species were prepared for light and scanning microscopy. The new species is most similar to *A.*

japonica but can be distinguished from the latter species based on its longer bothridia (196 – 232 vs. 316 – 435 µm), broader spinitriches on the apical organ, and less dense spinitriches covering the distal and proximal bothridial surfaces. This is the first record of *A. japonica* from outside Japan expanding its distribution south to Taiwan, and the third report of congeners in a single host species. Preliminary phylogenetic analyses of selected members of *Anteropora* suggest congeners from the same host species to not be each other's closest relatives, and that there is no phylogenetic signal for apical organ type or reproductive strategy. Moreover, *Anteropora* is monophyletic only if the aberrant *Sesquipedalapex comicus* Jensen, Nikolov and Caira, 2011 is transferred to the genus.

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ARRIVING DEAD CENTER OF A TARGET I DIDN'T KNOW I WAS AIMING FOR
(H.B. Ward Medal Lecture)

K. Jensen, University of Kansas

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CHALLENGES OF MENTORING PARASITOLOGISTS IN THE TROPICS
(Clark P. Read Mentor Lecture)

G.P. Ponce de León, Universidad Nacional Autónoma de México

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1927 Nashville TN
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1930 Cleveland OH *
1931 New Orleans LA
1932 Atlantic City NJ
1933 Boston MA
1934 Pittsburgh PA
1935 St Louis MO
1936 Atlantic City NJ
1937 Indianapolis IN
1938 Richmond VA
1939 Columbus OH
1940 Philadelphia PA
1941 Dallas TX
1942 No meeting
1943 No meeting
1944 Cleveland OH
1945 St. Louis MO
1946 Boston MA
1947 Chicago IL
1948 New Orleans LA *
1949 New York NY
1950 Cleveland OH
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1952 Ithaca NY †
1953 Madison WI †
1954 Memphis TN *
1955 Atlanta GA
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1957 Philadelphia PA *
1958 Bloomington IN †
1959 University Park, PA †
1960 Los Angeles CA *
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1962 Washington DC ‡
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1964 Boulder CO †
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1966 San Juan PR *
1967 Tucson AZ §
1968 Madison WI †
1969 Washington DC *
1970 Washington DC ¶
1971 Los Angeles CA
1972 Miami Beach FL *
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1996 Tucson AZ ††
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1998 Kona HI
1999 Monterey CA ‡‡
2000 San Juan PR ††
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2002 Vancouver BC, Canada ¶§§
2003 Halifax NS, Canada
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2005 Mobile AL
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2007 Merida Yucatan, Mexico §§¶ ¶
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2009 Knoxville TN
2010 Colorado Springs CO
2011 Anchorage AK
2012 Richmond VA
2013 Quebec City QB, Canada ***
2014 New Orleans LA
2015 Omaha NB

* 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 Associaton
** With American Association of Veterinary Parasitologists
†† With Society of Protozoologists
‡‡ With Society of Nematologists
§§ With Sociedád Méxicana de Parasitología
¶¶ With Parasitology Section, Canadian Society of Zoologists
*** With Québec Molecular Parasitology