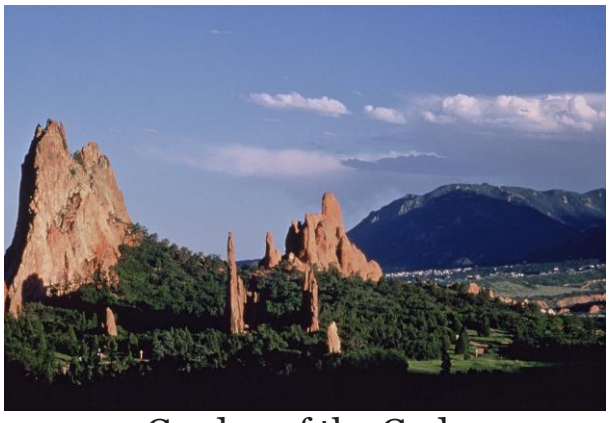
The 85th Annual Meeting of the American Society of Parasitologists

Crowne Plaza – Colorado Springs, Colorado
June 22 – 25, 2010


Downtown Colorado Springs


Colorado Columbine


Garden of the Gods

Program & Abstracts

Thanks to Everyone Who Helped Make This Meeting Possible…

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

The ASP Local Arrangements Committee
Dr. Ron Hathaway, Colorado College

ASP Scientific Program Officers
Dr. Herman Eure, Wake Forest University
Dr. Kelli Sapp, High Point University

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The American Society of Parasitologists
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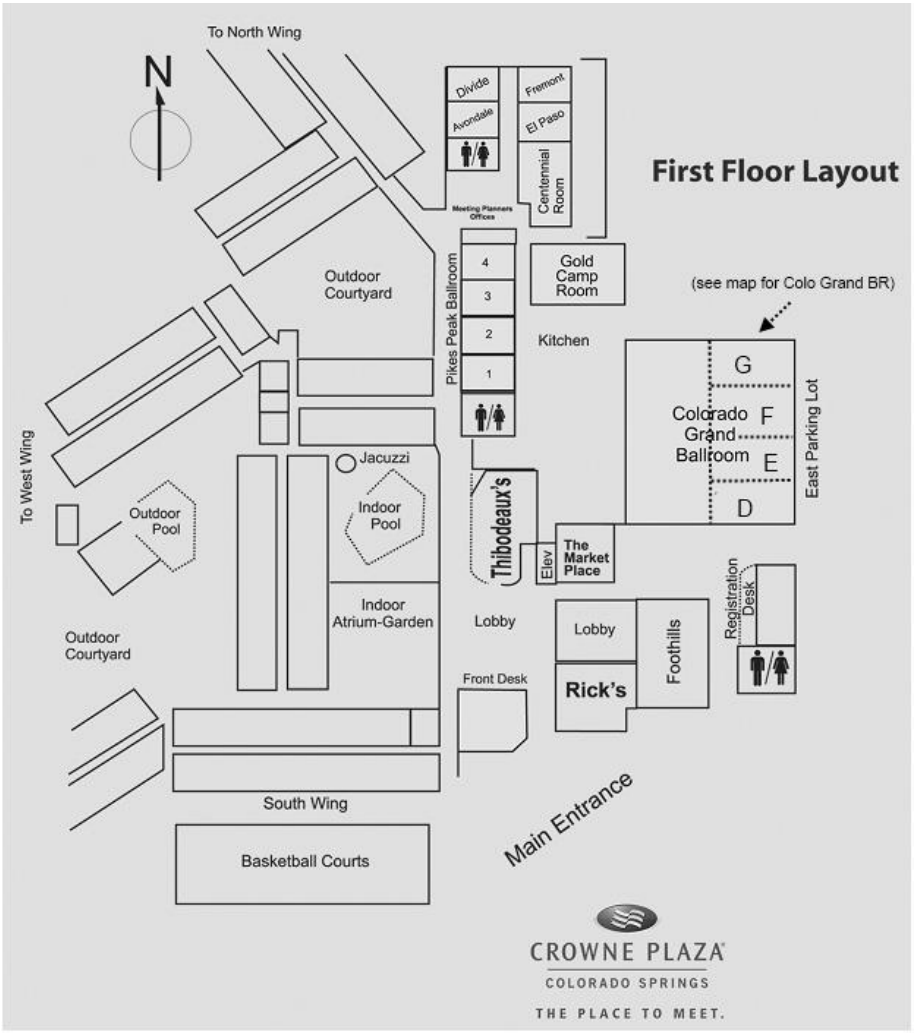
Welcome

We would like to welcome you to the 85th annual meeting of the American Society of Parasitologists (ASP).

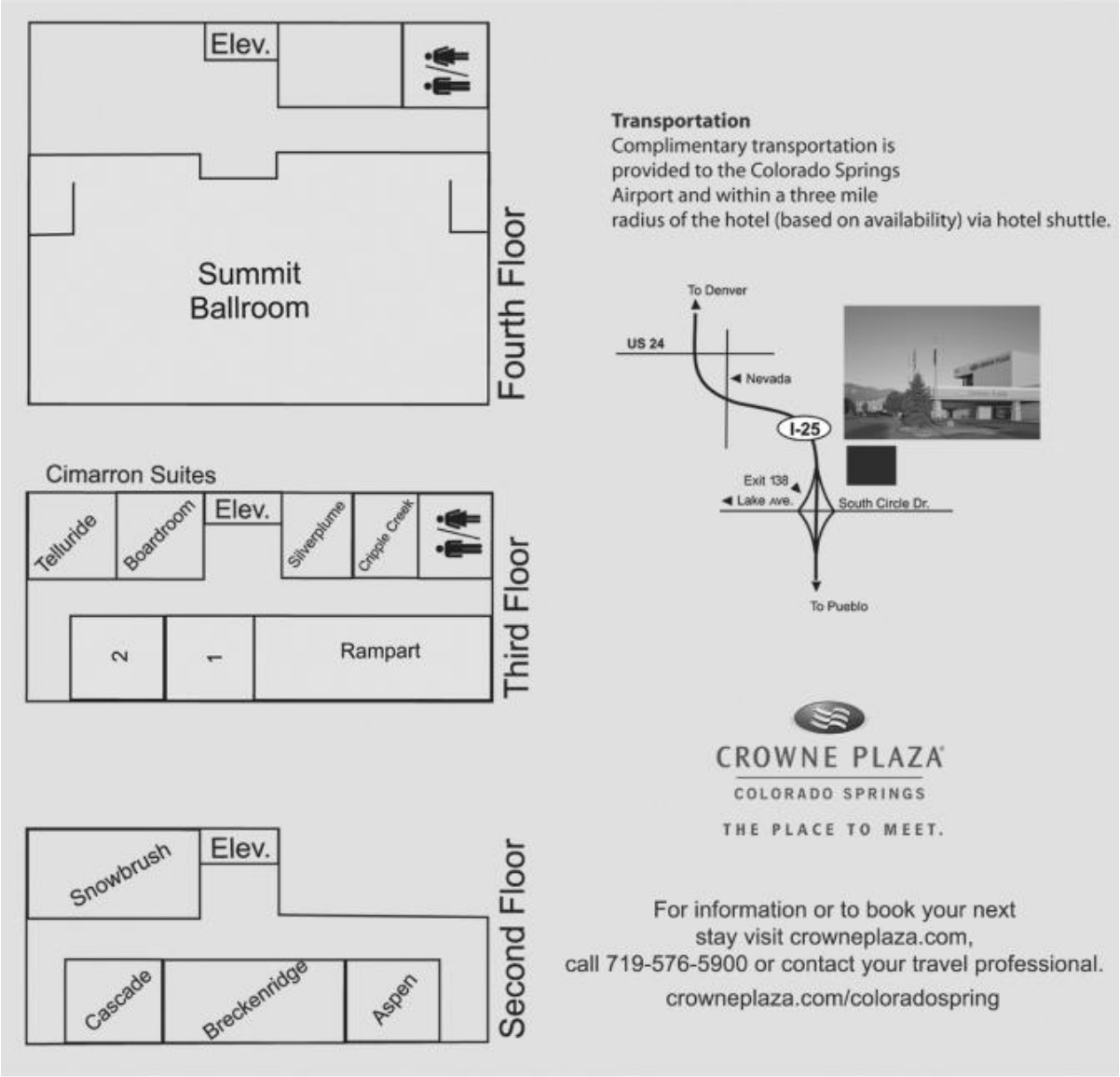
The ASP is a diverse group of over 1500 scientists from industry, government, and academia who are interested in the study and teaching of Parasitology. Founded in 1924, ASP members have contributed not only to the development of parasitology as a discipline, but also to primary research in systematics, medicine, molecular biology, immunology, physiology, ecology, biochemistry, behavior, and more.

Herman Eure and Kelli Sapp, Scientific Program Officers

ASP 2010 Conference Floor Plan

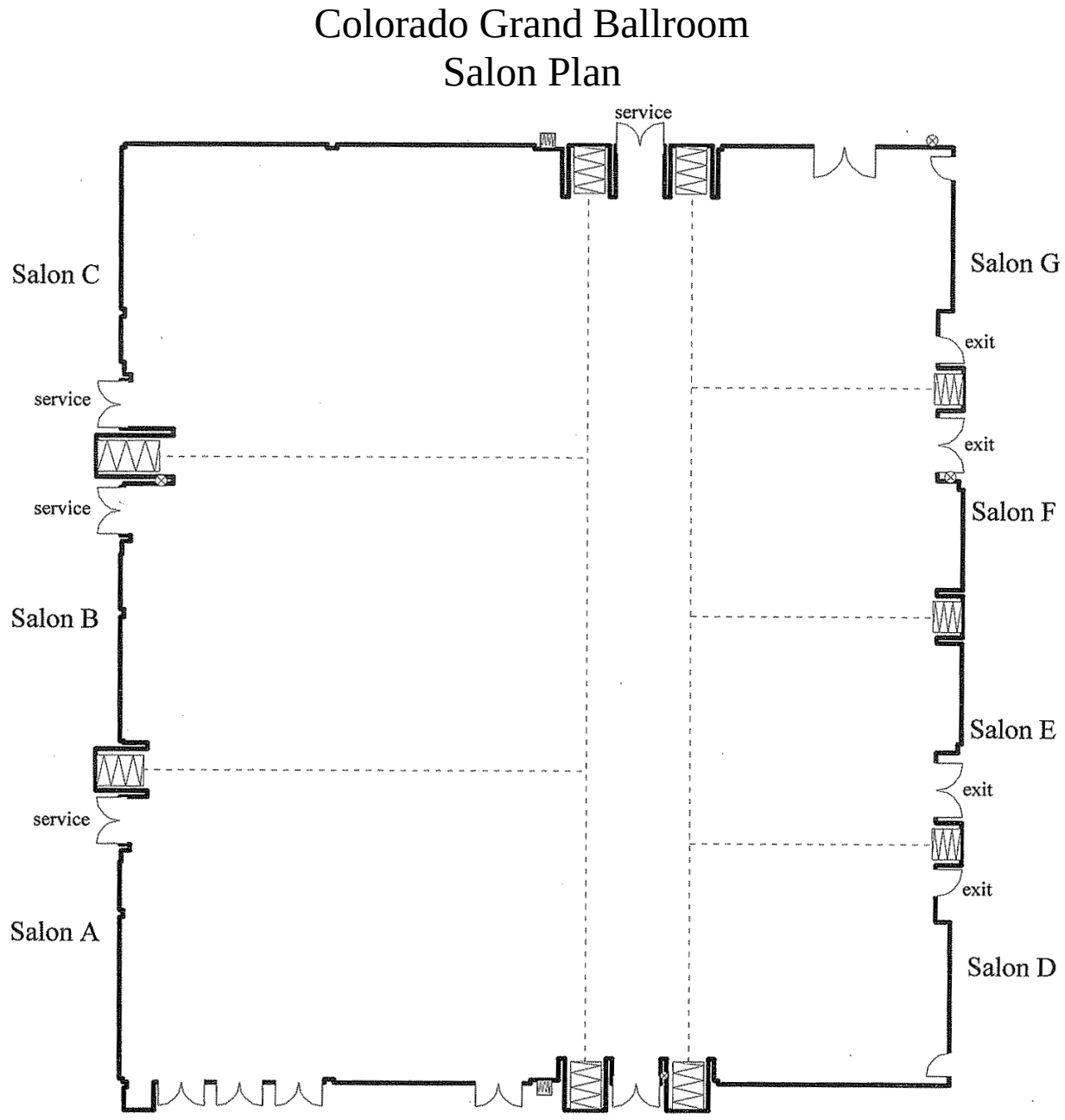


ASP 2010 Conference Floor Plan – upper section



Notes:

ASP 2010 Conference Floor Plan – Salons D, E, F, and G



Day/Times	Activity/Function	Room/Space
June 22 (Tuesday)		
8:00 a.m.-Noon	ASP Council	Rampart
1:00 -5:15 p.m.	Student Paper Competition I	Salon D
1:00-2:15 p.m.	Vector Bio, Cell Bio, Physiol	Salon E
1:00 – 5:15 p.m.	Teacher Education Workshop	Gold Camp
2:30-2:45 p.m.	Coffee Break	
2:45-5:15 p.m.	Genetics, Molec Bio, Immunology	Salon G
7:00 – 10:00 p.m.	Welcome Reception	Summit Ballroom
June 23 (Wednesday)		
7:00-8:30 a.m.	Editorial Board Breakfast	Rampart
8:30-10:30 a.m.	ASP President's Symposium	Colorado Grand Ballrm
10:30-11:00 a.m.	Coffee Break	
11:00-Noon	Stoll-Stunkard Lecture	Colorado Grand Ballrm
1:00-3:00 p.m.	Student Paper Competition II	Salon E
1:00-3:00 p.m.	Life Cycles, Epidemiology	Salon D
3:00-3:30 p.m.	Coffee Break	
3:30-5:00 p.m.	ASP Students' Symposium	Salon F/G
3:00-6:00 p.m.	Auction Set Up	Foothills
6:00-7:00 p.m.	Auction Preview	Foothills
7:00-9:00 p.m.	21st Annual ASP Student Auction	Foothills
June 24 (Thursday)		
8:00-10:00 a.m.	Associate Editors Symposium	Salon D
8:00 a.m.-12:00 p.m.	Host – Parasite Interactions	Salon F
8:30-11:45 a.m.	42nd Coccidiosis Conference	Salon E
10:00-10:15 a.m.	Coffee Break	
1:00-2:00 p.m.	ASP President's Address	Colorado Grand Ballrm
2:15-5:15 p.m.	Helminth - Amphibian Symposium	Salon D
2:15-5:00 p.m.	Ecology I	Salon F
2:15-5:00 p.m.	Taxonomy, Systematics, Phylogeny	Salon E
3:30-3:45	Coffee Break	
3:00-5:00 p.m.	Poster Boards delivered, authors may set up posters	Foothills
5:45-9:00 p.m.	Cheyenne Mountain Zoo	
June 25 (Friday)		
8:00-10:30 a.m.	Ecology II	Salon F
8:30-10:30 a.m.	Authors complete poster set up	
10:30-12:00	Poster Session, coffee, snacks	Foothills
1:00-2:30 p.m.	ASP Awards and Business Meeting	Colorado Grand Ballrm
8:00 a.m.-5:00 p.m. (Daily)	Speaker Ready Room	Avondale

Tuesday Morning, 2010-06-22

08:00 AM – Noon ASP Council Meeting, Rampart

Presiding: G.D. Cain, University of New Mexixo, Albuquerque, NM

Tuesday Afternoon, 2010-06-22

1:00-5:00 STUDENT COMPETITION I, Salon D

Presiding: J. Camp, Purdue University, West Lafayette, IN
K. Sapp, High Point University, High Point, NC

Time (Abstract No.)

1:00 (1) **J. J. Chaparro-Gutiérrez**, M. Wasserman, TWO GIANT PROTEASES IN AN EARLY-DIVERGENT PARASITE, GIARDIA INTESTINALIS.

1:15 (2) **E. Hoellerich**, C. Dunagan, D. Maring, Y. Wong, T. J. Albert, J. Milhon, NUCLEOLAR LOCALIZATION OF SMMAK16 PROTEIN FROM SCHISTOSOMA MANSONI IS NOT EFFECTED BY PH OR PHOSPORYLATION.

1:30 (3) **P. Vigueira**, K. S. Paul, ACETYL-COA CARBOXYLASE OF TRYPANOSOMA BRUCEI: A NEW DRUG TARGET FOR TREATMENT OF AFRICAN TRYPANOSOMIASIS.

1:45 (4) **M. R. Zimmermann**, K. E. Luth, G. W. Esch, INFECTION DYNAMICS OF DAUBAYLIA POTOMACA (NEMATODA:RHABDITIDA) IN HELISOMA ANCEPS.

2:00 (5) **K. E. Luth**, M. R. Zimmermann, G. W. Esch, FACTORS INFLUENCING THE COMMUNITY COMPOSITION OF PARASITIC AND FREE-LIVING NEMATODES IN A FRESH-WATER SYSTEM.

2:15 (6) **D. Szuroczki**, PRESENCE OF RIBEIROIA ONDATRAE IN THE DEVELOPING ANURAN LIMB DISRUPTS THE RETINOIC ACID SIGNALING CASCADE.

2:30-02:45 COFFEE BREAK

2:45 (7) **S. A. Coggins**, J. F. Hillyer, COMPARATIVE SUSCEPTIBILITY OF AEDES AEGYPTI AND ANOPHELES GAMBIAE MOSQUITOES TO BACTERIAL INFECTION.

3:00 (8) **H. R. Tracy**, M. G. Bolek, HELMINTH AND LEECH COMMUNITY STRUCTURE IN TWO SPECIES OF SYMPATRIC LARVAL AMPHIBIANS FROM WESTERN NEBRASKA.

3:15 (9) **H. R. Tracy**, M. G. Bolek, OBSERVATIONS ON THE NEMATODE GYRINICOLA BATRACHIENSIS (OXYUROIDEA: PHARYNGODONIDAE) IN EIGHT SPECIES OF LARVAL AMPHIBIANS FROM NEBRASKA.

3:30 (10) **A. K. Knipes**, J. Janovy, Jr., STREAM MORPHOLOGY, NICHE USE, AND OTHER FACTORS DETERMINING THE DISTRIBUTION OF DACTYLOGYRUS SPP. (MONOGENEA) ON NATIVE NORTH AMERICAN CYPRINIDS.

3:45 (11) **R. M. Fogelman**, THE BODY SIZES OF CYMOTHOID ISOPOD PARASITES.

4:00 (12) **H. A. Robinson**, M. A. Barger, T. J. Cook, ROLE OF ENVIRONMENTAL FACTORS IN STRUCTURING ENDOHELMINTH COMMUNITIES IN THE WESTERN MOSQUITOFISH, GAMBUSIA AFFINIS.

4:15 (13) **J. S. Carlson**, PHYLOGENETIC RELATIONSHIPS OF BLOOD PARASITES IN THE AVIFAUNA OF SOCORRO ISLAND, MÉXICO.

4:30 (14) **J. A. Ferguson**, J. Romer, C. B. Schreck, M. L. Kent, IMPACTS OF MULTIPLE PARASITE SPECIES INFECTION ON OREGON COASTAL JUVENILE COHO SALMON (ONCORHYNCHUS KISUTCH).

4:45 (16) **A. D. Stumbo**, TREMATODE-INDUCED OXIDATIVE STRESS IN LIVER TISSUE OF MINNOWS EXPOSED TO ORNITHODIPLOSTOMUM SP. CERCARIAE.

5:00 (17) **M. A. Thomson**, C. Goater, D. Colwell, TRANSMISSION BIOLOGY OF THE LANCET LIVER FLUKE (DICROCOELIUM DENDRITICUM) AMONG POTENTIAL DEFINITIVE HOSTS IN WESTERN ALBERTA, CANADA.

1:00-5:00 **VECTOR BIOLOGY, CELL BIOLOGY, PHYSIOLOGY, Salon E**

Presiding: J.F. Hillyer, Vanderbilt University, Nashville, TN

Time (Abstract No.)

1:00 (17) **R. H. Easy**, CHANGES IN ATLANTIC SALMON AND COD EPIDERMAL MUCUS PROTEINS IN RESPONSE TO STRESS.

1:15 (18) **R. H. Fetterer**, R. S. Schwarz, K. B. Miska, M. C. Jenkins, IDENTIFICATION AND PARTIAL CHARACTERIZATION OF AN EIMERIA SPECIFIC PROTEIN.

1:30 (19) **J. F. Hillyer**, J. W. Andereck, J. G. King, ABDOMINAL CONTRACTIONS FACILITATE EXTRACARDIAC RETROGRADE HEMOLYMPH PROPULSION IN THE MOSQUITO HEMOCOEL.

1:45 (20) **K. Tackett**, C. D. Davis, HIGH PREVALENCE OF BORRELIA BURGDORFERI IN TICKS RECOVERED FROM RACCOONS AND OPOSSUMS TRAPPED IN KENTUCKY.

2:00 (21) **S. M. Vetter**, J. L. Holmes, J. A. Montenieri, C. B. Graham, M. E. Woods, R. J. Eisen, K. L. Gage, EFFECTS OF TEMPERATURE ON TRANSMISSION OF YERSINIA PESTIS BY THE FLEA, XENOPSYLLA CHEOPIS.

1:00-5:15 TEACHER EDUCATION WORKSHOP, Gold Camp

Presiding: J. Serach, Aldo Leopold Chair
The Lawrenceville School, Lawrenceville, NJ

1:00 WELCOME AND OVERVIEW. **Ron Hathaway**, Professor of Biology, Colorado College, Colorado Springs, CO and **Jim Serach**, Aldo Leopold Chair, Lawrenceville School, Lawrenceville, NJ.

1:15 KEYNOTE ADDRESS: TOP TEN PARASITES. **John Janovy, Jr**., Varner Professor of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.

2:00 THE COOL, THE BAD, AND THE UGLY. **Matthew Bolek**, Assistant Professor of Zoology, Oklahoma State University, Stillwater, OK.

2:30-02:45 COFFEE BREAK

2:45-5:00 **"**INFECTING" THE NEXT GENERATION-PARASTIES IN THE CLASSROOM, LABORATORY AND FIELD. **J. Serach** and **Alaine Knipes**, PhD Graduate Student, University of Nebraska-Lincoln, Lincoln, NE.

5:00-5:15 Wrap up: Future Directions and Opportunities. **J. Serach**.

2:45-5:15 GENETICS, MOLECULAR BIOLGY, IMMUNOLOGY, Salon G

Presiding: C. Bayne, Oregon State University, Corvallis, OR
E.S. Loker, University of New Mexico, Albuquerque, NM

Time (Abstract No.)

2:45 (22) **F. O. Akinbo**, C. E. Okaka, R. Omoregie, L. Xiao, MOLECULAR EPIDEMIOLOGY OF CRYPTOSPORIDIOSIS AMONG HIV-INFECTED SUBJECTS IN BENIN CITY, EDO STATE, NIGERIA.

3:00 (23) **V. Gelmedin**, ROLE OF ANCYLOSTOMA CANINUM TRANSCRIPTION FACTOR DAF-16/FOXO DURING THE RESCUE OF DEVELOPMENTAL ARRESTED LARVAE.

3:15 (24) **M. C. Jenkins**, CHARACTERIZATION OF GIARDIN PROTEIN EXPRESSION DURING ENCYSTATION OF GIARDIA DUODENALIS TROPHOZOITES TO CYSTS.

3:30 (25) **S. F. Mossallam**, PROPHYLACTIC EFFECT OF BOVINE LACTOFERRIN AGAINST ACUTE TOXOPLASMOSIS IN IMMUNOCOMPETENT AND IMMUNOSUPPRESSED MICE.

3:45 (26) **S. Raiyawa**, R. Chawengkirttikul, IMMUNOBLOT PROFILES OF SERUM FROM PATIENTS WITH OCULAR ANGIOSTRONGYLIASIS AGAINST MALE AND FEMALE EXTRACTS.

4:00 (27) **J. F. Hillyer**, J. G. King, ANTIMICROBIAL FUNCTION OF SESSILE HEMOCYTES IN THE MOSQUITO HEMOCOEL.

4:15 (28) **A. Oladiran**, M. Belosevic, TRYPANOSOMA CARASSII CALRETICULIN BINDS HOST COMPLEMENT COMPONENT C1Q AND INHIBITS CLASSICAL COMPLEMENT PATHWAY-MEDIATED LYSIS.

4:30 (29) **J. Hines**, P. M. Cupit, A. D. Aragon, C. Cunningham, MICROARRAY ANALYSES OF SCHISTOSOMA MANSONI TREATED WITH PRAZIQUANTEL.

4:45 (30) **M. A. Forys**, P. C. Hanington, C. Lun, C. M. Adema, E. S. Loker, THREE DIFFERENT MODELS OF BIOMPHALARIA GLABRATA RESISTANCE TO TREMATODE INFECTION: COMMON UNDERLYING PATTERNS BASED ON MICROARRAY STUDIES.

5:00 (31) **P. C. Hanington**, M. A. Forys, C. M. Adema, E. S. Loker, FUNCTIONAL CHARACTERIZATION OF FREP3: A FIBRINOGEN RELATED PROTEIN ASSOCIATED WITH TREMATODE RESISTANCE IN BIOMPHALARIA GLABRATA.

Tuesday Evening, 2010-06-22

07:00 - 10:00 PM **WELCOME RECEPTION** - Summit Ballroom

Wednesday Morning, 2010-06-23

7:00 – 8:30 **Editorial Board Breakfast, Rampart**

8:30-10:30 **ASP PRESIDENT'S SYMPOSIUM, Colorado Grand Ballroom**

Presiding: A. Kuris, Marine Institute, University of California, Santa Barabara

Theme: Recent Discoveries in the Biology of Schistosomes.

Time (Abstract No.)

8:30 **A. Kuris**, Introduction.

8:35 (32) **J. H. McKerrow**, BIOCHEMICAL AND IMMUNOLOGICAL INSIGHTS INTO SCHISTOSOME HOST INVASION AND DEVELOPMENT.

9:05 (33) **P. T. LoVerde**, ROLE OF SIGNALING IN SCHISTOSOME MALE-FEMALE INTERACTIONS.

9:35 (34) **E. S. Loker**, S. V. Brant, SCHISTOSOME DIVERSITY.

10:05 Closing comments and questions.


Jane Carlton, NYU

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

11:00-Noon **STOLL STUNKARD LECTURE, Colorado Grand Ballroom**

Presiding: J. Bristol, University of Texas, El Paso

Time (Abstract No.)

11:00 **M. Siddall,** Introduction of **Dr. Jane Carlton**, Department of Medical Parasitology, New York University.

11:05 (35) **J. Carlton**. Parasite Genomics: The Next Generation.

Wednesday Afternoon, 2010-06-23

2:45-5:15 **STUDENT PAPER COMPETITION II, Salon E**

Presiding: G. Mayer, Virginia Commonwealth University, Richmond, VA
L.S. Roberts, Homestead, FL

Time (Abstract No.)

1:00 (36) **O. Jones-Nelson**, D. Minchella, TRANSMISSION DYNAMICS OF TWO STRAINS OF SCHISTOSOMA MANSONI UTILIZING NOVEL HOSTS.

1:15 (37) **C. Dold**, J. P. Cassidy, C. O'Farrelly, C. V. Holland, THE INNATE HEPATIC RESPONSE TO ASCARIS SUUM INFECTION IN THE MOUSE MODEL.

1:30 (38) **J. J. Cielocha**, K. Jensen, INVESTIGATING THE VALIDITY OF TWO QUESTIONABLE LECANICEPHALIDEA GENERA: HEXACANALIS AND CEPHALOBOTHRIUM.

1:45 (39) **C. Martinez**, MOLECULAR BASIS FOR HOST SPECIFICITY IN AVIAN MALARIA.

2:00 (40) **M. Pickering**, J. Caira, A CESTODE TEST OF NEWLY CIRCUMSCRIBED SPECIES BOUNDARIES IN THE SHARKS SQUALUS ACANTHIAS AND SQUALUS SUCKLEYI.

2:15 (41) **E. DiBlasi**, K. Dittmar, PHYLOGENETIC RELATIONSHIPS OF ECTOPARASITIC MITES (ACARI: ERYTHRAEOIDEA) ON ARGENTINE WALKING STICKS (INSECTA: PHASMIDA).

2:30 (42) **M. Pinto**, A PHYLOGENETIC RE-ASSESSMENT OF HYBRIDIZATION EVENTS AND SPECIES BOUNDARIES WITHIN TRYPANOSOMA CRUZI.

2:45 (43) **S. Jean**, CHARACTERIZATION OF NOVEL PEXEL-NEGATIVE P. FALCIPARUM EXPORTED PROTEIN, PFEXP250.

2:45-5:15 **LIFE CYCLES & EPIDEMIOLOGY, Salon D**

Presiding: B. Dixon, Health Canada, Ottawa, ON
A. Donoghue, Donoghue Consulting, LLC, Fort Collins, CO

Time (Abstract No.)

1:00 (44) **F. O. Akinbo**, PREVALENCE OF MALARIA AND ANAEMIA AMONG HIV INFECTED.

1:15 (45) **K. J. Reinhard**, EMERGENCE AND CONTROL OF GEOHELMINTHS IN HISTORIC ALBANY, NY, 1640-1920.

1:30 (46) **D. M. Roellig**, TRYPANOSOMA CRUZI IN THE UNITED STATES: MOLECULAR AND BIOLOGICAL CHARACTERISTICS OF SYLVATIC ISOLATES.

1:45 (47) **M. G. Bolek**, H. R. Tracy, THE ROLE OF DAMSELFLIES (ODONATA: ZYGOPTERA) AS PARATENIC HOSTS IN THE TRANSMISSION OF HALIPEGUS ECCENTRICUS (DIGENEA: HEMIURIDAE) TO ANURANS.

2:00 (48) **J. T. Payne**, J. Gunderson, METACESTODES OF BAIT SHRIMP IN THE GULF OF MEXICO.

2:15 (49) **B. Dixon**, L. Parrington, A. Cook, F. Pollari, J. Farber, CYCLOSPORA CAYETANENSIS, CRYPTOSPORIDIUM SPP. AND GIARDIA DUODENALIS IN PACKAGED READY-TO-EAT SALADS AND LEAFY GREENS FROM A SENTINEL SITE IN ONTARIO, CANADA.

2:30 (50) **S. F. Mossallam**, DETECTION OF SOME INTESTINAL PROTOZOA IN COMMERCIAL FRESH JUICES.

2:45 (51) **Y. Cruz**, L. Aguirre-Macedo, V. M. Vidal-Martínez, PANULIRUS ARGUS (LATREILLE, 1804) FROM BATABANO GULF, CUBA, PARASITIZED BY CYMATOCARPUS SOLEARIS (BRACHYCOELIDAE-METACERCARIA).

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

3:30-5:00 **ASP STUDENTS' SYMPOSIUM, Salon F/G**

Presiding: M. Pickering, University of Connecticut, Storrs, CT.

Theme: Accessing parasites from the comfort of your own home: an introduction to online parasite databases.

Time (Abstract No.)

3:30 **M. Pickering** , INTRODUCTION.

3:40 (51) **J. N. Caira**, ON-LINE CESTODE DATABASE RESOURCES.

4:10 (52) **J. C. Kissinger**, EUPATHDB – A EUKARYOTIC PATHOGEN DATABASE OF PROTIST "OMICS" DATA.

4:40 Questions, Closing Remarks**. M. Pickering**

Wednesday Evening, 2010-06-23

6:00-7:00 Auction Preview.

7:00-9:00 **21st ANNUAL ASP STUDENT AUCTION**, **Foothills**

Thursday Morning, 2010-06-24

8:00-10:00 **ASSOCIATE EDITORS SYMPOSIUM, Salon D**

Presiding: C. P. Goater, University of Lethbridge, Lethbridge, AB, Canada

Time (Abstract No.)

8:00 (54) **G. W. Esch, C. P. Goater**, ASSOCIATE EDITOR'S SYMPOSIUM – 2010

8:20 (55) **T. G. Geary**, C. ELEGANS AS A MODEL ORGANISM FOR ANTHELMINTIC RESEARCH: PROSPECTS AND PITFALLS.

8:50 (56) **A. W. Shostak**, PUTTING PARASITISM IN PERSPECTIVE: LESSONS FROM LARVAL TAPEWORMS.

9:20 (57) **K. Jensen**, MORPHOLOGICAL AND MOLECULAR APPROACHES TOWARDS UNDERSTANDING ADULT AND LARVAL ELASMOBRANCH TAPEWORM DIVERSITY.

9:50 **C. P. Goater**. Questions for the panel, summary and closing remarks.

8:00-12:00 HOST- PARASITE INTERACTONS, Salon F

Presiding: A. Didyk, University of New Brunswick, Moncton, NB
L. Durden, Georgia Southern University, Statesboro, GA

Time (Abstract No.)

8:00 (58) **M. N. Saudi**, A. M. Youssef, M. H. Badr, R. Y. Elbayaa, M. Z. El-azzouni, S. F. Mossallam, N. M. Baddour, M. M. Eissa, SYNTHESIS OF SUBSTITUTED PYRIMIDINEDIONE DERIVATIVES AS POTENTIAL SCHISTOSOMICIDAL AGENTS.

8:15 (59) **T. R. Platt**, E. Graf, A. Kammrath, D. A. Zelmer, DIURNAL MIGRATION OF ECHINOSTOMA CAPRONI (DIGENEA: ECHINOSTOMATIDAE) IN THE SMALL INTESTINE OF FEMALE ICR MICE.

8:30 (60) **D. Heins**, E. Birden, J. Baker, HOST MORTALITY AND VARIABILITY IN EPIZOOTICS OF SCHISTOCEPHALUS SOLIDUS INFECTING THE THREESPINE STICKLEBACK, GASTEROSTEUS ACULEATUS.

8:45 (61) **L. Durden**, S. Cannon, SIZE CORRELATIONS BETWEEN SUCKING LICE AND THEIR HOSTS INCLUDING A TEST OF HARRISON'S RULE.

9:00 (62) **M. L. Kent**, P. Rossignol, J. Ferguson, APOPHALLUS SP. METACERCARIAE IN COHO SALMON AND ASSOCIATIONS WITH OVER WINTER SURVIVAL IN A COASTAL RIVER IN OREGON.

9:15 (63) **J. Patonay**, C. A. Hall, THE ENHANCED ABILITY OF THE TYPE IIA STRAIN OF TRYPANOSOMA CRUZI TO BE CONGENITALLY TRANSFERRED IS CORRELATED TO ITS ABILITY TO INFECT PLACENTAL TROPHOBLAST CELLS.

9:30 (64) **W. Bullard**, C. Underhill, N. Acuff, C. A. Hall, EVALUATION OF THE ROLES OF COMPLEMENT AND TEMPERATURE IN AVIAN RESISTANCE TO TRYPANOSOMA CRUZI INFECTION.

9:45 (65) **D. Keeney**, A. Szymaniak, R. Poulin, COMPARATIVE PHYLOGEOGRAPHY OF TWO NEW ZEALAND INTERTIDAL SNAILS AND THEIR TREMATODES

10:00 COFFEE BREAK

10:15 (66) **K. Dittmar**, J. Mayberry, S. Morse, HOST-FINDING BEHAVIOR OF BAT FLIES (DIPTERA: HIPPOBOSCOIDEA).

10:30 (67) **G. Mayer**, CHARACTERIZATION OF PFEXP-250, A NOVEL PLASMODIUM FALCIPARUM EXPORTED PROTEIN.

10:45 (68) **S. E. Bush**, D. Kim, M. Reed, D. H. Clayton, EVOLUTION OF CRYPTIC COLORATION IN ECTOPARASITES.

11:00 (69) **A. Cruz-Reyes**, PREVALENCE OF TOXOCARA SPP. EGGS IN SOME PUBLIC PARKS OF MEXICO CITY.

11:15 (70) **B. Hanelt**, E. S. Loker, TRANSCRIPTOME PROFILES OF INTRAMOLLUSCAN DEVELOPMENTAL STAGES OF SCHISTOSOMA MANSONI IN BIOMPHALARIA GLABRATA.

11:30 (71) **K. Bichoupan**, LOCOMOTION IN BULINUS TRUNCATUS IS ALTERED BY INFECTION WITH SCHISTOSOMA HAEMATOBIUM.

11:45 (72) **M. E. Rowland**, J. Maloney, J. Huang, J. R. Dunn, R. Carpenter, T. F. Jones, A. C. Moncayo, SEROPREVALENCE OF RICKETTSIA IN CANINES FROM TENNESSEE.

8:30-11:45 **42nd COCCIDIOSIS CONFERENCE, Salon E**

Presiding: M.C. Jenkins, Animal Parasitic Diseases Laboratory, USDA
L. Xiao, CDC, Atlanta, GA

Time (Abstract No.)

8:30 (73) **Xin-zhuan Su**, MICROSATELLITE AND ITS APPLICATION IN GENETIC STUDIES OF MALARIA PARASITES.

9:00 (74) **M. E. Grigg**, N. Sundar, M. Miller, J. Wendte, P. Conrad and P. Keeling, VIRULENCE SHIFT IN A SEXUAL CLADE OF WILD TOXOPLASMA GONDII INFECTING MARINE MAMMALS.

9:30 (75) **L. Xiao**, GENETIC CHARACTERIZATIONS OF CRYPTOSPORIDIUM SPP. USING MICROSATELLITE AND MINISATELLITE MARKERS.

10:00 **COFFEE BREAK**

10:15 (76) **A. Tait**, A TALE OF TWO THEILERIAS: MICROSATELLITE GENOTYPING, WILD ANIMAL RESERVOIRS AND VACCINATION.

10:45 (77) **K. B. Miska**, STUDYING GENETIC DIVERSITY IN EIMERIA-PRESENT CHALLENGES AND FUTURE APPROACHES.

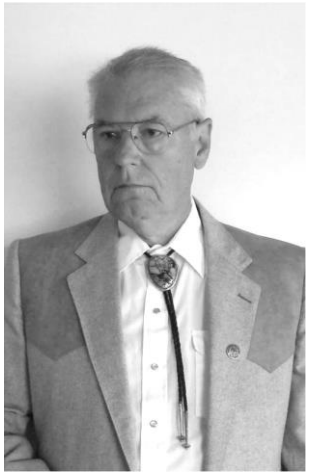
11:15 Roundtable discussion with all participants and audience members.

Thursday Afternoon, 2010-06-24

1:00-2:00 **ASP PRESIDENTIAL ADDRESS, Colorado Grand Ballroom**

Presiding: J. Oaks, University of Wisconsin-Madison, Madison, WI

1:00 Introduction of **Dr. George Cain**.
University of New Mexico, Department of Biology



George Cain, UNM

1:10 (78) **G. Cain**, Sanitizing Sewage Sludge: The Intersection of Parasitology, Civil Engineering and Public Health.

2:15-5:15 **CAUSES AND CONSEQUENCES OF HELMINTH INFECTIONS IN AMPHIBIANS SYMPOSIUM, Salon D**

Presiding: J. Koprivnikar, Brandon University, Canada
P. Johnson, University of Colorado, Boulder, CO
J. R. Rohr, University of South Florida

Time (Abstract No.)

2:15 **J. Koprivnikar, P. Johnson** and **J. R. Rohr**, Opening Remarks.

2:30 (79) **P. Johnson**, PARASITES AS METACOMMUNITIES: USING EXPERIMENTS AND MULTI-SCALE FIELD DATA TO UNDERSTAND VARIATION IN RIBEIROIA INFECTION AND AMPHIBIAN MALFORMATIONS.

2:45 (80) **D. J. Marcogliese**, K. C. King, A. D. Gendron, INTERACTIONS BETWEEN AGRICULTURAL ACTIVITY AND THE PARASITE FAUNA OF FROGS: NOT ALL PARASITES ARE EQUAL.

3:00 (81) **S. A. Orlofske**, R. C. Jadin, D. L. Preston, P. T.J. Johnson, PARASITE TRANSMISSION TO LARVAL AMPHIBIANS IS REDUCED BY ALTERNATIVE NATIVE AND NON-NATIVE HOSTS AND PREDATORS.

3:15 (82) **J. R. Rohr**, N. T. Halstead, J. T. Hoverman, T. McMahon, T. R. Raffel, J. M. Romansic, EFFECTS OF NATURAL AND ANTHROPOGENIC FACTORS ON AMPHIBIAN EXPOSURE AND SUSCEPTIBILITY TO TREMATODE INFECTIONS.

3:30 **COFFEE BREAK**

3:45 (83) **V. J. McKenzie**, LAND USE AND PATTERNS OF PARASITISM IN AMPHIBIAN HOSTS.

4:00 (84) **J. Koprivnikar**, INTERACTIONS OF ENVIRONMENTAL STRESSORS IMPACT SURVIVAL AND DEVELOPMENT OF PARASITIZED LARVAL AMPHIBIANS.

4:15 (85) **S. H. Paull**, P. T.J. Johnson, TEMPERATURE-DRIVEN CHANGES IN RIBEIROIA INFECTION: CONSEQUENCES FOR PARASITE TRANSMISSION AND AMPHIBIAN PATHOLOGY.

4:30 (86) **M. G. Bolek**, INTERACTIONS AMONG ABIOTIC FACTORS, AMPHIBIAN COMMUNITY STRUCTURE AND ADULT HELMINTH LIFE CYCLE STRATEGIES.

4:45 (87) **L. K. Belden**, METAGONIMOIDES OREGONENSIS (FAMILY: HETEROPHYIDAE) INFECTION IN AMPHIBIANS.

5:00 **J. Koprivnikar, P. Johnson** and **J. R. Rohr**, Closing remarks and informal discussion.

2:15-5:00 ECOLOGY I, Salon F

Presiding: N. Negovetich, St. Jude Children's Research Hospital, Memphis, TN
M. Zimmermann, Wake Forest University, Winston-Salem, NC

Time (Abstract No.)

2:15 (88) **M. Barger**, ECOLOGICAL EQUIVALENCE OF TWO TERRESTRIAL SNAILS AS SECOND INTERMEDIATE HOSTS OF PANOPISTUS PRICEI (TREMATODA).

2:30 (89) **C. L. Wall**, M. K. Jones, D. K. Cone, ECOLOGY OF ANGUILLICOLOIDES CRASSUS INFECTING THE AMERICAN EEL (ANGUILLA ROSTRATA) IN CAPE BRETON, NOVA SCOTIA.

2:45 (90) **I. F. Abou El Naga**, M. M. Eissa, S. F. Mossallam, S. I. Abd El-Halim, INHERITANCE OF SCHISTOSOMA MANSONI INFECTION INCOMPATIBILITY IN BIOMPHALARIA ALEXANDRINA SNAILS.

3:00 (91) **J. J. Daly Sr.**, TEMPERATURE QUOTIENT Q10 AND TREMATODE LARVAL STAGES OF EMERGENCE, SURVIVAL, AND INFECTIVITY.

3:15 (92) **J. J. Daly Sr.**, GLOBAL WARMING MEETS PARASITOLOGY: OR NOT?

3:30 COFFEE BREAK

3:45 (93) **T. Sato**, K. Watanabe, N. Tokuchi, H. Kamauchi, Y. Harada, K. D. Lafferty, A NEMATOMORPH PARASITE EXPLAINS VARIATION IN TERRESTRIAL SUBSIDIES TO TROUT STREAMS IN JAPAN.

4:00 (94) **D. Clayton**, J. Malenke, ANTAGONISTIC EFFECTS OF COMPETITION AND CLIMATE MAINTAIN THE DIVERSITY OF AVIAN LICE.

4:15 (95) **D. Clayton**, EXPERIMENTAL DEMONSTRATION OF THE FITNESS COSTS OF AN INTRODUCED PARASITE OF DARWIN'S FINCHES.

4:30 (96) **J. T. Detwiler**, D. J. Minchella, THE TRANSMISSION DYNAMICS OF CLONE ARMIES AND BEYOND: USING GENETIC DIVERSITY TO EVINCE THE COLONIZATION ROUTES OF LARVAL PARASITES.

4:45 (97) **H. M. Archer**, EFFECTS OF FOREST FRAGMENTATION ON THE PREVALENCE OF THE BLOOD PARASITES IN BIRDS OF COSTA RICA.

2:15-5:00 TAXONOMY, SYSTEMATICS, PHYLOGENY, Salon E

Presiding: L. Camp, University of California-Davis, Davis, CA
S. Seville, University of Wyoming, Laramie, WY

Time (Abstract No.)

2:15 (98) **S. A. Nadler**, A. Bieberich, C. Pagan, S. Naem, D. J. Richardson, EVOLUTIONARY GENETICS AND GEOGRAPHIC VARIATION OF BAYLISASCARIS SPECIES IN NORTH AMERICA.

2:30 (99) **R. Carreno**, L. Tuhela, RECOVERY OF 6 SPECIES OF THE THELASTOMATOIDEA (NEMATODA: OXYURIDA) BELONGING TO 6 DIFFERENT GENERA IN A WILD POPULATION OF THE PEPPERED COCKROACH ARCHIMANDRITA TESSELATA.

2:45 (100) **A. Jimenez**, F. Catzeflis, S. L. Gardner, THE PARASITE ASSEMBLAGES OF DIDELPHID MARSUPIALS ARE CLADE SPECIFIC.

3:00 (101) **T. Ruhnke**, J. Caira, RE-DISCOVERY OF PITHOPHORUS TETRAGLOBUS AND PHYLLOBOTHRIUM MINIMUM IN RHYNCHOBATUS DJIDDENSIS.

3:15 (102) **O. M. Amin**, UNUSUAL FEATURES IN THE ACANTHOCEPHALA AS REVEALED BY SEM AND TEM.

3:30 **COFFEE BREAK**

3:45 (103) **P. Hunt**, S. Cowen, T. Ruhnke, TAXONOMY OF ANTHOCEPHALUM SPECIES COLLECTED FROM SENEGAL, NORTHERN AUSTRALIA AND BORNEO.

4:00 (104) **F. Reyda**, HELMINTH DIVERSITY IN FISHES FROM OTSEGO LAKE, NEW YORK.

4:15 (105) **S. Brant**, E. S. Loker, DIVERSIFICATION OF SCHISTOSOMES: A SEARCH FOR PATTERNS.

4:30 (106) **R. E. Clopton**, T. J. Cook, J. J. Cielocha, REVISION OF NUBENOCEPHALUS: CANALIZATION, PLASTICITY, AND MORPHOMETRIC CHARACTER ANALYSIS IN GREGARINE TAXONOMY.

4:45 (107) **R. P. Scheibel**, F. A. Jiménez, EVALUATION OF SYNLOPHE AND BURSA AS TAXONOMIC CHARACTERS FOR VIANNAIINAE (NEMATODA: TRICHOSTRONGYLOIDEA).

Thursday Evening, 2010-06-24

5:45 PM - 9:00 PM **Evening at the Cheyenne Mountain Zoo**

Friday Morning, 2010-06-25

8:30-10:30 **Authors complete poster setup**

8:00-10:30 ECOLOGY II, Salon F

Presiding: K. Lafferty, University of California-Santa Barbara, Santa Barbara, CA
T. Platt, St. Mary's College, Notre Dame, IN

Time (Abstract No.)

8:00 (108) **C. E. Matisz,** C. P. Goater, MIGRATION, SITE SELECTION, AND DEVELOPMENT OF ORNITHODIPLOSTOMUM SP. METACERCARIAE (DIGENEA:STRIGEOIDEA) IN FATHEAD MINNOWS (PIMEPHALES PROMELAS).

8:15 (109) **J. T. Detwiler,** C. D. Criscione, UNEXPECTED ASEXUAL REPRODUCTION IN A TAPEWORM.

8:30 (110) **L. Aguirre-Macedo**, V. M. Vidal-Martínez, R. F. Hechinger, A. M. Kuris, TEMPORAL PATTERNS IN TREMATODE COMMUNITIES OF THREE GASTROPOD SPECIES FROM CELESTÚN, YUCATAN, MEXICO.

8:45 (111) **M. Torchin**, O. Miura, LATITUDINAL PATTERNS OF PARASITISM IN CONGENERIC MUD SNAILS IN THE ATLANTIC AND PACIFIC OCEAN.

9:00 (112) **R. F. Hechinger**, A. C. Wood, A. M. Kuris, EUSOCIALITY IN A FLATWORM: TREMATODE PARTHENITAE FROM SOLDIER AND REPRODUCTIVE CASTES.

9:15 (113) **I. D. Buller**, D. J. Larson, S. A. Orlofske, P. T.J. Johnson, A LOADED TOAD: PARASITE COMMUNITIES OF JUVENILE WESTERN TOADS (ANAXYRUS BOREAS) FROM CALIFORNIA AND OREGON.

9:30 (114) **S. E. Bush**, PARASITE DIVERSITY IN CHINA: CANARY LICE IN A COAL MINE.

9:45 (115) **V. M. Vidal Martinez**, L. Aguirre-Macedo, J. McLaughlin, A. Jaramillo, J. C. Shaw, A. K. James, K. D. Lafferty, A. M. Kuris, DIGENEAN SPECIES RICHNESS AND COMPOSITION OF PALMYRA ATOLL FISHES, EASTERN INDO-PACIFIC.

10:00 (116) **B. L. Fredensborg**, A. Silva, L. Garza, DEFYING THE RED QUEEN? REPRODUCTIVE STRATEGIES AND PARASITE INFECTIONS IN ASEXUAL AND SEXUAL MOLLIES IN THE RIO GRANDE VALLEY.

10:15 (117) **K. A. Hopperstad**, B. L. Fredensborg, PARASITES AND HOST ENERGETICS: EFFECTS OF A PARASITIC CASTRATOR ON CONSUMPTION AND METABOLISM IN AN AQUATIC SNAIL HOST.

10:30 - Noon POSTERS, COFFEE, SNACKS, FOOTHILLS

All authors must stand with your posters from 10:30-Noon.

BIOCHEMISTRY, PHYSIOLOGY

118 **S. S. Ray**, MECHANISM OF REGULATION OF TRYPANOSOMA BRUCEI ACETYL-COA CARBOXYLASE, THE KEY ENZYME FOR INITIATION OF FATTY ACID SYNTHESIS.

CELL BIOLOGY

119 **M. K. Larson**, R. C. Bender, C. J. Bayne, SELECTION AND EVALUATION OF REFERENCE GENES FOR SYBR GREEN QPCR STUDIES WITH HEMOCYTES FROM THE PULMONATE SNAIL, BIOMPHALARIA GLABRATA.

ECOLOGY

120 **K. L. Sheehan**, INTESTINAL PARASITES OF THE DOUBLE-CRESTED CORMORANT (PHALACROCORAX AURITUS), FROM NORTHERN ALABAMA, USA.

121 **B. F. Sears**, EVIDENCE THAT CERCARIAE CHOOSE THE MOST SUSCEPTIBLE AMPHIBIAN HOST SPECIES AND INDIVIDUALS.

GENETICS & MOLECULAR BIOLOGY

122 **K. Caban**, A. Mousley, A. G. Maule, A. M. Espino, DEVELOPMENTAL EXPRESSION AND SILENCING OF SAPOSIN AND FERRITIN LIKE ANTIGENS IN FASCIOLA HEPATICA.

HOST PARASITE INTERACTIONS

123 **S. Redón**, N. Berthelemy-Okazaki, B. Georgiev, G. Vasileva, P. Nikolov, F. Hontoria, F. Amat, CESTODES AND THE SUCCESS OF AN INVASION: THE CASE OF THE AMERICAN BRINE SHRIMP ARTEMIA FRANCISCANA IN A MEDITERRANEAN SALTERN.

124 **W. S. Buzetti**, M. da Silva Tenorio, M. F. Alves, M. dos Santos Paixao, D. T. da Silva, K. I. Tasca, N. M. de Queiroz, J. de Assis,VISCERAL LEISHMANIASIS IN CAPTIVE FOX CERDOCYON THOUS (CARNIVORA, CANIDAE).

125 **M. Amri**, C. Touil-Boukoffa, EVASION STRATEGIES OF ECHINOCOCCUS GRANULOSUS TO TH1 HOST PROTECTIVE RESPONSE DURING HUMAN INFECTION.

126 **J. A. Ferguson**, K. Woodberry, C. M. Gillin, D. H. Jackson, J. L. Sanders, W. Madigan, R. J. Bildfell, M. L. Kent, CYLICOSPIRURA SPECIES (NEMATODA:SPIROCERCIDAE) AND STOMACH NODULES IN COUGARS (PUMA CONCOLOR) AND BOBCATS (LYNX RUFUS) IN OREGON.

IMMUNOLOGY

127 **M. Amri**, C. Touil-Boukoffa, INTERLEUKIN 17 STIMULATES MONONUCLEAR CELLS TO KILL ECHINOCOCCUS GRANULOSUS PROTOSCOLECES BY NO-DEPENDENT MECHANISM.

128 **O. Figueroa,** A. Espino, POSSIBLE ROLE FOR TOLL LIKE RECEPTORS IN INTERACTION OF FASCIOLA HEPATICA EXCRETORY/SECRETORY PRODUCTS WITH MONOCYTE CELLS.

LIFE CYCLES & EPIDEMIOLOGY

129 **S. Ganguly**, INCIDENCE AND DIAGNOSIS OF PARASITIC ETIOLOGIES AMONG A SURVEILLANCE STUDY GROUP FROM INFECTIOUS DISEASE HOSPITAL, KOLKATA, INDIA.

TAXONOMY, SYSTEMATICS, PHYLOGENY

130 **J. Forest**, A TAXONOMIC REVISION OF OCTOMACRUM.

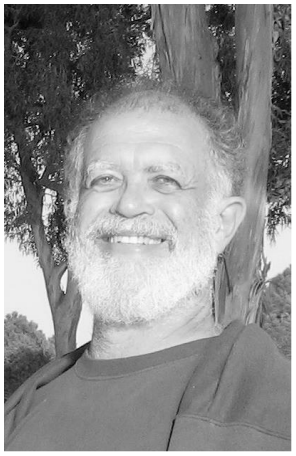
131 **B. Dixon**, J. Tetro, M. Ndao, S. Bidawid, J. Farber, THE FOOD AND ENVIRONMENTAL PARASITOLOGY NETWORK (FEPN) IN CANADA.

132 **C. M. Wiles**, F. Reyda, THE GREGARINE PARASITES OF ODONATA IN OTSEGO COUNTY (NEW YORK).

133 **M. Bergman**, L. Hendricks, F. Reyda, HOST USE AND MORPHOLOGICAL VARIATION OF LEPTORHYNCHOIDES THECATUS FROM OTSEGO LAKE, NEW YORK.

134 **L. E. Camp**, C. Pagan, S. A. Nadler, MOLECULAR SYSTEMATICS OF GEOGRAPHIC ISOLATES OF DAUBAYLIA SPP.

Friday Afternoon, 2010-06-25



Armand Kuris, UCSB

1:00 PM - 2:30 PM **ASP Awards and Business Meeting, Colorado Grand Ballroom**

ASP AWARDS

CLARK P. READ MENTOR AWARD LECTURE

Presiding: C. Criscione, Texas A&M University, College Station, TX

Time (Abstract No.)

1:00 **M. Torchin, V. McKenzie**. Introduction of Dr. ARMAND KURIS, University of California, Santa Barbara.

1:10 (135) **A. Kuris**. CLARK P. READ MENTOR AWARD LECTURE.

Dawn Roellig, CDC

ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: C. Davis, Western Kentucky University, Bowling Green, KY

The recipient of the 2010 New Investigator Award is **Dr. DAWN ROELLIG**, CDC, Atlanta, GA.

WILLIS A. REID JR., STUDENT RESEARCH GRANT AWARDS

Presiding: L. Couch, University of New Mexico, Albuquerque, NM

BEST STUDENT PRESENTAIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: Agustin Jimenez, Southern Illinois University, Carbondale, IL

ASP BUSINESS MEETING

Presiding: G. Cain, University of New Mexico, Albuquerque, NM

Thank you for attending this year's ASP meeting and have a safe trip home.
See you June 1-4, 2011 at our next meeting in Anchorage, AK!

Abstract Listings

Paper No.	Title	Authors
1	Two Giant Proteases in an Early-Divergent Parasite, Giardia intestinalis.	J. Chaparro-Gutiérrez, M. Wasserman
2	Nucleolar Localization of SmMAK16 Protein from Schistosoma mansoni is Not Effected by pH or Phosporylation.	E. Hoellerich, C. Dunagan, D. Maring, Y. Wong, T. Albert, J. Milhon
3	Acetyl-CoA Carboxylase of Trypanosoma brucei: A New Drug Target for Treatment of African Trypanosomiasis.	P. Vigueira, K. Paul
4	Infection Dynamics of Daubaylia potomaca (Nematoda: Rhabditida) in Helisoma anceps.	M. Zimmermann, K. Luth, G. Esch
5	Factors Influencing the Community Composition of Parasitic and Free-Living Nematodes in a Fresh-Water System.	K. Luth, M. Zimmermann, G. Esch
6	Presence of Ribeiroia ondatrae in the Developing Anuran Limb Disrupts the Retinoic Acid Signaling Cascade.	D. Szuroczki
7	Comparative Susceptibility of Aedes aegypti and Anopheles gambiae Mosquitoes to Bacterial Infection.	S. Coggins, J. Hillyer
8	Helminth and Leech Community Structure in Two Species of Sympatric Larval Amphibians from Western Nebraska.	H. Tracy, M. Bolek
9	Observations on the Nematode Gyrinicola batrachiensis (Oxyuroidea: Pharyngodonidae) in Eight Species of Larval Amphibians from Nebraska.	H. Tracy, M. Bolek
10	Stream Morphology, Niche Use, and Other Factors Determining the Distribution of Dactylogyrus spp. (Monogenea) on Native North American Cyprinids.	A. Knipes, J. Janovy, Jr.
11	The Body Sizes of Cymothoid Isopod Parasites.	R. Fogelman
12	Role of Environmental Factors in Structuring Endohelminth Communities in the Western Mosquitofish, Gambusia affinis.	H. Robinson, M. Barger, T. Cook
13	Phylogenetic Relationships of Blood Parasites in the Avifauna of Socorro Island, México.	J. Carlson
14	Impacts of Multiple Parasite Species Infection on Oregon	J. Ferguson, J. Romer, C. Schreck,

	Coastal Juvenile Coho Salmon (Oncorhynchus kisutch).	M. Kent
15	Trematode-Induced Oxidative Stress in Liver Tissue of Minnows Exposed to Ornithodiplostomum sp. Cercariae.	A. Stumbo
16	Transmission Biology of the Lancet Liver Fluke (Dicrocoelium dendriticum) Among Potential Definitive Hosts in Western Alberta, Canada.	M. Thomson, C. Goater, D. Colwell
17	Changes in Atlantic Salmon and Cod Epidermal Mucus Proteins in Response to Stress.	R. Easy
18	Identification and Partial Characterization of an Eimeria Specific Protein.	R. Fetterer, R. Schwarz, K. Miska, M. Jenkins
19	Abdominal Contractions Facilitate Extracardiac Retrograde Hemolymph Propulsion in the Mosquito Hemocoel.	J. Hillyer, J. Andereck, J. King
20	High Prevalence of Borrelia burgdorferi in Ticks Recovered from Raccoons and Opossums Trapped in Kentucky.	K. Tackett, C. Davis
21	Effects of Temperature on Transmission of Yersinia pestis by the Flea, Xenopsylla cheopis.	S. Vetter, J. Holmes, J. Montenieri, C. Graham, M. Woods, R. Eisen, K. Gage
22	Molecular Epidemiology of Cryptosporidiosis Among HIV-Infected Subjects in Benin City, Edo State, Nigeria.	F. Akinbo, C. Okaka, R. Omoregie, L. Xiao
23	Role of Ancylostoma caninum Transcription Factor DAF-16/FoxO During the Rescue of Developmental Arrested Larvae.	V. Gelmedin
24	Characterization of Giardin Protein Expression During Encystation of Giardia duodenalis Trophozoites to Cysts.	M. Jenkins
25	Prophylactic Effect of Bovine Lactoferrin against Acute Toxoplasmosis in Immunocompetent and Immunosuppressed Mice.	S. Mossallam
26	Immunoblot Profiles of Serum from Patients with Ocular Angiostrongyliasis Against Male and Female Extracts.	S. Raiyawa, R. Chawengkirttikul
27	Antimicrobial Function of Sessile Hemocytes in the Mosquito Hemocoel.	J. Hillyer, J. King
28	Trypanosoma carassii Calreticulin Binds Host Complement Component C1q and inhibits Classical Complement Pathway-Mediated Lysis.	A. Oladiran, M. Belosevic
29	Microarray Analyses of Schistosoma mansoni Treated with Praziquantel.	J. Hines, P. Cupit, A. Aragon, C. Cunningham
30	Three Different Models of Biomphalaria glabrata Resistance to Trematode Infection: Common Underlying Patterns Based on Microarray Studies.	M. Forys, P. Hanington, C. Lun, C. Adema, E. Loker
31	Functional Characterization of FREP3: a Fibrinogen Related Protein Associated with Trematode Resistance in Biomphalaria glabrata.	P. Hanington, M. Forys, C. Adema, E. Loker
32	Biochemical and Immunological Insights into Schistosome Host Invasion and Development.	J. McKerrow
33	Role of Signaling in Schistosome Male-Female Interactions.	Philip LoVerde
34	Schistosome Diversity.	Eric Loker, Sara Brant
35	**Stoll Stunkard Lecture**	J. Carlton

36	Transmission Dynamics of Two Strains of Schistosoma mansoni Utilizing Novel Hosts.	O. Jones-Nelson, D. Minchella
37	The Innate Hepatic Response to Ascaris suum Infection in the Mouse Model.	C. Dold, J. Cassidy, C. O'Farrelly, C. Holland
38	Investigating the Validity of Two Questionable Lecanicephalidea Genera: Hexacanalis and Cephalobothrium.	J. Cielocha, K. Jensen
39	Molecular Basis for Host Specificity in Avian Malaria.	C. Martinez,
40	A Cestode Test of Newly Circumscribed Species Boundaries in the Sharks Squalus acanthias and Squalus suckleyi.	M. Pickering, J. Caira
41	Phylogenetic Relationships of Ectoparasitic Mites (Acari:Erythraeoidea) on Argentine Walking Sticks (Insecta:Phasmida).	E. DiBlasi, K. Dittmar,
42	A Phylogenetic Re-Assessment of Hybridization Events and Species Boundaries within Trypanosoma cruzi.	M. Pinto
43	Characterization of Novel PEXEL-Negative P. falciparum Exported Protein, PfEXP250.	S. Jean
44	Prevalence of Malaria and Anaemia Among HIV Infected.	F. Akinbo
45	Emergence and Control of Geohelminths in Historic Albany, NY, 1640-1920.	K. Reinhard
46	Trypanosoma cruzi in the United States: Molecular and Biological Characteristics of Sylvatic Isolates.	D. Roellig
47	The Role of Damselflies (Odonata: Zygoptera) as Paratenic Hosts in the Transmission of Halipegus eccentricus (Digenea: Hemiuridae) to Anurans.	M. Bolek, H. Tracy
48	Metacestodes of Bait Shrimp in the Gulf of Mexico.	J. Payne, J. Gunderson
49	Cyclospora cayetanensis, Cryptosporidium spp. and Giardia duodenalis in Packaged Ready-To-Eat Salads and Leafy Greens from a Sentinel Site in Ontario, Canada.	B. Dixon, L. Parrington, A. Cook, F. Pollari, J. Farber
50	Detection of Some Intestinal Protozoa in Commercial Fresh Juices.	S. Mossallam
51	Panulirus argus (Latreille, 1804) from Batabano Gulf, Cuba, Parasitized by Cymatocarpus solearis (BRACHYCOELIDAE-METACERCARIA).	Y. Cruz, L. Aguirre-Macedo, V. Vidal-Martínez
52	On-Line Cestode Database Resources.	J. Caira
53	EuPathDB –A Eukaryotic Pathogen Database of Protist “Omics” Data.	J. Kissinger
54	Associate Editor’s Symposium – 2010	G. Esch, C. Goater
55	C. elegans as a Model Organism for Anthelmintic Research: Prospects and Pitfalls.	T. Geary
56	Putting Parasitism in Perspective: Lessons from Larval Tapeworms.	A. Shostak
57	Morphological and Molecular Approaches Towards Understanding Adult and Larval Elasmobranch Tapeworm Diversity.	K. Jensen
58	Synthesis of Substituted Pyrimidinedione Derivatives as	M. Saudi, A. Youssef, M. Badr,

	Potential Schistosomicidal Agents.	R. Elbayaa, M. El-azzouni, S. Mossallam, N. Baddour, M. Eissa
59	Diurnal Migration of Echinostoma caproni (Digenea: Echinostomatidae) in the Small Intestine of Female ICR Mice.	T. Platt, E. Graf, A. Kammrath, D. Zelmer
60	Host Mortality and Variability in Epizootics of Schistocephalus solidus Infecting the Threespine Stickleback, Gasterosteus aculeatus.	D. Heins, E. Birden, J. Baker
61	Size Correlations Between Sucking Lice and their Hosts Including a Test of Harrison's Rule.	L. Durden, S. Cannon
62	Apophallus sp. Metacercariae in Coho Salmon and Associations with Over Winter Survival in a Coastal River in Oregon.	M. Kent, P. Rossignol, J. Ferguson
63	The Enhanced Ability of the Type IIa Strain of Trypanosoma cruzi to be Congenitally Transferred is Correlated to Its ability to Infect Placental Trophoblast Cells.	J. Patonay, C. Hall
64	Evaluation of the Roles of Complement and Temperature in Avian Resistance to Trypanosoma cruzi Infection.	W. Bullard, C. Underhill, N. Acuff, C. Hall
65	Comparative Phylogeography of Two New Zealand Intertidal Snails and Their Trematodes.	D. Keeney, A. Szymaniak, R. Poulin
66	Host-Finding Behavior of Bat Flies (Diptera: Hippoboscoidea).	K. Dittmar, J. Mayberry, S. Morse
67	Characterization of PfEXP-250, a Novel Plasmodium falciparum Exported Protein.	G. Mayer
68	Evolution of Cryptic Coloration in Ectoparasites.	S. Bush, D. Kim, M. Reed, D. Clayton
69	Prevalence of Toxocara spp. Eggs in Some Public Parks of Mexico City.	A. Cruz-Reyes
70	Transcriptome Profiles of Intramolluscan Developmental Stages of Schistosoma mansoni in Biomphalaria glabrata.	B. Hanelt, E. Loker
71	Locomotion in Bulinus truncatus is Altered by Infection with Schistosoma haematobium.	K. Bichoupan
72	Seroprevalence of Rickettsia in Canines from Tennessee.	M. Rowland, J. Maloney, J. Huang, J. Dunn, R. Carpenter, T. Jones, A. Moncayo
73	Microsatellite and Its Application in Genetic Studies of Malaria Parasites.	Xin-zhuan Su
74	Virulence Shift in a Sexual Clade of Wild Toxoplasma gondii Infecting Marine Mammals.	N. Sundar, M. Miller, J. Wendte, P. Conrad, P. Keeling, M. Grigg
75	Genetic Characterizations of Cryptosporidium spp. Using Microsatellite and Minisatellite Markers.	L. Xiao
76	A Tale of Two Theilerias: Microsatellite Genotyping, Wild Animal Reservoirs and Vaccination.	A. Tait
77	Studying Genetic Diversity in Eimeria-Present Challenges and Future Approaches.	K. Miska
78	**ASP President's Address**	G. Cain
79	Parasites as Metacommunities: Using Experiments and	P. Johnson

	Multi-Scale Field Data to Understand Variation in Ribeiroia Infection and Amphibian Malformations.	
80	Interactions Between Agricultural Activity and the Parasite Fauna of Frogs: Not All Parasites Are Equal.	D. Marcogliese, K. King, A. Gendron
81	Parasite Transmission to Larval Amphibians is Reduced by Alternative Native and Non-Native Hosts and Predators.	S. Orlofske, R. Jadin, D. Preston, P. Johnson
82	Effects of Natural and Anthropogenic Factors on Amphibian Exposure and Susceptibility to Trematode Infections.	J. Rohr, N. Halstead, J. Hoverman, T. McMahon, T. Raffel, J. Romansic
83	Land Use and Patterns of Parasitism in Amphibian Hosts.	V. McKenzie
84	Interactions of Environmental Stressors Impact Survival and Development of Parasitized Larval Amphibians.	J. Koprivnikar
85	Temperature-Driven Changes in Ribeiroia Infection: Consequences for Parasite Transmission and Amphibian Pathology.	S. Paull, P. Johnson
86	Interactions Among Abiotic Factors, Amphibian Community Structure and Adult Helminth Life Cycle Strategies.	M. Bolek
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135	**Clark P. Read Mentor Award**	A. Kuris

1

TWO GIANT PROTEASES IN AN EARLY-DIVERGENT PARASITE, GIARDIA INTESTINALIS

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Giardia intestinalis is a protozoan parasite that causes a diarrheal disease in humans and animals worldwide. Moreover, *G. intestinalis* is considered an excellent model to study mechanisms involved in evolution of fundamental cellular processes of eukaryotic cells, because it represents the earliest divergent lines in the evolution of eukaryotic organisms. The *G. intestinalis* life cycle alternates between a vegetative form and an infectious cyst form. Encystation and excystation are crucial processes for the survival and transmission of this parasite and involves profound morphological and biochemical changes. These changes include specific degradation of proteins. Previous studies in our laboratory have shown that *G. intestinalis* has genes that code for components of the ubiquitin-proteasome system (UPS) and some of these are expressed during the life cycle of this protozoan. To address the question, what is the functionality of the UPS during *G. intestinalis* encystation?, we first evaluated the ubiquitination patterns, using a immunoblotting assays with a specific anti-ubiquitin antibody. Then, we quantified the proteasome-like activity in whole and fractionated protein extracts, using activity assays with fluorogenic peptides. Finally, we evaluated the effects of the proteasome inhibitors (MG132 and epoxomicin) on ubiquitination patterns, efficiency and quality of the encystation process. Interestingly our results show the presence of characteristic ubiquitination patterns and activity of proteasome 20S during encystation process. We demonstrated that the proteasome participate in turnover of cellular proteins via the ubiquitin pathway and its inhibition affect the quality of cysts produced. Moreover, we reported the presence of a new proteasome-like activity, which is up regulated during the encystation and its activity is essential for the stage-specific transformation. These results suggest the presence and activity of two giant proteases that probably have redundant roles in the UPS of this antique eukaryote.

2

NUCLEOLAR LOCALIZATION OF SMMAK16 PROTEIN FROM SCHISTOSOMA MANSONI IS NOT EFFECTED BY PH OR PHOSPORYLATION

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T. Albert, Roche NimbleGen Inc. and **J. Milhon**, Azusa Pacific University

SmMAK16 from the trematode *S. mansoni* is a protein that is known to localize in the nucleolus. Recent findings show that *Sm*MAK16 is involved in 60S ribosomal subunit synthesis. Parts of *Sm*MAK16 were cloned into plasmids in frame with Green Fluorescent Protein (GFP), and transfected into Cos-7 cells to isolate signals responsible for cellular localization. *Sm*MAK16 was found to contain two nuclear localization signals (NLS) and a separate nucleolar localization signal (NoLS). One of the NLSs contains a sequence identical to a published pH-dependent

nucleolar retention signal. The published signal directed proteins to the nucleolus only under acidic conditions. *Sm*MAK16/GFP constructs were transfected into Cos-7 cells and the cells were then transferred to acidic conditions; however, we found that it did not affect localization in *Sm*MAK16. It has also been reported that CKII can phosphorylate *Sm*MAK16 near one of the NLS at a site identical to one found in the SV40 LTA. Phosphorylation of this site in the SV40 LTA regulates the kinetics of the nearby NLS. To discover if kinetic regulation also occurs in *Sm*MAK16 mutant and wild type *Sm*MAK16 proteins were purified, phosphorylated, and injected into individual Cos-7 cells. Fluorescent images were then taken over time. No difference in the rate of transport was found between wild type and mutant *Sm*MAK16 proteins. Therefore, *Sm*MAK16 localizes to the nucleolus using three separate signals, two NLS and one NoLS, however, these signals are not affected by pH or phosphorylation at an adjacent CKII site.

3

ACETYL-COA CARBOXYLASE OF TRYPANOSOMA BRUCEI: A NEW DRUG TARGET FOR TREATMENT OF AFRICAN TRYPANOSOMIASIS

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Trypanosoma brucei is an early-branching, protozoan parasite transmitted by the tsetse fly to its mammalian hosts. The parasite causes fatal disease in humans and livestock. Current drugs are highly toxic and drug resistance is a growing problem. Vaccine development is confounded by the parasite's ability to undergo antigenic variation. Thus, investigation into novel drug targets is urgently needed. The parasite uses an unconventional elongase (ELO) pathway as the predominant mechanism of fatty acid synthesis. The ELO pathway is essential in both mammalian bloodstream (BSF) and tsetse fly procyclic forms (PCF), and is modulated in response to the availability of exogenous lipids. The two-carbon donor for the ELO pathway is malonyl-CoA, which is synthesized from acetyl-CoA by Acetyl-CoA Carboxylase (ACC). The *T. brucei* ACC protein sequence predicts a soluble cytosolic protein. Immunofluorescence microscopy and subcellular fractionation of myc-tagged ACC shows a cytoplasmic punctate pattern that does not co-localize with any marker proteins. These localization studies indicate a novel cytoplasmic localization pattern for ACC. We hypothesize ACC regulates the ELO pathway by controlling the availability of malonyl-CoA. To test our hypothesis, we generated ACC RNAi mutant cell lines that reduced ACC enzymatic activity (87% in BSF and 93% in PCF) resulting in a reduction in total ELO activity. Interestingly, induction of ACC RNAi in PCF parasites grown in normal media caused no growth defect. However, ACC knock down in low lipid media resulted in a 65% reduction in growth rate and was rescued by the addition of 35uM stearate. These data suggest the parasite is most dependent on the FAS pathway when exogenous lipids are limited. TOFA and Haloxyfop, two pharmacological inhibitors of ACC, were also effective in slowing parasite growth. *In vivo* studies demonstrate ACC to be essential in BSF parasites. RNAi of ACC resulted in delayed mortality in a murine model. This firmly validates ACC as pharmacological target for the treatment of African trypanosomiasis.

4

INFECTION DYNAMICS OF DAUBAYLIA POTOMACA (NEMATODA: RHABDITIDA) IN HELISOMA ANCEPS

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Daubaylia potomaca is an unusual parasite for a number of reasons. Specifically, it has a direct life cycle in which it uses a planorbid snail, *Helisoma anceps*, as the definitive host. Additionally, adult females have been shown to be both the infective stage, and the only stage documented to be shed from a live, infected host. Finally, adults, juveniles, and eggs have been observed in all tissues and blood spaces of the host, suggesting the parasite consumes and actively migrates through host tissue. The current study examined the population and infection dynamics of *D. potomaca* in Mallard Lake, a 4.9 ha public access pond in the Piedmont Region of North Carolina. In particular, this study determined the role of seasonality and co-infections with other parasites in the system on the prevalence and mean intensity of infection of *D. potomaca* in the snail host. Data collected from August 2008 to October 2009 suggest that prevalence and mean intensity were inversely related in the spring and fall. Prevalence in the fall of 2008 dropped to 10.3% while the mean intensity reached 52.4 ± 8.9 worms/infected host. However, prevalence jumped to 47.3% in March (2009) while mean intensity (3.1 ± 0.3 worms/infected host) was low. Co-infections of *D. potomaca* with an array of trematode parasites and a commensal, *Chaetogaster limnaei limnaei*, were found to have little impact on the infection dynamics of *D. potomaca* throughout the study. Analysis showed that snails infected with *D. potomaca* lived for a significantly shorter period of time under lab conditions than snails not infected with the parasite ($P<0.002$). However, the reproductive capabilities of the snail hosts were not affected by the presence of the nematode parasite in either the total number of eggs laid ($P>0.282$) or clutch size ($P>0.296$).

5

FACTORS INFLUENCING THE COMMUNITY COMPOSITION OF PARASITIC AND FREE-LIVING NEMATODES IN A FRESH-WATER SYSTEM

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A large number of studies have been undertaken to resolve the patterns of distribution and abundance of nematodes in marine and terrestrial habitats, however, relatively few exist for fresh-water systems. The current study sought to determine whether patterns of distribution, prevalence, and abundance existed for the nematode community in this system, and further, to determine what factors were driving such patterns. Focus was placed on the influences that seasonality, substratum-type, and nematode life history (feeding-type) have on these measures. Samples were collected from Mallard Lake, a 4.9 ha, eutrophic, public-access pond in the Piedmont region of NC over a 10 mo period (from 29 Jan to 18 Oct 2009). In total, 480 samples

were collected and placed in individual Baermann apparatus to isolate any nematodes. Nematodes were enumerated and categorized based on morphology, i.e., morphotyped. Overall, 2349 nematodes, belonging to 45 different morphotypes, were observed. Four morphotypes were parasitic (P), and accounted for 0.4% of the total number of nematodes identified. Of the remaining nematodes, 44.6% were designated as deposit feeders/swallowers (DF), 32.7% were chewers (C), 15.7% were suction feeders (SF), and 6.6% were epistrate feeders (EF). The mean abundance of P observed increased seasonally from spring to autumn, though the trend was not significant (P=0.10). Substratum-type did not significantly influence the prevalence of P (P=0.244); however, it did have a significant impact on the prevalence of C (P=0.00) and SF (P=0.00). Mean P abundance was not significantly influenced by substratum-type either (P=0.14-0.86). The mean abundance of C, however, was significantly greater in mixed substratum than mud/algae (P=0.04) or leaf (P=0.04). Additionally, the mean abundance of SF was significantly greater in mixed substratum than in leaf (P=0.00), mud/algae (P=0.01), and mud/clay (P=0.03). A combination of feeding behavior and substratum-type is likely driving the patterns observed in this system.

6

PRESENCE OF RIBEIROIA ONDATRAE IN THE DEVELOPING ANURAN LIMB DISRUPTS THE RETINOIC ACID SIGNALING CASCADE

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Increasing incidences of malformed frogs has sparked the interest of scientists worldwide to try and determine the causes of such grotesque malformations. *Ribeiroia ondatrae* is a digenetic trematode which has been implicated as one such cause, as this parasite encysts within the developing hind limb bud and inguinal region causing dramatic limb malformations. Currently, the mechanism involved in parasite induced limb deformities remains unclear; however, mechanical perturbation has been the prevailing hypothesis. In addition to parasitism and mechanical perturbation, environmental chemical pollutants have also been implicated as a possible explanation for the limb malformations. However, a third hypothesis exists which has received very little attention namely, the possibility that the parasite itself may modify the endogenous host growth factors to induce limb deformities. We sought to investigate whether endogenous retinoic acid a growth factor known to play a critical role in limb bud formation, is altered by the presence of *R. ondatrae* within the infected tadpole. Here we show through HPLC that limb bud tissue which has been parasitized contains 70% more retinoic acid compared to the control. Furthermore, encysted parasites or metacercariae, appear to contain substantially less retinoic acid (56%) than the free swimming cercariae. Taken together, these data illustrate for the first time that upon encystment, *R. ondatrae* may release retinoic acid into the host disrupting endogenous developmental cues in an effort to facilitate quicker transmission success into the definitive host.

7

COMPARATIVE SUSCEPTIBILITY OF AEDES AEGYPTI AND ANOPHELES GAMBIAE MOSQUITOES TO BACTERIAL INFECTION

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Mosquitoes defend themselves against invading pathogens by deploying a variety of cellular and humoral immune responses. Although many studies have characterized these responses in individual mosquito species, interspecific comparisons of immune responses are largely lacking. This study sought to compare the immune competencies of two mosquito species, *Aedes aegypti* and *Anopheles gambiae*, by observing their responses to bacterial infection. Initial experiments aimed to determine whether differences existed between the abilities of these two mosquito species to survive bacterial infections. Following infection with *Escherichia coli, Ae. aegypti* displayed greater survival when compared to *An. gambiae.* This survival correlated with quantitative analyses of bacterial killing, which showed that *Ae. aegypti* is more capable than *An. gambiae* at killing intrathoracically injected bacteria. In efforts to uncover mechanisms behind *Ae. aegypti*'s increased immune competence we began by assaying phagocytosis, which is a primary cellular immune response in the mosquito hemocoel. Assays of phagocytic activity within mosquito hemocytes demonstrated that both species are readily able to phagocytose large numbers of *E. coli*. However, preliminary data suggests that while *Ae. aegypti* hemocytes exhibit lower phagocytic indices, they are capable of internalizing larger numbers of bacteria than *An. gambiae* hemocytes. Together, these results show *Ae. aegypti*'s superiority over *An. gambiae* in resisting bacterial infection and reemphasize the integral role of phagocytosis as a rapidly-responding component of the mosquito's antibacterial defense.

8

HELMINTH AND LEECH COMMUNITY STRUCTURE IN TWO SPECIES OF SYMPATRIC LARVAL AMPHIBIANS FROM WESTERN NEBRASKA

H. Tracy and **M. Bolek**, Oklahoma State University

Currently no comparative studies exist on helminth community structure among sympatric tadpoles and salamander larvae. During June-August 2008-2009 we examined 50 bullfrog tadpoles, *Rana catesbeiana*, and 50 barred tiger salamander larvae, *Ambystoma tigrinum mavortium*, from Nevens Pond, Keith County, Nebraska for leech and helminth infections. The helminth and leech compound community of this larval amphibian assemblage consisted of at least 7 species: 4 in bullfrog tadpoles and 4 in barred tiger salamander larvae. The component community of bullfrog tadpoles was dominated by helminths acquired through active penetration, and/or incidentally ingested through respiratory currents and/or feeding on algae; whereas the component community of larval salamanders was dominated by helminths acquired through ingestion of intermediate hosts (χ^2 = 3,455.00, $P < 0.00001$). As a result of the longer developmental time of bullfrog tadpoles (2-3 years) verses a shorter developmental time of salamander larvae (2-5 months) and the ephemeral nature of

intermediate hosts in Nevens Pond, bullfrog tadpoles had significantly higher mean helminth species richness than larval salamanders ($t' = 12.31, P < 0.0001$). Differences in the herbivorous and carnivorous diet and time to metamorphosis among bullfrog tadpoles and barred tiger salamander larvae were important factors in structuring helminth communities among these sympatric larval amphibian species; whereas amphibian size was important in structuring helminth and leech communities in larval salamanders but not in bullfrog tadpoles. (Supported by NIH grant number 1 P20 RR16469 from the INBRE Program of the National Center for Research Resources)

9

OBSERVATIONS ON THE NEMATODE GYRINICOLA BATRACHIENSIS (OXYUROIDEA: PHARYNGODONIDAE) IN EIGHT SPECIES OF LARVAL AMPHIBIANS FROM NEBRASKA

H. Tracy and **M. Bolek**, Oklahoma State University

A total of 467 tadpoles and salamander larvae of 8 species were examined for the presence of *Gyrinicola batrachiensis* from 5 locations in Nebraska. Infection by *G. batrachiensis* occurred in tadpoles of *Rana blairi, R. catesbeiana* and *R. pipiens*, and *Bufo woodhousii*, whereas tadpoles of *Hyla chrysoscelis, Spea bombifrons* and *Pseudacris maculata* and larvae of *Ambystoma tigrinum mavortium* were not infected. In our study, female *G. batrachiensis* nematodes in *Rana catesbeiana, R. blairi*, and *R. pipiens* tadpoles were didelphic, but female nematodes in *B. woodhousii* tadpoles were monodelphic. Furthermore, only female nematodes were found in tadpoles of *B. woodhousii*. Such variations in nematode uterine morphology and nematode sex ratios among tadpole host of *R. catesbeiana, R. blairi, R. pipiens* and *B. woodhousii* are in accordance with the haplodiploid/autoinfective and apomictic/non autoinfective reproductive strategies previously reported for *G. batrachiensis*. Population structure defined as prevalence, mean abundance and frequency distribution of *G. batrachiensis* varied among species of tadpoles and was determined by long or short life cycle strategies of tadpole hosts and/or different reproductive strategies of *G. batrachiensis*. Populations of *G. batrachiensis* had a low or high prevalence and this was correlated to a short (*B. woodhousii*, and *R. pipiens*) or long (*R. catesbeiana*) tadpole life cycle strategy, whereas the distribution of *G. batrachiensis* followed a random distribution in tadpoles of *B. woodhousii* or a aggregated distribution in tadpoles of *R. catesbeiana* and *R. pipiens* which was correlated with the two different reproductive strategies of *G. batrachiensis*.

10

STREAM MORPHOLOGY, NICHE USE, AND OTHER FACTORS DETERMINING THE DISTRIBUTION OF DACTYLOGYRUS SPP. (MONOGENEA) ON NATIVE NORTH AMERICAN CYPRINIDS

A. Knipes and **J. Janovy, Jr.**, University of Nebraska-Lincoln

Dactylogyrus species' use of niches within a stream are dependent upon stream flow

characteristics and fish behavioral responses to those characteristics. A study of 7 *Dactylogyrus* spp. on *Pimephales promelas* (fathead minnow), *Notropis stramineus* (sand shiner) and *Semotilus atromaculatus* (creek chub), in the Salt Valley Watershed of Lancaster County, Nebraska have led to hypotheses as to factors exerting evolutionary pressures on parasite species in this system. In all, 93.5% of *P. promelas* (n=296) were infected with up to 3 species of *Dactylogyrus* including: *D. simplex* Mizelle, 1937; *D. bychowskyi* Mizelle, 1937; and *D. pectenatus* Mayes, 1977. In all, 48.2% of *N. stramineus* (n=274) were infected with a single species of *Dactylogyrus*, *D. rubellus* Mueller, 1938. In all, 58.7% of *S. atromaculatus* (n=99) were infected with up to 3 species of Dactylogyrus, including *D. microphallus* Mueller, 1938, *D. attenuatus* Mizelle, 1937, and *D. tenax* Mueller, 1938. At these 3 sites: (1) *Dactylogyrus* spp. are not shared among host species; (2) fish size and sex are not predictive of Dactylogyrus infection; (3) Dactylogyrus spp. vary (not always predictably) in their seasonal occurrence; (4) populations of *Dactylogyrus* spp. respond to environmental differences among sites; and (5) the community structure of *Dactylogyrus* spp. (order of abundance) on *P. promelas* and *S. atromaculatus* are independent of environment. These data from the Salt Valley Watershed suggest refuge-seeking behavior in fish translates into predictable increases in the number of parasites per fish and percentage of potential hosts that become infected in side pools of faster moving streams. Therefore, factors including stream morphology, niche use, and inherent differences among congeners are likely to play a role in the distribution of *Dactylogyrus* in nature and ultimately the evolution of parasite and host interactions.

11

THE BODY SIZES OF CYMOTHOID ISOPOD PARASITES

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Body size is a fundamental species trait. It has particular relevance for parasites, because their body size (both absolute and relative to their host) should directly reflect important aspects of the host-parasite relationship. Cymothoid isopods are parasites of fish. As a group, cymothoids encompass a range of parasitic strategies, ranging from ecto- to endoparasitism, and from being macroparasites to parasitic castrators. We used information from 283 studies to assemble a data set of body sizes for 325 cymothoid species (out of ~400 described species) and 480 host species. We first examine the frequency distributions of cymothoid species body sizes. We then examine factors potentially influencing cymothoid absolute and relative body size, paying particular attention to host body size, host taxon, site of infection, and biome. We also examine how body size influences their impact on the host, using the limited amount of information available. The distribution of cymothoid body sizes appears less skewed than the distributions characterizing most other animal groups. On average, cymothoids are larger than their free-living relatives. Cymothoid body sizes encompass about three orders of magnitude, ranging from 0.01 g to 25.2 g. Larger cymothoids are found on larger host species. However, the size increase is not isometric and the parasites are relatively smaller on larger hosts. Intermediate relative masses appear to most negatively impact host growth and reproduction. Cymothoid body size relative to host body size ranges from 1 to 58 %. Site of infection and biome also appear to influence cymothoid body size, but less strongly than host size. Cymothoids may provide a useful group to examine the

evolution of different parasitic strategies, because they encompass a wide range of absolute and relative body sizes and have a wide range of impacts on their hosts.

12

ROLE OF ENVIRONMENTAL FACTORS IN STRUCTURING ENDOHELMINTH COMMUNITIES IN THE WESTERN MOSQUITOFISH, GAMBUSIA AFFINIS

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Characteristics of the local environment undoubtedly influence the presence and abundance of helminths in freshwater fishes. This study examines the relationship between composition of endohelminth communities in western mosquitofish, *Gambusia affinis*, and a suite of environmental characteristics in an attempt to elucidate which features of the environment are most important in determining the structure of parasite communities. Seven hundred and twenty *G. affinis* were collected from 2 sites on each of 3 streams of the Trinity River system in southeastern Texas throughout 2009 and 2010. For each collection, water samples were analyzed for 18 environmental factors that collectively describe the biotic and abiotic components of the habitat. Patterns of similarity among helminth communities were examined using nonmetric multidimensional scaling (NMDS). These patterns were interpreted in terms of the environmental features by superimposing the values for each environmental variable on the NMDS ordination plot of community similarity. The pattern of similarity among endohelmnth communities most closely corresponded to canopy cover and pH. All of the helminth species examined in this study have indirect life cycles. It seems likely that these factors might affect the abundance of endohelminths by influencing the distribution of intermediate hosts or by directly affecting the free living stages of some species.

13

PHYLOGENETIC RELATIONSHIPS OF BLOOD PARASITES IN THE AVIFAUNA OF SOCORRO ISLAND, MéXICO

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The Socorro dove (*Zenaida graysoni*), endemic to Socorro Island, was last reported in the wild in 1972. The Island Endemics Foundation is planning the reintroduction of this species to its former habitat. Recently, the European Breeding Program for this species sent several doves to North America to establish a small population at the Rio Grande Zoo in Albuquerque, New Mexico. This will be the first known attempt to reintroduce a bird species extinct in the wild to its former island range. In order to assess the disease threats the Socorro dove may face, Socorro ground doves (*Columbina passerina socorrensis*) and mourning doves (*Zenaida macroura*) of Socorro Island, as well as the Socorro doves in captivity were screened for the avian haemosporidian blood parasites *Plasmodium*, *Haemoproteus* and *Leucocytozoon*. Here we report and compare the evolutionary relationships of haemosporidian blood parasites from birds of Socorro Island, the mainland, and other island populations. We found all three blood parasite

genera in the mourning doves and Socorro ground doves, and we discuss the implications for the reintroduction of the Socorro dove. In addition, we study the diversity of mosquito species of Socorro Island. We identified 1) *Aedes taeniorhynchus* (Wiedeman), a salt-marsh mosquito, and 2) *Culex quinquefasciatus* (Say); both species are known vectors for avian malaria parasites. These species are not endemic to the island, and therefore they must have been introduced by human activity sometime during the past fifty years.

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IMPACTS OF MULTIPLE PARASITE SPECIES INFECTION ON OREGON COASTAL JUVENILE COHO SALMON (ONCORHYNCHUS KISUTCH)

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Understanding the limiting factors for freshwater survival of wild coho salmon (*Oncorhynchus kisutch*) in Oregon has been crucial in managing these threatened Evolutionary Significant Unit stocks. The role of chronic parasite infections in survival has not been previously addressed. We have two main aims: 1) determine the identity and distribution of parasites in these fish, and 2) evaluate the impacts of these infections on various fish health and performance endpoints. Some of the most common and abundant parasites are metacercariae of *Nanophyetus salmincola*, *Apophallus* sp., and neascus (black spot). We also routinely find high numbers two myxozoans, *Myxobolus insidiosus* and *Myxobolus fryeri* in the somatic muscle. One river of particular interest is the West Fork Smith River (WFSR). Previous studies here have shown that coho have less than expected parr to smolt survival in the LMS vs. the UMS, and the former generally show higher parasite burdens. We therefore, evaluated the impacts of these infections in coho salmon under laboratory conditions. Naturally infected parr were collected in the fall from WFSR and held in captivity until the typical time of smoltification (the next spring). Fish were then evaluated for $Na^+ K^+$-gill ATPase activity, growth, and swimming stamina, which were used to compare to infection intensities. The LMS fish were more heavily infected than those from the UMS, particularly for *Apophallus* sp. (median of 48 vs 0 metacercariae/gram, respectively). The former showed less growth and swimming ability compared to the UMS fish, and both endpoints were correlated with parasitism (R^2 = 0.42 and 0.20, respectively). These results add support to our hypothesis that heavily parasitized fish have poorer overwintering survival, indicating the importance of including infection and disease in management programs.

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TREMATODE-INDUCED OXIDATIVE STRESS IN LIVER TISSUE OF MINNOWS EXPOSED TO ORNITHODIPLOSTOMUM SP. CERCARIAE

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The mechanisms underlying parasite-induced pathology on their hosts are rarely understood. This is especially so for natural host-parasite combinations where effects are often subtle, and where they are difficult to detect via crude assessment of host growth and survival. In this study,

we evaluated oxidative stress as an indicator of tissue damage caused by developing metacercariae of *Ornithodiplostomum* sp. in its intermediate host. Metacercarial development is complex in this species, involving an obligate period of growth within liver tissue of fathead minnows, followed by encystment within the body cavity. The growth phase is associated with extensive damage to tissue adjacent to developing worms. We evaluated lipid peroxidase (LPO) concentration as an indicator of oxidative stress in the livers of minnows exposed to low and high numbers of *Ornithodiplostomum* sp. cercariae. There was a sharp rise in liver LPO concentration at 5 days post-exposure relative to uninfected controls, even in hosts containing less than 20 metacercariae. LPO concentrations peaked at 5 days post-exposure and remained high through the encystment period when metacercariae were absent from the liver. These results indicate that developing metacercariae cause significant and long-term tissue damage to their intermediate hosts, likely mediated in part by oxidative stress associated with cell damage caused by rapidly growing worms. Results from this study also confirm those from field studies indicating that the LPO assay is an effective biomonitor for parasite-induced oxidative stress in fish.

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TRANSMISSION BIOLOGY OF THE LANCET LIVER FLUKE (DICROCOELIUM DENDRITICUM) AMONG POTENTIAL DEFINITIVE HOSTS IN WESTERN ALBERTA, CANADA

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The emergence of parasites and pathogens is a globally-recognized concern. A key shortcoming of models that attempt to forecast the spread and impact of emerging parasites, especially those that are host generalists, is that little data exists on the relative contribution of sympatric host species to the transmission of infective stages. The problem is acute in grazing systems where several species of potential definitive host share pasture. The lancet liver fluke, *Dicrocoelium dendriticum*, was identified as an emerging parasite in ungulates in Cypress Hills Provincial Park, Alberta around 1990. This study focused on the evaluation of the circulation of the *D. dendriticum* among potential definitive hosts within the park. Most wapiti, mule deer, white-tailed deer, and beef cattle have been identified as infected through necropsy, with worm intensities in individuals varying by 4 orders of magnitude. Individual definitive hosts are most at risk of infection when they graze within deciduous dominated habitats with preliminary results indicating this ecotype to have the highest prevalence of metacerariae-infected ants. To estimate the relative contribution of each species of definitive host to overall rates of transmission of eggs onto pasture, we evaluated worm burdens in the livers of hunter-shot definitive hosts and counted eggs in faecal samples. These data allowed a crude estimation of per capita worm fecundity in each species of definitive host. When combined with estimates of host population size, we calculated the relative contribution of each host species to the transmission of eggs. Our preliminary results indicate that beef cattle yearlings and a small number of heavily-infected deer are responsible for most transmission of *D. dendriticum* eggs onto pasture.

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CHANGES IN ATLANTIC SALMON AND COD EPIDERMAL MUCUS PROTEINS IN RESPONSE TO STRESS

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Fish epidermal mucus contains components that protect against negative environmental effects. The goal of this study is to provide a better understanding of the role of epidermal mucus in the response of Atlantic salmon (*Salmo salar*) and Cod (*Gadus morhua*) to stressors. Two dimensional gel electrophoresis was first used to examine the Atlantic salmon mucus proteome and identify target proteins to be used as putative stress biomarkers. The proteomic map identified an increase in transferrin cleavage products in infected fish, suggesting a potential protective response. Reverse transcription PCR identified transferrin expression in skin. Actin cleavage products were also identified, suggestive of proteolytic activity which is a novel observation for Atlantic salmon in response to sea lice infection. In a second study, fish were subjected to short and long-term handling stress. Western blotting with anti-actin antibodies presented unique protein profiles between mucus isolated from fish subjected to long-term handling stress and unstressed fish. Subsequent studies examined salmon mucus in response to injection with a vaccine and the effect of prior handling stress on the response to vaccination. Vaccination or PBS injection resulted in a complete loss of transferrin but not actin suggesting selective proteolysis. Short and long-term stress prior to vaccination attenuated the loss of transferrin suggesting that prior stress may alter protease activity triggered by vaccination. Actin profiles differed between PBS injected and vaccine injected groups, further demonstrating the specificity of protease activation. Ongoing studies include using signature proteins as biomarkers to identify changes in the cod epidermal mucus proteome in response to gyrodactylosis treatment. The current work sheds light on the complexity of fish epidermal mucus response to stressors.
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IDENTIFICATION AND PARTIAL CHARACTERIZATION OF AN EIMERIA SPECIFIC PROTEIN

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Avian coccidiosis is often caused by simultaneous infections with several members of the genus *Eimeria.* While their life cycles are very similar, different species inhabit distinct regions of the gut and have different pathological impacts on infected birds. In addition there appears to be little cross-immunity between species and significant immunovariability between strains of some species. Therefore, effective control of coccidiosis requires a control method that is effective against all the pathogenic species that may be present in a production facility. Key to development of vaccines or other novel controls is the identification of proteins common to

several *Eimeria* species and in particular those proteins that are unique to the parasite and dissimilar from the host. Comparative analysis of abundantly expressed transcripts from merozoites of *E. maxima*, *E. tenella* and *E. acervulina* revealed a novel transcript common to all three species and with no significant homology to any other sequence in public databases. This transcript encodes *Eimeria* specific protein (ESP) containing 166-178 amino acids with a 59 to 65% interspecific identity and the protein is predicted to be relatively unstable. A predicted signal peptide was identified consistent with the assumption that ESP is a secreted protein. Quantitative PCR analysis of developmental stages of these parasites indicated detectable levels of ESP transcription in sporulated oocysts (SO), sporozoites (SZ) and merozoites (MZ) and in general higher levels of expression were obtained in MZ or SZ relative to other stages examined. A polyclonal antibody prepared to recombinant ESP recognized a protein of 23 kDa in extracts of *E. maxima* and *E. tenella* SO and MZ. The antibody did not react with extracts from SO of *E. acervulina* or *E. praecox*. These results demonstrate the presence of a unique protein (ESP) common to at least three species of Eimeria. Current investigations are underway to further determine its biological function.

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ABDOMINAL CONTRACTIONS FACILITATE EXTRACARDIAC RETROGRADE HEMOLYMPH PROPULSION IN THE MOSQUITO HEMOCOEL

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Hemolymph circulation in mosquitoes is primarily driven by the contractile action of the dorsal vessel. This vessel is divided into a thoracic aorta and an abdominal heart that runs immediately underneath the dorsal midline of the tergum and pumps hemolymph in both anterograde (toward the head) and retrograde (toward the tip of the abdomen) directions. During our analyses of the functional mechanics of the mosquito heart, we observed that the ventral abdomen also periodically contracts and hypothesized that these contractions promote extracardiac hemolymph circulation in the abdominal hemocoel. To test this hypothesis, we devised methods to simultaneously analyze both heart and abdominal contractions, and to measure hemolymph flow in the mosquito hemocoel. Qualitative and quantitative analyses of mosquitoes restrained using non-invasive methods revealed that ventral abdominal contractions only occur in the retrograde direction. Interestingly, periods of ventral abdominal contraction begin only during periods of anterograde heart contraction and end immediately following heart contraction reversals, suggesting that ventral abdominal contractions function to propel extracardiac hemolymph in the retrograde direction. To test this functional role, we intrathoracically injected fluorescent microspheres into the hemocoel and allowed them to mix with the hemolymph. Quantitative measurements of microsphere speed and acceleration in extracardiac regions of the abdominal cavity showed that, during periods of abdominal contractions, hemolymph flows in dorsal and retrograde directions at a faster and more vigorous pace when compared to periods without abdominal contractions. Taken altogether, these data show that abdominal contractions play a fundamental role in hemolymph circulation. The implications of these findings on mosquito physiology, immune responses, and pathogen migration through the hemocoel will be discussed.

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HIGH PREVALENCE OF BORRELIA BURGDORFERI IN TICKS RECOVERED FROM RACCOONS AND OPOSSUMS TRAPPED IN KENTUCKY

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The incidence of tick-borne zoonoses such as Lyme disease has steadily increased in the southeastern United States in recent years. Although *Ixodes scapularis* is the most commonly recognized vector for the Lyme disease spirochete *Borrelia burgdorferi*, *Dermacentor variabilis* (a common vector for Rocky Mountain Spotted Fever) also has been shown to be a viable host for this pathogen. The purpose of the present study was to use PCR and DNA sequencing technologies to determine if *Borrelia burgdorferi sensu lato* is present in ticks removed from raccoons and opossums trapped in south-central Kentucky. Animals were trapped in Barren and Warren counties of Kentucky between June 2007 and June 2008. Ticks were removed and stored in 70% ethanol. Genomic DNA was extracted from the ticks using a QIAamp DNA mini kit (Qiagen). DNA samples were analyzed by polymerase chain reaction (PCR) for the presence of *B. burgdorferi* using primers specific for the OspA gene. Three different tick species were obtained from raccoons; *Dermacentor variabilis*, *Amblyomma americanum*, and *Ixodes sp*. *Dermacentor variabilis* was the only tick species found on opossums. Twenty-five percent (163/642) of the tick DNA samples were positive for *Borrelia burgdorferi*. Prevalence of *B. burgdorferi* by tick species was 24.4% (141/577) in *D. variabilis*, 40.6% (13/32) in *A. americanum*, and 27.6% (8/29) in *I. scapularis*. The high prevalence of *B. burgdorferi* in ticks common to raccoons and opossums observed in this study, as well as in a tick species that aggressively bites humans in the southeast U.S. (*A. americanum*), creates concern that there are ample opportunities for people to come in contact with the infected ticks on these animals. Future studies are urgently needed to fully assess the presence and prevalence of *B. burgdorferi* in Kentucky and other southeastern states in the U.S. Administrative support from NIH Grant 2 P20 RR-16481 from the National Center for Research Resources is gratefully acknowledged.

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EFFECTS OF TEMPERATURE ON TRANSMISSION OF YERSINIA PESTIS BY THE FLEA, XENOPSYLLA CHEOPIS

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Plague is a zoonotic disease caused by the gram-negative bacterium, *Yersinia pestis*. Infections are transmitted to rodents and other mammalian hosts, including humans, by flea vectors. Traditionally, the mechanism of flea transmission has been assumed to be dependent on overgrowth of the bacteria in the gut of the flea through a process commonly referred to as blockage. This process was previously shown to be temperature-regulated, with blockage failing to occur at temperatures above 30 °C. Recent work, however, has demonstrated efficient flea

transmission in the absence of blockage, demanding a re-examination of the transmission capabilities of fleas held at temperatures during which blockage is expected or not expected to form. We infected colony-reared fleas of *Xenopsylla cheopis* with a wild type strain of *Y. pestis* using an artificial feeding system, and maintained these infectious fleas at 10, 23, 27, or 30 °C. Naïve Swiss Webster mice were exposed to infected fleas on days 1-4 post-infection (p.i.), and every 3-4 days thereafter until day 14 p.i. for fleas held at 10 °C, or 28 days p.i. for fleas held at 23-30 °C. Exposed mice were monitored for signs of infection, and transmission was confirmed using *Y. pestis*-specific fluorescent antibody staining or a passive hemagglutination assay/hemagglutination inhibition test on tissues of mice. Fleas maintained at 23, 27, and 30 °C efficiently transmitted infections throughout the study period and median bacterial loads in these fleas remained high ($>10^4$ cfu/flea), although bacterial loads began to decline in fleas held at 27 and 30 °C by day 17 p.i. For fleas held at 10 °C, transmission was not observed until day 7 p.i. and their median bacterial loads were significantly higher ($>10^6$ cfu/flea) than those observed at the other temperatures. However, the survival of fleas maintained at 10 °C was also lower than fleas held at higher temperatures. Together, our results support the notion that blockage is not necessary for flea transmission at high temperatures, but that temperature does likely influence the dynamics of *Y. pestis* transmission by fleas by perhaps affecting the way the bacterium grows and persists in the flea gut at different temperatures.

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MOLECULAR EPIDEMIOLOGY OF CRYPTOSPORIDIOSIS AMONG HIV-INFECTED SUBJECTS IN BENIN CITY, EDO STATE, NIGERIA

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Molecular epidemiology of *Cryptosporidium* infection among HIV-infected patients was undertaken. Stool and blood samples were obtained from 500 HIV-infected patients. Demographics were obtained by means of a questionnaire. Presence of *Cryptosporidium* was detected in stool using SSU rRNA PCR-RFLP and DNA sequence of 60KDa glycoprotein (gp60) was used for subtyping. CD4 T-lymphocyte estimation from blood samples was done using flow cytometry. CD4 count < 200cells/µL was a significant risk factor for acquiring cryptosporidial infection (OR = 21.214 95% CI = 9.917, 45.381; P < 0.0001). Cryptosporidial infection was also associated with weight loss and diarrhea. Animal contact, especially with cattle, having streams or rivers as source of water and been divorced resulted in significantly higher prevalence of cryptosporidial infection. *C. hominis* (47.2%), *C. parvum* (44.4%), *C. felis* (5.6%) and *C. canis* (2.8%) were the species of *Cryptosporidium* observed. Genotyping of *C. hominis* revealed subtype families Ia, Ib and Ie, with Ie predominating and patients infected with it indicating streams and rivers as source of water. *C. parvum* has subtype families IIa, IIc and a yet unidentified subtype family. All *C. parvum* subtype families were from patients who used borehole water as source of water. *C. hominis* remains anthroponotic while *C. parvum* had a combination of zoonotic and anthroponotic subtypes.

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ROLE OF ANCYLOSTOMA CANINUM TRANSCRIPTION FACTOR DAF-16/FOXO DURING THE RESCUE OF DEVELOPMENTAL ARRESTED LARVAE

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Almost 800 million people are infected with the hookworms *Ancylostoma duodenale* and *Necator americanus,* causing disabling and persistent disease particularly in poor tropical regions. The infectious hookworm larvae (iL3) are soil-living, non-feeding and developmental arrested. They resume development to the reproductive stage in response to host-specific cues encountered during invasion. The underlying molecular mechanisms of the re-initiation of the developing process are mostly unknown. Similarities between the developmentally arrested stages, dauer stage from the non-parasitic *Caenorhabtidis elegans* and the hookworm L3, suggest that similar mechanisms might be involved. Exit from dauer arrest in *C. elegans* is dependant on the inactivation of the FoxO class forkhead transcription factor DAF-16. In the absence of insulin like signaling (ILS), DAF-16 enables the expression of dauer stage-associated genes, including genes involved in the heat shock response and metabolism. ILS starts a cascade of phosphorylation events that culminate in the phosphorylation of DAF-16 on conserved threonine or serine residues by AKT/ protein kinase B. Phosphorylated DAF-16 is escorted from the nucleus, resulting in expression of genes involved in reproductive development, and therefore recovery from dauer arrest. Our evidence suggests a similar role for DAF-16 in hookworms. The mechanism of phosphorylation and nuclear exclusion was investigated using heterologous expression systems, cellular fractionation, and imaging. Further, complementation assays of C. elegans dauer defective mutants with wild type and AKT phosphorylation site mutants of hookworm DAF-16 indicate functional orthology in the control of dauer recovery. The data suggest that the hookworm DAF-16 is a pivotal player in the hookworm infectious process and the transition to parasitism during infection.

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CHARACTERIZATION OF GIARDIN PROTEIN EXPRESSION DURING ENCYSTATION OF GIARDIA DUODENALIS TROPHOZOITES TO CYSTS

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Giardia duodenalis trophozoites attach to the gut surface by means of a ventral disk that contains various giardin proteins that are associated with structural microtubules and microribbons. Preventing giardiasis might rely on stimulating giardin-specific antibodies to block trophozoite attachment to the gut epithelium. Understanding giardin expression during encystation (cyst formation) or excystation (trophozoite release) might provide clues to the role of giardins in the *Giardia* life-cycle. In the present study expression of major giardin proteins during conversion of trophozoites to cysts was characterized. cDNA coding for beta, gamma, and alpha-2 giardin was

expressed in *Escherichia coli*, and antisera specific for each recombinant protein were prepared for immunolocalization and immunoblotting studies. Real-time PCR using giardin-specific primers provided data on the expression of each respective gene sequence relative to house-keeping genes over time. Immunoblotting revealed that expression of delta-giardin was restricted to trophozoites, whereas beta-giardin was present at all timepoints during encystation. This finding was confirmed by immunofluorescence assay, and also showed that beta-giardin was localized tp a well-defined ventral disk early in encystation, and then was increasingly localized to an amorphous structure inside the cysts as early as 48 hr during encystation.

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PROPHYLACTIC EFFECT OF BOVINE LACTOFERRIN AGAINST ACUTE TOXOPLASMOSIS IN IMMUNOCOMPETENT AND IMMUNOSUPPRESSED MICE

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Toxoplasma gondii is an important opportunistic agent in immunosuppressed (IS) individuals. Advances in modern medicine demand new compounds of stimulatory properties within the immune system. Recently, Lactoferrin (LF) gained interest as a promising immune-regulator against variety of diseases. This study aimed at evaluating the immune-potentiating effect of administering bovine LF to immunocompetent (IC) and IS mice prior to infection with tachyzoites of a RH strain of *T. gondii*. Mice were IS with cyclophosphamide. LF was given in seven oral doses on alternate days. Immunological and parasitological assessments established that LF induced statistically comparable resistance against acute toxoplasmosis in IC and IS mice. This was verified by elevated splenic CD4+ T lymphocytes, reduced tachyzoite viability and infectivity, with diminished parasite burdens. Consequently, mice mortality declined and their survival was prolonged. This encourages trying LF on cyst forming strains to determine its prophylactic efficacy against human toxoplasmosis in individuals at risk by alleviating their immune balance.

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IMMUNOBLOT PROFILES OF SERUM FROM PATIENTS WITH OCULAR ANGIOSTRONGYLIASIS AGAINST MALE AND FEMALE EXTRACTS

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Two case reports of ocular Angylostrongylus: The first case was sub-retinal and the second case was intravitreal. They were both serologically shown to be angylostrongylus and in the second, the parasite was surgically removed and was pathological identified. In the first case, the parasite found sub-retina in the inferonasal part of the fundus. The worm was lasered to death. The dead body was not removed. Six months later, there seemed to be a partial macular hole with a thin epi-macular membrane. The patient was lost to follow up for 11 years. When last seen in October

2008, there was a sub-macular scar and a thin epimacular membrane which was due to chronic sub-retinal inflammation. Only a segment the of infero-temperal visual field was intact with peripheral visual acuity at 20/200. The second case of ocular angiostrongyliasis, occuring in a 19 year old male, included severe proliferative vitreo retinopathy (PVR). The subject presented with a loss of vision of his right eye for two months. He had a history of consuming raw pillar snails and had developed eosinophic meningitis. A living parastie was observed upon ophthalamologic examination. The parasite ahd penetrated into the vitreous and created several holes on the retina, causing severe PVR. The parasite was extracted and indentified as an *Angiostrongylus cantoenesis* larva. This individual eventually went blind. Using an immunoblot analysis, both cases were positive for a 31 kDa component of female and male *A. cantoenesis*. Serological analysis also revealed a 38 kDa band in the patient infected with male *A. cantoenesis* larvae. Additional studies are needed to elucidate the significance of this band.

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ANTIMICROBIAL FUNCTION OF SESSILE HEMOCYTES IN THE MOSQUITO HEMOCOEL

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Mosquitoes hemocytes and other immune cells engage in the killing and sequestration of invading pathogens via phagocytic, melanization, and lytic pathways. To date, studies on cellular immunity in the mosquito hemocoel have so far revolved around visualizing static events after an immune challenge by extracting hemocytes that are circulating with the hemolymph. These experiments have described a broad range of immune responses but have not addressed the role of non-circulating cells in killing pathogens in the hemocoel. Here we will present data characterizing a poorly understood immune tissue in mosquitoes: sessile hemocytes. Histochemical labeling of live mosquito tissues uncovered immune cells attached to the viscera and the cuticular epithelium of the head, thorax, abdomen, legs, and antennae. Comparative analyses of circulating and sessile hemocytes showed that the two cell populations are morphologically and biochemically similar. In addition, similar to circulating hemocytes, sessile hemocytes respond to pathogens by forming cellular aggregates and engaging in phagocytosis. Interestingly, the largest aggregates develop in the periostial regions of the mosquito heart, an area ideal for pathogen sequestration because of its high rate of hemolymph flow. In summary, these data begin to characterize a previously unknown immune tissue in mosquitoes and suggest that the mosquito immune and circulatory systems work in concert to eliminate pathogens in the hemocoel.

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TRYPANOSOMA CARASSII CALRETICULIN BINDS HOST COMPLEMENT COMPONENT C1Q AND INHIBITS CLASSICAL COMPLEMENT PATHWAY-MEDIATED LYSIS

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Trypanosoma carassii is a parasite of economically important fish species that is evolutionarily related to *T. brucei* and *T. cruzi*. Since the surface coat of trypanosomes is of central importance to their immune evasion strategies, we performed proteomic study to identify proteins on the parasite surface and those found in excreted/secreted (ES) fraction of the in vitro cultured parasites. We identified *T. carassii* calreticulin (TcaCRT) in parasite ES and in the membrane protein fraction. We cloned and produced *T. carassii* calreticulin (rTcaCRT), and generated a rabbit polyclonal antibody to the recombinant protein. Incubation of parasites with rabbit anti-rTcaCRT affinity-purified IgG antibody indicated substantial CRT levels on the surface of trypanosomes, as well as internal structures of permeabilized organisms. Recombinant parasite calreticulin bound several molecules in host serum including the first complement component, C1q. The host C1q specifically interacted with parasite CRT since the C1q-dependent lysis of sensitized sheep erythrocytes was inhibited by rTcaCRT. Our findings suggest that CRT may be used by the parasite to inhibit hosts' classical complement pathway. [Supported by NSERC, CANADA]

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MICROARRAY ANALYSES OF SCHISTOSOMA MANSONI TREATED WITH PRAZIQUANTEL

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Schistosoma mansoni is one of the most common etiological agents of human schistosomiasis and is estimated to infect more than 83 million people in 54 countries. Praziquantel (PZQ) is the least expensive, easiest to use and most readily available of all current anti-schistosomal drugs. One problem associated with PZQ treatment is that it does not kill schistosomes for a period of 2-4 weeks after they infect the human host. A second potential problem is the presence of drug resistance traits in natural populations of worms. As a result there is an urgent need to develop a new generation of anti-schistosomal drugs, a task that will be made easier by understanding the mechanism of action of PZQ. As yet, neither the molecule to which PZQ binds nor the means by which it kills mature schistosomes is known. The overarching aim of our study is to understand the molecular basis of PZQ sensitivity in *S. mansoni*. We hypothesize that PZQ sensitivity is a reflection of the differential expression of a gene that encodes either the PZQ binding partner or a downstream component of a biochemical pathway whose activity is influenced by PZQ binding to its partner molecule. Four and six week post infection (p.i.) S. mansoni PR1 have been treated

in vitro with multiple sub-lethal as well as lethal doses of praziquantel. mRNA was extracted from replicate samples, cRNA prepared and labeled with Cy5 for transcriptomal analysis using a 44K *S. mansoni* microarray. All samples were compared against a common reference sample labeled with Cy3. Our initial analyses suggests that a number of genes associated with programmed cell death including cathepsins, Bax Interacting Factor 1 and death associated protein kinase (DAPK) are induced in 6 week (p.i.) praziquantel treated but not untreated schistosomes. DAPK has also been implicated in the phosphorylation of myosin light chains which has been reported to lead to vucuolation of cells and membrane blebbing - an often observed effect of PZQ on the mature but not juvenile worm tegument that may provide a more direct route to worm death.

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THREE DIFFERENT MODELS OF BIOMPHALARIA GLABRATA RESISTANCE TO TREMATODE INFECTION: COMMON UNDERLYING PATTERNS BASED ON MICROARRAY STUDIES

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As the intermediate host for the trematode *Schistosoma mansoni*, the freshwater snail *Biomphalaria glabrata* plays a significant role in the transmission of schistosomiasis to human populations. In the lab, *B. glabrata* has demonstrated its ability to defend against trematode infections by employing specific defense strategies to counteract parasite evasion or immuno-suppression. We here compare three different forms of resistance of *B. glabrata* to trematode infection: age-based, strain-based, and acquired resistance. To make these comparisons, we used a *B. glabrata* oligo-based microarray (1152 features) emphasizing stress and immune-response factors. We monitored the transcriptional profiles of *B. glabrata* from 0.5 up to 32 days post-exposure. The age-based array compared susceptible juvenile M-line snails (4-8mm) to adult, resistant snails (10-14mm), both exposed to the trematode *Echinostoma paraensei.* The strain-based array compared the responses to *S. mansoni* of resistant BS-90 snails with those of susceptible M line snails. Finally, our acquired resistance array examined the response of M-line snails that were first exposed to irradiated miracidia of *E. paraensei* and then 8 days later, challenged with viable miracidia. The three treatments each revealed a unique transcriptional profile, with each highlighting potential resistance-associated transcripts. We discovered a common pattern in which susceptible snails, at 2 days post-exposure, displayed a significant down-regulation of certain immune-associated transcripts (FREP3, C1q-like lectin, Dermatopontin, and others). In contrast, resistant snails at the same time point up-regulated many of the same transcripts and lacked the marked overall pattern of down-regulation associated with susceptibility. We hypothesize that this up-regulation has a significant impact on the ability of the snail to resist infection, and we are now looking further into the individual, functional roles of these molecules in resistance.

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FUNCTIONAL CHARACTERIZATION OF FREP3: A FIBRINOGEN RELATED PROTEIN ASSOCIATED WITH TREMATODE RESISTANCE IN BIOMPHALARIA GLABRATA

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Transcriptional analysis of *Biomphalaria glabrata* snails following challenge with the digenetic trematodes *Schistosoma mansoni* and *Echinostoma paraensei* resulted in discovery of a number of transcripts associated with snail resistance to infection. Comparison of the transcriptional profiles expressed by snails resistant to infection because of age/size, strain (BS-90/M-line) or prior exposure to homologous parasites (acquired resistance) yielded a pattern where some transcripts were commonly up regulated in resistant snails and down regulated in snails that were infected. From this comparison a number of resistance-associated transcripts were identified, some being commonly up regulated in all three types of resistant snails. One molecule displaying this type of pattern was fibrinogen related protein 3 (FREP3). The common recurrence of FREP3 in all of our transcriptional studies of snail resistance and the sequence heterogeneity that arises in FREP3 molecules due to a high incidence of point mutation and putative gene conversion events, made FREP3 a high priority for further functional analysis. *In situ* hybridization studies co-labeling for newly produced hemocytes (BrdU) and FREP3 suggest that newly developed hemocytes are involved in the production of FREP3. Using an anti-FREP3 antibody we purified native FREP3 from *B. glabrata* plasma and used both FREP3 and the antibody to it, to analyze FREP3 function. Thus far, we have demonstrated that FREP3 is involved in recognition and binding of galactose sugars, and that it can act as an opsonin to enhance phagocytosis of bound targets. Currently, proteomic analysis of FREP3 is underway to determine the level of protein variation that occurs within the FREP3 population of a single snail. We hypothesize that FREP3 represents a critical defense molecule that has an important role in protecting the snail against trematode infection.

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BIOCHEMICAL AND IMMUNOLOGICAL INSIGHTS INTO SCHISTOSOME HOST INVASION AND DEVELOPMENT

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Schistosome parasites begin infection of the host with invasion of skin and vasculature by multicellular larvae. Proteome analysis of this phenomenon has identified both parasite secretory molecules key to invasion and immune evasion, as well as host innate immune molecules serving as biochemical and immune barriers to parasitic infection. Following entry into blood vessels, schistosome parasites consume both red blood cells and serum proteins to support development into male and female worms, and production of large numbers of eggs for disease transmission. Proteome analysis of schistosome gut contents during residence in the vascular system has also led to insights into how these parasites efficiently degrade host blood proteins to

sustain development and egg production. A final remarkable adaptation of the schistosome is evasion and exploitation of the host immune response. Both gut derived and surface proteins are involved in immune evasion, yet without an intact host immune response schistosomula do not grow or differentiate into adult worms, and egg production is arrested.

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ROLE OF SIGNALING IN SCHISTOSOME MALE-FEMALE INTERACTIONS

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Schistosome parasites exhibit separate sexes and with the evolution of sex they have developed an intricate relationship between the male and female worms such that signals between the male and female that are initiated at the time of mating, regulate female reproductive development and subsequent egg production. As the egg stage is responsible for pathogenesis and transmission, understanding the molecular mechanisms of female reproductive development may identify novel targets for control of transmission and morbidity of this world public health problem. Recent data has demonstrated that the pairing process, proliferation and differentiation of vitelline cells, expression of female-specific genes and egg embryogenesis are regulated, in part, by the TGFb pathway. In functional assays it has been demonstrated *in vitro* and in the schistosome worm itself that human TGFb1 binds to the TGFb type II receptor (SmTbRII) and sends a signal that regulates target gene expression (Gynecophoric Canal Protein) and consequently elicits a specific TGFb effect.

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SCHISTOSOME DIVERSITY

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Schistosomes, the blood flukes of endotherms, comprise one of the best known families of parasitic helminths, presently with 14 genera, 9 in birds and 5 in mammals, together totaling about 100 described species. Recent collecting efforts coupled with molecular phylogenetics approaches suggest *Griphobilharzia* from crocodiles is a spirorchiid genus, and have resulted in identification and description of a new genus of avian schistosomes (*Allobilharzia*). They also indicate that the mammalian schistosome genus *Orientobilharzia* nests within *Schistosoma*, and that at least five additional genera of avian schistosomes may exist. Even in the relatively well-studied *Schistosoma*, three new species have been described in recent years, bringing the total for the genus to 22. A measure of the surprising diversity and ubiquity of schistosomes is that in a relatively arid state like New Mexico, 12 different lineages have been recovered, many previously overlooked because of their tendency to use the inconspicuous snail*Gyraulus parvus*. Mammalian schistosomes as thus far known are borne only by freshwater or amphibious snails whereas avian schistosomes cycle through freshwater and marine snails. Avian schistosomes have colonized a much broader range of snail hosts than species infecting mammals, and host

switching has been a prominent feature of schistosome-snail relationships. Adults of most schistosome species inhabit the mesenteric veins, but adoption of habitats in the nasal cavities, arterial system and urinary bladder has occurred. Schistosomes have also adopted a surprising variety of adult body forms (ranging from minimal to pronounced sexual dimorphism) and life history strategies (from parthenogenesis to short- or long-lived periods of egg production) in their definitive hosts. This study was supported by NIH grant R01 AI24340, and NIH grant number 1P20RR18754 from the Institutional Development Award (IDeA) Program of the National Center for Research Resources.

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STOLL STUNKARD LECTURE

PARASITE GENOMICS: THE NEXT GENERATION

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TRANSMISSION DYNAMICS OF TWO STRAINS OF SCHISTOSOMA MANSONI UTILIZING NOVEL HOSTS

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Parasites with complex life cycles must adapt to the genetic and phenotypic variability of their host. This study examines the interactions of a parasite with a homozygous genetic background when it encounters local and novel hosts. Both inbred and randomly breeding strains of *S. mansoni* were challenged with novel hosts to determine whether a lack of genetic variability constrains parasite infectivity in non-local hosts. The *B. glabrata* snails used as intermediate hosts consisted of a novel line recently derived from Brazilian field-collected snails and a local line that has been maintained in the laboratory for the last 20 years. Progeny from each snail line were exposed to *S.mansoni* larvae from either parasite strain and were monitored over a 10 week period for differences in both snail and parasite life-history parameters. As predicted there was a significant difference in parasite prevalence among the snails, as local snails exposed to the outcrossed parasites had a higher percentage of infected hosts. ($B=4.375$, $P= .016$). Parasite reproduction among the groups significantly varied as well, with local snails allowing the greatest parasite (cercariae) emergence ($F=15.92$, $P= .000$). Outcrossed parasites demonstrated higher levels of reproduction than inbred parasite strains ($F=6.265$, $p= 0.015$). Life history traits of the snail host were analyzed at weeks 5 and 10. Differences in life history traits occurred in growth, reproduction, and survival. Results demonstrate that parasite background has a strong influence on parasite infectivity and reproduction, and that outcrossed parasites may be better able to exploit novel hosts than inbred parasites.

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THE INNATE HEPATIC RESPONSE TO ASCARIS SUUM INFECTION IN THE MOUSE MODEL

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Ascaris lumbricoides and *Ascaris suum* are widespread parasitic nematode infections of humans and pigs respectively. This parasite exhibits an overdispersed frequency distribution in its hosts. Furthermore, observation of re-infection patterns post chemotherapy has indicated that individuals display a degree of predisposition to their worm burden status. The generative mechanism(s) of these observed phenomena are currently unknown and are difficult to elucidate in humans and pigs for ethical and logistical reasons. Comparative studies on larval migration demonstrated that the mouse is a suitable model for the early phase of *A. suum* infection. A murine model was recently developed and optimised and two inbred strains were identified as putatively susceptible (C57BL/6j) and resistant (CBA/Ca) to infection. Hepatic inflammatory responses and pathological damage were examined and the varying responses observed in each strain will be reviewed in light of larval burdens recovered. An earlier intense inflammatory response coupled with more rapid tissue repair in the hepatic lobes was detected in CBA/Ca mice, in contrast to C57BL/6j mice, and it is possible that these processes are responsible for restricting onward pulmonary larval migration in the resistant genotype. Hepatic cytokine levels produced in response to early infection in each mouse strain will also be discussed with reference to the inflammatory cellular infiltrate observed. Ongoing investigation of the hepatic innate immune response to infection in each strain will also be discussed.

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INVESTIGATING THE VALIDITY OF TWO QUESTIONABLE LECANICEPHALIDEA GENERA: HEXACANALIS AND CEPHALOBOTHRIUM

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The Lecanicephalidea are a well recognized, monophyletic order of elasmobranch tapeworms. Currently, twelve genera are considered valid and an additional nine are considered to be *genera inquirenda.* The taxonomic history of two of these *genera inquirenda*, *Cephalobothrium* and *Hexacanalis,* has been particularly intertwined and their validity has been questioned repeatedly. *Hexacanalis* was erected in 1931 for a species originally placed in *Cephalobothrium. Hexacanalis* has since been considered a synonym of *Cephalobothrium* while *Cephalobothrium* has been considered a synonym of *Lecanicephalum.* Most of the fifteen species of *Cephalobothrium* and eight species of *Hexacanalis* described appear to be inconsistent with the respective generic diagnosis. Type specimens and more recently collected specimens from Borneo and Australia were examined with light and scanning electron microscopy to address the validity of both genera as part of more comprehensive revisionary work. To our knowledge the

type specimens of the type species of *Cephalobothrium* do not exist. Examination of specimens consistent with the original description of the type species showed this genus to be distinct from *Hexacanalis* and *Lecanicephalum. Hexacanalis* was originally erected for specimens possessing six excretory vessels, rather than four, at that time a unique feature among Lecanicephalidea. *Hexacanalis* was recognized as valid based on examination of the type specimens of the type species and supported by discovery of a new species of this genus parasitizing the zone-tailed butterfly ray in Indonesia. Interestingly, one species currently placed in *Cephalobothrium* and newly collected specimens with similar morphology determined to be representatives of a new genus, also possess six excretory vessels. Future molecular and morphological studies will shed light on the utility of this feature uniting this subset of lecanicephalideans moving towards a revised familial classification.

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MOLECULAR BASIS FOR HOST SPECIFICITY IN AVIAN MALARIA

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The switching of pathogens to novel hosts is a characteristic of emerging diseases and, thus, is of great concern to human health and the management of wild and domesticated animal populations. Our previous work has shown that birds harbor well-characterized malaria parasites, some generalists and some host-specific, and thus are ideally suited for the study of how genes involved in host specificity vary in natural populations. Recent studies have identified genes that convey the host specificity of malaria parasites between humans and chimpanzees. While it is evident that the extracellular domain of Erythrocyte-binding antigen 175 (EBA-175) can account for the binding and host specificity of *Plasmodium falciparum* in humans, it is unclear how this and the rest of the erythrocyte binding-like (EBL) genes may act to preserve host specificity in natural ecological populations of birds. The EBA-175 Region two (RII; amino acids 145-760) was used as a reference sequence of amino acids in tblastn and DNA in blastn to find similar sequences in various *Plasmodium* species' genomic sequences. From the alignment we developed primers and have identified the first putative EBL gene in two avian parasites, *Plasmodium gallinaceum* and *Plasmodium relictum*. BLAST searches have identified the candidate genes to be orthologs of characterized EBL genes from *Plasmodium* parasites. The identification of an EBL gene in avian parasites will further enable us to isolate EBL family gene members with the intention to study differences in gene structure in parasites that differ in host specificity.

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A CESTODE TEST OF NEWLY CIRCUMSCRIBED SPECIES BOUNDARIES IN THE SHARKS SQUALUS ACANTHIAS AND SQUALUS SUCKLEYI

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Recently diverged species of hosts present an intriguing opportunity to explore the rates of divergence of their parasite lineages. The remarkably high degree of host specificity exhibited by many elasmobranch tapeworms makes them particularly ideal subjects for such studies. Recent re-examination of the global distribution of the spiny dogfish, *Squalus acanthias* has led to the North Pacific Ocean population now being recognized as a distinct species—*Squalus suckleyi*. This study explores this taxonomic decision from the standpoint of the cestode taxon *Trilocularia*, one of the components of the cestode fauna of these sharks. A total of 59 specimens of *Squalus suckleyi* from the North Pacific Ocean off of Vancouver Island and 217 specimens of *S. acanthias* from the North Atlantic Ocean off of Rhode Island were examined for *Trilocularia*. An integrative taxonomic approach was used to compare *Trilocularia* specimens between hosts. Specimens were examined with light and scanning electron microscopy, in addition, the D1-D3 portion of 28S rDNA was sequenced. Specimens from the 2 host species were morphologically similar in many respects, however those from *S. suckleyi* exhibited an ovary that was H-shaped, whereas the ovary of those from *S. acanthias* was U-shaped. Scanning electron microscopy revealed an unexpectedly wide array of morphologies both within and, in some cases, between host species. Small, but fixed differences were seen in the sequence data generated for *Trilocularia* specimens collected from the 2 host species. The paucity of historical records of *Trilocularia* from the North Pacific may at least in part account for the novelty of this finding. These results suggest that these cestodes may be speciating with, albeit perhaps more slowly than, their hosts.

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PHYLOGENETIC RELATIONSHIPS OF ECTOPARASITIC MITES (ACARI: ERYTHRAEOIDEA) ON ARGENTINE WALKING STICKS (INSECTA: PHASMIDA)

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Mites of the superfamily Erythraeoidea are found in a wide range of habitats where they frequently prey on and parasitize a significant number of arthropod hosts. Within Erythraeoidea lies the subfamily Leptinae (Southcott, 1957), composed of a single globally distributed genus *Leptus*. *Leptus* mites are protelean parasites, which are ectoparasitic only during the larval stages, yet generally free living as adults. This stark division of lifestyles makes it difficult to trace their development through all stages, and consequently their taxonomy and evolutionary history are poorly understood. Here, for the first time, phylogenetic relationships of Argentine New World *Leptus* spp. parasitizing walking sticks (*Agathemera* spp.) are explored, based on molecular data

from nuclear and mitochondrial genes. Preliminary data and analyses suggest the occurrence of five species of *Leptus* spp., all of which are new geographical records, and support *Leptus* monophyly. Characterization of morphology, evolutionary history and population structure of these mites provides novel insights into species boundaries, as well as phylogeographic and coevolutionary patterns respective to their hosts. Furthermore, the scope of this research is intended to add to the resolution of evolutionary relationships of Erythraeoidea mites in general.

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A PHYLOGENETIC RE-ASSESSMENT OF HYBRIDIZATION EVENTS AND SPECIES BOUNDARIES WITHIN TRYPANOSOMA CRUZI

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The protozoan parasite *Trypanosoma cruzi* is the causal agent of Chagas disease. It infects around 20 million people in the Americas and it is the tropical disease with the greatest economic burden in the New World. Variation among populations of *T. cruzi* has long been acknowledged, but questions still remain about the origin and maintenance of this genetic diversity. Seven discrete typing units, TcI to TcVI, and one subspecies *Trypanosoma cruzi marinkellei*, have been recognized within *T. cruzi*. Hybridization events among discrete typing units have been indicated. However, the possibility of ancestral retention of polymorphisms has not being totally ruled out. *T. cruzi marinkellei* has been found infecting only bats and shows remarkable levels of genetic differentiation, perhaps indicating that may be considered a valid species. Therefore, the objectives of this study are: 1) to distinguish if the genetic variation observed in *T. cruzi* is product of incomplete lineage sorting or hybridization events, and 2) to discern if *T. cruzi marinkellei* deserves specific status recognition. Sequences of 12 loci, including 2 mitochondrial and 10 nuclear fragments, were analyzed under phylogenetic and populations genetics approaches using Maximum Likelihood and Bayesian inference. Among discrete typing units there are several cases of incongruence on the gene tree topologies; the reasons behind these patterns are discussed. There are deep genetic divergences between *T. cruzi marinkellei* and the other lineages of *T. cruzi* suggesting that the full species status of *T. cruzi marinkellei* is warranted.

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CHARACTERIZATION OF NOVEL PEXEL-NEGATIVE P. FALCIPARUM EXPORTED PROTEIN, PFEXP250

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Plasmodium falciparum is the most virulent species of the genus *Plasmodium*, the protozoan parasite which causes malaria. During the blood stage of the parasitic infection, *P. falciparum* targets and invades erythrocytes where it secretes approximately 300 proteins from within a parasitophorous vacuole (PV) to the erythrocyte cytosol to regulate parasite growth and modify the host cell, resulting in disease. Recent discoveries of a PEXEL sequence shown to be

necessary for transport as well as a protease, Plasmepsin V and the translocon, shown to cleave and export PEXEL-positive proteins, respectively, fail to address a growing class of known exported proteins which lack the PEXEL sequence. These PEXEL-negative exported proteins (PNEP's) are known to play a role in host cell modification. In this study, a novel PNEP, PfEXP250 was identified and characterized. PfEXP250 is predicted to have a transmembrane domain and a calcium binding domain. We have determined the localization of PfEXP250 to be in the erythrocyte cytoplasm and possibly the erythrocyte membrane. The solubility of PfEXP250 was determined in order to resolve its location within the parasite. To further characterize the localization of PfEXP250, confocal immunofluorescence microscopy was used to determine association with the Maurer's Clefts (MC), parasite derived membranous structures in the erythrocyte cytoplasm, and erythrocyte membrane markers. We have found that PfEXP250 colocalizes with two MC proteins, REX1 and PfEMP1. Additionally, we have shown with solubility assays that PfEXP250 is associated with membranous structures of the parasite lysate. Based on these results, it appears that PfEXP250 is a *P. falciparum* exported protein that is associated with the membranous structures of Maurer's clefts.

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PREVALENCE OF MALARIA AND ANAEMIA AMONG HIV INFECTED

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The objective of this study was to determine the prevalence of malaria and anemia in HIV-infected persons and the effect of age, gender and CD4+T cell counts thereon. Blood samples were collected from 491 patients (240 female) attending an out patient clinic. Malaria parasitaemia was diagnosed by microscopy while anaemia was defined as a haemoglobin concentration of <130g/L in males and <120g/L in females. The CD4 + T cell count was estimated by flow cytometry. HIV infection was a risk factor for malaria infection (OR: 16.31; 95% CI: 7.41-35.87; $p < 0.0001$). CD4+T cell counts were equally a significant risk factor in malaria infection among HIVinfected patients (OR: 1.96; 95% CI: 1.28-3.02; $p = 0.002$). The prevalence of anaemia was significantly affected by HIV-infection (OR: 25.12; 95% CI: 11.42-55.28; $p < 0.0001$) while age was not associated with increased risk of malaria infection ($p=0.13$). A prevalence of 46.0% of malaria infection among HIV-infected was observed. HIV-infected patients were more likely to develop malaria and anaemia, while CD4+T cell counts < 200cells/μL were associated with an increased risk of malaria infection among HIV-infected. Age and gender did not affect the prevalence of malaria. HIV status should be considered early in the diagnostic evaluation of patients with suspected malaria and anaemia.

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EMERGENCE AND CONTROL OF GEOHELMINTHS IN HISTORIC ALBANY, NY, 1640-1920

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Extensive analyses of archaeological sediments excavated from Albany, New York were analyzed between 2006 and 2009. The sediments were recovered from latrines, drains, streets, yards, and industrial sites. The excavations covered the entire history of Albany from the 1640 Dutch Colony to early 20th century households. The large numbers of samples provides an opportunity to trace the emergence and establishment of geohelminths with European settlement and then trace the effects of war, socioeconomics, sanitation, and medical practices on geohelminth parasitism. This information provides the largest data base available for the study of parasite emergence in historic urban environments. The greatest numbers of eggs were in contexts related to the expansion of the city in the late eighteenth century. The number of eggs decreased during the nineteenth century during another period of rapid population growth. The city was able to control parasite infection during this period through several means, including new techniques of privy construction, new water supply systems, and medical treatments.

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TRYPANOSOMA CRUZI IN THE UNITED STATES: MOLECULAR AND BIOLOGICAL CHARACTERISTICS OF SYLVATIC ISOLATES

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Trypanosoma cruzi, the causative agent of Chagas disease, is a flagellated protozoan parasite endemic to Latin America; however, cases of autochthonously-acquired infections have been reported in the United States. Since January 2007, screening of US blood donors by the Chagas Disease Biovigilance Network has identified over 1,000 seropositive donations. In addition to confirmed and suspected autochthonous human cases, *T. cruzi* infections in domestic and wild animals and vectors in the region have been confirmed since 1916. Despite the documented *T. cruzi* cases in the US, limited research on isolates has been performed to better understand the molecular epidemiology of the parasite in this region. We have collected over 100 isolates of *T. cruzi* from wildlife reservoirs, vectors, domestic animals, vectors, and humans, and, in a series of research studies, the molecular and biological characteristics of several sylvatic isolates have been determined. Molecular analysis revealed a paucity of genotypes present in the region, evidence of genetic exchange, and strong evidence for a host-genotype association. Experimental infection studies of wildlife reservoirs further supported a host-genotype dichotomy, and infections in laboratory rodents suggested low virulence of sylvatic *T. cruzi* isolates from the United States. Differences in infectivity, replication, and growth rates were also observed in *in*

vitro experiments. Collectively this research suggests the sylvatic cycle of *T. cruzi* in the United States is perpetuated by a strong association between host species and genotype of the parasite that is evidenced by molecular and biological differences in isolates from different host species.

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THE ROLE OF DAMSELFLIES (ODONATA: ZYGOPTERA) AS PARATENIC HOSTS IN THE TRANSMISSION OF HALIPEGUS ECCENTRICUS (DIGENEA: HEMIURIDAE) TO ANURANS

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Halipegus eccentricus is a common hemiurid trematode in the eustachian tubes of North America frogs. However the life cycle of this species has never been completely elucidated. Studies on *H. eccentricus* suggest that it has a 3-host life cycle. Here, we show through fieldwork and host specificity experimental infections that the life cycle of *Halipegus eccentricus* utilizes 4 hosts. Metamorphosed anurans become infected with *H. eccentricus* by feeding on infected damselflies; worms resided in the stomach of anurans, migrate to the eustachian tubes within 32-39 days post-exposure (DPE), and release eggs 50-60 DPE. Cystophorous cercariae develop in *Physa gyrina* snails within 32-35 DPE, infect ostracod (*Cypridopsis* sp.) second intermediate hosts, and develop to metacercariae. Fifteen- to 19-dayold metacercariae from ostracods are infective to both damselfly larvae and metamorphosed anurans. Field surveys of damselflies and tadpoles along with laboratory exposure of damselfly larvae, metamorphosed anurans, and tadpoles with infected ostracods indicated that only metamorphosed anurans and damselflies become infected with *H. eccentricus*, whereas field collected tadpoles and laboratory exposed tadpoles were never infected with *H. eccentricus*. Because little morphological change occurred in the metacercaria stage of *H. eccentricus* between the ostracod second intermediate host and damselfly host, and metamorphosed anurans became infected with *H. eccentricus* metacercariae recovered from both host groups, we suggest that odonates serve as paratenic hosts in this life cycle. Additionally, our field work and experimental infections provide data on the use of odonates as the route of infection by another North American *Halipegus* sp. that matures in the stomach of frogs. Our data indicates that when the life cycles are known the use of odonates as the route of infection to anurans is common in life cycles of *Halipegus* spp.; and all species exhibit remarkable site fidelity in their amphibian hosts. (Supported by NIH grant number 1 P20 RR16469 from the INBRE Program of the National Center for Research Resources)

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METACESTODES OF BAIT SHRIMP IN THE GULF OF MEXICO

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Bait shrimp (*Farfantepenaeus aztecus*, *F. duorarum*, and *Litopenaeus setiferus*) obtained from several sites in the northern Gulf of Mexico (Apalachicola, Gulf Breeze, and Panacea, Florida; Ocean Springs, Mississippi) and from the Florida Keys (Key Largo) were examined for metacestodes belonging to groups other than the trypanorhynchs. Individual metacestodes were

frozen and the DNA was later extracted from them with a Qiagen QIAamp DNA Micro kit. The rRNA gene sequences of single larvae were then amplified by using primers complementary to conserved regions of the genes. DNA sequencing was carried out on a LI-COR 4200 automated sequencer. The geographic distribution of individual larval types was found to be highly localized; nerve cord metacestodes (described in a presentation at the 2009 ASP meeting) were found only in *F. duorarum* specimens collected in the vicinity of Panacea, one rhinebothriid species was found only in *F. duorarum* collected from Key Largo, and a second rhinebothriid was found in all three species of bait shrimp collected in Gulf Breeze and Ocean Springs, but not in *F. duorarum* from Key Largo. No rhinebothriids and no nerve cord metacestodes were found in shrimp from Apalachicola. We found developmental stages of the northern rhinebothriid in the spiral valve of the ray *Dasyatis sabina* but in no other rays examined by us, nor has its sequence been reported by investigators studying the cestodes of other rays.

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CYCLOSPORA CAYETANENSIS, CRYPTOSPORIDIUM SPP. AND GIARDIA DUODENALIS IN PACKAGED READY-TO-EAT SALADS AND LEAFY GREENS FROM A SENTINEL SITE IN ONTARIO, CANADA

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Numerous foodborne outbreaks of diarrheal illness associated with the consumption of produce contaminated with protozoan parasites have been reported in North America in recent years. In particular, foodborne cyclosporiasis outbreaks have occurred annually since 1995, and have generally been associated with fresh imported produce. Very few surveillance studies, however, have examined either imported or domestic produce in North America for the presence of these parasites. The present study is part of a comprehensive investigation of the incidence and exposure load of pathogens in the environment at a sentinel site in Ontario, Canada. In this study, we examined packaged ready-to-eat salads and leafy greens for the presence of *Cyclospora cayetanensis*, *Cryptosporidium* spp. and *Giardia duodenalis*. A total of 488 retail samples were collected between April, 2009 and February, 2010, and included a variety of blends of leafy greens including: iceberg lettuce, Romaine lettuce, baby lettuces, leaf lettuce, radicchio, endive, and escarole, as well as spinach and arugula. Most products were grown in the U.S., with the exception of a few items from Canada and Mexico. Samples were eluted in PBS-Tween 80 buffer using an orbital shaker, and then filtered through layers of gauze and centrifuged. Sample concentrates were then examined by immunofluorescence microscopy and polymerase chain reaction. DNA sequences were aligned with reference sequences in GenBank. *Cyclospora cayetanensis* was identified by microscopy and PCR in 6 (1%) samples, with two of the samples sequenced showing 100% homology with the reference sequence. *Cryptosporidium* spp. was identified in 33 (7%) samples; 3 were sequenced and aligned with the zoonotic species *C. parvum*. *Giardia duodenalis* was identified in 9 (2%) samples, 7 of which identified as the zoonotic Assemblages B (6) and A (1). The relatively high prevalence of these parasites in packaged leafy greens establishes a baseline for further studies, and suggests a need for research with respect to possible sources of contamination (human or animal) and the means to control them.

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DETECTION OF SOME INTESTINAL PROTOZOA IN COMMERCIAL FRESH JUICES

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Fresh fruit juices are popular, but not always safe. For assessing the likelihood of infection with newly emerging intestinal protozoa, commercial fresh orange, lemon, sugar cane, strawberry, and mango juices were screened by wet mounts, Weber's modified trichrome and modified Ziehl-Neelsen stains. Protozoal viability was done by fluorescine-diacetate/propidium-iodide staining, and infectivity was performed in Swiss albino mice. Results revealed that 35.43% of all samples were contaminated with one or more of *Cryptosporidia, Microsporidia,* and *Cyclospora*, as well as *Giardia spp.* Strawberry was the most contaminated juice (54.28%), while orange was the slightest (22.86%). *Cryptosporidia* was the highest contaminant (61.29%), and *Cyclospora* was the least (14.52%). *Microsporidia spp.* was the most robust contaminant which retained its viability and infectivity in juices in which it was detected. Moderately acidic strawberry and mango juices and alkaline sugar cane juice pose a possible threat, due to harboring the highest viable and infectious protozoa. Regarding highly acidic juices, viability and infectivity decreased in lemon, yet was still not risk free. Orange juice was comparatively safe, as viability dramatically declined, while infectivity was completely abolished. Hence consumers, especially high risk group, are placed at risk of contracting intestinal protozoal infections, especially through moderately acidic and alkaline juices.

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PANULIRUS ARGUS (LATREILLE, 1804) FROM BATABANO GULF, CUBA, PARASITIZED BY CYMATOCARPUS SOLEARIS (BRACHYCOELIDAE-METACERCARIA)

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Spiny lobsters are a very important fishery resource in Cuba as 70% of the income of this industry comes from the exportation of this crustacean to the European Union. Clearly, large parasites in the edible parts of lobsters are extremely important as they can produce rejection by the final consumer. This is the case of the metacercariae of *Cymatocarpus solearis*, which encysts in the musculature of lobsters. The cyst is large and evident to the naked eye. Thus, its presence can potentially affect the international price of spiny lobster. Adults of this trematode species have been found in the gut of wildlife marine turtles and metacercariae encysted has been found in the musculature of the spiny lobster in the Caribbean. Due to its potential economic importance, a preliminary study of the presence of this trematode in lobsters and crabs from Cuba was undertaken. Thirty spiny lobsters *P. argus* along with 35 Caribbean King crabs *Mithrax spinosissimus* from Batabano Gulf were surveyed. Several fragments of abdominal

muscle parasitized from *P. argus* were fixed to determine possible histological damage. The prevalence and mean abundance was 80% and 11.7 ± 9.6 for *P. argus* and 74.3% and 10.7 ± 15.9 for *M. spinosissimus*, respectively. The histological analysis showed hemocitic infiltration and encapsulation around the cysts. Two marine turtles, *Caretta caretta* and *Chelonia mydas*, were fed with heavily parasitized abdominal muscle of *P. argus* and five days after were necropsied. Eleven mature adults of *C. solearis* were collected from the gut of *Caretta caretta* but not in *Chelonia mydas*. This is the first record of *C. solearis* in *P. argus* from Cuba and *M. spinosissimus* as a new host. It is not known whether *C. solearis* could infect humans, but due to its industrial processing it is highly unlikely.

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ON-LINE CESTODE DATABASE RESOURCES

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Two related, but conceptually distinct, database systems of potential service to Parasitologists are described. (1) The Global Cestode Database (GCDB) is an on-line resource that will ultimately provide open access to taxonomic information and original descriptions of all nominal cestode taxa. The holdings of this database currently include 4,785 records, which are estimated to represent ~60% of existing nominal cestode taxa. The completion of up-to-date taxon entries, and verification of their associated data, is ongoing, with an expected "completion" date of 2013. These data will include access to original descriptions as well as images of type specimens from museums throughout the world. The database will ultimately provide a verified checklist of valid cestode taxa. (2) The associated host specimen databases for each of the 5 vertebrate classes (i.e., elasmobranchs, teleosts, mammals, birds, and herptiles) are more specifically project oriented, but perhaps provide an example of how host data might be managed on a relatively large scale. These databases provide access to collection data, a diversity of images, and molecular sequence verification data for each host specimen, from which cestode survey data were collected, thereby serving to voucher the identity of each host specimen. Among the 5 vertebrate host specimen databases, the elasmobranch host specimen database is currently most extensive, including records of over 5,700 elasmobranch host specimens. Both database systems take advantage of the open source MySQL platform, allowing unrestricted searching and viewing of existing data, and password protected uploading, of data. These databases are part of a collaborative effort involving Cestodologists from 15 countries around the world aimed at documenting global cestode diversity, host associations and distributions.

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EUPATHDB –A EUKARYOTIC PATHOGEN DATABASE OF PROTIST "OMICS" DATA

J. Kissinger, University of Georgia

EuPathDB is a freely accessible NIH-funded Bioinformatics Resource Center that currently

maintains and integrates data from 32 species in 11 genera including: *Entamoeba, Encephalitozoon, Giardia, Trichomonas,* the kinetoplastid parasites *Trypanosoma* and *Leishmania,* and the apicomplexan parasites, *Theileria, Plasmodium, Toxoplasma, Neospora* and *Cryptosporidium.* EuPathDB is designed to be a research platform that provides access to large genomic, comparative genomic, RNA expression (SAGE-tag, EST, RNA-seq, microarray), protein expression, ChIP-seq, SNP and parasite isolate data. Searches can be restricted to a single species, genus or all any combination of all organisms contained within the database. Our new strategy system allows researchers to ask complex questions like, "Find all proteins with a particular protein motif, evidence of expression and conservation within the genus but not outside of the genus" and retrieve a list of genes that satisfy the criteria. The strategy used to ask this question can be saved and shared with colleagues and be re-run as new data become available. EuPathDB is a collaborative undertaking between the University of Pennsylvania and the University of Georgia and is funded by NIH contract HHSN272200900038C.

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ASSOCIATE EDITOR'S SYMPOSIUM – 2010

G.W. Esch, Department of Biology, Wake Forest University, Winston-Salem, NC
C. Goater, Department of Biological Sciences, University of Lethbridge, Lethbridge, AB, Canada

Following a tradition established at the ASP annual meeting in 2008 (Arlington, Texas), each year three members of the Journal of Parasitology Editorial Board are invited to present a précis discussing the nature and scope of their personal research. This year, Dr. Tim Geary, McGill University, Dr. Kirsten Jensen, University of Kansas, and Dr. Al Shostak , University of Alberta will be the presenters. Their topics are as diverse as their backgrounds. Dr. Geary will talk about drugs and drug therapy in the treatment of parasitic helminths, using *Caenorhabditis elegans* as his animal model. Dr. Jensen will discuss her efforts in resolving the life cycles of tetraphyllidean cestodes in the Caribbean. Finally, Dr. Shostak will provide conceptual and experimental insight regarding the so-called 'crowding effect'. Esch will lead off with a presentation that will provide a 'back-drop' for each of the speakers; Cam Goater will introduce the speakers and handle the question-and-answer session that will accompany the symposium.

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C. ELEGANS AS A MODEL ORGANISM FOR ANTHELMINTIC RESEARCH: PROSPECTS AND PITFALLS

T. Geary, McGill University

Strategies for discovering and understanding anthelmintics evolved from work done on parasites in infected animals to research on the model nematode *Caenorhabditis elegans* to high-throughput screening against isolated nematode proteins produced through recombinant

technology. Only3 new classes of anthelmintics have been brought to market in the last 30 years; all were initially discovered in infected animal screens. The role of *C. elegans* in anthelmintic research has further evolved in this context. New data illuminate the potential and problems evident in the use of this remarkable animal in research on antiparasitic drugs.

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PUTTING PARASITISM IN PERSPECTIVE: LESSONS FROM LARVAL TAPEWORMS

A. Shostak, Department of Biological Sciences, University of Alberta

Parasites have garnered, in some cases deservedly, a poor reputation for their negative effects on host individuals. In turn, effects on host individuals are assumed to have downstream effects on host populations and communities. However, parasitism is not the only negative influence on their host. Assessment of the effects of parasitism on hosts can be made more robustly if placed in context with other influences on the host such as predation, food availability and environmental stresses. Three tapeworm-host relationships will be evaluated in this context: *Schistocephalus solidus* in fish, *Triaenophorus crassus* in copepods, and *Hymenolepis diminuta* in beetles. Larval parasites such as these are often capable of growing large relative to the size of their hosts and causing reductions in host survival, growth, and fecundity. Results from field and experimental studies on these systems confirm the existence of density-dependent mechanisms acting on parasites within individual hosts that moderate their effects on the host. Also, the effects of parasitism may not necessarily be more severe in stressed hosts.

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MORPHOLOGICAL AND MOLECULAR APPROACHES TOWARDS UNDERSTANDING ADULT AND LARVAL ELASMOBRANCH TAPEWORM DIVERSITY

K. Jensen, University of Kansas

Broad ecological or evolutionary studies involving marine tapeworms are often limited in their implications by our lack of understanding of the diversity present. This is especially true for elasmobranch tapeworms. Elasmobranch tapeworms currently constitute 17% of described cestode species diversity, compared to only 18% of described cestode species diversity parasitizing the speciose actinopterygians. Considerable progress has been made in the taxonomy and systematics of elasmobranch tapeworms over the past several decades and our understanding of the diversity and morphological disparity of these tapeworms is coming into focus. In general, shark and ray tapeworms form a paraphyletic group. Through a collaborative effort, much progress has been made bringing the classification in line with our understanding of interrelationships based on morphology and molecular sequence data. Our knowledge about elasmobranch tapeworm life-cycles, for most groups, is still surprisingly incomplete, but work towards the elucidation of some aspects of elasmobranch tapeworm life-cycles is ongoing. One of the orders of ray tapeworms, the Lecanicephalidea, remains particularly underestimated in terms of generic and species diversity. Moreover, the interrelationships of members of this order

are basically unknown and a familial classification outdated. In recent years, member of this order have been collected from mainly rays, primarily from Southeast Asia. Tapeworm specimens from this region exhibit particularly novel morphological features associated with the scolex and proglottids. These new collections suggest that the recognized generic diversity in lecanicephalideans, currently estimated at 14 genera, will increase by 100%, while species diversity, currently estimated at 75 species, will conservatively increase by 300%. In addition, research has focused on expanding of knowledge of geographic distributions and host associations of these species on a more global scale.

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SYNTHESIS OF SUBSTITUTED PYRIMIDINEDIONE DERIVATIVES AS POTENTIAL SCHISTOSOMICIDAL AGENTS

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Schistosomiasis, caused by *Schistosoma mansoni*, is a chronic, debilitating disease which affects 200 millions of people worldwide. It is a major disease of public health importance in humans occurring in over 70 countries of the tropics and subtropics regions. It is associated with a variety of clinical syndromes that may lead to severe morbidity. Remarkable achievements have been made in the control of the disease, with chemotherapy playing a crucial role. Praziquantel is the current drug of choice to control the disease; nevertheless, due to concerns about its tolerance or resistance, new drugs are still needed. A rational approach for the development of a new schistosomicidal agent might be derived from finding differences between the biochemistry of the host versus the parasite. It was recently reported that there is a difference in pyrimidine metabolism between schistosoms and mammalian cells. In mammals, orotatephosphoribosyltransferase and orotidylate decarboxylase exist as a multi-enzyme complex and the major orotate metabolism is uridine monophosphate which is essential for pyrimidine biosynthesis. In contrast, orotatephosphoribosyltransferase and orotidylate decarboxylase exist as separate enzymes in *S. mansoni* rather than a multi-enzyme complex as in mammalian cells. These differences in orotate metabolism, which are essential for DNA biosynthesis, may provide selective toxicity for a chemotherapeutic agent against schistosomes as compared to the host. Motivated by these findings, a study was designed to synthesize a novel series of substituted tetrahydropyrimidinedione derivatives (1-6) and evaluated their schistosomicidal activity both *in vitro* and *in vivo* using Praziquantel as a therapeutic control. Results of this study showed that all the tested compounds except compound 5 showed *in vitro* schistosomicidal activity. However, only compound 3 showed *in vivo* activity in Swiss strain albino mice as evidenced by significant reduction in worm load, tissue egg count, liver granuloma number and size, and histopathological study of the liver. Moreover, scanning electron microscopy of adult *S. mansoni* recovered from animals treated with compound 3 revealed tegumental changes. These data point to 2-(2,6-dioxo-1,2,3,6-tetahydropyrimidin-4-yl) isoindole-1,3-dione (3) as a promising new antischistosomal agent.

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DIURNAL MIGRATION OF ECHINOSTOMA CAPRONI (DIGENEA: ECHINOSTOMATIDAE) IN THE SMALL INTESTINE OF FEMALE ICR MICE

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We investigated the diurnal movement of *Echinostoma caproni* in ICR mice. Twelve mice were maintained on a 12/12 light-dark cycle and 12 mice were maintained on a 12/12 dark-light cycle for 7 days prior to infection. Animals were provided food and water *ad libitum* during all phases of the experiment. At the end of the acclimation period all mice were infected with 10 metacercariae via stomach tube. Mice were maintained under identical conditions for 28 days prior to necropsy. Three mice from each group were necropsied at 4 hr intervals beginning at 7 a.m. The intestine was removed, opened longitudinally and the position of each worm or worm group was determined to the nearest 0.1 cm. Each intestine was subsequently divided into 20 equal segments and each worm/worm group was assigned to a segment. All worms were restricted to the ileum (segments 10-20) and were highly aggregated. The distribution of worms over all time periods was random (Monte Carlo; $P=0.325$) within segments 10-17; however, the distribution of worms was not random (Monte Carlo; $P<0.001$) when all segments of the ileum (10-20) were analyzed. This reflects the absence of worms from segment 18 in all animals and a large contingent in segment 20 during the day when mice are inactive. Data were pooled to examine diurnal movements: morning (3 & 7 a.m.), day (11 a.m. & 3 p.m.), and night (7 & 11 p.m.). There was a significant anteriad shift during time when mice are active and feeding (night and morning) and a posteriad shift during the day. These data conform to results for the rat tapeworm, *Hymenolepis diminuta* tracking the availability of monosaccharides. *Echinostoma caproni* is a mucosal grazer and it is not known to what extent tegumental absorption is an important component of its energy budget. It is possible that *E. caproni* retreats to the ileo-cecal junction to deposit eggs prior to the next round of foraging activity by the definitive host.

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HOST MORTALITY AND VARIABILITY IN EPIZOOTICS OF SCHISTOCEPHALUS SOLIDUS INFECTING THE THREESPINE STICKLEBACK, GASTEROSTEUS ACULEATUS

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An analysis of the metrics of *Schistocephalus solidus* infection of the threespine stickleback, *Gasterosteus aculeatus*, in Walby Lake, Alaska, showed that an epizootic ended between 1996 and 1998 and another occurred between 1998 and 2003. The end of the first epizootic was associated with a crash in population size of the stickleback, which serves as the second intermediate host. The likely cause of the end of that epizootic is mass mortality of host fish over winter in 1996-1997. The deleterious impact of the parasite on host reproduction and increased

host predation associated with parasitic manipulation of host behaviour and morphology to facilitate transmission might also have played a role, along with unknown environmental factors acting on heavily infected fish or fish in poor condition. The second epizootic was linked to relatively high levels of prevalence and mean intensity of infection, but parasite: host mass ratios were quite low at the peak and there were no apparent mass deaths of the host. A number of abiotic and biotic factors are likely to interact to contribute to the occurrence of epizootics in *S. solidus*, which appear to be unstable and variable. Epizootics appear to depend on particular and, at times, rare sets of circumstances.

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SIZE CORRELATIONS BETWEEN SUCKING LICE AND THEIR HOSTS INCLUDING A TEST OF HARRISON'S RULE

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Ectoparasite size can be influenced by many factors; one is host size. Harrison's rule states that larger hosts typically have larger parasites. In this study, sucking lice (Insecta: Anoplura) were used to test this rule. Sucking lice should provide a good test for this rule because they are generally host-specific and because, as a group, they parasitize hosts of different sizes. Also, sucking lice use their tibio-tarsal claws to grasp host hairs; therefore, correlations between claw size and host hair diameters were also tested. Raw analyses for 206 species of slide-mounted sucking lice from throughout the world, followed by analyses of phylogenetically subtracted data, were used to test the hypotheses that sucking louse body size is correlated with host body size and that sucking louse claw size is correlated with host hair diameters. Data from 3 louse families, Hoplopleuridae, Linognathidae and Polyplacidae, were also analyzed separately. Raw data showed that louse body and claw size were positively correlated with host body and hair size, respectively. However, after phylogenetic subtraction, the overall data showed that another indicator of louse size, female louse second tarsal segment length, was positively correlated with both host body mass and length. Within the family Hoplopleuridae, both male and female louse thorax width was significantly correlated with host body mass and length, and with second tarsal segment length and host body length. Within the family Polyplacidae, male and female thorax width was positively correlated with host body length. Phylogenetically subtracted data revealed significant positive correlations for the families Hoplopleuridae and Polyplacidae between indicators of host and louse size. Overall, the data support the hypothesis that sucking lice have adapted morphologically to their hosts and conform to Harrison's rule.

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APOPHALLUS SP. METACERCARIAE IN COHO SALMON AND ASSOCIATIONS WITH OVER WINTER SURVIVAL IN A COASTAL RIVER IN OREGON

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For the last several years we have been evaluating the distribution and abundance of parasites in

coho salmon (*Oncohrynchus kistuch*) parr (underyearlings) and smolts (yearlings destined for ocean migration) in various coastal rivers in Oregon. Our goal was to determine the impact of certain parasites on the survival of these. Evaluating parasite-associated mortality on salmon populations is challenging. It is often difficult to obtain large numbers of fish samples and samples from various times may not represent the same population. We observed an extremely high abundance of *Apophallus metacercariae* (Heterophyidae) in the muscle of parr from multiple years from the lower main stem of the West Fork Smith River. Infections from ranged from 340-4,666 parasites/fish. In contrast, parr from upstream sites showed 0-342 parasites/fish. Other researchers have attributed poor overwinter survival of these parr to strong currents and poor habitat. We suggest that parasites may also play a role. Out migrating smolts collected each year in the following spring from a trap in the river mouth showed only 0-10 parasites/fish. In laboratory studies we previously demonstrated than there is minimal elimination of metacercariae from the parr to smolt stage. Given that there was only 10% overlap in abundance between main stem fish and smolts, probably only the very lightly infected parr from the main stem population survive to smolt stage. We analyzed smolt data compiled from multiple years using a variation of Crofton's truncation of the negative binomial. We concluded that the threshold of parasite associated mortality was approximately 400 metacercariae. As only 5% of the main stem parr had an abundance below this, the analysis suggests that most of these parr do not survive over the winter until smolt stage. The lower main stem of this river has been heavily logged and has high summer temperatures. The latter may directly enhance snails and *Apophallus* reproduction, which may explain the noteworthy abundance of this digenean in coho salmon at this location.

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THE ENHANCED ABILITY OF THE TYPE IIA STRAIN OF TRYPANOSOMA CRUZI TO BE CONGENITALLY TRANSFERRED IS CORRELATED TO ITS ABILITY TO INFECT PLACENTAL TROPHOBLAST CELLS

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Trypanosoma cruzi represents a genotypically diverse family of organisms with documented differences in tissue tropism and pathogenicity. Breeding experiments in mice comparing the relative abilities of North American isolates of Type I and Type IIa strains of *T. cruzi* to be congenitally transferred suggests that the Type IIa strain may have adaptations to facilitate transmission through the placenta. We describe here infection studies carried out in cultures of BeWo cells, an *in vitro* model for the human trophoblast cells barrier that form the interface between maternal and fetal tissues. Cultures of BeWo cells were exposed to either a Type I or Type IIa isolate of *T. cruzi* and assessed microscopically at 48, 72, and 96 hours for the percentage of trophoblast cells infected and the level of intracellular amastigote replication. Cultures exposed to the Type IIa isolate had a significantly higher percentage of infected cells, as well as higher average numbers of intracellular amastigotes. These differences in infection parameters between the two strains were lost when the procedure was repeated in DH-82 canine macrophages, suggesting that the Type IIa has adaptations that facilitate the invasion of placental tissues. This provides additional support that the Type IIa strain of *T. cruzi* that circulates in

North America may have evolved mechanisms to take advantage of congenital transmission in placental mammals.

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EVALUATION OF THE ROLES OF COMPLEMENT AND TEMPERATURE IN AVIAN RESISTANCE TO TRYPANOSOMA CRUZI INFECTION

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Although numerous mammalian species are known to serve as permissive hosts for *T. cruzi* infection, birds possess an innate resistance. Evidence suggests that the alternative pathway of the avian complement system is the mechanism largely responsible for this protection. In this study we used an *in vitro* system to assess the roles of complement and temperature in the killing *T. cruzi* epimastigotes (EMs) and blood stream form trypomastigotes (BSFs). We also made direct comparisons between avian sera to that of humans and raccoons (*Procyon lotor*), two permissive mammalian host species. Cultures of EMs and cBSFs were exposed *in vitro* to media containing 50% normal or heat inactivated serum for 1, 60, and 120 minutes at temperatures of 25, 37, or 40^0C. Parasite killing was then evaluated via hemocytometer counting at each temperature and time point and compared to control cultures in serum free media. Epimastigotes were greatly reduced by 60 min. in all cultures containing serum, regardless of species of origin, temperature, or heat inactivation. When cultures of BSFs were exposed to normal serum of humans and raccoons, parasite density declined approximately 30% by 60 min. at 37^0C. Under these same conditions, parasites in avian serum declined sharply within 1 min. of exposure, and the complete clearance of BSFs achieved after 60 min. Heat inactivation eliminated the ability of all three species of the sera tested to lyse BSFs at 25 and 37^0C. Interestingly, concentrations of BSFs cultured at 40^0C were greatly reduced independent of the presence of any serum in the media. These results confirm that a heat labile serum component contributes to the innate resistance to *T. cruzi* infection seen in birds. It also confirms that the complement system of mammals may possess some limited ability to lyse BSFs. More importantly, these results also suggest that the normal physiological body temperature of birds may contribute to their resistance, independent of serum proteins. This highlights the need for a greater understanding of the role of the fever in *T. cruzi* infected animals.

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COMPARATIVE PHYLOGEOGRAPHY OF TWO NEW ZEALAND INTERTIDAL SNAILS AND THEIR TREMATODES

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Comparing the phylogeographic structure of closely related host species can reveal the relative importance of common factors limiting their dispersal and unique events in their population histories. In addition, examining the geographic distribution of their parasites' genetic lineages can provide insights into the relative rates of gene flow and host-specificity within these systems.

The goals of the present study were to compare the broad-scale genetic structure of the New Zealand intertidal snails *Zeacumantus subcarinatus* and *Zeacumantus lutulentus*, determine the diversity of trematodes utilizing each species as first intermediate hosts throughout their ranges, and make preliminary investigations into the comparative geographic distribution of trematode genetic lineages versus host lineages. Analyses using cytochrome *c* oxidase subunit I (COI) gene sequences revealed strong genetic differentiation among populations of both snail host species. Both species possessed two major geographic groups of haplotypes (southern North Island/western North Island/northern South Island haplotypes versus the remainder of their distributions). The remaining *Z. lutulentus* haplotypes were localized on the eastern and northern North Island, while the more widespread *Z. subcarinatus* shared haplotypes among populations in the northern North Island and southern South Island. Diverse trematode assemblages were recovered from both host species, including representatives from the families Philophthalmidae, Echinostomatidae, Heterophyidae, Renicolidae, Microphallidae, and Schistosomatidae. Overall, trematode species were highly host-specific.

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HOST-FINDING BEHAVIOR OF BAT FLIES (DIPTERA: HIPPOBOSCOIDEA)

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Bat flies are obligate, blood-sucking, ectoparasitic Diptera that are exclusively adapted to bats. Recent research showed that bat flies are more host-specific than previously thought. Thus, finding the right bat species is critical, especially considering the ecology and biology of their hosts. Bats roost in clusters, and are moving targets, creating the need for multiple object separation and precise source identification for their parasites. This problem is further compounded by the peculiar reproductive strategy of these viviparous flies, which results in pupal deposition on a substrate removed from the host and the roost, thus continuously necessitating host-relocation. To date, only very few studies exist concerning bat fly host finding behavior. We here present behavioral data on the relative contributions of a variety of interacting sensory cues, including visual perception, olfaction, mechano-, and thermoreception. Specifically, we will address bat fly light responses and eye morphology, behavioral olfactory assays, as well as bat fly diurnal rhythms in the context of host activity and temperature.

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CHARACTERIZATION OF PFEXP-250, A NOVEL PLASMODIUM FALCIPARUM EXPORTED PROTEIN

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The pathogenesis of malaria, a prevalent and widely distributed infectious disease, is caused by the erythrocytic cycle of the parasite and is strongly correlated with export of *Plasmodium falciparum* proteins to the host cytosol and plasma membrane. *P. falciparum* causes the most

severe form of malaria in humans, with several hundred million infections each year and 1-3 million deaths. While most intracellular parasites grow in an active host, the asexual stages of the malaria parasite develop in a cell devoid of organelles or of a protein trafficking system. *P. falciparum* must remodel the erythrocyte by exporting proteins into the host cytoplasm and membrane. We have identified a novel *P. falciparum*-exported protein, PfEXP-250, which lacks a canonical N-terminal signal sequence and the obvious motifs described for PEXEL/VTS-positive and negative proteins. Our data show that PfEXP-250 is expressed and is exported to the host erythrocyte at all stages of the intraerythrocytic cycle. Moreover, we have shown that PfEXP-250 colocalizes and interacts with GBP130, a soluble PEXEL-positive *P. falciparum*-exported protein, RESA, *P. falciparum* skeleton-binding protein 1 (SBP1) and spectrin, a host cytoskeletal protein. This study identifies a novel *P. falciparum*-exported protein which interacts with PEXEL-positive and -negative *P. falciparum* proteins and the host cytoskeleton. Because PfEXP-250 lacks the motifs described in PEXEL/VTS-positive and -negative proteins, these data raise the likelihood of an additional export pathway in *P. falciparum*.

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EVOLUTION OF CRYPTIC COLORATION IN ECTOPARASITES

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The evolution of cryptic coloration is a classic example of evolution by natural selection. However, it has been studied almost exclusively in predator-prey systems, despite the fact that it may occur in other groups, such as ectoparasites of terrestrial or aquatic hosts. The principle defense of hosts against ectoparasites is grooming behavior, which has a visual component. Host-imposed selection should lead to the evolution of cryptic coloration if it helps ectoparasites escape from grooming. Here we use phylogenetically independent comparisons to show that avian feather lice (Phthiraptera: Ischnocera) have evolved coloration that matches the color of the host's plumage, except in the case of head lice, which are protected from grooming (preening). We further show that the colors of different subspecies of feather lice are correlated with the colors of their host species. Thus, cryptic coloration has evolved both within and between species of feather lice. Other examples of crypsis may exist among the 70,000 known species of ectoparasites that collectively represent five animal phyla.

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PREVALENCE OF TOXOCARA SPP. EGGS IN SOME PUBLIC PARKS OF MEXICO CITY

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Soil samples were collected from 8 public parks in Mexico City and examined for the presence of *Toxocara* spp. eggs. A total of 320 samples was analyzed using sedimentation (Ritchie method) and then the sediment was treated like feces sample with zinc sulfate flotation, and the

eggs were examined for their stage of development and viability. Overall, the samples were 15.93% positive for *Toxocara canis* and 3.6% for *Toxocra cati*. There was no significant difference in positivity among samples from different socioeconomic areas. The minimum and maximum number of eggs recovered from 20 g of soli was 1 and 3, respectively. The prevalence of non-embrionated and embrionated eggs was 73.33% and 26.67% in parks from middle socioeconomic zones, respectively, compared with 90.32% and 9.68% in parks from high socioeconomic zones. Viable eggs (eggs containing a motile L_2 larva) and therefore the risk of infection were present in both socioeconomic zones. Considering the high prevalence of this zoonotic parasite and its hygienic significance in causing human toxocariasis, particularly in children, plus the lack of control of stray dog populations, it is concluded that *T. canis* represents an overlooked public health risk in Mexico City.

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TRANSCRIPTOME PROFILES OF INTRAMOLLUSCAN DEVELOPMENTAL STAGES OF SCHISTOSOMA MANSONI IN BIOMPHALARIA GLABRATA

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Schistosomiasis is one of the world's great neglected diseases and remains deeply entrenched in many developing countries. It exemplifies a menacing, chronic, and debilitating infection with a life cycle that resists control. Schistosomes have a complex life cycle involving three highly divergent environmental niches; freshwater, the mammal host, and the snail host. Within the snail host, schistosomes undergo several distinct developmental stages, each of which must produce adequate defenses against ongoing assault by the snail's immune system. Currently, our understanding of the identity and succession of genes necessary for schistosomes to complete intramolluscan development is limited. A more complete characterization of this process could shed light on the parasite's general biology and on mechanisms of host-parasite compatibility, and could ultimately lead to a better understanding of how the parasite defends itself from the host, and how the parasite defends the host from invasion by other parasites and pathogens. Microarray analysis was used to profile *in vivo* intramolluscan developmental gene expression of *Schistosoma mansoni* in *Biomphalaria glabrata* snails. Total RNAs were isolated from infected snails 4, 8, 16, and 32 days post exposure (DPE) to probe arrays containing over 19,000 *S. mansoni* and *S. japonicum* target sequences. Single-channel array data was globally normalized using principal component analysis. Gene ontologies of the differentially expressed genes revealed a wide range of functions and processes, including various genes related to the trematode immune system and possible reaction to snail defenses. Since recent work has characterized the transcriptome profile of the host *B. glabrata* in response to infection with *S. mansoni*, our ultimate goal is to combine gene expression data from both parasite and host to test how the parasite-host unit responds to various biotic and abiotic perturbations.

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LOCOMOTION IN BULINUS TRUNCATUS IS ALTERED BY INFECTION WITH SCHISTOSOMA HAEMATOBIUM

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Bulinus truncatus serves as an intermediate host for *Schistosoma haemtobium,* a parasite capable of causing Schistosomiasis. This parasitic disease affects 200 million people globally. We investigate the effect of infection with *S. haematobium* on locomotion in the intermediate host *B. truncatus*. A total of 23 parasitized and 21 unparasitized snails were analyzed by being placed in clear plastic aquarium over a grid. Movements of each snail were recorded with a video camera over a ten-minute interval. Video clips of infected and uninfected snails were analyzed, compared and tested for differences in rate of travel, total distance traveled, rotation and rest phases. The total distance traveled, rate of travel and time in rest phases were not significantly different between the infected and uninfected snails. Unparasitized snails rotated a greater amount than infected snails and displayed less rest phases. Parasitized snails also displayed unique behavior in climbing walls when compared to unparasitized snails. Our results support alteration of the behavior of the snail host by the parasite as a result of infection. Previous studies of another human schistosome, *Schistosoma mansoni* and its intermediate host, *Biomphalaria glabrata* agree with these results. Understanding of this behavior may provide new implications for transmission and control.

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SEROPREVALENCE OF RICKETTSIA IN CANINES FROM TENNESSEE

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Rocky Mountain spotted fever (RMSF) is an important tick-borne disease throughout the southeastern United States and the most common tick-borne infection in Tennessee. RMSF is caused by *Rickettsia rickettsii*, a member of the spotted fever-group (SFG), and transmitted by *Dermacentor variabilis* ticks. Since 1990, RMSF incidence in Tennessee has increased making Tennessee one of the highest reporting states. In Tennessee a gradient is seen with increasing incidence from east to west. The reasons for this disease gradient remain elusive at this point. Domestic canines may be used as sentinels to assess geographic foci of RMSF. Additionally, dogs may play an important role in human RMSF as potential carriers of rickettsia-infected ticks. This study seeks to assess the prevalence *of Rickettsia* among dogs and relate canine prevalence to human RMSF cases. A survey was conducted to assess the seroprevalence of antibodies to *Rickettsia* among canines throughout the states of Tennessee. Serum samples were collected from 860 dogs and antibodies were detected using enzyme immunoassays (EIA). Samples were screened to assess rickettsial seroprevalence among the dogs in Tennessee. Preliminary data suggests that exposure to *Rickettsia* at the county level is 3-

64%. Our data indicate that *Rickettsia* exposure in domestic canines is wide-spread throughout the state of Tennessee.

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MICROSATELLITE AND ITS APPLICATION IN GENETIC STUDIES OF MALARIA PARASITES

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Microsatellites (MS) are simple sequence repeats (SSRs) such as (CA)n, (TAA)n, or (TA)n that have been found in all eukaryotes studied. MS are extremely abundance in the human malaria parasite *Plasmodium falciparum*, but the frequencies of MS are much lower in other *Plasmodium* species such as *Plasmodium vivax* and *Plasmodium yoelii*. MS are often polymorphic among parasite isolates because of variation in the length of the repeat. Genetic markers from MS have been employed to study population structure, evolution, transmission, and drug resistance of malaria parasites. Infections with multiple genotypes can be detected by typing 5-10 MS makers. Candidate drug resistant genes can be identified by searching for chromosomal regions with reduced MS diversity among drug resistant parasites, and the evolutionary history of a resistant gene among parasite populations can be investigated through analysis of MS haplotypes surrounding the resistant gene. MS are also useful for genetic mapping, particularly as genetic markers for typing DNA from progeny of genetic crosses. Although many high throughput methods such as microarray for typing single nucleotide polymorphism (SNP) and parallel sequencing are replacing MS in large-scale genome-wide studies, MS are still valuable for genetic studies of malaria and other parasites.

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VIRULENCE SHIFT IN A SEXUAL CLADE OF WILD TOXOPLASMA GONDII INFECTING MARINE MAMMALS

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Toxoplasma gondii-associated meningoencephalitis is a significant disease of California sea otters (*Enhydra lutris nereis*) and other marine mammals. *Toxoplasma* isolates have been obtained from Harbor Seals, California Sea Lions, and 80 California otters since 1998. Based on multi-locus PCR-DNA sequencing at 20 polymorphic genes across all 14 chromosomes, two distinct lineages have so far been identified: Type II and a new clade of strains, called Type X, that possess distinct alleles from archetypal strains at the majority of loci sequenced. Over 72% of marine mammal *Toxoplasma* infections were of Type X. No Type I or Type III genotypes were identified. Type X strains have also been identified infecting a variety of terrestrial animals

in the US, including humans and coastal bobcats and mountain lions, definitive hosts for this parasite. Phylogenetic analyses separated the Type X *Toxoplasma* isolates from archetypal Type I, II and III strains. When assayed through mice, a distinct subset of Type X strains were highly virulent in mice (LD_{100}= 1 parasite). The genetic basis for the altered virulence patterns among Type X strains is currently being assessed and will be presented.

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GENETIC CHARACTERIZATIONS OF CRYPTOSPORIDIUM SPP. USING MICROSATELLITE AND MINISATELLITE MARKERS

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Microsatellites and minisatellites are abundantly present in the small *Cryptosporidium* genome, most of which code for amino acids. They have been used to study population structure, host specificity, transmission, and virulence of *Cryptosporidium* spp. One of the most commonly used microsatellite markers is the gp60 gene, which is widely used in subtyping the two common human-pathogenic *Cryptosporidium* spp., *C. hominis* and *C. parvum*. Field molecular epidemiologic investigations have shown differences in clinical presentations, virulence, and outbreak potential among *C. hominis* subtype families. Likewise, host-adapted subtype families are present in *C. parvum*, which is responsible for reduced potential for both cross-species transmission of cryptosporidiosis among animals and zoonotic transmission of cryptosporidiosis in humans, especially in developing countries. Multilocus sequence typing (MLST) tools based on gp60 and other microsatellite and minisatellite markers have been developed to assess the population structure of *C. parvum* and *C. hominis* and track the temporal and geographic spread of pathogens. Their usage in epidemiologic investigations has significantly improved our understanding of the transmission of cryptosporidiosis in both outbreak and endemic settings. Genetic mapping of virulence genes on chromosome 6 (1.3 Mb) using microsatellite markers and analyses of haplotype diversity (Hd), linkage disequilibrium (LD), and extended haplotype homozygosity (EHH) suggests that the region surrounding gp60 is probably associated with the virulence of *C. hominis*. Thus, microsatellite and minisatellite analyses can provide valuable insight into cryptosporidiosis epidemiology.

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A TALE OF TWO THEILERIAS: MICROSATELLITE GENOTYPING, WILD ANIMAL RESERVOIRS AND VACCINATION

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The availability of the genome sequences of *T. parva* and *T. annulata* has facilitated a wide range of new research areas with these two parasite species. In terms of population biology and molecular epidemiology this has allowed the characterisation of highly polymorphic micro and minisatellite sequences which can be used to address both fundamental and more applied

questions. This paper will review our current state of knowledge of the molecular epidemiology of these parasites and illustrate how such markers have been used to address the following questions: (1) How frequently does genetic exchange occur and are populations sub-structured? (2) How diverse are infections and what is the multiplicity of infection? (3) Are wild buffalo a source of infection for cattle? (4) What are the consequences of live vaccination on parasite transmission and diversity? (5) Is there evidence for strain specific immunity? The conclusions will be discussed in relation to future developments in technology and how these could be applied to address some of the un-answered questions.

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STUDYING GENETIC DIVERSITY IN EIMERIA-PRESENT CHALLENGES AND FUTURE APPROACHES

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Coccidiosis in chickens remains the single most important parasitic disease afflicting the poultry industry. Although phenotypic, and limited genotypic differences between the *Eimeria* that cause the disease have been described, only anecdotal evidence has been presented describing intra-species diversity. It has long been thought that sufficient diversity exists among *Eimeria maxima* that immunizing birds with one isolate may not provide protection against a challenge with a second isolate. However, this diversity has never been documented at a molecular level. The difficulty in carrying these studies in *Eimeria* has been several-fold. First, it is difficult to establish, propagate, and maintain pure isolates. Additionally, other approaches such as Random Amplification of Polymorphic DNA **(**RAPD) and Amplified Fragment Length Polymorphism (AFLP) have very low reproducibility. Approaches, such as identification of Single Nucleotide Polymorphisms (SNPs) at a specific locus have not yielded any "strain-specific" differences. In the last several years, great steps have been achieved in the ability to produce whole genome sequence using Illumina technology. It is possible that using this technology can help us not only determine the genome sequence of additional *Eimeria* species, but also the techniques utilized in related protozoa (e.g. *Plasmodium*, *Toxoplasma*) for which whole genome sequences are available can be extended to identification of strain differences among species. Current research toward achieving this goal will be discussed in relation to studies of *E. maxima* diversity.

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PARASITES AS METACOMMUNITIES: USING EXPERIMENTS AND MULTI-SCALE FIELD DATA TO UNDERSTAND VARIATION IN RIBEIROIA INFECTION AND AMPHIBIAN MALFORMATIONS

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Amphibians serve as intermediate or definitive hosts for a diverse assemblage of helminth parasites. Among those that use amphibians as intermediate hosts, the trematode *Ribeiroia ondatrae* has emerged as one of the more pathogenic species, causing both mortality and severe limb malformations in a variety of frogs, toads, and salamanders. Recent experimental and field work has helped advance our understanding of infection dynamics and the factors that control variation among host species and individuals. Differences in the levels and timing of parasite exposure, for example, help to explain variation in pathology among individuals within a species, among species within a community, and between years at a wetland. Experimental results also indicate that host species can vary in infection resistance and tolerance, such that the composition of amphibian communities can profoundly affect parasite transmission and host pathology (e.g., the 'dilution effect' hypothesis in which more diverse communities engender a reduction in overall transmission). More challenging, however, have been efforts to understand the relative importance of factors that control host-parasite interactions in natural systems and how they vary as a function of scale. Alongside changes in amphibian host communities, wetlands vary in abiotic and biotic characteristics, including water chemistry (nutrients and pesticides), parasite community, and non-host community (including predators and decoys). Ultimately, interactions among these factors will combine to determine local and regional patterns of parasite abundance and malformations. Using *Ribeiroia*-amphibian interactions as a case study, we emphasize the importance of coupling mechanistic experiments with a 'disease metacommunity approach', in which host-pathogen-environment interactions are compared across multiple spatial scales (i.e., wetland, landscape, continental). This approach has already provided valuable insights into the dynamics of communities of free-living organisms and holds great application potential for parasite ecology. The increasing availability of data and models to apply this approach will facilitate a broader understanding of the scale-dependency of transmission and the determinants of spatial variation in environmental 'hotspots'.

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INTERACTIONS BETWEEN AGRICULTURAL ACTIVITY AND THE PARASITE FAUNA OF FROGS: NOT ALL PARASITES ARE EQUAL

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Agricultural activities can affect the parasite communities in amphibians. A reduction in parasite diversity and infracommuntity species richness in metamorph leopard frogs (*Lithobates pipiens*)

and adult bullfrogs (*Lithobates catesbeianus*) was associated with use of pesticides and agricultural development. In both host species, nematodes with direct life cycles and echinostomes were more common in agricultural wetlands contaminated with pesticides than in reference wetlands. In contrast, the lungflukes *Haematoloechus* spp. were more abundant in reference wetlands, which may be linked to the distribution and abundance of their odonate second intermediate hosts. Mean infracommunity richness in both frog species was negatively correlated with the agricultural and urban area immediately surrounding the wetlands. This is believed to be due to fragmentation of the landscape, limiting access to the wetlands by various avian and mammalian definitive hosts. Results suggest that pesticide exposure affects certain aspects of the immune response, but it is difficult to disentangle ecotoxicological from ecological effects. Furthermore, parasitic infections may affect the immune response and other biomarkers of animal health in a context-dependent fashion, leading to unpredictable interactions between effects of parasites and pesticides.

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PARASITE TRANSMISSION TO LARVAL AMPHIBIANS IS REDUCED BY ALTERNATIVE NATIVE AND NON-NATIVE HOSTS AND PREDATORS

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Parasites and hosts interact with a diverse community that can influence transmission. The dilution effect hypothesis describes the reduction in disease risk due to biodiversity. Current investigations of this hypothesis have focused on the effect of alternative hosts on vector-borne diseases. However, parasites with free-living stages, such as trematode cercariae, provide a good model to examine mechanisms of the dilution effect. Two important mechanisms are predation leading to increased mortality of free-living stages and alternative hosts leading to encounter reduction. To evaluate the effects of predators and alternative hosts on transmission, we measured the ability of aquatic invertebrate and vertebrate predators to consume or serve as alternative hosts for *Ribeiroia ondatrae* in the laboratory. To determine if these mechanisms influenced transmission to Pacific chorus frog (*Pseuacris regilla*) hosts, we conducted a second experiment in which tadpoles were exposed to *R. ondatrae* cercariae alone, in the presence of predators/alternative hosts, or predator/alternative host effluent (to simulate presence but without consumption or infection). The predator survey showed that approximately 15% of cercariae remained after trials with California newts (*Taricha torosa*) or non-native mosquitofish (*Gambusia affinis*), whereas ~40% remained after trials with California clam shrimp (*Cyzicus californicus*) or damselfly nymphs (Lestidae and Coenagrionidae). Necropsies revealed that 65% of cercariae removed had infected the newts. In the transmission experiment, damselfly nymphs reduced transmission of *R. ondatrae* to tadpoles by 50% compared to controls without predators present. However, mosquitofish did not significantly influence transmission, either as predators or alternative hosts. Collectively, these results show that members of the broader community can significantly influence parasite transmission. Describing the significance of community structure on the transmission of trematode parasites is important considering biodiversity loss and species invasions.

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EFFECTS OF NATURAL AND ANTHROPOGENIC FACTORS ON AMPHIBIAN EXPOSURE AND SUSCEPTIBILITY TO TREMATODE INFECTIONS

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Previous research has shown that the herbicide atrazine and fertilizer can increase amphibian trematode infections, but we still lack a broad understanding of how natural factors, such as seasonality, competition, and predation, or agrochemicals, in general, affect amphibian exposure and susceptibility to trematodes. Here I present an overview of four experiments intended to address these aims. In experiment one, increasing tadpole density increased the number of metacercarial infections in tadpoles, despite no evidence for stress-induced immunomodulation. Instead, this effect was explained by competition delaying tadpole development, which increased both the duration of exposure to cercariae and susceptibility to infection, because tadpoles spent more time in highly susceptible early stages. In study two, we used a combination of a field survey, lab experiment, and modeling to reveal that the best predictor of the age-metacercarial-intensity relationship in tadpoles was seasonality of cercarial shedding from snails (first intermediate host), followed secondarily by stage-dependent susceptibility. In experiment three, we examined the effects of 12 pesticides, at expected environmental concentrations, on amphibian exposure and susceptibility to trematodes. There were two pesticide types (insecticides and herbicides), two classes within each pesticide type (triazine herbicide, chloroactenilide herbicide, carbamate insecticide, organophosphate insecticide), and three different pesticides in each of the four classes. We generally found consistency in responses within pesticide classes. Organophosphate insecticides and triazine herbicides increased the abundance of snails through top-down and bottom-up effects, respectively. By delaying development, herbicides, in general, increased time at early, trematode-susceptible stages where eosinophil densities were low. In experiment four, we examined how atrazine and fertilizer alone and in combination affect potential exposure to trematodes by quantifying the abundance of three different snail species. Atrazine generally elevated snail abundance, but the combination of atrazine and fertilizer caused a 40-fold, synergistic increase in the abundance of *Planorbella trivolvis* snails. These experiments reveal general mechanisms, such as seasonality, stage-dependent susceptibility, and top-down and bottom up effects on exposure, by which natural and anthropogenic factors can alter amphibian trematode infections.

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LAND USE AND PATTERNS OF PARASITISM IN AMPHIBIAN HOSTS

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Depending on the type of land use and the life histories of parasites and hosts, parasitism may increase or decrease in response to changes in land use patterns. For amphibians, the interactions between parasites and pathogens, the environment, and host immunity are becoming key issues in understanding threats to amphibian welfare. The conversion of natural habitats to agricultural or urbanized landscapes can influence both water quality in amphibian habitats and the surrounding faunal communities. These changes can result in shifts in the abundance of hosts for complex life cycle parasites, direct effects on free-living parasitic stages in the environment, and/or impacts on amphibian immune systems. By comparing several studies of amphibian parasite responses to land use disturbances, this study presents a synthesis that informs the overall impacts on amphibians. Trophically transmitted parasites that use amphibians as intermediate hosts will often respond to land use-imposed changes mediated by the response of the definitive host vertebrates (e.g. birds, mammals, and reptiles that prey on amphibians) and intermediate hosts (e.g. molluscs and insects). In highly disturbed sites devoid of vertebrate activity, these parasites may be absent, but amphibians often have to contend with poor water quality and toxicants. Alternatively, parasites that use amphibians as definitive hosts respond to land use-imposed changes mediated by the response of intermediate hosts. In this case, parasites can be significantly more abundant in agricultural, nutrient-rich water bodies. Overall, land use disturbances can create parasite "hotspots", challenge amphibian immune systems with toxicants, or allow both sets of problems to act concurrently.

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INTERACTIONS OF ENVIRONMENTAL STRESSORS IMPACT SURVIVAL AND DEVELOPMENT OF PARASITIZED LARVAL AMPHIBIANS

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Infected hosts are exposed to many environmental stressors that must be taken into account in order to determine the importance of disease, as various combinations can interact in unpredictable ways. Here, northern leopard frog (*Lithobates pipiens*) tadpoles, a species in decline, were exposed to stressors singly or in combination. Stressors included infection by *Echinostoma trivolvis* (a trematode), exposure to predator chemical cues (larval dragonflies), and exposure to varying concentrations of the herbicide atrazine. Parasitism decreased survival only in combination with exposure to 3 µg/L atrazine, with a negative interaction observed for mass as well. Similarly, a negative interaction of parasitism and predation on survival occurred. These results indicate that certain stressor combinations are particularly deleterious for young parasitized tadpoles. Notably, very common low-intensity parasite infection can be particularly

harmful in certain situations. Such negative impacts on larval amphibians in certain scenarios may contribute to ongoing amphibian population declines, emphasizing that the combination of environmental stressors must be considered when evaluating the general role of disease in species extinctions.

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TEMPERATURE-DRIVEN CHANGES IN RIBEIROIA INFECTION: CONSEQUENCES FOR PARASITE TRANSMISSION AND AMPHIBIAN PATHOLOGY

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The complexity of many parasite life cycles and uncertainties associated with climate predictions make understanding the net effect of climate change on host-parasite interactions challenging. Warmer temperatures may enhance parasite transmission as well as the immune response of ectothermic hosts, and mechanistic studies of the influence of temperature on host-parasite interactions can clarify which aspects of transmission dynamics are most likely to be influenced by changing climate. We assessed short-term transmission success in 60 *Pseudacris regilla* tadpoles exposed to 25 *Ribeiroia ondatrae* cercariae at three temperatures (17, 20, and 26 °C) by filtering the water for parasites after 45 minutes of exposure, and dissecting all tadpoles after 48 hours. We exposed an additional 96 tadpoles to 28 *R. ondatrae* to measure the long-term effects of temperature on infection and malformation levels at metamorphosis. The highest temperature significantly enhanced both transmission efficiency and tadpole immune response. In the 26°C treatment, 66% of parasites penetrated tadpoles compared to 53% at 17°C; however, a lower proportion of parasites that penetrated tadpoles successfully encysted inside the tadpoles at warmer temperatures. While there were no differences in survival among treatments at metamorphosis, parasite-induced deformities were highest in the 20°C treatment. Tadpoles in the cooler treatments were at earlier developmental stages on average during the 9 day infection period. Malformation prevalence may have peaked at the middle temperature treatment because infection of early-stage hosts at cooler temperatures increased the likelihood that they would develop malformations, but lower temperatures also reduced transmission efficiency. The changes in transmission efficiency and immune response along with changes in the developmental rates of both hosts and pathogens in response to changing temperatures may translate into altered amphibian pathology under future climate change.

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INTERACTIONS AMONG ABIOTIC FACTORS, AMPHIBIAN COMMUNITY STRUCTURE AND ADULT HELMINTH LIFE CYCLE STRATEGIES

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Previous studies on helminth communities of amphibian hosts indicate that most amphibian parasites are not host specific and are associated with host habitat. Aquatic amphibian species are

dominated by trematodes, whereas terrestrial amphibian species are dominated by nematodes, and semi-terrestrial amphibian species are infected with a combination of trematodes and nematodes. We examined the helminth communities of aquatic, semi-terrestrial, terrestrial, semi-arboreal, and arboreal amphibian species from three different ecological habitats differing in their amphibian species composition and amount of annual precipitation. Our results indicate that in a moist environment amphibian helminth communities were dominated by trematodes and direct life cycle nematodes that develop in the soil, whereas amphibian helminth communities in a dry environment were dominated by trematodes. However, in a semi-dry environment direct life cycle nematodes switched hosts from terrestrial amphibians to aquatic and semi-terrestrial amphibians. In order to understand how amphibians become infected with different helminth species, we completed the life cycles of ten species of trematodes and a two species of nematodes in multiple species of hosts varying in ecological habitats, to determine their host specificity and life cycle plasticity. Our study indicates that transmission events are favored by regional environmental conditions and definitive host species composition where factors influence probabilities of transmission at one or more stages during their life cycle. These data allows us to generate hypotheses about the mechanisms that drive transmission events in amphibian parasite life cycles.

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METAGONIMOIDES OREGONENSIS (FAMILY: HETEROPHYIDAE) INFECTION IN AMPHIBIANS

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We know very little about most of the hundreds of trematode species that use amphibians as either intermediate or definitive hosts. One of these little known trematodes is *Metagonimoides oregonensis* (Family: Heterophyidae), which was first described in 1931. *Metagonimoides oregonensis* uses raccoons and mink as definitive hosts, and stream snails and amphibians as intermediate hosts. Some variation regarding the life cycle has been noted for populations across the range in the U.S., specifically in terms of whether cercariae can develop directly into metacercariae within the rediae in the snail host. We have been studying *M. oregonensis* in Virginia and North Carolina for the past several years. In this part of the range, *Desmognathus* spp. stream salamanders are commonly used as second intermediate hosts. We have found individual salmanders with over 1000 metacercarial cysts, which form in between the muscle fibers throughout the body. There is a strong correlation between the number of visible cysts on live salamanders and the total number of cysts identifiable after clearing and staining, which will allow us to study infection dynamics in natural salamander populations over time using mark-recapture techniques. We have experimentally examined the ability of *M. oregonensis* cercariae from North Carolina to infect *Rana* spp. tadpoles, which are a natural host of *M. oregonensis* in the Western U.S., but did not see any evidence of infection. Landscape level surveys of first intermediate host snail infection in streams indicate large variation in infection prevalence among sites, but GIS analysis did not indicate any correlations between snail infection prevalence and land cover. We still have a lot to learn about the causes and consequences of

infection with *M. oregonensis* in amphibians, but work in this system shows promise for elucidating the abiotic and biotic factors that can impact infection dynamics.

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ECOLOGICAL EQUIVALENCE OF TWO TERRESTRIAL SNAILS AS SECOND INTERMEDIATE HOSTS OF PANOPISTUS PRICEI (TREMATODA)

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Panopistus pricei (Trematoda) occurs in shrews in North America and uses terrestrial gastropods as both first and second intermediate hosts. In southeastern Nebraska, metacercariae of *P. pricei* are found commonly in *Neohelix albolabris* and *Webbhelix multilineata*. Because of their similar size and ecological habits, it was hypothesized that *N. albolabris* and *W. multilineata* are ecologically equivalent second intermediate hosts of *P. pricei*, and a field study was conducted to test this hypothesis. At the microhabitat level, metacercariae were distributed similarly in the kidneys and primary ureters of *N. albolabris* and *W. multilineata*. Prevalence and mean abundance did not differ between host species at any of 6 sites, nor did the relationship between host size and parasite abundance. Prevalence in *N. albolabris* was tightly correlated with prevalence in *W. multilineata* across sites; the same was true for mean abundance. The slope of each relationship was very close to 1.0, suggesting nearly exact ecological equivalence of these two snail species. The only results inconsistent with ecological equivalence were analyses of demographics of worms at 2 of 6 sites, but it is not known whether the observed differences persist or are transient. Overall, the study suggests that *N. albolabris* and *W. multilineata* are equivalent second intermediate hosts of *P. pricei* in southeastern Nebraska.

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ECOLOGY OF ANGUILLICOLOIDES CRASSUS INFECTING THE AMERICAN EEL (ANGUILLA ROSTRATA) IN CAPE BRETON, NOVA SCOTIA

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The American eel (*Anguilla rostrata*) is listed as 'Special Concern' by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), and it is currently being considered for listing under the federal Species at Risk Act (SARA). It is believed that the North Atlantic Oscillation (NAO), as well as natural causes such as migrational barriers, habitat loss, reduction in available prey, and predation may be affecting recruitment and survival of these eels. In addition, it has been suggested that infection by the swimbladder parasite, *Anguillicoloides crassus* (Kuwahara, Niimi et Itagaki, 1974), is playing a role in the decline of American eel. Infection of the swimbladder by *A. crassus* can cause thickening, disruption, or even rupture of the bladder wall, secondary bacterial infections, decreased host activity level, and possibly interfere with eel migration to spawning grounds in the Sargasso Sea. In the summer of 2007,

American eels, from 2 localities on Cape Breton Island were found to be infected with *A. crassus* and this prompted a more extensive survey in 2008 on the distribution of this exotic parasite throughout Cape Breton Island. During 2008 and 2009, 29 localities around Cape Breton Island were examined for *A. crassus*. Prevalence of *A. crassus* on Cape Breton was 43.1%, having a mean intensity of 4.5 ± 5.0, with a maximum of 32 nematodes being found in one eel from the Mira River. Analysis of *A. crassus* mitochondrial DNA identifies Japanese populations of the nematode to be the most similar, suggesting that invasion of Cape Breton eels did not occur via Europe but rather from Asia or the eastern US. These scenarios are discussed.

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INHERITANCE OF SCHISTOSOMA MANSONI INFECTION INCOMPATIBILITY IN BIOMPHALARIA ALEXANDRINA SNAILS

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This work aimed at studying the inheritance of susceptibility and resistance in the first generation of crossbred *Biomphalaria alexandrina* snails to *Schistosoma mansoni* infection, for use as a control method for schistosomiasis. Laboratory bred snails were infected with S. *mansoni* miracidia and examined for cercarial shedding to determine susceptibility and resistance. Five parental groups were used; Group I contained 30 susceptible snails, group II contained 30 resistant snails, group III contained 15 susceptible and 15 resistant snails, group IV contained 27 susceptible and 3 resistant snails, while group V contained 3 susceptible and 27 resistant snails. The percentage of resistant snails in the resulting progeny varied according to the ratio of susceptible and resistant parents per group, being 7%, 100%, 68%, 45%, and 97% from groups I, II, III, IV, and V respectively. On increasing the parent resistant snails, the percentage of their progeny that were resistant increased, while cercarial production of their susceptible progeny decreased.

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TEMPERATURE QUOTIENT Q10 AND TREMATODE LARVAL STAGES OF EMERGENCE, SURVIVAL, AND INFECTIVITY

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Q10 is a formula that measures the change in metabolic or other biological processes over a change in temperature. As a rule, metabolic processes double with an increase in 10^{o} giving a Q10 of 2. A Q10 of 1 indicates no or little effect of temperature and Q10s much higher than 2 are considered to be unusual or out of balance. Poulin (Parasitology, 2006: 236:151) reported 1/3 of Q10s that were calculated from the literature at "around" 20^{o} C for cercarial emergence from molluscan hosts. Emergence is only one facet of a larval trematode's cycle; survival of cerariae outside the host and cercarial (or miracidial) infectivity being two other important stages. Q10s presented herein were calculated for all three stages for all temperature ranges found in the

literature with N = 81 for emergence, 51 for survival and 45 for infectivity. Emergence was found to have the highest percentage of Q10s of >5 (43%), followed by Infectivity (38%), and survival (10%). Q10 averages and SD were emergence 21 ± 62, survival 3.4 ± 5.1 and infectivity 20.6 ± 37. Survival Q10 was found to be statistically different from emergence and infectivity (*P* = < 0.001) but there was no difference between emergence and infectivity. The Q10 values were subdivided into three categories by temperature range, 10 - 20, 20 - 25, and >30° C. The majority of Q10s, but not all, were in the 0 - 20° C range. Emergence and infectivity involve interaction between both a host and the trematode which may influence production of high Q10s whilst survival involves only the parasite. The high Q10s in the 10 - 20° C range may represent an acceleration process geared to environmental changes to reach an optimum metabolic rate.

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GLOBAL WARMING MEETS PARASITOLOGY: OR NOT?

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A report in 2006 (Parasitology 132:143) used data from the literature on emergence of trematode larvae from molluscan hosts at different temperatures to calculate Q10 values. Many of these values were much higher than normal leading to the conclusion that such increased reproduction due to a rise in temperature would result in more human and veterinary trematode infections as a result of global warming. However, emergence is only one factor in the trematode life cycle that affects population numbers. Survival of cercariae and miracidia in the external environment and infection of the next host are also important factors. A review of the literature presented herein shows that although emergence increases with increasing temperature it may also reach an apex and decrease. Survival, however, rapidly decreases. Infectivity also increases but also decreases at increasing temperatures. As some have pointed out, the effect of all three stages results in a trade-off which may be different depending upon the trematode species. Too many variables involving temperature effects on trematode larvae are involved to make any valid generalizations regarding the effects of future global warming on increasing trematode infections.

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A NEMATOMORPH PARASITE EXPLAINS VARIATION IN TERRESTRIAL SUBSIDIES TO TROUT STREAMS IN JAPAN

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Nematomorph parasites alter the behavior of their orthopteran hosts, driving them to water and creating a source of food for endangered trout. We investigated whether nematomorphs could explain variation in the amount of terrestrial subsidy across several streams. In nine study streams, orthopterans composed the large fraction of the stomach contents of trout (46 ± 31% on average). Total mass of ingested prey per trout biomass positively correlated with the orthopterans ingested, suggesting that the orthopterans enhanced absolute mass of prey consumption by the trout population. The orthopterans ingested per trout biomass positively

correlated with the abundance of nematomorphs in the stream, but not with the abundance of camel crickets (the dominant hosts) around the streams. Streams in conifer plantations had fewer nematomorphs than streams in natural deciduous forests. These results provide the first quantitative evidence that a manipulative parasite can explain variation in the energy flow through and across ecosystems.

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ANTAGONISTIC EFFECTS OF COMPETITION AND CLIMATE MAINTAIN THE DIVERSITY OF AVIAN LICE

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Parasite diversity is often attributed to the specificity of parasites, reflecting unique adaptations to particular features of the host. Other biotic and abiotic factors also have the potential to influence host use, but these factors are more poorly understood. We investigated the influence of such factors on the specificity of two species of feather lice (Phthiraptera: Ischnocera) that share a single host species, the Mourning Dove *(Zenaida macroura)*. We show that relative humidity is responsible for restricting the range of one species, *Columbicola macrourae3*, to the more humid eastern U.S.A. The second species, *C. baculoides,* is restricted to drier regions of the western United States by *C. macrourae3,* which out-competes *C. baculoides* in competition experiments. Thus, arid conditions in the west provide *C. baculoides* with a climatic refuge from the competitively superior *C. macrourae3,* effectively doubling parasite diversity on this host. Reductions in humidity predicted to accompany global warming will likely exclude *C. macrourae3* from North America, allowing *C. baculoides* to spread across the continent, reducing parasite diversity on Mourning Doves. Ectoparasite communities on other terrestrial hosts may also be vulnerable to a loss of diversity in the face of climate change.

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EXPERIMENTAL DEMONSTRATION OF THE FITNESS COSTS OF AN INTRODUCED PARASITE OF DARWIN'S FINCHES

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Introduced parasites are a threat to hosts living on islands, where parasite-mediated extinction can occur before hosts have a chance to mount effective defenses. The parasitic fly *Philornis downsi*, recently introduced to the Galápagos Islands, feeds on nestlings of Darwin's Finches and other land birds. Several studies have reported inverse correlations between fly load and host fitness. However, a rigorous assessment of the direct impact of a parasite on host fitness requires experimental manipulation of the parasite. We conducted an experiment with medium ground finches *(Geospiza fortis)* to measure the direct impact of the fly, while controlling for other factors that may influence correlations between parasite load and host fitness. Our results show that *P. downsi* has a significant direct effect on nestling growth and fledging success. Only five of 24 (21%) heavily parasitized nests may have fledged young, compared to 12 of 24 (50%)

nests treated to reduce parasites (but not eliminate them entirely). Of these, only one of 24 (4%) heavily parasitized nests was confirmed to have fledged young, compared to 8 of 24 (33%) nests treated to reduce parasites. *P. downsi* is clearly a serious threat to Darwin's Finches and other species of Galápagos land birds.

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THE TRANSMISSION DYNAMICS OF CLONE ARMIES AND BEYOND: USING GENETIC DIVERSITY TO EVINCE THE COLONIZATION ROUTES OF LARVAL PARASITES

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Assessing the genetic diversity of parasite populations among and within hosts is essential to understanding the transmission dynamics of trematode parasites. Previous studies suggest two factors that may increase parasite diversity (both within and among species) during transmission to second intermediate hosts: vagility of the second intermediate hosts, and flow rate of the medium they live in. Freshwater echinostomes can occur in ponds with minimal water flow, so that the distribution of parasites is largely dependent upon the biology of the hosts. The freshwater snail, *Lymnaea elodes* can serve simultaneously as a first and second intermediate host, and additional snail species can be second intermediate hosts. We used microsatellite and mitochondrial markers to evince the colonization routes of larval parasites between the molluscan hosts (1st intermediate and second intermediate) in the parasite life cycle. We compared clonal diversity of infection for one parasite species, *Echinostoma revolutum*, as well as haplotype richness among echinostome species between first and second intermediate hosts. Simultaneous first and second intermediate hosts were dominated by a single *E. revolutum* clone, while second intermediate hosts with infected with a mix of clones. Similarly, echinostome haplotype richness was higher in second intermediate hosts as compared to first intermediate hosts. Relative to other parasite systems, low levels of clonal diversity were found in both first and second intermediate hosts. Yet, the within and between species haplotype diversity in individual hosts results in the simultaneous transmission of an array of larval parasites to vertebrate definitive hosts where sexual reproduction occurs. This mixing favors mating among diverse haplotypes within a species, and provides opportunities for potential hybridization events.

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EFFECTS OF FOREST FRAGMENTATION ON THE PREVALENCE OF THE BLOOD PARASITES IN BIRDS OF COSTA RICA

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Using the birds of Costa Rica, we determine how forest fragmentation, landscape mosaics, and the life history characteristics of avian hosts can affect the prevalence of haemosporidian blood parasites. Birds were sampled from 2004-2010 at Las Cruces Biological Station in southern

Costa Rica. Habitats include coffee plantations, riparian zones, undisturbed contiguous forest and disturbed forest fragments. Target species include 4 species of manakins, 2 thrush species and the silver-throated tanager. We have collected over 1200 blood samples from these birds. Some of these species are sedentary and others are highly vagile. Preliminary data show prevalences range from 0-55% for *Plasmodium* and *Haemoproteus* species. Some of the parasite lineages and their evolutionary relationships are described here for the first time. Interestingly, we find a paucity of parasites in recaptured birds. This study is unique in that avian blood parasites are studied in a single tropical habitat over multiple seasons.

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EVOLUTIONARY GENETICS AND GEOGRAPHIC VARIATION OF BAYLISASCARIS SPECIES IN NORTH AMERICA

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Species of *Baylisascaris* have frequently been reported from different mammalian host species in North America, often at high prevalence. *Baylisascaris procyonis* has been reported from raccoons throughout the United States and is considered to be an important agent of visceral larva migrans (VLM) with predilection for tissues of the human central nervous system. Despite their importance as potential causative agents of VLM, investigations of the systematics and genetic structure of *Baylisascaris* species have been limited.To address this problem, nuclear and mitochondrial gene sequences were used to delimit species, assess host-fidelity of species, infer phylogenetic relationships, and examine geographic variation of mitochondrial DNA from *Baylisascaris* samples obtained from ten U.S. states. Population samples of *Baylisascaris* from raccoons (*B. procyonis*) and skunks (*B. columnaris*) were characterized for a species-diagnostic region of ITS ribosomal DNA (by sequence or RFLP-typing), and individuals were sequenced for a region of *cox*-1. Most individuals of *B. procyonis* and *B. columnaris*, as assessed by genetic markers, showed fidelity to their expected definitive host species. However, 10 individual nematodes from raccoon hosts were hybrids as assessed by ITS ribosomal DNA. These hybrid individuals included mtDNA haplotypes from both *B. procyonis* and *B. columnaris*, indicating that females of both species had mated with males of the other species. Geographic distributions of mtDNA variation in populations sampled in the eastern and midwestern U.S. suggest that *B. procyonis* and *B. columnaris* have been characterized by high levels of gene flow, perhaps reflecting the high vagility and recent geographic expansion of host populations. In contrast, some highly divergent mtDNA haplotypes were discovered in the western United States, indicating geographic and/or historical discontinuities.

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RECOVERY OF 6 SPECIES OF THE THELASTOMATOIDEA (NEMATODA: OXYURIDA) BELONGING TO 6 DIFFERENT GENERA IN A WILD POPULATION OF THE PEPPERED COCKROACH ARCHIMANDRITA TESSELATA

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Six species of thelastomatid pinworms belonging to 6 different genera were collected from the peppered cockroach *Archimandrita tesselata* at the Area de Conservación Guanacaste, Costa Rica, from 2003 to 2006. A new species of *Aoruroides* was recovered. This species differs from other described members of this genus in having different morphological dimensions including a shorter esophagus than that of *A. philippinensis* (Chitwood and Chitwood, 1933) and *A. queenslandensis* Jex, Cribb, & Schneider, 2004, longer esophageal corpus and isthmus than in *A. legionarius* Kloss, 1966, and a much shorter male tail than that of *A. legionarius*. The five additional species recovered included *Buzionema validum*, *Protrelleta floridana*, *Cranifera cranifera*, *Hammerschmidtiella* sp., and an unknown Thelastomatidae sp. These species are redescribed by light and scanning electron microscopy and constitute new host and geographic records.

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THE PARASITE ASSEMBLAGES OF DIDELPHID MARSUPIALS ARE CLADE SPECIFIC

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Didelphidae (Marsupialia) includes 91 species distributed across the New World showing several lifestyles and morphological adaptations. However, the metazoan parasite assemblages are known for only a handful of large sized species that include the Virginia opossum and its relatives. I herein compare the structure of 13 parasite assemblages of large sized opossums present in nine different localities across the New World. These assemblages occur in four species that form a monophyletic group within Didelphinae. The effect of host phylogeny and habitat on the taxonomic structure and species richness of the assemblages was tested. First, qualitative similarity was calculated using the Jaccard similarity index comparing all possible pairs of assemblages. Second, an area cladogram approach was used to test the historic relationships among parasite assemblages. Third, the effect of host phylogeny on the structure of the assemblages was tested by linear regression under an independent contrast frame and finally, the effect of each of the nine localities on species richness was tested by Welch's ANOVA. Our results suggest that 1) species of parasites infecting marsupials depend on their localities, showing high levels of endemism; 2) sympatric species of marsupials share a high proportion of parasites (>60%), whereas assemblages occurring in co-specific marsupials from different localities share relatively few species, and 3) species richness of parasite assemblages occurring in didelphid opossums is not an attribute of the host species. Analysis of parasite faunas from

other species of marsupials with different habits and adaptations will help in determining the role of the locality and phylogeny on the historic associations between these metazoans in the New World.

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RE-DISCOVERY OF PITHOPHORUS TETRAGLOBUS AND PHYLLOBOTHRIUM MINIMUM IN RHYNCHOBATUS DJIDDENSIS

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The Giant guitarfish, *Rhynchobatus djiddensis* is the type host to five phyllobothriid tapeworm species: *Marsupiobothrium karbharii*, *Marsupiobothrium rhynchobati*, *Phyllobothrium minimum*, *Pithophorus tetraglobus* and *Spongiobothrium lintoni*. *Marsupiobothrium karbharii* , *M. rhynchobati* and *S. lintoni* should be considered *incertae sedis* members of their respective genera. Discovery of *P. minimum* and *P. tetraglobus* from specimens of *R. djiddensis* taken from the coast of northern Australia allows for a resolution of their systematic status. Type specimens of *P. tetraglobus* were examined, however, their condition did not allow for definitive resolution of bothridial morphology. Examination of the newly collected specimens of *P. tetraglobus* verified the presence of a prominent bothridal muscle bundle and a posterior bothridial opening. The proglottid morphology of the new specimens is also consistent with those of the type specimens. Examination of specimens of *P. minimum* revealed that they are consistent in morphology with species of *Orectolobicestus.* Scanning electron microscopy of the scolex of *P. minimum* will be critical so that the bothridial spinithrix morphology of it can be compared to that of *Orectolobicestus* species. Ribosomal DNA sequencing of both species is in progress.

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UNUSUAL FEATURES IN THE ACANTHOCEPHALA AS REVEALED BY SEM AND TEM

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A few unusual anatomical features and their functional relationships were observed in various species of Acanthocephala in the course of recent taxonomic studies. These include: (1) the para-receptacle structure in *Neoechinorhynchus qatarensis* collected from the flame parrot fish in the Arabian Gulf, among other eoacanthocephalans, (2) microtrichs on the tegument of *Rhadinorhynchus ornatus* collected from skip jack tuna in Pacific South America off the coasts of Ecuador, Peru, and Colombia, (3) striations in the proboscis hooks of *Rhadinorhynchus ornatus* collected from the same host and locations, (4) lobulation of the giant nuclei and its relationships with the reproductive cycle in eoacanthocephalans, (5) the reproductive function of the para-vaginal muscles in species of *Neoechinorhynchus* with subventral gonopore, (6) the

histolytic secretory/glandular function of the apical organ of the proboscis of *Polyacanthorhynchus kenyensis* from the body cavity of paratenic freshwater fish hosts in Lake Naivasha, Kenya, (7) the prominent expansion of the dorsal inner receptacle wall (PEDIRW) in the anterior proboscis of *Sphaerirostris picae* from magpie, *Pica pica*, in northern Iran. Additional unusual features in *Acanthocephalus lucii*, *Acanthocephaloides propinquus*, and *Acanthosentis tilapiae* are also presented.

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TAXONOMY OF ANTHOCEPHALUM SPECIES COLLECTED FROM SENEGAL, NORTHERN AUSTRALIA AND BORNEO

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The genus *Anthocephalum* was erected by Southwell (1925) for worms taken from the Roughtail stingray, *Dasyatis centroura* and the genus currently houses nine species. Species of *Anthocephalum* are most distinctively characterized by the marginally loculate morphology of their bothridia, in addition to the possession of a genital pore located in the posterior half of the proglottid and a sinuous vagina. Review of collections of *Anthocephalum* from additional dasyatid hosts have so far revealed seven new species of the genus. Two species have been identified from *Dasyatis* c.f. *centroura* and *D. margaritella* taken from the coast of Senegal. Four new species have been identified from *Himantura draco*, *H. jenkinsii*, and *Neotrygon kuhlii*, taken from the coast of northern Australia. A seventh species was collected from *H. pastinacoides*, taken from the coast of malaysian Borneo. Scanning electron microscopy of three of the new species revealed that the distribution of microtriches on their scolices is similar to those for existing species. These new species can be differentiated from one another and from existing species of *Anthocephalum* in characteristics such as total length, apical sucker diameter, marginal loculi number, proglottid dimenstions and testes number. The average ND1 sequence pair-wise distance between samples of five of the new species was 22 percent. Additional DNA sequencing of ND1 and lsrDNA for new and existing species of *Anthocephalum* is ongoing.

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HELMINTH DIVERSITY IN FISHES FROM OTSEGO LAKE, NEW YORK

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A survey of the helminth parasites of the fishes of Otsego Lake and nearby water bodies in Otsego County, New York was undertaken from September 2008 to the present in order to characterize species diversity. Otsego Lake, an oligotrophic finger lake, is part of the Mid-Atlantic drainage basin. It serves as the headwaters of the Susquehanna River, which drains into the Chesapeake Bay. Fish were collected by hook and line, seine or by gill net during fall, winter, spring and summer. Over three hundred individual fish representing nine species were necropsied for helminths. These included: *Micropterus salmoides* (Largemouth bass);

Ambloplites rupestris (Rock bass); *Lepomis macrochirus* (Bluegill); *Lepomis gibbosus* (Pumpkinseed); *Lepomis auritus* (Redbreast sunfish); *Perca flavescens* (Yellow perch); *Esox niger* (Chain pickerel); *Catostomus commersoni* (Common White sucker) and *Ictalurus nebulosus* (Brown bullhead). Multiple species of metazoan parasites were encountered, including nematodes (e.g., *Spinitectis*, *Philometra*), digeneans (e.g., *Clinostomum*, *Crepidostomum* and *Azygia*), cestodes (e.g., *Proteocephalus*), and acanthocephalans (e.g., *Leptorhynchoides thecatus* and *Neoechinorhynchus*). Fish helminth diversity (or lack thereof) is discussed with respect to other studies in similar North American lakes.

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DIVERSIFICATION OF SCHISTOSOMES: A SEARCH FOR PATTERNS

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Factors responsible for the evolutionary diversification of parasites remains poorly explored. Schistosomes display a range of morphological and reproductive variation, and use a range of phylogenetically disparate hosts. The dominant mechanisms responsible for the radiation of this group are not known. Phylogenetic patterns shed some light on possible mechanisms that might have been significant for the evolutionary diversification of this group of trematodes. *Trichobilharzia* and *Schistosoma*, the two most speciose genera in the family Schistosomatidae, highlight patterns that imply attributes that may have contributed to their radiation. Closely related species in each genus often differ in specialization of some features, for example, in reproduction and both intermediate and definitive host use. These differences when placed in a phylogenetic context permit us to estimate ancestral conditions and hence the direction of trends in degree of specialization that may have been significant in their radiation. Three major patterns that may have been significant in the radiation of these two genera will be discussed: host use, reproductive biology, and relative timing of diversification. For example, within *Schistosoma*, closely related species use congeneric snail hosts. However, in *Trichobilharzia*, some closely related species use different genera and families of snail hosts. Genetic differences between sister species of *Schistosoma* tend to be higher than those between *Trichobilharzia*. Therefore snail host use suggests that the range of ability to utilize snails so far is not reflected in genetic variation. But, species within the genus *Trichobilharzia* are presumed evolutionarily younger than *Schistosoma*. By contrasting the current data on phylogeny, biology, and distribution of *Schistosoma* and *Trichobilharzia*, it seems that the acquisition of novel snail hosts provides one of the major pathways leading to diversification.

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REVISION OF NUBENOCEPHALUS: CANALIZATION, PLASTICITY, AND MORPHOMETRIC CHARACTER ANALYSIS IN GREGARINE TAXONOMY

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Gregarines exhibit the 2 classic problems of alpha taxonomy in a diverse but poorly known group: first, taxa are diagnosed using unique suites of non-unique characters; and second, there is no consensus of relative character weight across taxonomic levels. Morphometric analyses are valuable pragmatic taxonomic tools in such systems and permit the accumulation of distinct taxa for larger scale character analysis within the group. The general utility of this strategy is demonstrated with a character analysis of species comprising *Nubenocephalus* (Apicomplexa: Eugregarinida: Actinocephalidae). Gregarines of the genus *Nubenocephalus* are primarily distributed in the New World and are known only from species of *Argia* (Odonata: Zygoptera: Coenagrionidae) in the Nearctic. Their host distribution expands to include species of *Hetaerina* (Odonata: Zygoptera: Hetaerinidae) in the Neotropics. Diagnosis within the Actinocephalidae has been confounded by the practice of heavily weighting suites of non-unique epimerite and gametocyst characters and a similar approach has been used in *Nubenocephalus*. The similarity and overlap of these characters in large population samples necessitates a more complex morphometric solution to species diagnosis within *Nubenocephalus*. This is a common taxonomic problem as known diversity within a genus increases: proliferating diversity reveals increasingly complex patterns of variation partitioned by an escalating diagnostic character set. Plane shape classification analysis reveals the uncorrelated plasticity in epimeritic characters as well as the relatively high level of canalization in oocyst and gamontic characters. Distinct and consistently diagnosable differences between species are established using centroid cluster analyses.

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EVALUATION OF SYNLOPHE AND BURSA AS TAXONOMIC CHARACTERS FOR VIANNAIINAE (NEMATODA: TRICHOSTRONGYLOIDEA)

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The superfamily Trichostrongyloidea (Travassos, 1937) Durette-Desset, 1985 includes numerous diverse groups of parasites divided into 14 families and 24 subfamilies. Each family contains genera of varied morphology, yet much emphasis has been placed on characters of the caudal bursa and the synlophe as keys to classifying the nematodes and understanding their morphological evolution. Bursal arrangement types based on disposition of rays came about in order to group the parasites according to family and subfamily. However, variation in bursal arrangement can exist even within a genus, as in the case of *Viannaia* Travassos, 1914. In this study, I compare and contrast the similarities and differences in bursal arrangement and synlophe

in Viannaiinae Neveau-Lemaire, 1934. The examination of representative species of *Travassostrongylus* Orloff, 1933, *Viannaia*, and *Hoineffia* Diaw, 1976, allows the understanding of the intra and interespecific variability of this structure. I hypothesize that significant bursa type variation exists between the genera in this subfamily. Inconsistencies in bursa types across Viannainae would suggest that bursal arrangements are not reliable diagnostic characteristics. Additionally, the positions of cuticular ridges on the synlophe are structures that provide another level of analysis. In examining these parasites I attempt to answer the following question: is bursal variability also observed in sister genera? In general, this study would reexamine the key characters of Trichostrongyloid classification and work towards a taxonomic revision of the family Viannaidae Durette-Desset, 1982.

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MIGRATION, SITE SELECTION, AND DEVELOPMENT OF ORNITHODIPLOSTOMUM SP. METACERCARIAE (DIGENEA: STRIGEOIDEA) IN FATHEAD MINNOWS (PIMEPHALES PROMELAS)

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The traditional view of trematode metacercariae as a developmental resting stage is inaccurate. Rather, the metacercariae of some species undergo tremendous development within specific tissues of their second intermediate host prior to reaching infectivity in their definitive host. Our understanding of migration, site selection and development of these types of metacercariae is known for only a few species. In this study, we characterize the invasion and development of *Ornithodiplostomum* sp. metacercariae in their second intermediate host, the fathead minnow. Diplostomules completed their migration into the abdominal cavity between 15 minutes and 48 hours post-infection (p.i.). Most diplostomules migrated along muscular and connective tissue then penetrated the peritoneal lining of the abdominal cavity en route to the liver or pancreas. Alternatively, some diplostomules migrated within the host's circulatory system, including the heart and arteries of the hepatic portal system. Metacercarial development within the liver and pancreas was complex, involving distinct growth, encystment and consolidation phases. Metacercariae volume increased 15-fold between 48 hours and 4 weeks p.i., presumably due to absorptive and/or ingestive feeding activities within host tissues. By 2 weeks p.i., metacercariae were enveloped within a cyst wall and they were found loosely attached to the surfaces of internal tissues or unattached within the body cavity. These results emphasize the complex nature of metacercariae migration and growth and demonstrate that their biphasic nature of development is associated with a micro-habitat shift within their intermediate hosts.

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UNEXPECTED ASEXUAL REPRODUCTION IN A TAPEWORM

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While parasites have been invoked as a mechanism for the maintenance of sex in their hosts, little attention has been given to the evolution of sex among parasites themselves. Current theoretical work largely predicts that sexual reproduction is favored in parasites. Yet, this prediction has not been adequately examined in parasitic species. Indeed, we know very little about modes of reproduction in adult parasitic flatworms. Cytogenetic observations in a handful of species indicate the possibility of asexual reproduction (offspring genetically identical to their parents). Also, the presence of triploidy in some cestodes and digeneans has been used to infer the possible presence of asexual reproduction. However, among flatworms, direct genotype comparisons between adults and their offspring to test for clonality are nonexistent. Furthermore, the extent and persistence of clonal lines within natural populations remains unknown. Population genetics data from a study initially designed to test mating system dynamics of a presumed hermaphroditic sexual parasite, the tapeworm *Oochoristica javaensis*, has yielded unexpected patterns. Here we present data such as identical multilocus genotypes between parent-offspring comparisons that support asexual reproduction. As data are preliminary, we cannot rule out the occurrence of sexual reproduction across the tapeworm's range. Nonetheless, asexual reproduction is present and raises important questions about the mechanism of asexual reproduction, the persistence and variation in reproductive success among clonal lineages, and the opportunity for selection on sex allocation between male and female gonads.

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TEMPORAL PATTERNS IN TREMATODE COMMUNITIES OF THREE GASTROPOD SPECIES FROM CELESTúN, YUCATAN, MEXICO

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Monthly surveys of the snails *Cerithidea pliculosa* (2001 to 2009; n= 40-211 per month), *Melampus coffeus* (2006-2009; n= 29-126), and *Pyrgophorus coronatus* (2007-2009; n= 174-230) indicated depauperate parasite communities in Celestún, Yucatan Mexico. Although a total of 20 trematode species were identified over the entire sampling period: 5 from *C. pliculosa* (mean±sd/ month, 1.3 ± 1.2), 2 from *M. coffeus* (0.7± 0.6) and 13 from *P. coronatus* (3.3 ± 2), monthly samples did not exceed 2 for *M. coffeus*, 4 in *C. pliculosa* and 6 in *P. coronatus*. The species composition of trematode communities in the three host species was relatively constant over time, dominated by one or two species. Switching of the numerically dominant species occurred from time to time, with no consistent trend. Numerically dominant species spanned several trematode families, but usually had birds as definitive hosts. No double infections were recorded for any of the three parasite communities. Prevalence of individual trematode species in each host did not show clear temporal patterns. However the monthly prevalence of all

trematodes combined (total percentage of infected host) seemed to regularly increase during the rainy season.

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LATITUDINAL PATTERNS OF PARASITISM IN CONGENERIC MUD SNAILS IN THE ATLANTIC AND PACIFIC OCEAN

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The latitudinal gradient in species diversity is a robust and general pattern which extends across a broad range of animal and plant taxa. Species richness is negatively correlated with latitude and, in general, the tropics harbor more species compared to temperate regions. However, it is often difficult to evaluate species richness in a standardized way within the same habitat type across a broad latitudinal range. Two geminate snail species, *Cerithidea californica* (= *mazatlanica*) and *C. pliculosa* offer such a possibility. *Cerithidea californica* and *C. pliculosa* are sister species which were separated by the rise of the Isthmus of Panama over 3 million years ago. Both snails have an extremely broad geographic range, extending over 30 degrees of latitude and they share a similar suite of trematode parasites making this an ideal system to test patterns of species richness. We quantified parasitism in over 50,000 snails from over 30 locations across 6 countries in North and Central America. We show that counter to conventional patterns of species richness, trematode richness in both snail species is positively correlated with latitude, where the tropics are relatively depauperate in trematode species compared to temperate regions. We discuss potential factors which might drive this unusual biogeographical pattern.

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EUSOCIALITY IN A FLATWORM: TREMATODE PARTHENITAE FROM SOLDIER AND REPRODUCTIVE CASTES

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In some of the most complex animal societies, individuals exhibit a cooperative division of labor to form castes. The most pronounced types of caste formation involve a reproductive division of labor among individuals that also possess discrete morphologies underlying their different functional roles. In colonies comprised of potentially mobile individuals, this type of caste formation has been recognized only among the arthropods, sea anemones, and mole-rats. Here, we present experimental and observational data demonstrating the existence of physical and behavioral castes in a digenean trematode flatworm. Trematode parasites undergo repeated clonal reproduction of 'parthenitae' within their first intermediate hosts. The mass of parthenitae form a colony, although not typically recognized as such. We document specialization among trematode parthenitae to form distinct soldier and reproductive castes for an echinostomatid trematode (*Himasthla* sp. B) that uses the California horn snail (*Cerithidea californica*) as first intermediate host. Unlike reproductives, soldiers do not reproduce, have relatively large

mouthparts, and are much smaller and thinner. Soldiers are also more active, and are disproportionally common in areas of the host where new trematode infections frequently occur. Further, only soldiers readily and consistently attack heterospecifics and conspecifics from other colonies (other infected snails). The division of labor described here for trematodes has strong parallels to other social systems with a soldier caste. The parallel caste formation in these systems, despite varying reproductive mode and taxonomic affiliation, indicates the general importance of ecological factors in influencing the evolution of social behavior. A division of labor is likely widespread among trematodes. Trematodes conservatively include 20,000 species, each of which as a rule forms colonies in their first intermediate host. Therefore, trematodes should provide new, fruitful systems to investigate the ecology and evolution of sociality.

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A LOADED TOAD: PARASITE COMMUNITIES OF JUVENILE WESTERN TOADS (ANAXYRUS BOREAS) FROM CALIFORNIA AND OREGON

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From June to August 2009, four hundred and thirteen Western toad, *Anaxyrus boreas*, tadpoles and recent metamorphs were collected from 31 locations in California and Oregon, United States. A total of 8 different taxa were recovered including 7 larval digenean trematodes and 1 nematode. The larval digeneans include *Ribeiroia ondatrae*, *Echinostoma* spp., *Alaria* sp., *Manodistomum syntomentera*, *Apharyngostrigea pipientis*, *Glypthelmins* sp., and an unknown Plagiorchidae. The nematode was an unknown Spiruridae. The most prevalent parasites among sites were *Echinostoma* spp. (63% prevalence among sites), *R. ondatrae* (56%), *M. syntomentera* (10%), and *Alaria* sp. (5%). *Glypthelmins* sp., *A. pipientis*, the unknown Plagiorchidae, and the unknown Spiruridae were observed but at low prevalence and intensity. *Echinostoma* spp. and *R. ondatrae* exhibited the highest intensity among sites at 12.5 and 7.3 respectively. This survey is the first known to examine the parasite communities of *A. boreas* tadpoles and recent metamorphs. We discuss patterns of infection prevalence, infection intensity, and infection aggregation (k) for each site and parasite group. Given the declining status of Western toads across many parts of their geographic range, it is important to know which parasites are using juvenile *A. boreas* as intermediate hosts and whether they induce pathology, as suspected for *R. ondatrae* and the echinostomes.

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PARASITE DIVERSITY IN CHINA: CANARY LICE IN A COAL MINE

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Studies of biodiversity traditionally focus on charismatic megafauna, such as birds and mammals. By comparison, little is known about the biodiversity of parasites. Recent studies demonstrate

significant coextinction of host specific parasites with their hosts. Indeed, under conditions of poor host habitat quality, parasites may go extinct before their hosts, but this hypothesis has seldom been tested. Here I will present data on parasite diversity among several sites in southern China, a biodiversity hotspot. In this study, ectoparasite species correlates with forest size. In small forests parasites appear to precede their hosts into local extinction. Indeed, parasite diversity may even be useful as an indicator of the health of host populations. Thus, a thorough understanding of the biology of host specific parasites may aid in the conservation of these parasite species as well as the hosts they infest.

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DIGENEAN SPECIES RICHNESS AND COMPOSITION OF PALMYRA ATOLL FISHES, EASTERN INDO-PACIFIC

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Palmyra Atoll is a wildlife refuge located 1680 km SW of Hawaii closed to fishing since 2001. It has been established that reef fishes there have a higher diversity of helminth parasites compared to heavily fished locations, but the parasites had not yet been identified by taxonomic experts. During a survey on helminth parasites of Palmyra Atoll fishes, we collected a large number of digenean species. Our objectives were to identify them, to determine their mean number of species and individuals, and to establish their zoogeographical affinities within the Indo-Pacific region. The fishes were collected by seine, spear, hook and line from the lagoon flats in October and November, 2009, and examined for helminths at the laboratory of the Palmyra Atoll Research Consortium (PARC). We examined 231 individuals from 35 fish species and identified 24 species of digeneans among 23,547 worms. Metacercariae (21 spp., 23,388 individuals) vastly outnumbered the adult digeneans (3 spp., 159 individuals). The most prevalent (5-100%) and abundant (1-2279 ± 1615) species was *Bucephalus* sp. 2. The overall mean number of species of digeneans per fish species was 2.5 ± 2.9, while the mean number of individuals was 604.5 ± 1652.8. The mean number of species of digeneans in the metacercarial stage was 2.5 ± 2.7, while the mean number of individuals was 617.3 ± 1673.1. For the adult stages, the mean number of species was 0.1 ± 0.3, and the mean number of individuals was 4.9 ± 5.2. The digenean species composition of Palmyra fishes showed strong affinities with that of the Hawaiian Islands, which is not surprising due to their geographical proximity. The mean number of species of digeneans in this atoll and that of coral reef fishes from the Great Barrier Reef (GBR, 2.61 species per fish species) was similar. However, in Palmyra digenean species were mostly metacercariae, while in GBR most of the digeneans reported there are adults. A possible explanation for this contrast is that our samples were limited to fishes of the lagoon sand flats rather than of the reef itself.

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DEFYING THE RED QUEEN? REPRODUCTIVE STRATEGIES AND PARASITE INFECTIONS IN ASEXUAL AND SEXUAL MOLLIES IN THE RIO-GRANDE VALLEY

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Ecological theory predicts that the evolution and maintenance of sex is driven by a selective advantage of maintaining a high genetic diversity to evolve in response to parasites and infectious disease (the Red Queen Hypothesis). While the Red Queen Hypothesis has been supported from invertebrate host-parasite models it has not been adequately addressed among vertebrates where very few asexual species exist. In this study, we compared the parasite fauna of two closely related mollies (Poecilidae) co-existing in South Texas. *Poecilia formosa* exclusively reproduces asexually while *P. latipinna* only reproduces sexually. As a starting point for our investigation, we specifically addressed two questions: 1) Does the asexually reproducing *P. formosa* harbor more macroparasites than the sexually reproducing *P. lattipina*? 2) Does the sexually reproducing host species display a higher variation in the number of parasites reflecting the higher genetic variation observed in that species? We collected 50 specimens of each species by seining from five irrigation canals in the Rio Grande Valley in the fall of 2009. Metacercariae of *Centrocestus formosanus* encysted in gill tissue, and *Diplostomum* sp. encysted in the eyes were widely distributed and they were used for comparison between *P. formosa* and *P. latipinna*. We found significant effects of both location and parasite species. While a significantly higher mean abundance of *Diplostomum* sp. was found in *P. formosa* a significantly higher mean abundance of *C. formosanus* metacercariae was found in *P. latipinna*. The mean abundance of *C. formosanus* was much more variable in *P. latipinna* compared to *P. formosa*. Ongoing research is investigating the susceptibility to parasite infection of the two species using experimental infection challenges.

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PARASITES AND HOST ENERGETICS: EFFECTS OF A PARASITIC CASTRATOR ON CONSUMPTION AND METABOLISM IN AN AQUATIC SNAIL HOST

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Parasites are widespread and ubiquitous organisms, contributing a substantial amount of biomass to both aquatic and terrestrial ecosystems. Since biomass and energetics are related, we conjecture that parasites would have a considerable impact on the flow of energy through food webs. In order to study how parasitism influences energy available to other trophic levels, the consumption and metabolism of the freshwater snail red-rim melania (*Melanoides tuberculatus*), host to the Oriental avian eye fluke (*Philophthalmus gralli*), was determined. Methodology was developed to quantify snail consumption and, in a separate experiment, the effect of infection on snail consumption was studied. Dried samples of algae were added to 60 cups, 30 cups

containing snails and 30 cups containing no snails. Algal consumption was measured over a period of 7, 10, or 14 days. Data showed snail treatment resulted in a significant reduction of algae at 7, 10, and 14 days ($p = 0.0112$, 0.00019, < 0.0001, respectively) when compared to control treatment. Using the developed methodology, the effect of snail size and infection status on consumption was tested over a period of 14 days. Results showed snail size affected consumption ($p < 0.001$), but that snail infection status had no significant effect on consumption ($p = 0.841$). Future studies will address differences in the metabolism of infected and uninfected snails using a respirometer. The results of the experiments will be discussed in relation to potential effects of parasites on host energetics.

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MECHANISM OF REGULATION OF TRYPANOSOMA BRUCEI ACETYL-COA CARBOXYLASE, THE KEY ENZYME FOR INITIATION OF FATTY ACID SYNTHESIS

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Trypanosoma brucei is one of the major causes of death in some parts of Africa. Transmitted by Tse Tse fly, these parasites cause fatal disease in humans (sleeping sickness) and in livestock. Current drugs are toxic and drug resistance is growing. Vaccine development is unlikely because the parasites undergo antigenic variation. Fatty acids are implicated in antigenic variation, hence fatty acid synthesis (FAS) could present novel targets for therapeutic intervention. Trypanosomes prefer to rely on fatty acids from the host. However, under limiting conditions, *T. brucei* can synthesize its own fatty acids by an unconventional FAS pathway. The 2-carbon donor of FAS is malonyl-CoA, which is synthesized from Acetyl-CoA by Acetyl-CoA Carboxylase (ACC). We hypothesize that ACC is negatively regulated by phosphorylation. We are testing our hypothesis using three approaches. First we are using a bioinformatic approach to examine potential phosphorylation sites. Although *T. brucei* ACC lacks the canonical serine phosphorylation site present in mammals, phospho-prediction algorithms show 53 Ser, 33 Thr, and 19 Tyr sites with high predictive scores. Second, we are analyzing *T. brucei* lysates by immunoblotting with phospho-specific antibodies. To date we see no reactivity of the correct size (243 kD) with anti-Ser-P or anti-Thr-P antibodies. We do see a large >200 kD band react with anti-Tyr-P antibodies, suggesting ACC may be phosphorylated on Tyr. Third, we plan to use direct metabolic radiolabeling with ^{32}P followed with partial purification of myc-tagged ACC and autoradiography. Currently, we are continuing our bioinformatic analysis of potential phosphorylation sites, probing lysates and partially-purified native ACC with an expanded panel of phospho-specific antibodies and attempting to label ACC with [32P] phosphate in order to elucidate the extent to which ACC is phosphorylated, and what role phosphorylation plays in the regulation of ACC and FAS.

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SELECTION AND EVALUATION OF REFERENCE GENES FOR SYBR GREEN QPCR STUDIES WITH HEMOCYTES FROM THE PULMONATE SNAIL, BIOMPHALARIA GLABRATA

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Quantitative real-time PCR is a powerful tool for examining relative gene expression. Accurate comparison of samples depends on carefully chosen reference genes. Ideal reference genes have steady expression regardless of experimental conditions and are used to normalize target gene levels. GeNorm has become a standard program for analyzing reference gene stability. It calculates a gene-stability measure (M) defined as the average pair-wise variation of a particular gene with all other genes. We used GeNorm to rank expression stabilities of seven putatively identified reference genes in *Biomphalaria glabrata* hemocytes. The three best reference genes were then used, in various combinations, to adjust the relative constitutive expression of hemocyte superoxide dismutase (SOD1). The gene candidates ranked by GeNorm from least to most stable were *tyrosine 3-monooxygenase, elongation factor-1-α, β-actin, glyceraldehyde-3-phosphate dehydrogenase 3, guanine nucleotide binding protein-β polypeptide,* and the combination of *60S ribosomal protein L32* and *myoglobin*. Consistent with GeNorm's analysis, we found that the relative expression of SOD1 was similar when normalized with the geometric mean of *L32* and *myoglobin*, or the geometric mean of the top three reference genes (*gnb, L32, myo*). Supported by NIH award AI016137.

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INTESTINAL PARASITES OF THE DOUBLE-CRESTED CORMORANT (PHALACROCORAX AURITUS), FROM NORTHERN ALABAMA, USA

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The intestines of double-crested cormorants (*Phalacrocorax auritus*) collected in fall 2009 from Lake Guntersville, Alabama, were assessed for disease and parasitic infection. Abnormal appearance of tissues, fat content (for body condition assessment), and eukaryotic parasites were documented in young of the year (YOY), sexually immature adults (over 1 year old; IM & IF), and sexually mature adults (M & F). Platyhelminthes [digenean trematodes] and nematodes were found in nearly all birds assessed. Cestodes were also documented in a number of adult cormorants. Ectoparasitic and non-parasitic arthropods were collected from the digestive tract, although their presence was likely due to ingestion during grooming activities or indirectly thought feeding activities. Relationships between parasite variables (abundance, richness, and relative biomass) and intestinal fat content (proportion of biomass) will be explored for different sexes and age classes (YOY, IM, IF, M, and F). Implications of parasite infections on body

condition of the double-crested cormorant will be discussed in light of the ecology of each parasitic group and/or species.

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EVIDENCE THAT CERCARIAE CHOOSE THE MOST SUSCEPTIBLE AMPHIBIAN HOST SPECIES AND INDIVIDUALS

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A parasite that can infect multiple host species is likely to encounter varying levels of host susceptibility. Such parasites might therefore face selective pressure to discriminate among hosts in order to infect those that will maximize the parasite's reproductive success. Trematode cercariae often follow water-borne cues to detect their hosts, but whether they demonstrate a preference among suitable host species has not been tested. When exposed to four different tadpole species, armatae-type cercariae consistently chose among amphibian hosts, preferring tadpoles in the following order: southern toads (*Bufo terrestris*), squirrel tree frogs (*Hyla squirrella*), southern leopard frogs (*Rana sphenocephala*), and Cuban tree frogs (*Osteopilus septentrionalis*). Host attractiveness to cercariae was negatively correlated with time to metamorphosis in each species, with the exception of *O. septentrionalis*, an introduced species. Furthermore, trials examining host species resistance to this trematode revealed that cercarial preference was generally negatively related to host species' resistance to infection, suggesting that cercarial choice is adaptive and that models assuming random host choice might be underestimating parasite transmission rates. Finally, there was consistent variation among individual hosts within a species in their attractiveness to cercariae a pre-requisite for natural selection to act on this trait. Hence, if attractiveness to cercariae is heritable, there might be an evolutionary arms race between host evasion of parasites through altered chemical cues and parasite tactics to identify and infect hosts**.**

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DEVELOPMENTAL EXPRESSION AND SILENCING OF SAPOSIN AND FERRITIN LIKE ANTIGENS IN FASCIOLA HEPATICA

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Fasciola hepatica is an important disease of livestock and a recognized food-borne zoonotic disease affecting approximately 2.4 million people. Growing resistance to the drug of choice, Triclabendazole, is compromising control options and underscores the need to discover novel chemo-and/or immunotherapeutics. The excretory/secretory (ES) products produced by *F. hepatica* are key players in the host-parasite interaction and offer appealing targets for chemo/immunotherapy. We have identified two ES antigens with potential roles in nutrient acquisition: (i) FhFrr, a Ferritin-like protein that is involved in iron (Fe) metabolism; and, (ii) FhSAP2, a member of the Saposin-like protein family (SAPLIP). However, the function of both antigens during the early stages of infection remains unknown. RNA interference (RNAi)

provides a tool with which to probe gene function /validate drug/vaccine targets, and has been successfully employed to silence genes in the infective stage (newly excysted juvenile, NEJ) of *F. hepatica*. Using quantitative (q)PCR we demonstrate *FhSAP2 and FhFrr* expression in NEJs and adults of *F. hepatica*. Immunocytochemical studies using rFhSAP2-antiserum revealed gut and tegument localization. To probe the function of FhFrr and FhSAP2 in both life stages, we exposed NEJs and adults to double stranded RNA (dsRNA, 100 ng/ul); qPCR confirmation of gene silencing in NEJs is ongoing. Preliminary results obtained by qPCR for adults RNAi revealed knockdown of 93% (~15-fold) in the levels of *FhSAP2* transcripts and no significant knockdown for the *FhFrr* target. However, this finding demonstrated for the first time the knockdown of gene transcript in the adult stage of the parasite which provides a new platform for gene function studies in this developmental stage. These preliminary data suggest that RNAi will facilitate functional studies on FhFrr and FhSAP2 in *Fasciola* and highlight these ES as potential vaccine/drug targets.

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CESTODES AND THE SUCCESS OF AN INVASION: THE CASE OF THE AMERICAN BRINE SHRIMP ARTEMIA FRANCISCANA IN A MEDITERRANEAN SALTERN

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The American brine shrimp *Artemia franciscana* became an invasive species in the Iberian Peninsula and in the Western Mediterranean salterns, where is eradicating autochthonous *Artemia* species. Brine shrimps act as intermediate hosts of several water bird cestodes (Cyclophyllidea). When invasive species leave their origin and escape from their coevolved parasites, they can experience a demographic release (enemy release hypothesis) in the new range, becoming highly competitive and threatening biodiversity there. The aim of this work was to assess whether the invasive *A. franciscana* is affected by avian cestode cysticercoids to the same extent as the native *A. salina*. The natural infection of both bisexual species was studied in La Trinitat salterns (Tarragona Province, Spain) from January until May when they cooccur. The additional purpose of this work was to afford the first data on the cestode parasitism found in *A. franciscana* in its native range (Great Salt Lake, Utah). The morphological identification of the cysticercoids was based on previous descriptions (Georgiev et al., 2005; Vasileva et al., 2009). In La Trinitat salterns, levels of overall infection are markedly lower in the invasive than in the native brine shrimp species. The prevalence ranged between 0.6 and 37.2 for *A. franciscana* and between 0.9 and 75.3 for *A. salina*. The mean intensity varied between 1 and 1.24 for the invasive species and between 1 and 1.98 for the native one. *Flamingolepis liguloides*, parasitizing flamingos, showed significantly higher prevalences and mean abundances in *A. salina* than in the American brine shrimp. Cysticercoids from mainly dilepidid species (mostly *Eurycestus avoceti*) were parasitizing the invasive *A. franciscana*. However, only *Confluaria podicipina* (parasitizing grebes) and *Wardium* spp. (parasitizing gulls) were recorded in the *A. franciscana* native range. Our results suggest that cestodes play an important role in the

competitive interaction between native and alien brine shrimps and they could partially explain the *A. franciscana* invasion success.

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VISCERAL LEISHMANIASIS IN CAPTIVE FOX CERDOCYON THOUS (CARNIVORA, CANIDAE)

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Visceral Leishmaniasis (VL) is an important worldwide disease and also affects wild animals with the fox *Cerdocyon thous* considered a wild reservoir of many zoonotical diseases, particularly VL. The aim of this study was to report the presence of *Leishmania* amastigotes in different organs of one *C. thous* found dead in the Zoo of Ilha Solteira, SP, Brazil. This animal was positive by IFAT (indirect fluorescence antibody test) and had many clinical signs of VL. After the natural death, this animal was autopsied and tissue samples from many organs were collected and examined by direct parasitological and immunhistochemical methods and PCR. Intact amastigote forms of *Leishmania* were seen inside the neutrophils and macrophages in sample tissues from skin, lymph nodes (popliteal, submandibular, prescapular, and mesenteric), spleen, liver, kidneys and lungs. Higher numbers of infected neutrophils with *Leishmania* amastigotes in comparison with macrophages were seen in submandibular and prescapular lymph nodes, but in the other organs (spleen, liver and mesenteric lymph nodes) the numbers of infected macrophages were superior to neutrophils. In addition, PCR demonstrated extensive distribution of *Leishmania sp.* DNA in *C. thous* tissues from many organs. Intact *Leishmania* inside neutrophils and macrophages and DNA of this parasite in many organs characterized the presence of VL in *C. thous* in Brazil.

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EVASION STRATEGIES OF ECHINOCOCCUS GRANULOSUS TO TH1 HOST PROTECTIVE RESPONSE DURING HUMAN INFECTION

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Human cystic hydatid disease constitutes a major health problem in Algeria. More recently, we have highlighted an evident role of IFN-γ (Th1 cytokine) in parasite killing by the NOS2 (Nitric oxide Synthase2) pathway. Moreover, IL-10 (Treg cytokine) production seems to be an evasive mechanism taken by the parasite to establish in the host by Arginase pathway (Amri et *al.*, 2007 & 2009). Of note, NOS2 and Arginase are known to compete for the common substrate, L-Arginine. Moreover, IL-10 downregulates IFN-γ production. Indeed, more research is required to identify factors present in the parasite cyst which affect protective Th1 response in *Echinococcus granulosus* human infection. We investigate the effect of laminated-layer (accelullar layer of hydatic cyst) extract (LLs) on Th1/Treg and NOS2/Arginase balance in culture performed with

mononuclear cells (PBMC) of hydatid patients and healthy donors. Furthermore, we have investigated the effect of LLs on parasite viability in PBMC-parasite cocultures. Our results demonstrated that LLs reduced IFN-γ/NO production and enhanced IL-10 production and Arginase activity. In addition, LLs enhanced parasite survival *in vitro*. Similar findings are observed in cultures and cocultures performed with PBMC of patients and healthy donors. Moreover, the major antigenic fraction in LLs: the fraction 4 (12kDa, purified by chromatography) has the same effect as LLs. Collectively, the present study provides evidence that *Echinococcus granulosus* laminated layer impairs Th1 protective response and allows the parasite to survive. Inhibition of these mechanisms seems to be an important issue to address during the design of anti-hydatic treatment.

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CYLICOSPIRURA SPECIES (NEMATODA: SPIROCERCIDAE) AND STOMACH NODULES IN COUGARS (PUMA CONCOLOR) AND BOBCATS (LYNX RUFUS) IN OREGON

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The stomachs and proximal duodena of 160 cougars (*Puma concolor*) and 17 bobcats (*Lynx rufus*), obtained throughout Oregon between 1999 and 2007, were examined for *Cylicospirura* spp. and their associations with nodules. Prevalence in cougars was 73%, with a range in intensity from 1 to 562 worms. The mean diameter of nodules was 1.2 cm (SD; 0.5) and many extended through the submucosa to the muscularis. The majority of nodules contained worms, but some of the smaller nodules contained porcupine quills instead. A mean of 12.4 worms/nodule (SD; 34.1) was observed, with a maximum of 340 worms/nodule. Prevalence in bobcats was 53%, with intensity ranging from 1 to 25 worms. About 65% of bobcats had nodules. Nodules in bobcats were slightly smaller than those in cougars and appeared to involve similar layers of gastrointestinal tissue. One to 25 *Cylicospirura* sp. were found in all but two small nodules in bobcats. A statistical analysis revealed that cougars killed for livestock damage or safety concerns had a higher median worm intensity than those that died of other causes. Also, the median worm intensity of older cougars was higher than that of younger lions. There were more males killed for livestock damage or safety concerns than females. The cylicospirurid from cougars was identified as *C. subaequalis* and that of bobcats was *C. felineus*. These two similar species were separated morphologically by differences in tooth and sex organ morphology. They were also differentiated by DNA sequence analysis of the mitochondrial cytochrome *c* oxidase subunit 1 gene (*cox1*). We found that worm sequences from cougars differed from those from bobcats by 11%, while no difference was found amongst worms from the same host. A phylogenetic analysis showed that within the order Spirurida, they were most closely related to *Spirocera lupi* based on this gene sequence.

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INTERLEUKIN 17 STIMULATES MONONUCLEAR CELLS TO KILL ECHINOCOCCUS GRANULOSUS PROTOSCOLECES BY NO-DEPENDENT MECHANISM

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Human echinococcosis is one of the world's major zoonotic infections. It usually manifests as unilocular cyst(s) mainly located in the liver. Surgery is the main therapeutic approach; however dissemination of protoscoleces (cystic components) constitutes a source of relapse. More recently, we have highlighted an evident role of IFN-γ in protoscoleces killing by NOS2 (Nitric Oxide Synthase2) induction (Amri et al., 2007) and Arginase inhibition. Discovery of the Th17 cell lineage and functions in immune responses of man prompted us to investigate the role of IL-17 in host defense during human echinococcosis. We have investigated the effect of IL-17 on protoscoleces co-cultured with PBMC of hydatic patients (before and after surgery) and healthy donors. After 20h, NO and urea are evaluated, respectively for NOS2 and Arginase activities. Our results demonstrated that IL-17 decrease protoscoleces viability (from 53.37±7.96 to 17.7±3.99 %, $p<0.0001$). Moreover, we observed a concomitant elevation of NO levels (from 77.36±18.18 to 133.85±22.59 µM, $p<0.0001$) and a decrease in urea levels (from 50.26±8.35 to 18.08±2.99 mM, $p<0.001$). Interestingly, inhibition of the IL-17 responses enhanced protoscoleces survival. This effect is associated with a decrease in NO level and an elevation in urea level. Similar findings are observed in the cases of PBMC of patients and healthy donors. The results reported here show that IL-17 plays a relevant role in the protective immune response during human echinococcosis. This role may be mediated by NOS2 up-regulation. Our findings provide useful tools for the development of therapeutic strategies.

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POSSIBLE ROLE FOR TOLL LIKE RECEPTORS IN INTERACTION OF FASCIOLA HEPATICA EXCRETORY/SECRETORY PRODUCTS WITH MONOCYTE CELLS

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Fasciola hepatica, the common liver fluke, causes widespread disease in farm animals as well as in man. *F. hepatica* is able to immunomodulate its host secreting products that often polarize the immune responses toward the Th2 end of the spectrum. These polarized immune responses may be associated with the development of chronic infections while avoiding the clearance by the host. Because the innate immunity constitutes the first line of defense against infections and molecules produced during innate immune responses stimulate and influence the nature of adaptive immune response, it's possible to hypothesize that the *F. hepatica* ES products (FhES) are responsible to interact with the cells of innate system resulting in a favorable immunological response that facilitate the parasite survival into the host. In the current study, we present data examining the interaction of total and molecular mass-fractioned ES antigens on human

monocyte cell line (THP1-CD14) which express different TLRs. After screening the interaction of the antigens in conjunction with the corresponding agonist and antagonist of all TLRs we stated that ES antigens stimulate positively the TLR-4 and TLR-8 and possibly also interact with the TLR-2 and TLR-5. We also stated that ES antigens in the range of 10-30kDa and 30-100KDa are involved in the interaction with these TLRs. Further studies are in progress to elucidate the complete TLRs signaling pathways stimulated by these antigens during the active infection and its influence on the adaptive immune response.

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INCIDENCE AND DIAGNOSIS OF PARASITIC ETIOLOGIES AMONG A SURVEILLANCE STUDY GROUP FROM INFECTIOUS DISEASE HOSPITAL, KOLKATA, INDIA

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In the developing countries, diarrhea is one of the major and common causes of death and is the major cause of infant death in global perspective. Enteric parasites are among the commonest cause of diarrhea. Among the common enteric parasites *Entamoeba histolytica*, *Giardia lamblia* and *Cryptosporidium* sp. are mostly causing diarrhea in developed and developing countries. During the last 24 months (Nov 07 to Jan 10) a total of 49904 diarrheal cases were admitted in the I. D. Hospital, Kolkata out of which 2709 diarrhea patients were enrolled in a joint surveillance program for finding out common diarrheogenic etiologies in this area. For treatment, patients have received ofloxacin-ornidazole or ciprofloxacin-metronidazole. The death rate was 1% among the enrolled cases. We have screened these fecal samples for finding out common parasitic etiology causing diarrhea. Samples have been screened with three different techniques. Microscopic detection, molecular detection by PCR using standardized primers for all the parasites including their non-pathogenic variants and antigen capture ELISA using specific commercial kits (TECHLAB, VA, USA). Out of the 2709 samples screened *E. histolytica* (3.2%), Cryptosporidium sp. (6.1%) and *Giardia lamblia* (11.1%) constitute the major parasitic load. Apart from that, parasitic infections were the most common incidence of mixed infection (29.5%), not only with other parasites but also with common virus (34.3% with Rotavirus) and bacteria (36% with *Vibrio cholerae* and 8.3% with *Shigellae*). *Giardia lamblia* and *Cryptosporidium* have been seen to be the most abundant etiology among all parasitic infections. Total isolation rate of Giardia was the third highest (after *V. cholerae* and Rotavirus) and Cryptosporidium was the fifth among all diarrheogenic etiologies, even Giardia is the forth major cause of diarrheal illness (after *V. cholarae*, Rotavirus and *Shigellae*) as a sole pathogen among our surveillance study group. Among the two different age groups (≤5 years and >5 years) under our surveillance study it has been observed that age group of <5 years were more susceptible to Giardiasis and Cryptosporidiosis. Among all the patients admitted under our surveillance program in I.D. hospital there was almost equal distribution of male and female patient and the most prevalent areas as suggested from GIS map are Rajarhat, Tangra and Tiljala followed by Beliaghata, Salt Lake City and Dumdum for Giardiasis. Rajarhat, Tiljala, Dumdum, Narkeldanga and Salt Lake City were the most prevalent areas for Cryptosporidiosis. Within these twelve months period *Giardia lamblia* occurrence remained almost unchanged throughout the year whereas *Cryptosporidium* sp. and *Entamoeba histolyticaoccurrence* showed differential

distribution. While comparing our detection rate with that of preceding years in the same area among similar group of patients we have observed that there might be a trend of change in the pattern of infection (etiology) with time. Though *Giardia* and *Cryptosporidium* have shown a trend of increasing infection rate but *Entamoeba histolytica* as well as its non pathogenic asymptomatic variant *E. dispar* infections have been seen to be decreased with time. This observation might be very striking leading us to a new thought of drug sensitivity and other environmental issues which might have some good relevance in this slow but obvious change in the infection pattern.

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A TAXONOMIC REVISION OF OCTOMACRUM

J. Forest, Saint Mary's University

Preliminary data for a proposed revision of the polyopisthocotylid genus *Octomacrum* Mueller, 1934, a small genus of six nominal species found on gills of cypriniform fishes in North America and Europe is presented. Since May 2008, 315 host fish from 5 different genera (*Semotilus*, *Catostomus*, *Notropis*, *Phoxinus*, *Notemigonus* from Ontario and Nova Scotia) have been necropsied yielding 2 of the 6 known species of *Octomacrum* (*O. microconfibula*, *O. semotili*). Museum specimens of the remaining 4 species (*O. lanceatum*, *O. europaeum*, *O. spinum*, *O. mexicanum*) have also been examined. A revised diagnosis of the genus based on a consistent terminology of the whole body anatomy as well as on the diagnostically important haptoral clamps is proposed. Comparative morphometrics show significant variation among the six species in terms of overall body size and in the size and form of the clamps. SEM reveals what appears to be a massive tactile organ forming a band around the body, and which appears new for the Monogenea. Work is underway to prepare a molecular phylogeny of the genus.

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THE FOOD AND ENVIRONMENTAL PARASITOLOGY NETWORK (FEPN) IN CANADA

B. Dixon, Health Canada, **J. Tetro**, University of Ottawa, **M. Ndao**, McGill University, **S. Bidawid** and **J. Farber**, Health Canada

A network of Canadian researchers, regulators, and public health officials with an active involvement in issues related to food and environmental parasitology has recently been established by Health Canada in Ottawa, Ontario. The Food and Environmental Parasitology Network (FEPN) currently has over 50 members from across Canada representing federal and provincial government, academia, and industry. The Network focuses on issues such as contaminated foods and infected food animals (e.g., imported produce, raw meats, fish and shellfish), potable and non-potable water, northern and aboriginal issues, zoonotic transmission (e.g., livestock, wildlife, fisheries and aquaculture, companion animals), and epidemiology. The objectives of the Network are (i) to identify and communicate risks and research / surveillance gaps; (ii) to facilitate discussion, collaborative research, and development of grant applications amongst members and external researchers; (iii) to develop and validate standardized methods

for the isolation, detection, characterization and control of foodborne and waterborne parasites; (iv) to develop and validate methods for the surveillance and investigation of parasitic infection in humans; (v) to generate data for risk assessment and policy development; and (vi) to provide expert advice and testing in support of outbreak investigations and surveillance studies. Meetings are held at least twice a year by teleconference, and *ad hoc* face-to-face meetings are held in conjunction with scientific conferences. A future goal of the Network includes the establishment of a national reference laboratory for food and environmental parasitology, which would include a centralized culture collection and a database for laboratory testing results and parasite genotyping data. The Network is particularly interested in establishing linkages with similar international networks and databases. For more information on the FEPN, please contact the Network Chair, Dr. Brent Dixon, at: Brent.Dixon@hc-sc.gc.ca, or visit our website at: http://www.medicine.uottawa.ca/crem/eng/FEPN.html.

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THE GREGARINE PARASITES OF ODONATA IN OTSEGO COUNTY (NEW YORK)

C. Wiles and **F. Reyda**, State University of New York at Oneonta

Gregarines have a rich species diversity and are highly host specific (Clopton, 1995). Little is known about how many different gregarine species exist in the United States because many insects species have not been examined for parasites. In fact, no studies have been done in the Northeastern United States. This survey of damselflies and dragonflies (Insect: Odonata) and their gregarines was conducted at the State University of New York at Oneonta Biological Field Station in Otsego County, New York. Sampling was done using aquatic and aerial bug nets to catch both the larval and adult stages of the odonates. The dissections were done by dragging the gut of the insects across a slide and then teasing the gut apart to look for parasites. Any gregarines found were stained with Semichon's Carmine Stain, dehydrated, made transparent in xylene, and mounted in Canada balsam. Approximately twenty-one different odonate species were encountered. Previously described species and some possible new species of gregarines were found in the odonates. For example two species of the previously described *Prismatospora* spp. Ellis, 1914 were encountered in Cherry-faced Meadowhawk dragonfly, *Sympetrum internum* Montgomery, 1943. This survey revealed the presence of undescribed gregarine species, but more research is needed to better understand the gregarine diversity in the odonates of Otsego County.

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HOST USE AND MORPHOLOGICAL VARIATION OF LEPTORHYNCHOIDES THECATUS FROM OTSEGO LAKE, NEW YORK

M. Bergman, **L. Hendricks and F. Reyda,** State University of New York at Oneonta

A survey of the helminth parasites of the fishes of Otsego Lake and nearby water bodies in Otsego County, New York was undertaken from September 2008 to the present. Fish were

collected by hook and line, seine, or by gill net. Over three hundred individual fish representing nine species were examined for intestinal helminths. Among helminths encountered, species of acanthocephalans were further investigated for potential taxonomic work. Seven of the nine fish species examined were infected with adult specimens of the acanthocephalan *Leptorhynchoides thecatus*. However, gravid female *L. thecatus* were only found in the Largemouth bass, *Micropterus salmoides*. In each of the seven fish species infected with *L. thecatus*, worms were more frequently located in the intestine rather than in the pyloric cecae. Morphological features of the *L. thecatus* specimens encountered were compared with *L. thecatus* reported elsewhere. Of note was a conspicuous dorsal-ventral hook asymmetry on the proboscis. The variation in host use and morphological features of *L. thecatus* encountered in this study supports other recent studies that suggest *L. thecatus* represents several morphologically distinguishable species in North America.

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MOLECULAR SYSTEMATICS OF GEOGRAPHIC ISOLATES OF DAUBAYLIA SPP

L. Camp, **C. Pagan** and **S. Nadler,** University of California, Davis, Department of Nematology

Nematodes from the genus *Daubaylia* are parasites of freshwater planorbid snails. *Daubaylia* spp. have a worldwide distribution, having been recovered from infections in snails on four continents. *Daubaylia potomaca* was initially discovered infecting *Helisoma trivolvis* in the Potomac River and was subsequently recovered from snails in northern Michigan in the 1950s and from the Piedmont region of North Carolina in 2004. Characteristics of *Daubaylia* spp. were established in investigations of the life cycle of *D. potomaca* as well as morphological and molecular characterizations of this species. Recently, nematodes presumed to be *Daubaylia* spp. have been found infecting planorbid snails in Wisconsin and in the central valley of California. Molecular prospecting was performed in order to determine if the putative *Daubaylia* spp. are different lineages compared to *D. potomaca* based on nuclear rDNA. In addition, morphological data was obtained and compared with characteristics of known *Daubaylia* spp.

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CLARK P. READ MENTOR AWARD

A. Kuris, University of California, Santa Barbara

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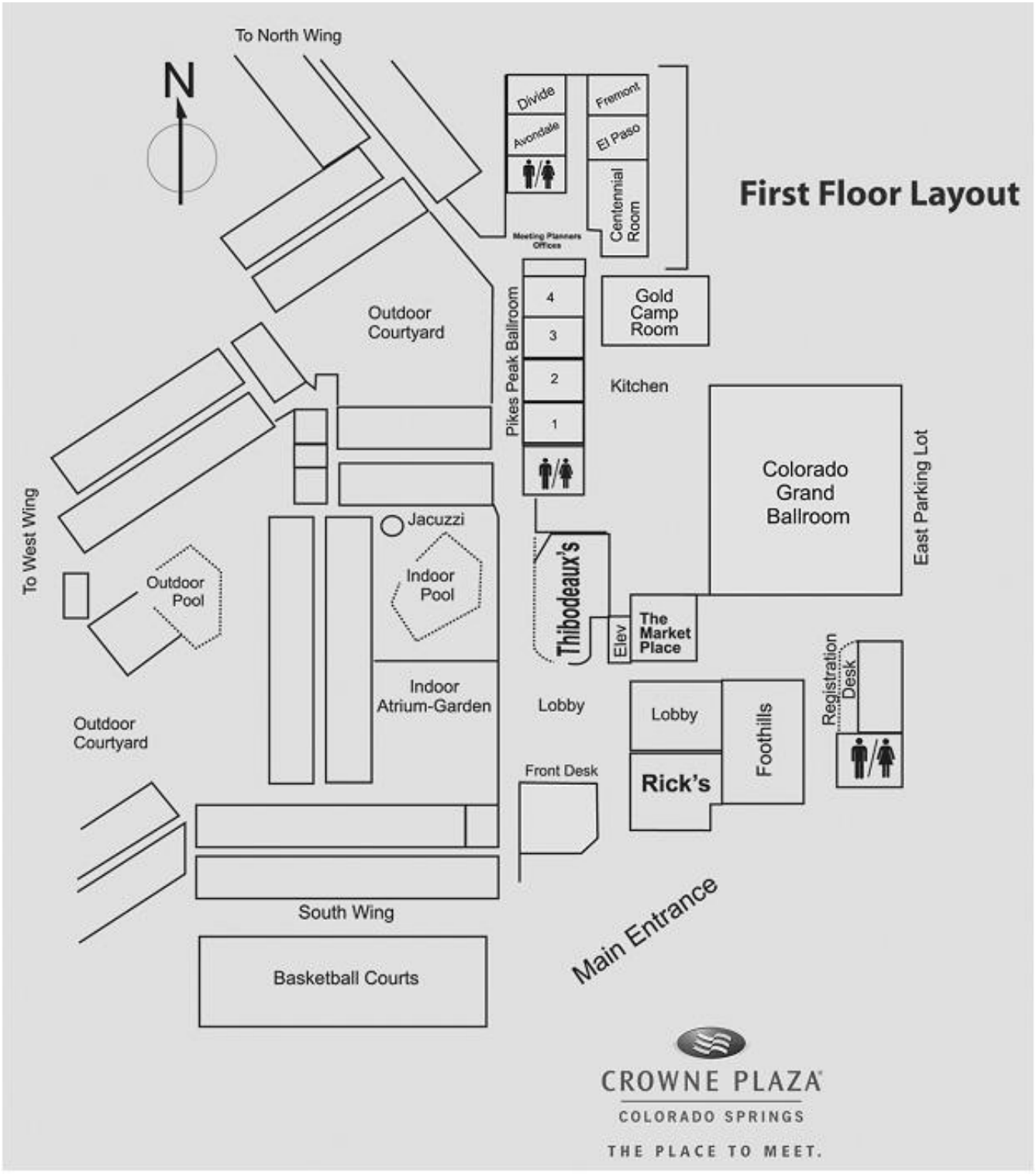
Notes:


First Floor Layout
To North Wing
N
Divide
Avondale
Fremont
El Paso
Centennial Room
Meeting Planners Offices
Outdoor Courtyard
Pikes Peak Ballroom
4
3
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Kitchen
Colorado Grand Ballroom
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Lobby
Lobby
Foothills
Registration Desk
Outdoor Courtyard
Front Desk
Rick's
South Wing
Main Entrance
Basketball Courts
CROWNE PLAZA
COLORADO SPRINGS
THE PLACE TO MEET.

ASP Meeting History

1925 Kansas City MO
1925 Philadelphia PA
1927 Nashville TN
1928 New York NY
1928 Des Moines IA
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
1043 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
1951 Chicago IL *
1952 Ithaca NY †
1953 Madison WI †
1954 Memphis TN *
1955 Atlanta GA
1956 Storrs CT †
1957 Philadelphia PA *
1958 Bloomington IN †
1959 University Park PA †
1960 Los Angeles CA *
1961 Lafayette IN †
1962 Washington DC ‡
1963 Chicago IL *
1964 Boulder CO †
1965 Atlanta GA
1966 San Juan PR *
1967 Tucson AZ §
1968 Madison WI †
1969 Washington DC *
1970 Washington DC ¶
1971 Los Angeles CA
1972 Miami Beach FL *
1973 Toronto, ON, Canada
1974 Kansas City MO
1975 New Orleans LA *
1976 San Antonio TX
1977 Las Vegas NV
1978 Chicago IL *
1979 Minneapolis MN
1980 Berkeley CA
1981 Montreal, QB, Canada
1982 Toronto, ON, Canada ¶
1983 San Antonio TX *
1984 Snowbird UT
1985 Athens GA
1986 Denver CO *
1987 Lincoln NE #
1988 Winston-Salem NC
1989 Vancouver, BC, Canada
1990 East Lansing MI
1991 Madison WI
1992 Philadelphia PA
1993 Atlanta GA *
1994 Ft. Collins CO
1995 Pittsburgh PA **
1996 Tucson AZ ††
1997 Nashville TN
1998 Kona HI
1999 Monterey CA ‡‡
2000 San Juan PR ††
2001 Albuquerque NM
2002 Vancouver, BC, Canada ¶§§
2003 Halifax, NS, Canada
2004 Philadelphia PA **
2005 Mobile AL
2006 Glasgow, Scotland ¶
2007 Merida, Yucatan, Mexico §§¶ ¶
2008 Arlington TX
2009 Knoxville TN
2010 Colorado Springs, CO
2011 Anchorage, AK

* 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