The 86th Annual Meeting of the American Society of Parasitologists

Sheraton Anchorage Hotel and Spa
Anchorage, Alaska, June 1-4, 2011

Chugach State Park

Alaska Native Heritage Center

Program & Abstracts

Thanks to Everyone Who Helped Make this Meeting Possible …

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

ASP Local Arrangements Committee and Scientific Program Officers

Dr. Herman Eure, Wake Forest University

Dr. Kelli Sapp, High Point University

In Anchorage …

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The American Society of Parasitologists
ESTABLISHED 1924

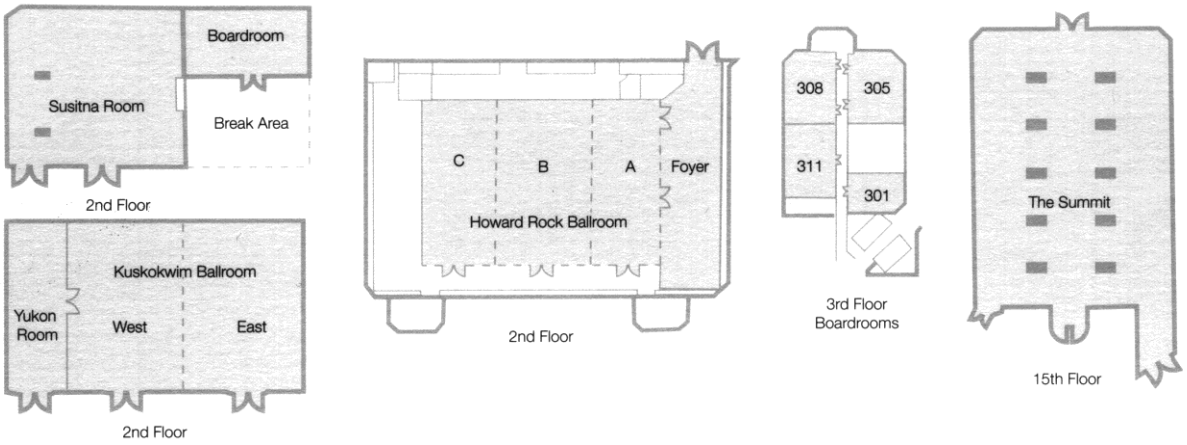
Welcome

We would like to welcome you to the 86th annual meeting of the American Society of Parasitologists (ASP).

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

Herman Eure and Kelli Sapp, Scientific Program Officers

Floor Plan, Sheraton Anchorage Hotel & Spa



Day/Times	Activity/Function	Room/Space
June 1 (Wednesday)		
8:00 a.m.-Noon	ASP Council	Boardroom 305
1:00 – 4:45 p.m.	Arctic Passages Symposium	Susitna Room
1:00 -5:00 p.m.	Host Parasite Interactions I	Kuskokwim East
1:00-4:45 p.m.	Life Cycles and Epidemiology	Kuskokwim West
2:45-3:15 p.m.	Coffee Break	
7:00 – 10:00 p.m.	Welcome Reception	The Summit
June 2 (Thursday)		
7:00-8:30 a.m.	Editorial Board Breakfast	Yukon Room
8:30-10:30 a.m.	ASP President's Symposium	Howard Rock Ballroom
10:30-11:00 a.m.	Coffee Break	
11:00-Noon	Eminent Parasitologist Lecture	Howard Rock Ballroom
1:00-3:00 p.m.	Taxonomy, Systematics, Phylogeny I	Kuskokwim East
1:00-3:00 p.m.	Biochemistry, Cell Biology, Physiology	Kuskokwim West
3:00-3:30 p.m.	Coffee Break	
3:45-5:30 p.m.	ASP Students' Symposium	Kuskokwim East/West
5:30-6:30 p.m.	ASP Student Social	Susitna Room
3:00-6:00 p.m.	Auction Set Up	Howard Rock A & Foyer
6:00-7:00 p.m.	Auction Preview	Howard Rock A & Foyer
7:00-9:00 p.m.	22nd Annual ASP Student Auction	Howard Rock A & Foyer
June 3 (Friday)		
8:00-10:00 a.m.	Associate Editors Symposium	Susitna Room
8:30-11:45 a.m.	Genetics and Molecular Biology	Kuskokwim East
8:30-11:30 a.m.	43rd Coccidiosis Conference	Kuskokwim West
10:00-10:15 a.m.	Coffee Break	
1:00-2:00 p.m.	ASP President's Address	Howard Rock Ballroom
2:15-5:45 p.m.	Ecology I	Susitna Room
2:15-5:45 p.m.	Taxonomy, Systematics, Phylogeny II	Kuskokwim East
2:45-5:00 p.m.	Vector Bio., Immuno., Chemotherapy	Kuskokwim West
3:45-4:00 p.m.	Coffee Break	
3:00-5:00 p.m.	Poster Boards delivered, authors may set up posters	Foyer
7:00-10:00 p.m.	Anchorage Museum	
June 4 (Saturday)		
8:00-11:30 a.m.	Ecology II	Kuskokwim West
8:00-12:00 p.m.	Host Parasite Interactions II	Kuskokwim East
9:45-10:00 a.m.	Coffee Break	
8:30-10:30 a.m.	Authors complete poster set up	
12:00-1:30 p.m.	Poster Session, coffee, snacks	Foyer
2:00-3:30 p.m.	ASP Awards and Business Meeting	Howard Rock Ballroom

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

Wednesday Morning, 2011-06-01

08:00 AM – Noon ASP Council Meeting, Boardroom 305

Presiding: J. Caira, The University of Connecticut

Wednesday Afternoon, 2011-06-01

1:00-4:45 pm Arctic Passages Symposium

Location: Susitna Room

Presiding: E.P. Hoberg, Animal Parasitic Diseases Laboratory, USDA

Time (Abstract No.)

1:00 (1) **J.A. Cook**, E.P. Hoberg, S.O. MacDonald, A.G. Hope, N.G. Dawson, ZV. Fedorov. BERINGIA: HISTORY AND CLIMATE STRUCTURE NORTHERN ASSEMBLAGES OF MAMMALS AND PARASITES AT THE NEXUS OF ASIA AND NORTH AMERICA.

1:25 (2) **S.L. Talbot**, S.A. Sonthagen, N.G. Dawson J.M. Pearce, G.K. Roffler, G.K. Sage, E.S. Martinsen, R.C. Fleischer. INTEGRATING TO MANAGE FOR CHANGE: INCORPORATING PARASITES INTO MANAGEMENT AND CONSERVATION PLANS.

1:50 (3) **K.E. Galbreath**, E.P. Hoberg. A WORM WITH A VIEW: PARASITE PERSPECTIVES ON BERINGIAN BIOGEOGRAPHY.

2:45-3:15 pm COFFEE BREAK

3:15 (4) **B.M. Rosenthal**, PAST AND PRESENT CHANGES IN THE DISTRIBUTION OF *TRICHINELLA* SPP. IN THE ARCTIC.

3:40 (5) **S. Kutz** . ARCTIC CHANGE – A DRIVER FOR PARASITE EMERGENCE, INVASION AND EXTINCTION?

4:10-4:45 Questions, Closing Remarks.

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

Location: Kuskokwim East

Presiding: S.C. Datta, West Bengal University
K. Sapp, High Point University

Time (Abstract No.)

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

1:00 (6) **R. Kortet**, A. Hedrick, A. Vainikka. PARASITES AND PATHOGENS ARE IMPORTANT PLAYERS IN EVOLUTION OF ANIMAL PERSONALITY TRAITS?

1:15 (7) **A. Schmidt-Rhaesa**, FROM TINY TO LONG – THE DEVELOPMENT OF HORSEHAIR WORMS (NEMATOMORPHA) WITHIN THEIR HOST.

1:30 (8)† **M. Tellez**, ANNUAL HOST-PARASITE DISTRIBUTION PATTERNS OF *ALLIGATOR MISSISSIPPIENSIS* IN LOUISIANA.

1:45 (9)† **A. Morgan**, T. Cook. GREGARINE HOST USE AND DISTRIBUTION WITHIN *CALOPTERYX* DAMSELFLIES OF THE SOUTHEASTERN UNITED STATES.

2:00 (10)† **J. Palladino**, R. Poulin, D. Keeney. GENETIC DIVERSITY AND HOST SPECIFICITY OF ECHINOSTOMATID TREMATODES IN NEW ZEALAND INTERTIDAL SNAILS.

2:15 (11) **M.A. Forys**, P.C. Hanington, E.S. Loker. AN EXAMPLE OF MODULATED HOST SUSCEPTIBILITY: SENSITIZATION WITH ECHINOSTOMES REDUCES THE RESISTANCE OF BS-90 STRAIN *BIOMPHALARIA GLABRATA* TO *SCHISTOSOMA MANSONI*.

2:30 (12) **J.A. Ferguson**, C.B. Schreck, K.C. Jacobson, P.A. Rossignol, S. St-Hilaire, K.J. Rodnick, J. Rommer, M.L. Kent. IMPACTS OF MULTISPECIES PARASITISM ON JUVENILE COHO SALMON (*ONCORHYNCHUS KISUTCH*) IN OREGON.

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

3:15 (13)† **K.L. Sheehan**, P. Jodice. INTESTINAL PARASITE ASSEMBLAGES OF DOUBLE-CRESTED CORMORANTS: A COMPARISON OF THREE LAKE COLONIES IN MINNESOTA USA.

3:30 (14) **K.M. Bichoupan**, O. Varechtouk, S.B. Muench. LOCOMOTIVE BEHAVIOR IN *BULINUS TRUNCATUS* IS ALTERED BY INFECTION WITH *SCHISTOSOMA HAEMATOBIUM*.

3:45 (15) **M. Sterner**, C. Roderick, N. Thomas, R.A. Cole. COMPARISON OF THE GASTROINTESTINAL PARASITE FAUNA OF ALASKAN AND WASHINGTON SEA OTTERS (*ENHYDRA LUTRIS KENYONI*) SUBMITTED TO THE NATIONAL WILDLIFE HEALTH CENTER FROM 1991-2010.

4:00 (16)† **C. Niebuhr**. DETECTING SPINOSE EAR TICK (*OTOBIUS MEGNINI*) PRESENCE USING HOST AND HABITAT CHARACTERISTICS.

4:15 (17)† **M. Dodge**, R. Sehgal. THE EFFECTS OF MIGRATION ON THE SPREAD OF AVIAN MALARIA IN NEOTROPICAL BIRDS.

4:30 (18)† **K. Coyne**, J. Laursen, T. Yoshino. *FASCIOLOIDES MAGNA* MIRACIDIA ARE DAMAGED IN VITRO BY MUCUS FROM INCOMPATIBLE SNAIL *HELISOMA TRIVOLVIS*, BUT NOT FROM COMPATIBLE SNAIL HOST, *LYMNAEA PALUSTRIS*.

4:45 (19)† **M.S. Sokolowski**, T.H. Cribb, S.B. Munch. WHICH CONTRIBUTES MORE TO TOTAL PARASITE DIVERSITY, DIVERSITY WITHIN OR AMONGST HOSTS?

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

Location: Kuskokwim West

Presiding: R. Fayer, USDA-ARS
L. Measures, Fisheries and Oceans Canada

Time (Abstract No.)

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

1:00 (20) **S. Brant**, N. Davis. ITCHY KIWIS: SWIMMER'S ITCH AND SCHISTOSOME DIVERSITY IN NEW ZEALAND.

1:15 (21) **R.M. Kocan**, P. Hershberger. EXPERIMENTAL EVIDENCE FOR THE EXISTENCE OF A CIRCULATING BLOOD STAGE OF *ICHTHYOPHONUS* SP. IN ORALLY EXPOSED PACIFIC STAGHORN SCULPINS (*LEPTOCOTTUS ARMATUS*).

1:30 (22)† **T. Roberts**, J. Harkness, J. Ellis, D. Stark. MOLECULAR EPIDEMIOLOGY AND CLINICAL ASPECTS OF *BLASTOCYSTIS* SP.- AN AUSTRALIAN PERSPECTIVE.

1:45 (23) **W. Miller**. FECAL PROTOZOA AS PART OF A FUTURE WATER QUALITY FRAMEWORK.

2:00 (24) **M. Santin**, D. Dargatz, R. Fayer. *GIARDIA DUODENALIS* ASSEMBLAGES IN WEANED CATTLE ON COW-CALF OPERATIONS IN THE UNITED STATES.

2:15 (25) **W. Li**, N.M. Kiulia, J.M. Mwenda, A. Nyachieo, M.B. Taylor, M. Eberhard, X. Zhang, L. Xiao. IDENTIFICATION OF CYCLOSPORA PAPIONIS AND HUMAN-PATHOGENIC GENOTYPES AND SUBTYPES OF *CRYPTOSPORIDIUM* AND *ENTEROCYTOZOON BIENEUSI* IN CAPTIVE BABOONS IN KENYA.

2:30 (26) † **M.A. Thomson**, D.D. Colwell. S.Z. Kienzle, C.P. Goater. LANDSCAPE EPIDEMIOLOGY OF AN EMERGING PARASITE: THE LANCET LIVER FLUKE, *DICRCOELIUM DENDRITICUM*, IN CYPRESS HILLS PARK, ALBERTA.

2:45-3:15 pm COFFEE BREAK

3:15 (27) **A. Choudhury**, R. Cole, A. Makinster. THE LIFE CYCLE OF THE CECAL TROUT NEMATODE, *TRUTTAEDACNITIS TRUTTAE* (NEMATODA: CUCULLANIDAE) IN NORTH AMERICA.

3:30 (28) **C.T. Faulkner**, R. Donnell. *DIROFILARIA IMMITIS* IN WILD CANIDAE FROM KNOX AND SURROUNDING COUNTIES IN EAST TENNESSEE.

3:45 (29) **K. Marshall**, K. Taylor, V.D. Faulkner. KNOWLEDGE AND PERCEPTIONS OF TOXOPLASMOSIS AMONG MEDICAL AND VETERINARY PERSONNEL IN AN APPALACHIAN COMMUNITY.

4:00 (30) **R.A. Cole**, L. Nico. EXAMINATION OF IMPORTED ASIAN SWAMP EELS (SYNBRANCHIDAE: *MONOPTERUS (AMPHIPNOUS) CUCHIA*) FROM TWO MARKETS IN THE SOUTHEASTERN UNITED STATES FOR THE PRESENCE OF ADVANCED L3 OF *GNATHOSTOMA* SPP.

4:15 (31) **T.R. Olariu**, G. Darabus, D. Teodorescu Brinzeu, A. Koreck, C. Petrescu. GIARDIASIS IN INSTITUTIONALIZED ROMANIAN CHILDREN.

4:30 (32) **F.O. AKINBO**, C.E. Okaka, R. Omoregie. PREVALENCE OF INTESTINAL PARASITES IN RELATION TO CD4 COUNTS AND ANAEMIA AMONG HIV-INFECTED PATIENTS IN BENIN CITY, EDO STATE, NIGERIA.

Wednesday Evening, 2011-06-01

07:00 - 10:00 PM WELCOME RECEPTION – The Summit

Thursday Morning, 2011-06-02

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

8:30-10:30 am ASP PRESIDENT'S SYMPOSIUM

Location: Howard Rock Ballroom

Presiding: E.S. Loker, University of New Mexico

Theme: Parasitology at the Boundary of Ecology and Evolution.

8:30 INTRODUCTION.

8:40 (33) **M.V. Sukhdeo**. SKIRMISHES ON THE BORDER BETWEEN PARASITOLOGY AND COMMUNITY ECOLOGY: THE NEED FOR NATURAL HISTORY.

9:10 (34) **S.A. Nadler**. PHYLOGENETIC SYSTEMATICS: AN ESSENTIAL FRAMEWORK FOR UNDERSTANDING HOST-PARASITE ECOLOGY.

9:40 (35) **R. Poulin**. HOST SPECIFICITY AT THE INTERFACE OF ECOLOGY AND EVOLUTION.

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

10:30-11:00 am COFFEE BREAK

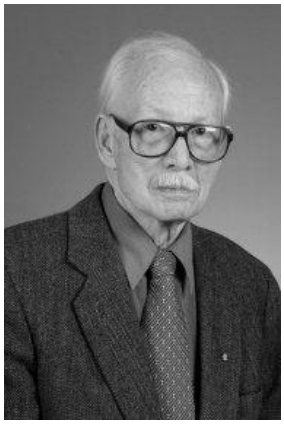
11:00 am-NOON Eminent Parasitologist Lecture

Location: Howard Rock Ballroom

Presiding: W.O. Granath, University of Montana

11:10 Introduction. E.P. Hoberg and A. Adams.

11:10 (36) **R.L. Rausch**. "From the Arctic to the Tropics."



R. L. Rausch, *Emminent* Parasitologist

Thursday Afternoon, 2011-06-02

1:00-3:00 pm Taxonomy, Systematics, Phylogeny I

Location: Kuskokwim East

Presiding: A. Jiménez, Southern Illinois University, Carbondale
V. Tkach, University of North Dakota

Time (Abstract No.)

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

1:00 (37)† **C. Bochte**, S. Brant, J. Leonard, E.S. Loker. OBSERVATIONS ON THE MORPHOLOGY, BEHAVIOR AND PHYLOGENETIC POSITION OF THREE LARGE-TAILED STRIGEID CERCARIAE FROM SMALL PLANORBID SNAILS (TRIBE PLANORBINI).

1:15 (38)† **K. Bell**, E. Hoberg, J. Demboski, J. Cook. COMPARATIVE PHYLOGEOGRAPHY OF TWO PINWORM SPECIES THAT INFECT CHIPMUNKS.

1:30 (39) **M. Garcia-Varela**, F.J. Aznar, G. Pérez Ponce de León, S.A. Nadler. MOLECULAR PHYLOGENY OF POLYMORPHIDAE (ACANTHOCEPHALA) A FAMILY OF PARASITES OF MARINE MAMMALS, WATERFOWL AND FISH-EATING BIRD INFERRED FROM NUCLEAR AND MITOCHONDRIAL GENE SEQUENCES.

1:45 (40)† **L. Babcock**, R.E. Clopton. FENCES IN THE COMMON GARDEN: SUBOPTIMAL FITNESS OF *BLABERICOLA PRINCISI* AND *BLABERICOLA BLABERAE* EXPERIMENTALLY INFECTING ABNORMAL COCKROACH HOSTS.

2:00 (41)† **M. Pickering**, J.N. Caira. EXPANSION OF THE CESTODE GENUS *TRILOCULARIA*: AN INVESTIGATION ACROSS SHARK HOSTS AND OCEANS.

2:15 (42)† **A.J. Phillips**, S. Kvist. DO GAPS BETWEEN GEOGRAPHIC DISTRIBUTIONS OF *PHILOBDELLA* SPECIES CORRELATE WITH ENVIRONMENTAL DATA?

2:30 (43)† **J. Bernot**. CESTODE MORPHOLOGY AS PREDICTED BY ELASMOBRANCH RELATIONSHIPS: *CALLIOBOTHRIUM* IN SMOOTH HOUND SHARKS OF THE GENUS *MUSTELUS*.

2:45 (44) **A.P. Shinn**, G. Paladini, M. Rubio-Godoy, I.D. Whittington, J.E. Bron. MONODB: WORK IN PROGRESS FOR A CENTRALIZED WEB-BASED RESOURCE FOR THE CLASS MONOGENEA.

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

1:00-3:00 pm Biochemistry, Cell Biology, Physiology

Location: Kuskokwim East

Presiding: J. Camp, Purdue University
T. Yoshino, University of Wisconsin, Madison

Time (Abstract No.)

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

1:00 (45) **D. Macarisin**, C. O'Brien, G. Bauchan, M. Jenkins, R. Fayer. SPATIAL LOCALIZATION OF δ-GIARDIN WITHIN THE VENTRAL DISC OF *GIARDIA DUODENALIS* USING LASER SCANNING CONFOCAL MICROSCOPY.

1:15 (46) **J.A. Flaspohler**, B. Jensen, T. Saveria, C. Kifer, M. Parsons. CHARACTERIZATION OF A NOVEL PROTEIN KINASE LOCALIZED TO LIPID BODY MEMBRANES OF *TRYPANOSOMA BRUCEI*.

1:30 (47) **G. Mayer**, HAEMOSPORIDIA PREVALENCE IN BREEDING PROTHONOTARY WARBLERS.

1:45 (48)† **S. Jean**. DETERMINATION OF THE FUNCTIONALITY OF THE C2 DOMAIN OF NOVEL *P. FALCIPARUM* EXPORTED PROTEIN, PFEXP-250.

2:00 (49) **S. Cai**, FRACTIONATION OF LIFE CYCLE STAGES OF *NOSEMA BOMBYCIS* (MICROSPORIDIA) FROM *BOMBYX MORI* BY PERCOLL DENSITY GRADIENT.

2:15 (50) **I.G. Tsarukyanova**, H. van Keulen, T.A. Paget, K. Harris, E.L. Jarroll, B. Goldberg. EFFECT OF NITROSYLATION ON ENCYSTMENT REGULATION IN THE PROTOZOAN *GIARDIA INTESTINALIS*.

2:30 (51) **E.S. Mo**, E.L. Jarroll, M. Watson, T.A. Paget. METABOLIC VARIATION BETWEEN HUMAN INFECTIVE *GIARDIA* ASSEMBLAGES.

2:45 (52)† **S.S. Ray**. REGULATION OF *TRYPANOSOMA BRUCEI* ACETYL-COA CARBOXYLASE, THE KEY ENZYME FOR INITIATION OF FATTY ACID SYNTHESIS.

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

3:45-5:30 pm ASP Students' Symposium

Location: Kuskokwim East/West

Time (Abstract No.)

3:45 pm **J. Cielocha**, Introduction.

3:50 (53) **A.M. Adams**. REGULATORY IMPACTS ON PREVALENCE AND TREATMENT OF FOODBORNE PARASITES.

4:20 (54) **T.V. Rajan**. THE VIGILANT GENOTYPE.

4:50 (55) **R.R. Dunn**. THE WILD LIFE OF OUR BODIES-CONSEQUENCE OF HAVING EVOLVED IN THE WILD FOR OUR MODERN, CLEAN, LIVES.

5:20 Questions, Closing Remarks**.**

5:30-6:30 pm *ASP Students' Social*

Location: Susitna Room

Thursday Evening, 2011-06-02

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

7:00-9:00 pm **22nd ANNUAL ASP STUDENT AUCTION**

Location: Howard Rock A & Foyer

Friday Morning, 2011-06-03

8:00-10:00 Associate Editors Symposium

Location: Susitna Room

Presiding: G.W. Esch, Wake Forest University
M. Sukhdeo, Program in Ecology and Evolution, Rutgers University

Time (Abstract No.)

8:00 (56) **G.W. Esch, M. Sukhdeo**. Introduction, EDITORS SYMPOSIUM – 2011.

8:20 (57) **W.O. Granath**. ECOLOGY OF SALMONID WHIRLING DISEASE IN A WESTERN MONTANA STREAM: A LONG-TERM STUDY (AKA: A TWISTED TAIL).

8:40 (58) **J.T. Sullivan**. RESPONSES OF THE AMEBOCYTE-PRODUCING ORGAN OF *BIOMPHALARIA GLABRATA* TO NONSELF.

9:00 (59) **J. Sakanari**. MACROFILARICIDAL DRUG STUDY FOR THE TREATMENT OF HUMAN ONCHOCERCIASIS AND LYMPHATIC FILARIASIS.

9:20 (60) **A.W. Shostak**. *HYMENOLEPIS* AND *TRIBOLIUM* AS A MODEL SYSTEM IN PARASITE ECOLOGY.

9:40 Questions, Closing Remarks**.**

10:00-10:15 am **COFFEE BREAK**

8:30-11:45 am Genetics and Molecular Biology

Location: Kuskokwim East

Presiding: J.M. Porter-Kelley, Winston-Salem State University
B. Sears, University of South Florida

Time (Abstract No.)

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

8:30 (61) **X. Gao**, K. Goggin, J.M. Hawdon. DAF-16/FOXO TARGET GENE REGULATION DURING EARLY PARASITIC DEVELOPMENT OF HOOKWORMS.

8:45 (62) **V. Gelmedin**, X. Gao, T. Brodigan, M. Krause, J. Hawdon. HOOKWORM TRANSCRIPTION FACTOR DAF-16 WILD-TYPE AND AKT- PHOSPHO- MUTANTS RESTORE DEVELOPMENTAL ARREST IN *C. ELEGANS* MUTANTS.

9:00 (63) **J.D. Stoltzfus**, H.C. Massey Jr., J.B. Lok. *STRONGYLOIDES STERCORALIS* AGE-1: A POTENTIAL REGULATOR OF INFECTIVE LARVAE DEVELOPMENT.

9:15 (64) **T.A. Lyda**, A.Y. Kelada, Y. Hernandez, M.B. Joshi, P.A. Bates, D.M. Dwyer. MOLECULAR AND FUNCTIONAL CHARACTERIZATION OF A UNIQUE DEVELOPMENTALLY EXPRESSED SECRETORY INVERTASE FROM *LEISHMANIA MEXICANA*.

9:30 (65)† **L.I. McCall**, G. Matlashewski. INVOLVEMENT OF THE *LEISHMANIA DONOVANI* VIRULENCE FACTOR A2 IN THE PARASITE STRESS RESPONSE: PROTECTION AGAINST HEAT SHOCK AND OXIDATIVE STRESS.

9:45 (66) **I. Blasco-Costa**, J.M. Waters, R. Poulin. HOW DO HABITAT FEATURES AFFECT PARASITE POPULATION CONNECTIVITY?

10:00-10:15 am COFFEE BREAK

10:15 (67) **P. Lee**, Y. Nagashio, K. Nakagaki. IDENTIFICATION AND CHARACTERIZATION OF *DIROFILARIA IMMITIS* MICROFIALRIAL CHITINASE.

10:30 (68) **J.M. Porter-Kelley**, S.H. Kanan, M.J. Woodard. MICRORNAS IN *LEISHMANIA BRAZILIENSIS*.

10:45 (69) **C.L. Valentim**, T.C. Anderson, J.I. Tsai, M. Berriman, P.T. LoVerde. FORWARD GENETICS AS A TOOL TO MAP OXAMNIQUINE RESISTANCE IN *SCHISTOSOMA MANSONI*.

11:00 (70) **K.M. Bonner**, C.J. Bayne, M.S. Blouin. ASSESSING FITNESS CONSEQUENCES OF RESISTANCE ALLELES AT CU/ZN SUPEROXIDE DISMUTASE (SOD1) IN THE *S. MANSONI*/*B. GLABRATA* MODEL PARASITE SYSTEM.

11:15 (71) **R.B. Beckstead**. MOLECULAR CHARACTERIZATION OF *HISTOMONAS MELEAGRIDIS*.

11:30 (72)† **C. Martinez**, C. Loiseau, R. Sehgal. IDENTIFICATION OF MAEBL, AN ERYTHROCYTE BINDING PROTEIN, IN *PLASMODIUM GALLINACEUM*.

8:30-11:30 pm *43rd Coccidiosis Conference (sponsored by Bayer and Merial)*

Location: Kuskokwim West

Presiding: G. Zhu, Texas A&M University
R. Beckstead, The University of Georgia

Time (Abstract No.)

8:30 am Introduction.

8:45 (73) **D.S. Roos.** DESIGNING AND MINING GENOME DATABASES: FROM GENES TO DRUGS AND VACCINES.

9:10 (74) B. Striepen. GENETIC DISSECTION OF APICOPLAST FUNCTION AND BIOGENESIS.

9:35 (75) **L. Cui**, J. Miao, L. Cui. THE ROLE OF TRANSLATIONAL REGULATION IN SEXUAL DEVELOPMENT OF MALARIA PARASITE.

10:00-10:15 am **COFFEE BREAK**

10:15 (76) **X. Suo**, X. Liu, G. Yin, X. Huang, Y. Chen. CONSTRUCTION OF TRANSGENIC *EIMERIA* PARASITES AND STUDY OF THEIR ELICITATION OF MUCOSAL IMMUNITY.

10:40 (77) **G. Zhu**. *CRYPTOSPORIDIUM*: UNIQUE EVOLUTIONARY POSITION AND METABOLIC FEATURES FOR DRUG DEVELOPMENT.

11:05 Questions, Closing Remarks.

Friday Afternoon, 2011-06-03

Janine Caira, ASP President

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

Location: Howard Rock Ballroom

Presiding: D. Duszynski, Univerisity of New Mexico

1:00 Introduction of **Dr. Janine Caira**.
The University of Connecticut

1:10 (78) **J. Caira**. "
The American Society of Parasitologists: Who are we now?"

2:15-5:45 pm *Ecology I*

Location: Susitna Room

Presiding: K.D. Lafferty, Univeristy of California-Santa Barbara, USGS
K.L. Sheehan, Clemson University

Time (Abstract No.)

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

2:15 (79)† **M.R. Zimmermann**, K.E. Luth, G.W. Esch. COMPLEX INTERACTIONS AMONG A NEMATODE PARASITE (*DAUBAYLIA POTOMACA*), A COMMENSALISTIC ANNELID (*CHAETOGASTER LIMNAEI LIMNAEI*), AND TREMATODE PARASITES IN A SNAIL HOST (*HELISOMA ANCEPS*).

2:30 (80)† **K.K. Herrmann**, R. Poulin. WHEN A TREMATODE SKIPS A HOST: PROGENESIS AS AN ALTERNATIVE LIFE CYCLE STRATEGY.

2:45 (81)† **B. Johnson**, M. Sukhdeo. THE IMPACTS OF URBAN WETLANDS ON MOSQUITO POPULATION DYNAMICS AND DISEASE RISK FOR WEST NILE VIRUS.

3:00 (82)† **W. Rossiter**, M.V. Sukhdeo. PATTERNS IN THE DISTRIBUTION OF PARASITE BIOMASS IN A RIVERINE FOOD WEB.

3:15 (83)† **J. Hogan**, M. Daniels, F. Watson, P. Conrad, W. Miller. WATERBORNE PROTOZOAL REMOVAL BY COASTAL CALIFORNIA WETLANDS.

3:30 (84) **M. Johnson**, K.D. Lafferty, C. Oosterhout, J. Cable. SOCIALITY DRIVES EXPERIMENTAL EPIDEMICS IN GUPPIES.

3:45 – 4:00 pm **COFFEE BREAK**

4:00 (85)† **C. Boesen**. HELMINTH COMMUNITY STRUCTURE IN THREE SPECIES OF COLUMBIDS THAT CO-OCCUR IN EAST TEXAS.

4:15 (86)† **A.D. Stumbo**, C.T. James, C.P. Goater, B.D. Wisenden. SAFETY IN NUMBERS: SHOALING AS AN ANTI-PARASITE DEFENSE IN FATHEAD MINNOWS EXPOSED TO TREMATODE CERCARIAE.

4:30 (87)† **B.F. Sears**, J. Rohr, L.B. Martin. RESISTANCE TO TREMATODE PARASITES CARRIES A DEVELOPMENTAL COST IN ANURAN TADPOLES.

4:45 (88)† **J.P. Losee**, K.C. Jacobson. USING TROPHICALLY TRANSMITTED PARASITES TO ESTABLISH LINKS BETWEEN PACIFIC SALMON AND VARIABILITY IN OCEAN CONDITIONS.

5:00 (89)† **B. Walker**, G. Sandland, J. Nissen. SEASONAL AND SPATIAL DISTRIBUTIONS OF AN INVASIVE SNAIL (*BITHYNIA TENTACULATA*) AND ITS PARASITIC HITCHHIKERS IN THE UPPER MISSISSIPPI RIVER NATIONAL WILDLIFE AND FISH REFUGE (UMRWFR).

5:15 (90) **R.F. Hechinger**, K. Lafferty, A. Dobson, J. Brown, A. Kuris. A COMMON SCALING RULE FOR THE ABUNDANCE AND ENERGETICS OF PARASITIC AND FREE-LIVING SPECIES.

5:30 (91) **A.T. Claxton**, M. Bhuthimethee, D. Teel, K.C. Jacobson. PARASITE ASSEMBLAGES AND JUVENILE CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) HABITAT USE IN THE COLUMBIA RIVER ESTUARY IN 2004 AND 2005.

2:15-5:45 pm Taxonomy, Systematics, Phylogeny II
Location: Kuskokwim East

Presiding: M. Siddall, Sackler Institute of Comparative Genomics
S. Seville, University of Wyoming

Time (Abstract No.)

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

2:15 (92) **M. Rubio-Godoy**, G. Paladini, .A. Freeman, A. García-Vásquez, A.P. Shinn. DESCRIPTION OF A NEW STRAIN OF *GYRODACTYLUS SALMONIS* (PLATYHELMINTHES, MONOGENEA) COLLECTED IN MEXICO FROM RAINBOW TROUT (*ONCORHYNCHUS MYKISS WALBAUM*): MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION.

2:30 (93)† **A.C. Begay**, A. Schmidt-Rhaesa, M.G. Bolek, B. Hanelt. NEW SPECIES OF *GORDIONUS* (NEMATOMORPHA: GORDIIDA) FROM THE SOUTHERN ROCKY MOUNTAINS.

2:45 (94) **B. Hanelt**, A. Schmidt-Rhaesa, M.G. Bolek. HIDDEN DIVERSITY IN *GORDIUS ROBUSTUS* (NEMATOMORPHA: GORDIIDA); HOW MOLECULAR DATA IS SHEDDING LIGHT ON A CRYPTIC SPECIES COMPLEX.

3:00 (95) **C.J. Healy**. RHINEBOTHRIIDEAN CESTODES FROM RAYS (ELASMOBRANCHII: BATOIDEA) IN VIETNAM AND A COMPARISON OF PARASITE FAUNAS FROM THREE LOCALITIES ACROSS THE INDO-WEST PACIFIC: VIETNAM, BORNEO AND AUSTRALIA.

3:15 (96)† **A.F. Oceguera-Figueroa**. PHYLOGENY OF THE LEECH FAMILY GLOSSIPHONIIDAE (ANNELIDA: RHYNCHOBDELLIDA) BASED ON MOLECULAR DATA.

3:30 (97) **E.E. Pulis**, V.V. Tkach, R.M. Overstreet. HELMINTH PARASITES OF THE ALLIGATOR SNAPPING TURTLE (*MACROCLEMYS TEMMINCKII* HARLAN, 1835) FROM THE PASCAGOULA RIVER.

3:45 – 4:00 pm COFFEE BREAK

4:00 (98) **F. Reyda**. A TWO-YEAR SURVEY OF THE FISH PARASITES OF OTSEGO LAKE, NEW YORK.

4:15 (99) **S.E. Greiman**, V.V. Tkach, S.D. Snyder. NEW *DRACOVERMIS* (DIGENEA, LIOLOPIDAE) FROM AUSTRALIAN CROCODILES AND ITS PHYLOGENETIC AFFINITIES.

4:30 (100) **R.P. Scheibel**, F. Jiménez. EVOLUTIONARY RELATIONSHIPS OF NEMATODES IN THE FAMILY VIANNAIIDAE (NEMATODA: TRICHOSTRONGYLINA) BASED ON THE FIRST MOLECULAR PHYLOGENY.

4:45 (101) **M.G. Bolek**, B. Hanelt, A. Schmidt-Rhaesa, C. Szmygiel. UNRAVELING A GORDIAN KNOT: BIODIVERSITY OF GORDIAN WORMS, PHYLUM NEMATOMORPHA.

5:00 (102) **M. Siddall**. FRONTEIRS IN PARASITE PHYLOGENOMICS - EXPRESSED SEQUENCE TAGS AND THE NEXT 5 YEARS.

5:15 (103) **A. Jiménez**, M. Robles. HOST USE AND GEOGRAPHIC DISTRIBUTION OF TWO SPECIES OF PINWORMS (*SYPHACIA*: OXYURIDAE) IN SOUTH AMERICA.

5:30 (104) **V.V. Tkach,** J. Schroeder, J.A. Vaughan. DISTRIBUTION OF *NEORICKETTSIA* AMONG DIGENEANS: EVOLUTIONARY AND ECOLOGICAL CONSIDERATIONS.

2:45-5:00 pm Vector Biology, Immunology, Chemotherapy

Location: Kuskokwim West

Presiding: L. Camp, University of California, Davis
J.F. Hillyer, Vanderbilt University

Time (Abstract No.)

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

2:45 (105) **J.F. Hillyer**, J.G. King. INFECTION-INDUCED HEMOCYTE AGGREGATION ON THE SURFACE OF THE MOSQUITO HEART.

3:00 (106) J.A. Greenberg, M.A. DiMenna, H.J. Wearing, **B.V. Hofkin**. EVALUATION OF WEST NILE VIRUS VECTORS IN BERNALILLO COUNTY, NEW MEXICO, USA: IMPLICATIONS FOR DISEASE TRANSMISSION.

3:15 (107)† **L.T. Sigle**, M. Robles-Murguia, N. Sharma, M. Ramalho-Ortigao. KAZAL-TYPE SERINE PROTEASE INHIBITORS IN *PHLEBOTOMUS PAPATASI* MIDGUT.

3:30 (108) **S.I. Jarvi**, M.E. Farias, C.T. Atkinson. EFFECTS OF CO-INFECTION WITH AVIPOXVIRUS ON DIVERSITY OF *PLASMODIUM RELICTUM* IN NATIVE HAWAIIAN FOREST BIRDS.

3:45 – 4:00 pm COFFEE BREAK

4:00 (109) **J.F. Hillyer**, T.Y. Estevez-Lao. ROLE OF MOSQUITO EGF-REPEAT CONTAINING PROTEINS IN THE ANTIBACTERIAL IMMUNE RESPONSE IN THE HEMOCOEL

4:15 (110)† **J. Edwards**, W.T. Watford, M.J. Yabsley. DIVERGING IMMUNE RESPONSES IN BALB/C MICE TO INFECTION WITH DISTINCT *TRYPANOSOMA CRUZI* STRAINS FROM THE UNITED STATES AND SOUTH AMERICA.

4:30 (111) **E.N. Villegas**, M.W. Ware, U. Nwa, C.C. Brescia, S. Augustine, L.F. Villegas, M.J. See, S.L. Hayes, H.A. Lindquist, F.W. Schaefer, III, J.P. Dubey, ALTERNATIVE APPROACHES TO EVALUATE THE EFFECTS OF CHEMICAL AND PHYSICAL DISINFECTANTS ON WATERBORNE PROTOZOA.

4:45 (112) **S.C. Datta**. MOMORDICATIN IS A NOVEL AND EFFECTIVE CHEMOTHERAPEUTIC AGENT TO TREAT VISCERAL LEISHMANIASIS.

3:00-5:00 pm Poster DisplayBoards delivered

Location: Foyer (adjacent to the Howard Rock Ballroom)

Authors may set up posters during this time

Friday Evening, 2011-06-03

7:00 – 10:00 pm An Evening at the Anchorage Museum

About the museum—
The Anchorage Museum shares and connects Alaska with the world through art, history and science. Permanent exhibits include an Alaska history gallery, Alaska art galleries, the Imaginarium Discovery Center science galleries and the Smithsonian Arctic Studies Center, which features Alaska Native artifacts on long-term loan from the Smithsonian Institution.

The Smithsonian Institution's Arctic Studies Center conducts public programs and collaborative research programs to increase understanding of northern peoples, cultures and environments

Web site http://www.anchoragemuseum.org

Saturday Morning, 2011-06-04

8:00-11:30 am Ecology II

Location: Kuskokwim West

Presiding: K. Luth, Wake Forest University
G. Sandland, University of Wisconsin, La Crosse

Time (Abstract No.)

8:00 (113) **C.A. Blanar**, D.J. Marcogliese. MAJOR CHANGES IN PARASITE COMMUNITY STRUCTURE IN TROUT-PERCH (*PERCOPSIS OMISCOMAYCUS*) ON THE ATHABASCA RIVER: EFFECTS OF OIL SANDS OPERATIONS?

8:15 (114) **S. Kaunisto**, R. Kortet, L. Härkönen, S. Härkönen, H. Ylönen, S. Laaksonen. A NEW METHOD TO DIAGNOSE DEER KED (*LIPOPTENA CERVI*) INFECTION IN CERVIDS DURING WINTER TIME.

8:30 (115) **J. Koprivnikar**, C. Gibson. INFECTIOUS PERSONALITIES: LARVAL AMPHIBIAN BEHAVIOURS AND RISK OF PARASITISM.

8:45 (116) **R.N. Sehgal**, C. Loiseau, A. Chasar, G. Valkiunas, T.B. Smith. EFFECTS OF HABITAT CHANGE ON AVIAN BLOOD-PARASITES.

9:00 (117) **S.K. File-Emperador**. *BIOMPHALARIA GLABRATA* IN PUERTO RICO: WHERE AND HOW THEY SURVIVE TODAY.

9:15 (118) **H. Randhawa**, R. Poulin. TAPEWORMS IN ELASMOBRANCH FISHES: RICHNESS CORRELATES AND SPECIES DISCOVERY.

9:30 (119) **G.J. Sandland**, M. Laidemitt. NUTRIENT RESTRICTION ALTERS THE INTERACTION BETWEEN AN AQUATIC SNAIL, *BIOMPHALARIA GLABRATA*, AND ITS TREMATODE PARASITE, *SCHISTOSOMA MANSONI*.

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

10:00 (120) **K.C. Jacobson**, D. Bryan, J. Buchanan, M.B. Rew. PLEUROCERCOIDS OF THE TRYPANORHYNCH CESTODE *NYBELINIA SURMENICOLA* IN PACIFIC HAKE (*MERLUCCIUS PRODUCTUS*) CAUGHT OFF OREGON AND WASHINGTON.

10:15 (121) **R. Bernot**. ECOLOGICAL CONSEQUENCES OF TREMATODE-SNAIL ELEMENTAL MISMATCHES: STOICHIOMETRY FOR PARASITOLOGISTS.

10:30 (122) **R.E. Baldwin**, M.B. Rew, M.L. Johansson, M.A. Banks, K.C. Jacobson. MIGRATION PATTERNS AND STOCK STRUCTURE OF PACIFIC SARDINES (*SARDINOPS SAGAX*) USING PARASITE COMMUNITY AND POPULATION GENETICS.

10:45 (123) **D. Zelmer**. ECOLOGICAL DRIFT IN PARASITE INFRACOMMUNITIES.

11:00 (124) **J.S. Hernández-Orts**, E.A. Crespo, J.T. Timi, J.A. Raga, F.J. Aznar. STATIC AND ONTOGENETIC ALLOMETRY OF TRUNK SPINES IN TWO SPECIES OF *CORYNOSOMA* (ACANTHOCEPHALA: POLYMORPHIDAE): ATTACHMENT STRATEGIES TO THE DEFINITIVE HOST MAY DIFFER BETWEEN SPECIES AND SEXES.

11:15 (125) **V.M. Vidal-Martinez**, A.L. May-Tec, D.P. Pool, M.L. Aguirre-Macedo, J.W. Lewis. TEMPORAL VARIATION IN THE INFECTION PARAMETERS OF *MEXICONEMA CICHLASOMAE* (NEMATODA: DANICONEMATIDAE) IN THE MAYAN CICHLID *CICHLASOMA UROPHTHALMUS* FROM YUCATAN, MEXICO.

8:00-12:00 pm Host Parasite Interactions II

Location: Kuskokwim East

Presiding: T. Ruhnke, West Virginia State University
M. Zimmerman, Wake Forest University

Time (Abstract No.)

8:00 (126) **D.J. Larson**, P.G. Johnson, D.R. Sutherland. STANDARDIZED METHOD FOR AMPHIBIAN METAMORPH NECROPSIES.

8:15 (127) **I. Eleftherianos**. INSECT IMMUNE RESPONSES TO ENTOMOPATHOGENIC NEMATODES AND THEIR SYMBIOTIC BACTERIA.

8:30 (128) **P.C. Hanington**, M. Forys, E.S. Loker. FREP3 (FIBRINOGEN-RELATED PROTEIN 3) IS AN IMPORTANT COMPONENT OF SNAIL RESISTANCE TO DIGENTIC TREMATODE INFECTION.

8:45 (129) **M.L. Kent**, S.E. Benda, C.B. Schreck. PARASITES AND PRESPAWNING MORTALITY IN CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) IN THE WILLAMETTE RIVER, OREGON.

9:00 (130) **R.H. Easy**. THE PROTEOMIC INTERFACE OF STRESS, PARASITES, AND HOSTS: LESSONS FROM SALMON AND COD.

9:15 (131) **G. Mayer**. EXPRESSION AND LOCALIZATION OF *PLASMODIUM*-EXPORTED PROTEINS IN THE LIVER STAGES.

9:30 (132) **P.J. Skelly**, R. Bhardwaj, G. Krautz-Peterson, Z. Faghiri, A. Da'darah. MOLECULAR CHARACTERIZATION OF THE SCHISTOSOME SURFACE.

9:45-10:00 am COFFEE BREAK

10:00 (133) **M.G. Bolek**, M.S. Vhora, H. Robinson, C. Wiles. SITE FIDELITY OF AMPHIBIAN HEMIURID TREMATODES IN THE GENUS *HALIPEGUS*: DOES AMPHIBIAN HOST MATTER?

10:15 (134) **C.M. Adema**, G.H. Rosenberg, S.K. Buddenborg. LONGTERM *BIOMPHALARIA GLABRATA/SCHISTOSOMA MANSONI* INFECTIONS STUDIED BY RNA-SEQ.

10:30 (135) **S.K. Buddenborg**, J.W. Dragoo, G.H. Rosenberg, C.M. Adema. DOES PARASITE IMMUNE FUNCTION CONTRIBUTE TO SURVIVAL OF LONG-TERM *SCHISTOSOMA MANSONI*-INFECTED *BIOMPHALARIA* SNAILS?

10:45 (136) **J. Nolan**, J.W. Dragoo, S.K. Buddenborg, C.M. Adema. MICROARRAY TRANSCRIPTION PROFILES OF *BIOMPHALARIA GLABRATA* RESISTANT AND SUSCEPTIBLE FOR *SCHISTOSOMA MANSONI*.

11:00 (137) **J.W. Dragoo**, J. Nolan, C.M. Adema. *BIOMPHALARIA GLABRATA* SNAIL HOSTS OF *SCHISTOSOMA MANSONI* ARE IMMUNOLOGICALLY DIVERSE.

11:15 (138) **M.C. Curran**, K.L. Yozzo, S. Ebanks, M.J. Partridge, T.M. Modeste, P.L. Pennington. HOW DOES THE BOPYRID PARASITE *PROBOPYRUS PANDALICOLA* AFFECT THE DAGGERBLADE GRASS SHRIMP *PALAEMONETES PUGIO*: A CLOSER LOOK AT ABUNDANCE, GROWTH RATES, BEHAVIOR, AND PREDATION.

11:30 (139) **D. Heins**, J. Baker, D. Green. PROCESSES INFLUENCING THE DURATION AND DECLINE OF EPIZOOTICS IN *SCHISTOCEPHALUS SOLIDUS* INFECTING THREESPINE STICKLEBACKS.

11:45 (140) **J. Kvicerova**, A. Macova, V. Hypsa. *APODEMUS* AND *EIMERIA*: POPULATION STRUCTURE, HOST SPECIFICITY AND BIOGEOGRAPHY.

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

Friday Afternoon, 2011-06-04

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

Location: Foyer (adjacent to the Howard Rock Ballroom)

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

CELL BIOLOGY

141 **A. Sulemana**, T. Paget, E. Jarroll. BISTABILITY IN *GIARDIA LAMBLIA* ENCYSTMENT.

ECOLOGY

142 **A.V. Koehler**, R. Poulin. PHENOTYPIC AND GENETIC VARIATION OF CERCARIAE: CONSTRAINTS OF HOST SPECIFICITY?

143 **A. Zavala Lopez**, C. Hogue. THE EFFECT OF TEMPERATURE ON SHEDDING RATE OF *EUHAPLORCHIS CALIFORNIENSIS* CERCARIAE.

144 **C.R. Rouco**, A. Bertó-Morán, E. Serrano, S. Moreno. COMBINED EFFECT OF PARASITES AND VIRAL DISEASES ON SURVIVAL OF EUROPEAN WILD RABBITS.

145 **R. Míguez-Lozano**, T.V. Pardo-Carranza, J.A. Balbuena, I. Blasco-Costa. HELMINTH COMMUNITIES OF THE GOLDEN GREY MULLET *LIZA AURATA* (ACTINOPTERYGII: MUGILIDAE) IN TWO WESTERN MEDITERRANEAN LOCALITIES: WHY CARE ABOUT TRANSMISSION?

146 **R. Quiñones**, A. Giovannini, J. Hernández-Orts, A. Raduán, J.A. Raga, M. Fernández. INTESTINAL HELMINTH FAUNA FROM MEDITERRANEAN BOTTLENOSED DOLPHIN (*TURSIOPS TRUNCATUS*) AND COMMON DOLPHIN (*DELPHINUS DELPHIS*).

147 **K.C. Shim**, M.R. Forbes. ROLE OF TEMPERATURE ON THE TRANSMISSION AND IMPACT OF A PARASITE TO ITS HOST.

148 **J.S. Hernández-Orts**, F.E. Montero, M.S. Leonardi, J.A. Raga, F.J. Aznar, E.A. Crespo. INTESTINAL HELMINTHS FROM THE SOUTH AMERICAN SEA LION, *OTARIA FLAVESCENS*, FROM NORTH PATAGONIA, ARGENTINA.

149 **G. Vélez-Rubio**, L. Fernández-Porras, N. Muriel, M. García-Varela, J.S. Hernández-Orts, J.A. Raga, F.J. Aznar. BIOMASS INEQUALITIES IN THE ACANTHOCEPHALAN *CORYNOSOMA CETACEUM*: POPULATION SIZE AND HABITAT VARIABILITY INCREASE INEQUALITIES IN REPRODUCTIVE FEMALES.

150 **A. Khan**, A.L. Johnson, K.R. Jones, M.S. McCravy, J.M. Grisham, J.R. Davis, S.A. Boyle, L.E. Luque de Johnson. AN INTEGRATIVE ASSESSMENT OF SNAKE PARASITISM IN AN URBAN ENVIRONMENT.

151 **M. Sanz-Sebastián**, A. Saint-Pierre, C. Luciani, J.S. Hernández-Orts, J.A. Raga, T. Kuiken, F.J. Aznar. HABITAT SELECTION AND POPULATION STRUCTURE OF *CORYNOSOMA STRUMOSUM* (ACANTHOCEPHALA) IN COMMON SEALS (*PHOCA VITULINA*) FROM THE NETHERLANDS.

GENETICS AND MOLECULAR BIOLOGY

152 **K. Caban-Hernandez**, J.F. Gaudier, J.N. Quetell, A.M. Espino. MOLECULAR CLONING AND CHARACTERIZATION OF A CDNA ENCODING A YOLK FERRITIN PROTEIN OF *FASCIOLA HEPATICA*.

153 **J.O. Odera**, J. Porter-Kelley. LEISHMANIA VIRUS 1 MICRORNA IN *LEISHMANIA GUYANENSIS*.

154 **A. Besné-Mérida**, C. Rico-Torres, C. Cedillo-Peláez, D. Correa. GENOTYPING OF *TOXOPLASMA GONDII* FROM DOMESTIC CATS OF THREE REGIONS OF MEXICO.

155 **C. Cedillo-Pelaez**, C.P. Rico-Torres, G.C. Salas-Garrido, D. Correa. ACUTE TOXOPLASMOSIS IN SQUIRREL MONKEYS (*SAIMIRI SCIUREUS*) IN MéXICO.

156 **C. Rico-Torres**, C. Cedillo-Peláez, I. Cañedo-Solares, H. Luna-Pastén, R. López-Reboseño, R. Figueroa-Damián, D. Correa. MOLECULAR DIAGNOSIS AND GENOTYPING OF HUMAN CASES OF PERINATAL TOXOPLASMOSIS.

HOST-PARASITE INTERACTIONS

157 **S. Zuray**, R.M. Kocan, P. Hershberger. LONG-TERM EPIDEMIOLOGICAL TRENDS IN *ICHTHYOPHONUS* SP.-INFECTED CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) IN THE YUKON RIVER, ALASKA; 1999–2010.

158 **A.M. Fedynich**, S.M. Villarreal, D. Rollins. *TETRAMERES PATTERSONI* IN A NORTHERN BOBWHITE POPULATION FROM TEXAS.

159 **M. McGrier**, J. Laursen. SNAIL HOST FINDING BY MIRACIDIA OF *FASCIOLOIDES MAGNA*.

160 **W.A. Buzetti**, D.T. Silva, M.F. Neves, N.P. Queiroz, R.V. Silveira. PRESENCE OF *LEISHMANIA* AMASTIGOTES IN INTESTINE OF DOGS.

161 **R.A. Dalloul**, E.R. Gilbert, C.M. Cox, P.M. Williams, A.P. McElroy, W.K. Ray, A. Barri, D.A. Emmerson, E.A. Wong, K.E. Webb. SERUM PROTEOME OF *EIMERIA*-INFECTED BROILER CHICKENS.

162 **X. Wu**, H. Liu, L. Gonzalez, A.M. Deelder, C.H. Hokke, T.P. Yoshino. GLYCOTOPE SHARING BETWEEN LARVAL *SCHISTOSOMA MANSONI* AND HEMOLYMPH OF SUSCEPTIBLE AND RESISTANT *BIOMPHALARIA GLABRATA* SNAILS.

163 **A. McElroy**, G. Lehman, R. Dalloul, A. Cowieson. PERFORMANCE, INTESTINAL MORPHOLOGY, AND AMINO ACID DIGESTIBILITY OF BROILERS ADMINISTERED A LIVE COCCIDIA VACCINATION AND FED DIETARY PHYTIC ACID.

164 **C. Cedillo-Pelaez**, C.P. Rico-Torres, I. Rangel-Rodriguez, D. Espinosa-Aviles, G. Salas-Garrido, D. Correa. TOXOPLASMOSIS IN CAPTIVE AUSTRALIAN MARSUPIALS IN MéXICO.

165 **I. Canedo-Solares**, M. Calzada-Ruiz, L.B. Ortiz-Alegría, H. Luna-Pastén, D. Correa. INVASION KINETICS OF *TOXOPLASMA GONDII* RH AND ME49 STRAINS TO HUMAN ENDOTHELIAL CELLS.

166 **J.V. Hopper** .WINNER TAKES ALL: INTERSPECIFIC AND INTRASPECIFIC COMPETITION AMONG AUSTRALIAN PARASITOIDS FOR THEIR HOST, THE LIGHT BROWN APPLE MOTH.

IMMUNOLOGY

167 **L.G. Arlian**, M.S. Morgan, B. Elder, D.L. Vyszenski-Moher. COMPARATIVE EVOLUTION OF PARASITIC SCABIES MITES AND FREE-LIVING HOUSE DUST MITES.

168 **A. Morales**, A.M. Espino. IMMUNODIAGNOSIS OF HUMAN FASCIOLIASIS USING A TEGUMENTAL SOLUBLE EXTRACT AS ANTIGEN.

169 **O. Figueroa-Santiago**, A.M. Espino. ROLE OF THE *FASCIOLA HEPATICA* ES PRODUCTS IN TLR INTERACTION.

170 **M.K. Saifullah**, G. Ahmad, S.M. Abidi. IMMUNODIAGNOSIS OF BUFFALO AMPHISTOMOSIS BY COPROANTIGEN DETECTION.

LIFE CYCLES AND EPIDEMIOLOGY

171 **S.M. Gennari**, A.B. Cassinelli, A.H. Minervino, H.S. Soares, J.T. Lima, A.F. Malheiros. PREVALENCE OF ANTIBODIES ANTI-*TOXOPLASMA GONDII* IN DOGS FROM THE TAPIRAPE INDIGENOUS COMMUNITY IN THE STATE OF MATO GROSSO, AMAZON REGION OF BRAZIL.

172 **A.M. Cassinelli**, A.F. Malheiros, A.H. Minervino, H.S. Soares, J.T. Lima, S.M. Gennari. PREVALENCE OF ANTIBODIES ANTI-*NEOSPORA CANINUM* IN DOGS FROM THE TAPIRAPé INDIGENOUS COMMUNITY IN BRAZILIAN AMAZON REGION.

173 **H. Caballero-Ortega**, S. Murrieta, E. Calderón-Segura, H. Luna-Pastén, R. Castillo-Cruz, C.J. Conde-González, D. Correa. EVALUATION OF ELISA AND WESTERN BLOT FOR ANTI-*TOXOPLASMA GONDII* IGG ANTIBODIES IN HUMAN SERUM SAMPLES FROM THE WHOLE POPULATION OF MEXICO.

174 **H. Caballero-Ortega**, F.J. Uribe-Salas, H. Luna-Pastén, C. Cedillo-Pelaez, J.A. Vargas-Villavicencio, I. Cañedo-Solares, L.B. Ortiz-Alegría, E. Calderón-Segura, C.J. Conde-González, D. Correa. SEROPREVALENCE AND NATIONAL DISTRIBUTION OF HUMAN TOXOPLASMOSIS IN MEXICO: ANALYSIS OF THE 2000 AND 2006 NATIONAL HEALTH SURVEYS.

175 **H. Randhawa**, P. Brickle. UNDERSTANDING THE ROLE OF SQUID IN THE TRANSMISSION OF CESTODES IN FALKLAND ISLANDS' SHELF WATERS USING A PHYLOGENETIC APPROACH.

176 **A.U. Opara**, A.D. Acholonu. URINARY SCHISTOSOMIASIS AND BACTERIAL CO-INFECTION AMONG SCHOOL CHILDREN IN NDONI LOCAL GOVERNMENT AREA OF RIVERS STATE, NIGERIA.

177 **J.A. Raga**, A.E. Ahuir-Baraja, N. Sánchez-García, F.E. Montero. THE DEVELOPMENT OF *LEPEOHTHEIRUS NORDMANNI* (H. MILNE-EDWARDS, 1840) (COPEPODA: CALIGIDAE) ON THE SKIN AND MOUTH OF THE SUNFISH (*MOLA MOLA* L.).

178 **N. Sanchez-Garcia**, A.E. Ahuir-Baraja, J.A. Raga, F.E. Montero. DEVELOPMENT OF THE HAPTOR AND THE COPULATORY ORGAN OF TWO SPECIES OF *LAMELLODISCUS* (DIPLECTANIDAE, MONOGENEA).

179 **N.E. Davis**. ITCHY KIWIS. RESEARCH ACCOMPLISHED IN NEW ZEALAND FROM 1990 THROUGH THE PRESENT. WHERE TO FROM HERE?

TAXONOMY, SYSTEMATICS AND PHYLOGENY

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***Bruce Christensen**, C.P. Read Mentor Award*

ASP AWARDS

CLARK P. READ MENTOR AWARD LECTURE

Presiding: J.F. Hillyer, Vanderbilt University

Time (Abstract No.)

2:00 Introduction of 2011 C.P. Read Mentor Award

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ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: J.F. Hillyer, Vanderbilt University

The recipient of the 2011 New Investigator Award is **Ms. Chelsea Matisz**, Department of Physiology & Pharmacology, University of Calgary.

***Chelsea Matisz**, New Investigator Award*

WILLIS A. REID JR., STUDENT RESEARCH GRANT AWARDS

Presiding: S. Seville, University of Wyoming

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: K.C. Jacobson, NOAA Fisheries

ASP BUSINESS MEETING

Presiding: J. Caira, The University of Connecticut

Thank you for attending this year's ASP meeting and have a safe trip home.
*See you **July 12-17, 2012** at our next meeting in **RICHMOND, VA***

NOTES:

Abstract Listings

(1)

BERINGIA: HISTORY AND CLIMATE STRUCTURE NORTHERN ASSEMBLAGES OF MAMMALS AND PARASITES AT THE NEXUS OF ASIA AND NORTH AMERICA

J.A. Cook, University of New Mexico
E.P. Hoberg, USDA National Parasite Laboratory
S.O. MacDonald, University of New Mexico
A.G. Hope and **N.G. Dawson,** University of New Mexico; Alaska Science Center, U. S. Geological Survey
V. Fedorov, Institute of Arctic Biology, University of Alaska

The profound influence of history and climate on high latitude biotas emphasizes the need to understand drivers in evolutionary time as the foundation for contemporary diversity. We explore historical processes across Beringia, an iconic geographic province spanning eastern Asia and northwestern North America that remained ice-free during repeated glacial cycles during the Pleistocene. Beringia served as a high latitude refugium and as the crossroads (Bering Land Bridge) of the northern continents for the boreal biota. Numerous questions persist regarding the importance of this region in the evolution of high latitude faunas. Integrated inventory over the past decade, in conjunction with molecular phylogenetics of diverse mammalian and parasite clades, reveal new insights about historical biogeography. Beringia's impact on generating diversity as well as the sequence, direction, and number of colonization events linking Old World and New World faunas are demonstrated. A central theme is one of biotic interchange, geographic and host colonization defined by episodes of climate change and ecological perturbation. Patterns established in Beringia set the stage for defining contemporary diversity, frame important questions about conservation biology, and identify a path to predicting responses in complex systems that are now under a regime of accelerated environmental change.

(2)

INTEGRATING TO MANAGE FOR CHANGE: INCORPORATING PARASITES INTO MANAGEMENT AND CONSERVATION PLANS

S.L. Talbot and **S.A. Sonthagen,** Alaska Science Center, U. S. Geological Survey
N.G. Dawson, U. S. Geological Survey and University of New Mexico
J.M. Pearce, **G.K. Roffler** and **G.K. Sage,** Alaska Science Center, U. S. Geological Survey
E.S. Martinsen and **R.C. Fleischer,** National Zoological Park, Smithsonian Institution

Many resource managers and conservation biologists are working to formulate plans that will help predict the response of target species and ecological communities to rapidly changing environmental conditions expected under climate change scenarios. Prescriptive actions that support adaptation of species to climate change, such as identifying macro- and microrefugia, applying measures aimed at maintaining biodiversity, or monitoring dynamic transition zones, would benefit from a greater understanding of the implication of change for interspecies interactions. One particular type of interspecies interaction that remains little studied, but that could be affected by climate change, is the relationship between hosts and their associated pathogens or parasites. Despite a general understanding of the importance of parasites to disease transmission or as a marker of coevolutionary processes or contemporary movement, few management plans targeting species of conservation concern integrate information about parasites. The application of appropriate genetic markers targeting different temporal scales, and different genes, for both host and parasite can aid in understanding contemporary demographic and adaptive responses.

Studies focusing in this area have shown that species and associated pathogens vary in response to climate fluctuations, including rapid adaptation *in situ*, to parasite colonization and expansion, hybridization, and finally, complete population demise. This precludes the application of general prescriptive actions targeted toward one species or group. We present a series of collaborative studies that highlight the complexity of contemporary host-parasite relationships associated with boreal and arctic species, including terrestrial large- and meso-carnivores and herbivores, marine mammals, and migratory birds. These studies illustrate how pathogen/parasite studies incorporating a molecular approach can be used by resource managers and communities to help prepare for possible changes in vertebrate communities and assess the potential hazards of emerging or persistent zoonotic diseases in a region already experiencing profound changes associated with global climate change. These studies serve to emphasize the importance of historical processes as a foundation for understanding the structure and future of contemporary ecological communities.

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(3)

A WORM WITH A VIEW: PARASITE PERSPECTIVES ON BERINGIAN BIOGEOGRAPHY

K.E. Galbreath, Western Washington University
E.P. Hoberg, Animal Parasitic Diseases Laboratory, USDA

Perspectives drawn from the endoparasitic helminths of northern mammals reveal complex histories of diversification and colonization that challenge traditional models of Beringian biogeography. The cestode *Arostrilepis horrida* was once thought to be a widespread generalist in arvicoline rodents (voles and lemmings) but is now recognized as a complex of 10 or more cryptic species specializing on separate host clades. This considerable diversity was structured by deep and shallow episodes of climate-driven range expansion across Beringia, overlain by various coevolutionary processes (e.g., cospeciation, host-switching, “missing-the-boat”). Diversification therefore occurred as a consequence of the dynamic interplay between fluctuating Beringian paleoenvironments and the deterministic and stochastic factors governing species responses to those changes. By providing independent perspectives on host biogeography, parasites have also illuminated histories that studies of hosts alone fail to resolve. Genetic signatures from multiple discrete parasite lineages show that North American pikas from low latitudes expanded northward to colonize eastern Beringia. Persisting there over the course of multiple glacial cycles, the population diverged from southern conspecifics. This new understanding inverts the typical narrative of north to south pika colonization, which is based on traditional models of Beringian biogeography but little data. Our examination of the diverse parasite faunas associated with arvicolines and pikas reveal the important role of geographic range expansion, driven by episodes of climate change during the Quaternary, in promoting differentiation across the Beringian nexus. These complex systems demonstrate that host-parasite comparative analyses enrich our understanding of general processes that underlie diversity.

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(4)

PAST AND PRESENT CHANGES IN THE DISTRIBUTION OF *TRICHINELLA* SPP. IN THE ARCTIC

B.M. Rosenthal, Agricultural Research Service, USDA

Although all parasites in the genus *Trichinella* were once attributed to a single species, genetic evidence has served as the basis to subdivide the genus into several distinct species. Each of these is transmitted via a cycle of predation and/or scavenging, and forceful cycles of transmission occur in the Arctic where such feeding habits typify resident mammals. When people consume incompletely cooked meats, zoonotic

infection and clinical disease can ensue. The geographic distributions and evolutionary interrelationships among these lineages provide evidence that the parasite community in the Arctic is composed of a mosaic. One lineage (*Trichinella nativa*) probably became established in North America when its rodent or carnivore hosts first migrated from Eurasia through Beringia; another (the T6 genotype) evolved *in situ* after *T. nativa* became established here; a third (*Trichinella spiralis* sensu strictu) was introduced to North America only within the last 500 years, most probably via trans-Atlantic shipment of infected pigs and/or rats. Analyses of allelic nuclear genes generally affirm the subdivision freeze resistant parasites into *T. nativa* and the T6 genotype. However, introgression has blurred the distinction between these parasite taxa, at least where their ranges overlap. Consequently, diagnoses based on nuclear and maternally inherited markers can conflict. The viability of hybrid progeny has been found wanting in experimental crosses; nevertheless, such hybrids clearly have contributed to certain extant populations. Taken together, the phylogenetic histories of hosts and parasites in this region should reinforce one another, contributing to our more general understanding of the biotic responses to climate variation as well as its practical consequences for food safety.

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(5)

ARCTIC CHANGE – A DRIVER FOR PARASITE EMERGENCE, INVASION AND EXTINCTION?

S. Kutz, Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Climate change at northern latitudes is resulting in dramatic perturbations in the biotic and abiotic environment, including changes in the ecology of infectious diseases. Host-parasite interactions are highly sensitive to climate change and general predictions include reduced generation times and increased diversity, abundance and severity of pathogens in northern wildlife. During the past decade several examples of climate-linked parasite and/or disease emergence have been reported for arctic ungulates. The response of these host-parasite systems to climate change is complex, not uniform across taxa, and not always intuitive. For example, consistent with general climate change predictions, the generation time has decreased and the geographic range has expanded for *Umingmakstrongylus pallikuukensis*, the protostrongylid lungworm of muskoxen. Similarly, *Setaria tundra* emerges as a disease causing agent of reindeer following unusually warm summers. Contrary to predictions, however, research on *Ostertagia gruehneri,* the Trichostrongylid abomasal nematode of caribou, suggests that generation times may be unaffected by climate change and increased temperatures could actually reduce availability of infective larvae at certain times of the year. We use these and other case studies of endemic and invasive northern parasites to explore the impacts of climate change on parasite biodiversity and host-parasite interactions at high latitudes.

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(6)

PARASITES AND PATHOGENS ARE IMPORTANT PLAYERS IN EVOLUTION OF ANIMAL PERSONALITY TRAITS?

R. Kortet, University of Eastern Finland
A. Hedrick, University of California Davis
A. Vainikka, University of Oulu

Animal personalities (consistent, individually characteristic expression of behavioral traits) and their evolutionary importance are currently a topic of extreme interest among ecologists. One of the most important open questions is to ultimately understand why animal personalities are found in the wild. Existence of personalities does not appear evident, since for example, a bold and aggressive individual can pay a notable cost for its bold behavior in the presence of predators. Our recent idea suggests that parasites and pathogens may provide an ultimate explanation for the evolution and diversification of animal personalities. This proposition is based on the negatively frequency-dependent selection generated

by parasites and pathogens - that are present ubiquitously. By generating genetic variation in host immune function, parasites affect the optimal behavior of individuals. This occurs, if the personality-indicating behaviors are dependent on individuals' immunological capacity. In this scenario, individuals that are inherently resistant or able to improve parasite resistance through high food intake rate behave more boldly than less resistant individuals. Moreover, we predict that the stronger is the risk of parasitism, the more strictly individuals should follow their optimal trajectories, which can then seen as highly consistently behaving individuals. Our approach acknowledges the condition-dependence of immune function and co-evolutionary dynamics between hosts and parasites.

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(7)

FROM TINY TO LONG – THE DEVELOPMENT OF HORSEHAIR WORMS (NEMATOMORPHA) WITHIN THEIR HOST

A. Schmidt-Rhaesa, Zoological Museum, University Hamburg

Horsehair worms (Nematomorpha) are parasites in the body cavity of arthropods as juveniles, but emerge from their host to reproduce in water. The tiny, morphologically distinct larvae infect (intermediate) hosts. During the parasitic phase, a considerable growth from about 100 µm larval length to 10, sometimes more than 100 cm adult length takes place. During this phase, there is sufficient evidence that nutrients are taken from the host's body cavity through the nematomorph integument. The cuticle is thin and is replaced by a thick protective cuticle towards the end of the parasitic phase. At this time, the epidermis becomes less physiologically active and shrinks in size. The musculature develops gradually, the nervous system moves from an intraepidermal to a submuscular position. The intestine appears physiologically active in early stages, but obviously becomes inactive in later stages. The development of the gonads starts early, in mature animals gonads occupy the majority of space in the animal. In summary, the development of organ systems reflects rapid growth of the reproductive system. Nutrients are absorbed in the parasitic, but not in the free-living phase, as is reflected by the structure of the integument and intestine.

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(8)

ANNUAL HOST-PARASITE DISTRIBUTION PATTERNS OF *ALLIGATOR MISSISSIPPIENSIS* IN LOUISIANA

M. Tellez, Department of Ecology and Evolutionary Biology, UCLA

As the sole surviving reptilian archosaurs of an ancient phylogenetic lineage, it is probable that the interaction between crocodilians and their parasites has developed over evolutionary time, allowing them to adapt to changing environments and novel pathogens. However, these relationships may vary among size, gender and location of crocodilian hosts due to different life-history patterns. Investigating the extent of host-parasite relations among these groups is pertinent to identify unstable distribution patterns in crocodilian populations by using parasites as bio-indicators of a disturbed environment. My research investigates intestinal helminths to assess annual host-parasite distribution patterns in populations of *A. mississippiensis* in Louisiana to evaluate environmental and anthropogenic impacts on the host. Intestinal tracts of alligators of various size, gender and locations will be collected annually for three years during the Louisiana wild alligator harvest with the assistance of Louisiana Department Fisheries and Wildlife (LDFW). To date, specimens from two harvests have been collected, and data from the first harvest have been analyzed. Trematode intensity between geographic zones, and trematode intensity between males and females within the East Zone were significantly different (P=0.03, P=0.02 respectively). Overall parasitism was higher in the East Zone, and in male alligators. A significant finding

was 100% parasitic prevalence. Continual data collection and assessment will be vital for local wildlife and wetland management agencies as they continue wetland restoration processes from past hurricane activity, and urbanization management.

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(9)

GREGARINE HOST USE AND DISTRIBUTION WITHIN *CALOPTERYX* DAMSELFLIES OF THE SOUTHEASTERN UNITED STATES

A. Morgan and **T. Cook**, Sam Houston State University

Gregarines (Apicomplexa: Eugregarinida) are parasites of invertebrates, particularly insects, and are thought to exhibit strict host specificity, thus suggesting that gregarine assemblages are the product of cospeciation. This host-specificity has been demonstrated in several cross-infection laboratory experiments. However, experimental demonstration of host specificity is not possible in those systems where the hosts are not readily domesticated, for example among the gregarines parasitizing hosts in the order Odonata. In such cases, patterns of host use and distributional data from large scale, intensive field survey can be evaluated for trends that indicate the influences of coevolution and ecological fitting in structuring gregarine assemblages and thus can shed light on the nature of gregarine host specificity. This study surveys the gregarine assemblages in broadwing damselflies, *Calopteryx* spp. throughout the Southeastern United States from Texas to Florida. We specifically suggest that similarities in gregarine assemblages in closely related species of *Calopteryx*, despite broad geographical separation, provide evidence of a strong coevolutionary influence on community structure; whereas similarities in gregarine assemblages in geographically close or ecologically similar habitats suggest that community structure is at least partially dependent on the surrounding environment. To date, only one gregarine species has been described from any species of *Calopteryx* in the U.S.: *Calyxocephalus karyopera* infecting *C. maculata*. In 2010, we recovered *Calyxocephalus karyopera* from *C. maculata* in Texas, Mississippi, and Alabama, representing new geographic records for this gregarine species. Additionally, we recovered an undescribed gregarine co-occurring with *C. karyopera*. *Calopyterx dimidiata* was collected from only a single location in Mississippi and was not infected with any gregarine species. We present morphometric analyses of the undescribed gregarine, discuss basic parasite population biology, and present directions for future work.

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(10)

GENETIC DIVERSITY AND HOST SPECIFICITY OF ECHINOSTOMATID TREMATODES IN NEW ZEALAND INTERTIDAL SNAILS

J. Palladino, Le Moyne College, **R. Poulin**, University of Otago, **D. Keeney**, Le Moyne College

The host specificity of parasites can be influenced by the likelihood of a parasite encountering potential hosts and physiological interactions between potential hosts and parasites after encounter. Molecular studies often identify previously unrecognized levels of trematode diversity within intermediate hosts, altering conceptions of host specificity in these host-parasite systems. The goals of the present study were to identify the number of genetic lineages of echinostomatid trematodes infecting the New Zealand intertidal mud snails *Zeacumantus subcarinatus* and *Zeacumantus lutulentus* and to determine the host specificity of each parasite lineage. Analysis of the cytochrome *c* oxidase subunit I (COI) gene identified two major groups of haplotypes possessing distinct patterns of genetic diversity and host specificity. The first group consisted of a single, geographically widespread species. This species was found in both snail hosts, with the vast majority recovered from *Z .lutulentus*. The second group of haplotypes consisted of multiple genetically distinct species, including members of a recently identified

Acanthoparyphium species complex. Each species was specific to either *Z. subcarinatus* or *Z. lutulentus*, and individual species were recovered from varying geographic scales. The comparison of parasite lineage distributions to host geographic distributions may shed light on the factors influencing host specificity in this system.

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(11)

AN EXAMPLE OF MODULATED HOST SUSCEPTIBILITY: SENSITIZATION WITH ECHINOSTOMES REDUCES THE RESISTANCE OF BS-90 STRAIN *BIOMPHALARIA GLABRATA* TO *SCHISTOSOMA MANSONI*

M.A. Forys, Center for Evolutionary and Theoretical Immunology (CETI), University of New Mexico
P.C. Hanington, University of Alberta
E.S. Loker, Center for Evolutionary and Theoretical Immunology (CETI), University of New Mexico

The freshwater snail, *Biomphalaria glabrata* is the intermediate host for several trematode species, including the human pathogen *Schistosoma mansoni*. The outcome of trematode challenge of *B. glabrata* is dependent on certain compatibility criteria. The age, strain, and previous exposure history of an individual, as well as the species of trematode presenting the challenge, can all influence the success or failure of the snail to clear the infection. Compatibility between the snail host and the parasite is based on whether or not the snail can overcome the tactics employed by the parasite to evade or suppress the snail's defense response. Failure to control the infection early on results in measurable transcriptional patterns that vary depending on the trematode species and snail strain. For example, challenge a juvenile M-line *B. glabrata* with the trematode *Echinostoma paraensei*, results in observable immunosuppression that interferes with immune molecule production as well as hemocyte functioning. When the snail's immune response has been suppressed, it can allow for other infections, including those by trematodes that would previously have been successfully cleared. Here, following the design of classic experiments by Lie et al (1977), we explore this phenomenon in more detail by exposing the BS-90 strain of *B. glabrata* to irradiated miracidia of *E. paraensei* (compatible but developmentally suppressed), and then secondarily challenge them 4 days later to viable miracidia of *S. mansoni* (normally incompatible with the BS-90 strain). We hypothesized that by suppressing the snail's immune system with irradiated *E. paraensei*, that *S. mansoni* would then be able to establish an infection to the point of shedding schistosome cercariae, which would not otherwise happen, thus making a normally resistant snail susceptible. The results of this experiment supported our hypothesis: 46% of the experimental BS-90s became infected and shed *S. mansoni* cercariae, as compared to 0% of the control snails exposed only to *S. mansoni*. Further analyses of snails that were unable to clear the *S. mansoni* infection, based on transcriptional profiling and histology, may provide insight towards determining the major players in compatibility.

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(12)

IMPACTS OF MULTISPECIES PARASITISM ON JUVENILE COHO SALMON (*ONCORHYNCHUS KISUTCH*) IN OREGON

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C.B. Schreck, Dept. Fisheries and Wildlife, Oregon State University
K.C. Jacobson, NOAA Fisheries; Oregon State University
P.A. Rossignol, Oregon State University
S. St-Hilaire, Idaho State University
K.J. Rodnick, Dept. Biological Sciences, Idaho State University
J. Rommer, Oregon Dept. Fish and Wildlife
M.L. Kent, Oregon State University

We assessed the impacts of multispecies parasitism on a threatened stock of juvenile coho salmon (*Oncorhynchus kisutch*). An essential first step of this research was to document the geographic distribution and histopathologic changes of infections in these fish across different Oregon coastal streams. We found 21 different parasite species in parr (resident underyearlings) and smolts (migrating yearlings) from 10 different rivers. Some parasites, such as *Apophallus* sp., were more common in parr than smolts and had a more restricted geographic distribution. We then focused our research on parasitized coho salmon from one river, the West Fork Smith River (WFSR). The lower abundance of some parasites in smolts, compared to parr suggested parasite associated mortality. Therefore, we evaluated the persistence of these parasites, as this trend could also be explained by infection recovery. The parasites in our study persisted throughout the overwintering period in captive coho salmon. We conducted the retrospective analysis of Crofton's truncation of the negative binomial distribution to evaluate parasite associated mortality. Results indicated that up to 95% of parr from the lower mainstem of the WFSR had infections levels of *Apophallus* sp. that were associated with mortality. We also conducted a laboratory study on wild-caught coho salmon from two consecutive year classes and fish experimentally infected with *Nanophyetus salmincola*. Parasite associations were evaluated for the following fish performances: size, growth, swimming stamina, and gill Na^+,K^+-ATPase activity. Parasites were most negatively associated with size and growth, which was remarkably consistent between study years and likely influenced swimming stamina and ATPase activity levels. Taken together, results from the population, individual, and tissue levels, all indicate that these parasites impact this threatened stock of juvenile coho salmon. These results may have implications for fishery management, as it represents a previously unrecognized limiting factor for this recovering population.

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(13)

INTESTINAL PARASITE ASSEMBLAGES OF DOUBLE-CRESTED CORMORANTS: A COMPARISON OF THREE LAKE COLONIES IN MINNESOTA USA

K.L. Sheehan, Clemson University Department of Forestry and Natural Resources South Carolina Cooperative Fish and Wildlife Unit
P. Jodice, USGS

The Double-crested cormorant, *Phalacrocorax auitus* is a prolific avian species that is lethally managed in the U.S. High colony densities of birds within closed lake systems are suggested to encourage increased transmission of infectious agents such as parasites and lethal viruses like virulent-type Newcastle's disease. Furthermore, transmission of disease over migratory ranges is possible. On the contrary, the stress of long-distance migration could allow for cormorants to rid themselves of parasites, particularly species that infect the digestive tract. Here, we compare assemblages of intestinal parasite in cormorants collected from three breeding colonies in Minnesota. All birds were sampled immediately after arriving to the breeding grounds following spring migration with the exception of birds from Leech Lake, where birds were also collected in late fall prior to colony dispersal. The fish communities in the lakes sampled are thought to be significantly different (mostly associated with lake morphology and anthropogenic influences), but parasite species composition was similar among lakes in spring, signifying similar diet composition of cormorants among lakes or a lack of host-specificity during the parasites' life stages within fish. Dissimilar parasite diversity was found between seasons from the Leech Lake colony, specifically, an increased abundance of dilepidid cestodes and trematodes within the fall samples. A higher diversity of tapeworms was observed in the fall in Leech Lake cormorants and the variance in the size of *Drepanocephalus* sp. trematodes in those birds suggests novel infections occur at that breeding site. The mechanism behind the increased seasonal parasitism within-site may be associated with 1) increased ability to remove parasites during migration, 2) decreased immune function post-migration, and/or 3) a result of increased parasite abundance specific to cormorants in the lakes from the breeding range when compared to wintering locations. Parasite assemblages of cormorants sampled in the fall were similar to those observed in a resident colony in Alabama. Our findings agree with the suggestion that many parasites are removed from the gastrointestinal system during migration.

(14)

LOCOMOTIVE BEHAVIOR IN *BULINUS TRUNCATUS* IS ALTERED BY INFECTION WITH *SCHISTOSOMA HAEMATOBIUM*

K.M. Bichoupan, **O. Varechtouk** and **S.B. Muench,** SUNY Geneseo

Bulinus truncatus serves as an intermediate host for *Schistosoma haemotobium*, a parasite capable of causing Schistosomiasis. This parasitic disease affects 200 million people globally and is responsible for 200,000 deaths a year. A better understanding of the effects this parasite has on the behavior of its intermediate hosts may provide alternative routes towards its prevention. In this study we investigate the effect of infection with *S. haematobium* on locomotion in the intermediate host *B. truncatus*. Movement and behaviors of the snail were analyzed for a total of 23 parasitized and 21 unparasitized snails through video recording for ten minutes. Video clips were analyzed in order to determine total distance traveled, time in resting phase, degree of rotation in movement, and climbing behavior. Statistical analysis was used to compare the groups of snails. Total distance traveled and time spent in rest phase was not significantly different between parasitized and unparasitized snails. Unparasitized snails rotated a significantly greater amount than infected snails ($p < 0.05$). Interestingly, significantly more parasitized snails than unparasitized snails displayed climbing activity ($p < 0.01$). 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 but do not show climbing behavior. Understanding of this behavior may provide new implications for transmission and control.

(15)

COMPARISON OF THE GASTROINTESTINAL PARASITE FAUNA OF ALASKAN AND WASHINGTON SEA OTTERS (*ENHYDRA LUTRIS KENYONI*) SUBMITTED TO THE NATIONAL WILDLIFE HEALTH CENTER FROM 1991-2010

M. Sterner, **C. Roderick, N. Thomas and R.A. Cole,** United States Geological Service National Wildlife Health Center

Since 1991 as part of a health surveillance program, the National Wildlife Health Center has received carcasses of sea otters from Alaska and Washington to determine cause of death. As part of the necropsy, the gastrointestinal tract was removed and examined for parasites. A total of 41 otters from Washington and 6 from Alaska were examined. Twenty-six of 41 Washington otters and 4 of 6 Alaskan otters were positive for 12 genera of helminthes and 2 genera of mites. The parasite richness of the two groups is quite different. The majority of the Washington otters had only a single parasite genus present with only one individual infected with parasites belonging to two genera. Unlike the Washington otters the Alaskan otters were commonly found to have 2 or 3 parasite genera with one otter harboring 5 helminth genera. Two genera of helminthes were common to both populations (*Corynosoma sp.* and *Micropallus sp.*) while 5 genera of helminthes were unique to Washington (*Polymorphus sp., Levinseniella sp., Maritrema sp., Spelotrema sp.,* and *Androcotyle sp.*) and 4 genera of helminthe *sp.*) and 2 genera of mites (*Orthohalarchne sp.* and *Halarachne sp.*) were unique to Alaska. The parasite communities reflect the food habits of the two different groups of otters. Off the coast of Alaska the majority of otters feed on fish while the Washington group feeds primarily on sea urchins, bi-valves, crabs and fish. Knowing the parasite fauna of each group of otters can provide additional information on the otters' range expansion or if populations are mixing between Alaska and Washington. Determining the parasite communities will also shed more light on food habits of individual otters.

(16)

DETECTING SPINOSE EAR TICK (*OTOBIUS MEGNINI*) PRESENCE USING HOST AND HABITAT CHARACTERISTICS

C. Niebuhr, Tarleton State University

Otobius megnini (Dugès), the spinose ear tick, is a one‐host tick recently observed in the ears of a variety of threatened and endangered ungulate species at Fossil Rim Wildlife Center (FRWC) in Glen Rose, Texas. Infestations of this tick species can cause severe irritation and stress in host animals leading to lack of thrift, affecting breeding behavior. Since the animals at FRWC are found in large free-roaming pastures and not regularly handled by staff, and since the adult stage of *O. megnini* does not feed and thus is found off the host, traditional on-host tick management strategies are not practical. Preliminary research was conducted to help define temporal and spatial patterns of *O. megnini* by detecting presence on and off host animals. In addition to FRWC's exotic animals, native wildlife species within the facility were examined to identify alternate hosts. Traditional tick survey methods and initial small mammal and raccoon trapping produced multiple tick species, but not *O. megnini*. However adult stages of *O. megnini*were found by filtering debris collected from specific microhabitats within animal‐use structures, such as wall crevices and corner spaces. This information may prove important for facilities attempting to manage spinose ear tick infestations. Results are from one component of a larger two year study.

(17)

THE EFFECTS OF MIGRATION ON THE SPREAD OF AVIAN MALARIA IN NEOTROPICAL BIRDS

M. Dodge and **R. Sehgal,** San Francisco State University

We examined the phylogenetic relationships among Cytochrome *b* lineages of the avian blood parasite genera *Haemoproteus*, *Plasmodium* and *Leucocytozoon* from three sites across the range of the swainson's thrush. To determine whether transmission of these parasites occurs on breeding or wintering grounds, we collected blood samples from both hatch year and adult birds in Alaska and California, and adult birds in Costa Rica. If parasite transmission occurs on breeding grounds, hatch year birds will be found to harbor local lineages of these parasites. Specifically, we examine the extent to which avian blood parasite lineages migrate with the swainson's thrush. Preliminary data reveal a high diversity of blood parasites in this host, and we assess the parasite-host specificity to these and other migratory and non-migratory passerines. Understanding how avian blood parasites are spatially distributed will help us to predict how migration can affect host switching and range expansion events.

(18)

FASCIOLOIDES MAGNA MIRACIDIA ARE DAMAGED IN VITRO BY MUCUS FROM INCOMPATIBLE SNAIL *HELISOMA TRIVOLVIS*, BUT NOT FROM COMPATIBLE SNAIL HOST, *LYMNAEA PALUSTRIS*

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To elucidate some of the complex mechanisms by which trematode parasites and their snail intermediate hosts maintain specific compatibility relationships and to investigate what barriers may play an important role in excluding trematodes from incompatible snails, we studied the effects of snail mucus, the first physical barrier presented by the snail to the parasite, on the snail-infective *Fascioloides magna*stage, the miracidia. *In vitro* assays were used to quantify the damage suffered by *F. magna* miracidia after 4 hrs of exposure to the mucus of a compatible snail host, *Lymnaea palustris*, and an incompatible snail, *Helisoma trivolvis*, including experiments in which the mucus had been either diluted to several different concentrations, heat treated (65°C for 35 min), or subjected to proteinase K digestion. Parasite eggs were collected from adult flukes harvested in St. Croix State Park from hunter-killed white-tailed deer livers, embryonated, and stored at 4°C. Snails were wild-caught and screened for patent parasitic infections prior to laboratory culture and use in experiments. Mean rates of miracidial damage were dramatically different for the two snail species when mucus was moderately diluted with Chernin's Balanced Salt Solution, but rates were similar when mucus was highly diluted. Miracidial damage rates of 1.4%, 0.0%, 71.9%, and 100% were observed in *H. trivolvis* mucus at dilutions of 1/3000, 1/300, 1/30, and 1/3, respectively, and 0.0% miracidial damage was seen in *L. palustris* mucus at all the same dilutions. Mean damage rates also were 0.0% in mucus from both snail species when heated or digested with proteinase K, strongly suggesting that a proteinaceous component(s) of *H. trivolvis* mucus may be mediating *F. magna* miracidial damage, thereby possibly functioning to prevent *F. magna* larval penetration of the mantle surface in this incompatible snail species.

(19)

WHICH CONTRIBUTES MORE TO TOTAL PARASITE DIVERSITY, DIVERSITY WITHIN OR AMONGST HOSTS?

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Total parasite diversity (gamma diversity) can be partitioned into within host (alpha) and amongst host (beta) components. Which component (alpha or beta) contributes the most to parasite gamma diversity remains an outstanding question (Dove and Cribb 2006). The numbers equivalents for species richness, Shannon and Simpson indices (Jost 2007) were used to analyze the partitioning of diversity in gastro-intestinal digenean communities of several fish host from Heron Island and Lizard Island, Australia. The numbers equivalent is the number of equally likely elements needed to produce a given index value. Beta diversity is then interpreted as the effective number of distinct parasite communities and the inverse of beta can be interpreted as the proportion of total diversity within the average host (Jost 2007). The mean (standard deviation) beta diversity for species richness, Shannon and Simpson indices were 3.44 (1.71), 1.96 (0.86) and 2.31 (2.56), respectively. As for the inverse of beta, if we make 0.5 the point at which alpha and beta diversity are equal, a value of <0.5 means that beta diversity is the major component of gamma diversity, whereas >0.5 the major component is alpha diversity. Out of the 14 communities analyzed beta diversity was the major component 11 times for species richness, 6 times for the Shannon index and 4

times for the Simpson index. All three indices were in agreement for 7 communities with beta diversity being the major component 4 times and alpha diversity 3 times. As for the other 7 communities in which the diversity indices disagreed, species richness was consistently beta dominant and the Simpson index was consistently alpha dominant, while the Shannon index agreed with species richness 2 times and the Simpson index 5 times. Thus, the parasite communities analyzed here run the spectrum from having diversity primarily within the host to where diversity is mainly amongst host, while several communities are in between with a mix of high and low prevalent and/or abundant species.

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(20)

ITCHY KIWIS: SWIMMER'S ITCH AND SCHISTOSOME DIVERSITY IN NEW ZEALAND

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Cercarial dermatitis, or swimmer's itch, is a global problem, and New Zealand is no exception. In several lakes, swimmers were complaining of itchy, red papules after leaving the water. However, until recently, it was unknown, which species or how many species of schistsomes might be responsible for the current outbreaks or even what hosts were involved. Surveys of birds and snails were conducted on Lake Wanaka, one of the key lakes for itch outbreaks. The endangered New Zealand scaup was most commonly infected and was host to a new species of visceral *Trichobilharzia*, a nasal schistosome, *T. regenti* and *Dendritobilharzia* sp. Prevalence for both species of *Trichobilharzia* in the scaup was close to 100%. In a survey of snails, only *Lymnaea tomentosa* were shedding schistosomes, which served as the host for both species of *Trichobilharzia*. The new species of *Trichobilharzia* is closely related both genetically and morphologically to species occurring in North America (using physid snails) and Europe (using different species of lymnaeid snails). Given that both species of these *Trichobilharzia* species use the same snail host, it is unknown which schistosome is responsible for most of the itch outbreak. The implications of snail host use and host shifting will be discussed.

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(21)

EXPERIMENTAL EVIDENCE FOR THE EXISTENCE OF A CIRCULATING BLOOD STAGE OF *ICHTHYOPHONUS* SP. IN ORALLY EXPOSED PACIFIC STAGHORN SCULPINS (*LEPTOCOTTUS ARMATUS*)

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Ichthyophonus sp. was first described over 100 years ago, yet much of its life-history remains enigmatic. The most convincing evidence for the route of infection is by ingestion of infected tissues (e.g. oral), but the infectious stage, as well as the mechanism for exiting the infected host is still unknown. The tissue stages within the fish host have been extensively described with numerous descriptions and photographs, including verbal descriptions of a circulating blood stage, variously described as "numerous", "common", and being "spherical with a diameter ranging from 10µm to 90 µm". Curiously, there are no photographs or drawings of the circulating stage(s) even though every other morphological stage is extensively represented in the literature. We attempted to identify this mysterious "circulating blood stage" by feeding tissues from infected Pacific herring (*Clupea pallasii*) to 25 Pacific staghorn sculpins (*Leptocottus armatus*), a natural host for *Ichthyophonus*. Exposures consisted of a single feeding followed by daily sampling for 32d. Samples consisted of (1) blood smears stained with Giemsa's stain & PAS, (2) explant cultures of heart, liver, spleen and kidney, (3) blood cultures (50-100 µL), and (4) histological sections of

heart, liver, spleen, kidney, stomach and muscle stained with H&E and PAS. Explant cultures of all tissues were positive for *Ichthyophonus* beginning 24h post-exposure (p.e.) and every day thereafter for 32d. Blood cultures were positive in 12 of the 25 positive fish beginning 24h p.e., and peaking between 48 and 120h p.e. From 144h to 32d p.e. blood cultures were positive on only 3 days, suggesting a waning of the stage after 120h p.e. All blood smears were negative and *Ichthyophonus* was first observed in histological sections 25d post-exposure. The existence of a circulating blood stage of *Ichthyophonus* has now been confirmed, but its morphological form remains elusive.

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(22)

MOLECULAR EPIDEMIOLOGY AND CLINICAL ASPECTS OF *BLASTOCYSTIS* SP.- AN AUSTRALIAN PERSPECTIVE

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Blastocystis is a single-celled enteric protozoan that has a world-wide distribution. *Blastocystis* is the most common parasite isolated from human stool samples with prevalence of infection varying from 3.3% in developed countries, up to 53.8% in developing countries. Recent in vivo and in vitro studies strongly suggest that this organism has pathogenic potential and it has been suggested that pathogenicity could be related to subtype infection. *Blastocystis* has shown to exhibit extensive genetic diversity and all isolates from humans and animals can be assigned to one of ten subtypes. Molecular diagnosis by PCR using the small subunit (SSU) ribosomal (r) RNA gene is gaining popularity for the detection of enteric parasites. This study aimed to look at the molecular epidemiology of *Blastocystis sp.* in the Sydney population and comment on the pathogenic potential of this parasite. The study included 510 stool samples submitted to St.Vincent's Hospital, Sydney Australia over a ten month period. All samples were submitted to direct smear, xenic culture, PCR and DNA sequence analysis. There was a 19% incidence rate of *Blastocystis* seen in the Sydney population. There were six different subtypes identified (1, 2, 3, 4, 6 and 8). Subtype 3 was the predominant subtype found in clinical samples from this Sydney population with 45% of isolates belonging to this group. There was a much higher incidence of symptoms seen from patients infected with subtype 2, 4 and 8 which could suggest that these subtypes have pathogenic potential. This is the first molecular epidemiological study of *Blastocystis* from Sydney, Australia. It was shown that subtype 3 is the most common subtype found in the Sydney population. This study highlights the pathogenic potential of *Blastocystis* and shows that symptoms could be subtype related.

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(23)

FECAL PROTOZOA AS PART OF A FUTURE WATER QUALITY FRAMEWORK

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The difficulties in quantifying pathogens include (1) even the most comprehensive monitoring toolkit cannot measure all pathogens of concern, (2) those pathogens that are targeted can be difficult to detect and quantify, (3) lack of pathogen detection is not necessarily evidence of absence of pathogenicity, and (4) pathogens that are detected by methods that do not require culturing might not be infective. Therefore we proposed to supplement available pathogen and indicator data with additional testing of fecal discharge sources for protozoa (e.g. *Cryptosporidium, Giardia),* bacteria (e.g.

Salmonella, *Campylobacter jejuni)* and viruses (e.g. noroviruses, rotaviruses) as well as indicator bacteria, including host-specific *Bacteroidales* that allows for identification and quantification of animal sources. The specific objectives were: (1) to identify and address data gaps pertaining to concentrations of waterborne pathogens and indicators from various discharges to recreational waters, and (2) to compile, analyze and synthesize the data in waterborne risk management frameworks. Sampling was directed toward discharges-of-concern rather than receiving waters. Conducting robust quantitative microbial risk assessment (QMRA) requires capturing and quantifying data for many variables including contributing fecal sources, types of pathogens, individual exposure levels, dose responses, and differential immunity. To adequately inform risk management, QMRA must proceed through six steps: (i) establish the context; (ii) identify the hazards (pathogens); (iii) assess exposures; (iv) assess dose-response; (v) characterize risks; and (vi) communicate those risks. The risk characterization step is the "engine room", in which "Monte Carlo" modeling is usually performed, by making repeated random draws from statistical distributions of the key variables, accounting for both variability and uncertainty. A key feature of our approach is that the QMRA does *not* depend on gaining pathogen data from receiving waters. Rather, these data are *predicted* using influent and effluent data, and appropriate environmental models. These predictions are used to quantify individuals' exposures, in step (iii). This study hás increased knowledge about relationships between pathogen indicators, source identifiers, and pathogens to support QMRA efforts and the implementation of revised recreational water quality criteria.

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(24)

GIARDIA DUODENALIS ASSEMBLAGES IN WEANED CATTLE ON COW-CALF OPERATIONS IN THE UNITED STATES

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To determine the prevalence of *Giardia duodenalis* in weaned beef calves in cow-calf operations, fecal specimens were collected from 819 6- to 18-month-old calves in 20 states. After cleaning and concentrating cysts from feces, DNA was extracted from each specimen. The presence of *G. duodenalis* was determined by nested PCR of a fragment of the SSU rRNA gene. All positive PCR products were subjected to sequence analysis. The overall prevalence of *Giardia* was 33.5 % with prevalence ranging from 0 to 100% among 49 operations. The highest prevalence was found in operations from Georgia, Idaho, Nebraska, and Iowa with 100, 90, 87.5, and 85% of the animals infected, respectively. *Giardia* was not detected in 7 operations, 2 operations each from Louisiana and Oklahoma, and 1 each from Texas, South Dakota, and California. The molecular analysis of the 274 *Giardia*-positive samples identified Assemblage E in 260 (31.7%) and Assemblage A in 10 (1.2%). Four calves from Nebraska had a mixed infection with Assemblages A and E. The potentially zoonotic assemblage A was detected in specimens from 4 operations in Nebraska, and 1 each in Iowa and Oregon. These findings indicate that most *G. duodenalis* found in beef calves was Assemblage E, presenting no known zoonotic threat. However, the presence of Assemblage A in a small number of animals poses a potential risk for human infection.

(25)

IDENTIFICATION OF *CYCLOSPORA PAPIONIS* AND HUMAN-PATHOGENIC GENOTYPES AND SUBTYPES OF *CRYPTOSPORIDIUM* AND *ENTEROCYTOZOON BIENEUSI* IN CAPTIVE BABOONS IN KENYA

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To assess the potential for transmission of cryptosporidiosis, microsporidiosis, and cyclosporiasis between humans and non-human primates that are in close contact with humans, 235 fecal specimens from captive baboons in Kenya were analyzed for *Cryptosporidium* spp., *Enterocytozoon bieneusi*, and *Cyclospora* spp. by PCR and DNA sequence analysis of the small subunit (SSU) rRNA gene, internal transcribed spacer (ITS) region of the rRNA gene, and the SSU rRNA gene, respectively. *Cryptosporidium hominis* was identified in six (2.6%) of the specimens. DNA sequence analysis of the 60kDa glycoprotein (gp60) gene of five *C. hominis* specimens revealed the presence of three subtypes in subtype families, Ib, If and a novel subtype family. *Enterocytozoon bieneusi* was detected in 29 (12.3%) specimens, belonging to 11 genotypes (four known genotypes: A, D, Peru 7 and Peru 11; seven new genotypes: KB-1 to KB-7) that formed two phylogenetic clusters. All the *E. bieneusi* genotypes were previously found in humans or were genetically related to those in humans. Only one species of *Cyclospora*, *C. papionis*, was identified in 42 (17.9%) specimens. Results of this study indicated that non-human primates in Kenya were infected with human-pathogenic *Cryptosporidium* genotypes and subtypes and *E. bieneusi* genotypes. Thus, cross-species transmission of cryptosporidiosis and microsporidiosis is possible between humans and non-human primates that are in close contact with each other.

(26)

LANDSCAPE EPIDEMIOLOGY OF AN EMERGING PARASITE: THE LANCET LIVER FLUKE, *DICRCOELIUM DENDRITICUM*, IN CYPRESS HILLS PARK, ALBERTA

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Advances in our understanding of parasite population dynamics at the landscape scale have been aided by the availability of geographical information systems (GIS) and remote sensing. These tools have been used to characterize spatial patterns of infection and to identify environmental risk factors for the transmission of malaria, lyme disease, and chagas disease. The approach is less common for macroparasites. *Dicrocoelium dendriticum* is an invasive trematode in Cypress Hills Park (CHP) in southern Alberta, Canada. It was absent in the park prior to approximately 1990, but is now present in at least 70% of elk, white-tailed deer, mule deer, and beef cattle sampled since 2005. We used standard GIS methods to characterize the presence and intensity of metacercariae-infected ants (*Formica* spp., second intermediate hosts) within this complex landscape, with the aim of developing a risk map for co-grazing cattle and wildlife. ArcMap was used to randomly select 100 sites within the park that encompassed the range of ecotypes within the park (mixed stands of deciduous and coniferous forests, interspersed with fescue grasslands and wetlands). Ant nest density, terrestrial snail (*Oreohelix* spp., first intermediate

host) density, canopy characteristics, and ground cover were assessed at each site. Standard regression methods were used to assess environmental risk factors for hotspots of metacercariae-to-ungulate transmission within the park. Our analyses identified the presence of pure or mixed stands of aspen and balsam poplar as hotspots of metacercariae-to-ungulate transmission within the park. Large tracts of grassland, pine, and spruce never contained infected ants. Establishing a link between environmental covariates and the presence of infective intermediate hosts allow us to infer the underlying processes determining the current distribution and potential spread of *D. dendriticum* within and beyond CHP.

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(27)

THE LIFE CYCLE OF THE CECAL TROUT NEMATODE, *TRUTTAEDACNITIS TRUTTAE* (NEMATODA: CUCULLANIDAE) IN NORTH AMERICA

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Truttaedacnitis truttae is a characteristic cucullanid nematode of salmonine fishes, particularly rainbow trout (*Oncorhynchus mykiss*) in North America. The only major study on the life cycle of this nematode showed that brown trout become parasitized by ingesting lampreys serving as intermediate hosts. The distribution of *T. truttae* in North America suggests an alternative life cycle. High abundances of *T. truttae* in rainbow trout and its potential impact on the fishery in the Colorado River drainage in Grand Canyon prompted a focused study on its transmission dynamics. Eggs of *T. truttae*, collected from gravid females were incubated in the laboratory. Two species of *Physa* (the most common native snail genus in Grand Canyon), were exposed to *T. truttae* containing infective larvae, 3-4 weeks later. Exposed snails (and controls) were maintained and checked for infections. Active larvae of *T. truttae* were seen penetrating the intestinal wall of exposed snails and larvae were found in the visceral tissues when examined one week after exposure. Larvae in snails showed minimal growth and development and correspond to L3 larvae. Infected snails were fed to hatchery reared juvenile rainbow trout. L3 and L4 larvae were subsequently found in the mucosal lining of the trout intestines. Adult male and female (gravid) worms were found in trout examined 5-6 months after infection. *T. truttae* larvae, found in pepsin/trypsin digests and mucosal scrapings of trout intestines from naturally infected trout, corroborate laboratory findings. *T. truttae* is similar to *T. clitellarius* of lake sturgeon in infecting a snail host and to other cucullanid species in having a histotropic phase of development.

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(28)

DIROFILARIA IMMITIS IN WILD CANIDAE FROM KNOX AND SURROUNDING COUNTIES IN EAST TENNESSEE

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The canine heart worm *Dirofilaria immitis* is an insidious disease producing agent in the companion animal population. The apparent increased incidence of heartworm infection in endemic areas and its occurrence in previously undocumented localities has prompted concern among veterinarians and the pet owning public to better understand the epidemiology of infective reservoirs and the importance of following effective prophylactic programs for its prevention in companion animals. Carcasses of live-trapped nuisance coyotes, gray, and red foxes from Knox and surrounding counties in East Tennessee are being examined to estimate the prevalence of heartworm infection in the wild canine population. To date, the occurrence of heartworm in coyotes is 37% (10/27), while a single gray fox (1/12) and red fox (1/7) were each infected with 1 worm.

(29)

KNOWLEDGE AND PERCEPTIONS OF TOXOPLASMOSIS AMONG MEDICAL AND VETERINARY PERSONNEL IN AN APPALACHIAN COMMUNITY

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Toxoplasmosis is a zoonotic disease resulting from infection with the protozoan parasite *Toxoplasma gondii*. *Toxoplasmosis*is considered too be the third leading cause of death attributed to food borne illness in the United States infecting more than 60 million persons. It is important that physicians, veterinarians and their respective medical staff be knowledgeable about the basic facts concerning zoonotic diseases. As part of an ongoing effort to appreciate the public health significance of toxoplasmosis in rural Appalachian communities, medical professionals were surveyed for information relevant to their understanding of the biology of the parasite, the primary populations at risk for infection, mechanisms of transmission, and recommendations for prevention of infection. Preliminary results suggest that most respondents (71%) recognize *T. gondii* as a protozoan parasite and its zoonotic origin with cats as the primary animal host. In order of decreasing importance respondents thought the majority of infections in people result from contact with their pets, followed by soil related contact through gardening, and ingestion of undercooked meat. Overwhelmingly respondents recognized pregnant women and immunocompromised persons as the primary population at risk for toxoplasmosis. Although most (84%) knew that there is no vaccine for prevention of infection with the parasite, the low recognition of undercooked meat as a source of toxoplasmosis demonstrates the need for increased awareness of this important transmission pathway.

(30)

EXAMINATION OF IMPORTED ASIAN SWAMP EELS (SYNBRANCHIDAE: *MONOPTERUS (AMPHIPNOUS) CUCHIA*) FROM TWO MARKETS IN THE SOUTHEASTERN UNITED STATES FOR THE PRESENCE OF ADVANCED L3 OF *GNATHOSTOMA* SPP.

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L. Nico, US Geological Survey

Over the last two decades large numbers of wild caught and farmed live swamp eels (*Monopterus* spp) have been imported from countries in Asia into the United States and parts of Canada. The eels are sold in ethnic food markets and are on occasion retained live by customers and released into the wild. *Monopterus* spp. are not native to North America however there are 5 documented wild populations of this eel in the continental United States. It is most likely that ethnic food markets are the source for the majority of introductions of these fish into North America. There is no information on the species of parasites in eels from markets in the United States, therefore the potential of eels to serve as sources of exotic parasites or intermediate hosts of zoonotic parasites is not known. We conducted a pilot study to examine 20 *Monopterus cuchia* from markets in Atlanta, Georgia (N = 12) and Orlando, Florida (N = 8) for the presence of advanced L_3 of *Gnathostoma* spp which has been reported as a human pathogen at high prevalences in Mexico, Japan, Thailand and Vietnam. Liver, kidney, gastrointestinal tracts and musculature were separated and removed from eels immediately after euthanization. Individual tissues were examined grossly then macerated and subjected to pepsin hydrochloric acid digest at 37° C for up to 24 h. Seven of the 12 eels (58%) from the Atlanta market were infected with *Gnathostoma* spp. Livers from the 7 eels in addition to muscle from one of the eels were the only tissues infected. The maximum intensity of L_3 was 14. One of the 8 eels (12.5%) purchased from the Orlando market was infected with 2 L_3. Additional work is ongoing to further characterize the extent of infected eels in live markets and in wild populations in the United States.

(31)

GIARDIASIS IN INSTITUTIONALIZED ROMANIAN CHILDREN

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Parasitic diseases have a worldwide distribution and represent an important public health problem. The aim of the present study was to evaluate the prevalence of intestinal parasitic infections in a Romanian Children Care Unit. Clinical and routine laboratory investigations were also conducted to evaluate symptoms and eosinophil count in the infected children. One hundred sixty-four institutionalized children aged 2-8 years were investigated. Stool examinations were performed using the iodine staining for the identification of protozoan cysts and the Willis-Hung concentration method for the identification of helminth eggs. Eosinophil values were determined in the peripheral blood by differential white blood cell count with May-Grunwald-Giemsa staining. The control group consisted of 58 healthy children age matched. Intestinal parasitic infections were diagnosed in 47 cases (28.6%). *Giardia lamblia* (25%), *Entamoeba coli* (3%), *Blastocystis hominis* (1.2%), *Ascaris lumbricoides* (0.6%) and *Trichuris trichiura* (0.6%) were the only parasites identified. *Giardia lamblia* was diagnosed in 41 (87.2%) of 47 infected children. Among the children with parasitic infections we have determined association of two parasites in 7 (14.9%). Diarrhea (38.8%), weight loss (41.6%), nervous disorders (33.3%), and cutaneous manifestations (16.6%) were the most frequent clinical signs in children with giardiasis. We have found that in children with giardiasis the eosinophil number was increased (5.54% +/-4.21%) compared to controls (3.69+/-1.48%) ($p<0.01$). Laboratory results revealed that 61% of the children with giardiasis had the eosinophil count in normal range (≤4%). In conclusion, parasitic infections were diagnosed in a significant number of institutionalized children. *Giardia lamblia* was the parasite identified most frequently in this Pediatric Care Unit.

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PREVALENCE OF INTESTINAL PARASITES IN RELATION TO CD4 COUNTS AND ANAEMIA AMONG HIV-INFECTED PATIENTS IN BENIN CITY, EDO STATE, NIGERIA

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R. Omoregie

Parasitic infections continue to take their toll on HIV positive patients by influencing the blood qualitatively and quantitatively. The objective of this study was to assess the intestinal parasitic infections in relation to anaemia and CD4 counts among HIV-infected patients in Benin City, Nigeria. This was a study involving 2000 HIV-infected patients on their first visit prior to highly active anti-retroviral therapy (HAART) at the University of Benin Teaching Hospital between August 2007 and August 2009. A serial sampling method was used. Stool and blood samples were collected from each patient. The stool samples were processed using the modified Ziehl-Neelsen staining technique to microscopically identify the oocysts of *Cryptosporidium* species, *Isospora belli*, *Cyclospora* species and spores of *Microsporidium* species while saline and iodine preparations were used for identifying the ova, cysts and parasites of *Ascaris lumbricoides*, hookworm, *Taenia* spp. and other parasites. The blood specimens were equally analyzed using flow cytometry for $CD4^+$ T-lymphocyte counts and auto analyzer – sysmex kx – 21 for haemoglobin concentration. The overall prevalence of anaemia was 93.3% while 18% had parasitic infections. There was a significant relationship between CD4 count < 200cells/μL and anaemia ($p < 0.0001$). *Cryptosporidium* species, *A. lumbricoides* and hookworm ($p=0.027$, $p=0.005$, $p=0.035$)

were associated with anaemia. Anaemia was associated with CD4 count
while *Cryptosporidium* species, *Ascaris lumbricoides* and hookworm were the intestinal parasitic agents associated with anaemia.

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(33)

SKIRMISHES ON THE BORDER BETWEEN PARASITOLOGY AND COMMUNITY ECOLOGY: THE NEED FOR NATURAL HISTORY

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Over the last three decades, parasites have quietly become included and recognized as important in almost all areas of ecology and evolution, and particularly at the levels of organismal and population studies. However, the integration of parasites into community ecology has been much more problematic, even though it is widely recognized that we need to integrate parasites into the larger picture of community interactions and ecosystem function. Despite much effort by numerous ecologists and parasitologists, it is still not clear how to include parasites in food webs, or in ecological models of community function. Part of the problem may lie in fundamental differences in the approach and the critical questions in each field, and this is further complicated by inadvertent barriers to entry from both sides. This talk will summarize some of the major ideas published in the last 5 years that relate to parasites and their place in food webs. I will illustrate some of the complications that arise from attempts at integration, and opine on alternative viewpoints. A general conclusion is that before this matter is resolved, much more data will be required on the natural history of parasites… and this bodes well for field parasitologists.

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(34)

PHYLOGENETIC SYSTEMATICS: AN ESSENTIAL FRAMEWORK FOR UNDERSTANDING HOST-PARASITE ECOLOGY

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Ecological investigations can encompass a wide range of biotic and abiotic interactions. Within parasitology, biological associations between parasite species and host species are often at the forefront of ecological studies, for example, when investigators evaluate the abundance and host-associations of parasite species across geographic space or their variation over time (e.g., seasonality, longer-term trends). In addition, ecological interpretations of different host-parasite interactions may benefit from understanding the origin and duration of the association, for example, association by descent (cophylogeny) versus colonization (host-switching). Thus, accurate parasite (and host) systematics is key to analyzing host-parasite ecological interactions both at and beyond the species level. The increasingly frequent detection of cryptic parasite species indicates that ecological studies of host-parasite interactions will also benefit from application of molecular systematics. The utility of molecular systematics for understanding host-parasite associations is illustrated herein by an investigation of *Uncinaria* hookworms from pinniped hosts. These adult hookworms can cause significant pathology in juvenile pinnipeds, contributing to the deaths of pinniped pups on rookeries. In addition, recent documentation of extra-intestinal hookworm migrations in pinnipeds with fatal peritonitis have raised questions regarding which *Uncinaria* species are responsible for such unexpected behavior. To address these and other questions, hookworms were sampled from 8 pinniped host species, including the northern fur seal (*Callorhinus ursinus*), South American sea lion (*Otaria flavescens*), Steller sea lions *(Eumetopias jubatus*), California sea lions (*Zalophus californianus*), South American fur seals (*Arctocephalus australis*), Australian fur seals (*Arctocephalus pusillus*), New Zealand sea lions (*Phocarctos hookeri*) and southern elephant seals (*Mirounga leonina*). Approximately 200 individual

hookworms were sequenced for 5 genes representing 2 loci (mtDNA and nuclear rDNA). Phylogenetic analysis of these data yielded strong evidence for 6 distinct *Uncinaria* species. The 2 described *Uncinaria* species each matured in 2 different host species: *U. lucasi* parasitized *C. ursinus* and *E. jubatus*, and *U. hamiltoni* parasitized *O. flavescens* and *A. australis*. The other 4 undescribed species were each associated with a unique host species. Molecular diagnostics based on RFLP analysis did not support the hypothesis that peritoneal infections were caused by a novel host-parasite association. Patterns of *Uncinaria* host-sharing and phylogenetic relationships of species inferred from gene sequences revealed a strong geographic component to host-sharing, and in one case the potential directionality of a host-switching event.

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HOST SPECIFICITY AT THE INTERFACE OF ECOLOGY AND EVOLUTION

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Host specificity, i.e. the extent to which parasites can exploit different host species, is one of their most fundamental properties, as it affects their population dynamics, their chances of local or global extinction, and the probability that they persist following their introduction to new areas. I will discuss the evolution and ecology of host specificity, ranging from the genetics of intraspecific variation in host use all the way to large-scale patterns of host specificity and their ecological consequences. First, at a microevolutionary level, I will report on experimental studies aiming at understanding why different trematode genotypes do not succeed equally in different hosts. Taking advantage of the fact that cercariae come in genetically-identical replicates, these experiments test the hypothesis that phenotypic plasticity and/or high heterozygosity allow an escape from strict specificity and the invasion of new hosts. Second, at a macroevolutionary level, I will review evidence that host specificity is a phylogenetic dead-end, i.e. that it is evolutionary irreversible once adopted by a lineage. Comparative evidence will also be used to test the 'jack-of-all-trades-master-of-none' principle, which suggests that evolution might favor specialization. Finally, at the ecological level, I will dissect host specificity into its various components, each manifested at different spatial scales, and relate various facets of host specificity to basic ecological and biogeographical properties of parasites. My goal throughout will be to show that a few fundamental principles unite all levels, whether one approaches host specificity from an evolutionary or ecological perspective, whatever the temporal or spatial scale.

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FROM THE ARCTIC TO THE TROPICS

EMINENT PARASITOLOGIST LECTURE

R.L. Rausch, Department of Comparative Medicine, University of Washington School of Medicine

Dr. Rausch's research includes zoonotic diseases and the natural history and taxonomy of their mammalian hosts. The field and laboratory investigations by Dr. Rausch have emphasized various diseases, including rabies, brucellosis, and tularemia, that affect indigenous peoples in the Arctic and Subarctic. Since 1950, sustained research has concerned cestodes of the genus *Echinococcus*, each species of which causes a distinctive disease in people. Investigations begun in 1950 on St. Lawrence Island (Bering Sea) led to recognition of *E. multilocularis* as an independent species, resolving a century-long controversy as to the etiology of alveolar echinococcosis, and to elucidation of the natural cycle of that cestode. From 1970 to 1996, in collaboration with physicians at the Alaska Native Medical Center (Anchorage), investigations concerned methods of diagnosis, chemotherapy, and prevention of alveolar

echinococcosis. Related studies were also undertaken in the field in Japan, People's Republic of China, and NE Siberia (in collaboration with V. R. Rausch). Since 1950 also, the investigation of cystic echinococcosis has been conducted concurrently. In 1972, a neotropical species, *E. vogeli*, was described by Rausch and Bernstein from a wild canid, *Speothos venaticus*, captured in Ecuador. In collaboration with A. D'Alessandro, Tulane University, and V. R. Rausch, the cycle was defined during the late 1970's in Colombia. Polycystic echinococcosis caused by that cestode is now known to be a severe disease occurring in people in northern countries of South America, and as far north as Panama. A project in progress since 1949 concerns cestodes (Diphyllobothriidae) transmitted from fishes to people and other mammals, and to piscivorous birds, mainly in the northern hemisphere. Several new species, some occurring in people, have been described in Alaska. Basic investigations on the taxonomy of helminths and of mammals are continuing. reference: http://depts.washington.edu/compmed/faculty/faculty/rausch.html

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OBSERVATIONS ON THE MORPHOLOGY, BEHAVIOR AND PHYLOGENETIC POSITION OF THREE LARGE-TAILED STRIGEID CERCARIAE FROM SMALL PLANORBID SNAILS (TRIBE PLANORBINI)

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We provide observations regarding three unusual, large-tailed, strigeid cercariae, all from small planorbid snails (Tribe Planorbini). The first, from *Gyraulus parvus* from New Mexico, resembles *Cercaria bulbocauda* described by Miller (1927). It is unusual for its large overall size, long tail stem, and for the peculiar bulge in the tail stem just anterior to the furcae. It resembles a copepod while swimming. The second cercaria, also from New Mexican *G. parvus*, was distinctive for its inflated tail stem that has in its anterior half numerous spherical structures filled with refractile bodies. We know of no other cercariae with similar bodies in the tail stem. The third cercariae from *Ceratophallus natalensis* from Kenya, was unusual in having a wide tail stem, thick furcae and slow swimming speed. The 28S rRNA sequences obtained for the three cercariae had as their closest match the European strigeid *Apharyngostrigea cornu*, which also has an unusual tail stem. Although it is clear the three cercariae we found are related, more sequence data from additional strigeids is needed to determine if they might form a monophyletic group. All of these cercariae differ from more typically recovered strigeid cercariae in having unusual modifications to their tail stems. They serve to accentuate the point that the cercarial tail is an organ capable of remarkable morphological and behavioral plasticity in response to selection in strigeids.

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COMPARATIVE PHYLOGEOGRAPHY OF TWO PINWORM SPECIES THAT INFECT CHIPMUNKS

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A parasite's geographic distribution is shaped by complex interactions. While parasites may track a host, they may be more dependent on a particular host resource than a specific host. We examine the biogeographic history of two species of pinworms (*Heteroxynema cucullatum* and *Syphacia eutamii*) that infect western chipmunks (subgenus *Neotamias*) to address questions about the evolutionary and geographic history of this host-parasite association. In particular, do pinworm and chipmunk phylogeographies suggest similar responses to past changes in populations, such as expansion and isolation? Are pinworm phylogeographic patterns strictly

associated with host lineages? Or, have changes in chipmunk populations led to host-switching? We use DNA sequences from pinworms to compare phylogeographic patterns for both parasites and hosts in the Western U.S., with most samples from the Southern Rocky Mountains. Preliminary phylogeographic relationships suggest that within both pinworm species some genetic lineages have been associated with a host species or host lineage, while others are structured geographically. While both species of pinworm are associated with the same host subgenus, each parasite species has different phylogeographic patterns, suggesting that each has had a different biogeographic history.

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MOLECULAR PHYLOGENY OF POLYMORPHIDAE (ACANTHOCEPHALA) A FAMILY OF PARASITES OF MARINE MAMMALS, WATERFOWL AND FISH-EATING BIRD INFERRED FROM NUCLEAR AND MITOCHONDRIAL GENE SEQUENCES

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Acanthocephalans of the family Polymorphidae Meyer, 1931 are obligate endoparasites with complex life cycles. These worms used alternatively vertebrates (marine mammals, fish-eating birds and waterfowl) as definitive host and invertebrates (amphipods and decapods) as intermediate host to complete their life cycle. The family contains 12 genera, with approximately 127 species diagnosed by having a spinose trunk, bulbose proboscis, double-walled proboscis receptacle, and usually 4 to 8 tubular cement glands. In the current study sequences of the small-subunit (SSU) and large-subunit (LSU) ribosomal DNA and cytochrome *c* oxidase subunit 1 (*cox* 1) were generated for individuals of 27 taxa representing 10 of 12 genera of Polymorphidae, plus other 3 species of acanthocephalans that were used as outgroups. Maximum parsimony (MP), maximum likelihood (ML) and Bayesian analyses were conducted on the nuclear rDNA (SSU + LSU) and the combined sequence dataset (SSU + LSU + *cox* 1 genes). Phylogenetic analyses support the monophyly of Polymorphidae and nine genera are recovered as monophyletic: *Andracantha*, *Corynosoma*, *Bolbosoma*, *Profilicollis*, *Pseudocorynosoma*, *Southwellina*, *Arhythmorhynchus*, *Hexaglandula* and *Ibirhynchus*. However, *Polymorphus* is polyphyletic, suggesting that the genus represents a complex of species that should be re-examined and re-classified using morphological, ecological, and molecular data. Our data suggest that the fish-eating birds and amphipods were initially colonized during the evolutionary history of the group and that the association with other definitive (marine mammals and waterfowl) and intermediate (decapods) hosts, represent episodes of secondary colonization and diversification via host-switching.

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FENCES IN THE COMMON GARDEN: SUBOPTIMAL FITNESS OF *BLABERICOLA PRINCISI* AND *BLABERICOLA BLABERAE* EXPERIMENTALLY INFECTING ABNORMAL COCKROACH HOSTS

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Gregarines are nearly ubiquitous apicomplexan intestinal parasites of arthropods. Gregarine species isolation is usually ascribed to host specificity: the failure of two gregarine species to infect and overlap in a single host species effectively prevents gene flow. Recent empirical work demonstrates that gregarine

host specificity is not always strict, suggesting that other mechanisms maintain gregarine species isolation in the presence of cross-transmission. Gregarine species of *Blabericola* are restricted to cockroach hosts but may not adhere to a paradigm of strict host specificity. New World cave roaches of the genus *Blaberus* are a closely related group of species that often overlap in distribution and habitat use and their gregarines are an ideal model to test host-specificity and relative fitness in normal and abnormal hosts. *Blabericola princisi* infects the Bolivian cave cockroach, *Blaberus boliviensis,* while *Blabericola blaberae* infects the death's head cockroach, *Blaberus craniifer*. Experimental infections were conducted to assess the relative host specificity of these gregarines and their relative fitness in both their normal and abnormal host species. In experimental control- and cross-infections, both species of *Blabericola* established infections in normal and abnormal hosts, confirming a lack of strict host specificity among *Blabericola* species. However, subsequent growth, development, and reproduction of both species was significantly reduced or eliminated in the abnormal host. We propose that these differences in relative fitness play a role in maintaining unique species identities among gregarine species.

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EXPANSION OF THE CESTODE GENUS *TRILOCULARIA*: AN INVESTIGATION ACROSS SHARK HOSTS AND OCEANS

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The elasmobranch cestode *Trilocularia gracilis* (=*acanthiaevulgaris*) has been reported from the spiny dogfish, *Squalus acanthias*, throughout the global antitropical distribution of this shark. While there have been some studies of this hyperapolytic cestode in the N. Atlantic Ocean, studies across disparate localities are lacking, and it has remained a monotypic genus since its description in 1867. Recent re-examination of the global distribution of the host, *Squalus acanthias* has led to the N. Pacific Ocean population being recognized as a distinct species, *S. suckleyi*, prompting a closer look at the cestodes of these shark species and a congener, *S.* cf. *mitsukurii*. This study uses an integrative taxonomic approach to compare *Trilocularia* specimens among these 3 host species from localities around the world. A total of 6 specimens of *Squalus* cf. *mitsukurii* from the Indian Ocean; 59 specimens of *S. suckleyi* from the North Pacific Ocean; 20 specimens of *S. acanthias* from the South Pacific Ocean; 217 specimens of *S. acanthias* from the North Atlantic Ocean; and 19 specimens of *S. acanthias* from the Black Sea were necropsied for *Trilocularia*. Specimens were examined with light and scanning electron microscopy, in addition, sequence data were generated for partial 16S rDNA and partial 28S rDNA genes. Differences in morphological characters of the cestode specimens, including ovary size and shape, dehiscence pattern, and size of anterior attachment region of the free proglottids, suggest the cestodes examined may represent upwards of 3 new species. This is supported by the molecular data which shows 4 distinct clusters of *Trilocularia*: (1) specimens from the Indian Ocean (*S.*cf. *mitsukurii*), (2) specimens from the N. Pacific Ocean (*S. suckleyi*), (3) specimens from the S. Pacific Ocean (*S. acanthias*), and (4) a mixed cluster containing specimens from the N. Atlantic Ocean (*S. acanthias*) and the Black Sea. Thus there is a high likelihood that the examination of other species of *Squalus* will reveal additional diversity in the cestode genus *Trilocularia*.

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DO GAPS BETWEEN GEOGRAPHIC DISTRIBUTIONS OF *PHILOBDELLA* SPECIES CORRELATE WITH ENVIRONMENTAL DATA?

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Geographic data of the North American leech species *Philobdella floridana* and *Philobdella gracilis* were compared to environmental GIS data to determine if the geographic distributions of these sister species correlate with environmental indicators or are the result of other processes (e.g. competition). *Philobdella floridana* is distributed in coastal areas along the eastern coast from the Carolinas south to Florida. *Philobdella gracilis,* on the other hand, is distributed along the Mississippi River from New Orleans, Louisiana north to Illinois. There is a clear gap between the distributions of the two species in the area of the Mobile Basin which has not been explained by poor sampling efforts or other phenomenon. The region not inhabited by *Philobdella* species is, however, inhabited by *Macrobdella ditetra* of the sister genus, demonstrating that the region is habitable by leeches and well-sampled for leech fauna. The distribution of *M. ditetra* overlaps the entire range of *P. floridana* and a large portion of *P. gracilis*. With over 60 unique locality records derived from museum collections and recent expeditions, we assessed the correspondence between WorldClim data sets and locality records for these three species.

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CESTODE MORPHOLOGY AS PREDICTED BY ELASMOBRANCH RELATIONSHIPS: *CALLIOBOTHRIUM* IN SMOOTH HOUND SHARKS OF THE GENUS *MUSTELUS*

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The first formal, comprehensive phylogenetic analysis of the triakid shark genus *Mustelus* based on NADH2 sequence data generated for 18 of its 31 valid species, suggests that this genus consists of 2 distinct clades of smooth hound sharks, one consisting of 11 species and the other of 7 species. This result prompted a closer look at the cestodes of the sharks comprising these 2 clades. In total, the cestode faunas of the following shark species were examined: *M. californicus* and *M. albipinnis* collected from the Gulf of California in 1996, *M. canis* collected from the Long Island Sound in 1998, *M. manazo* collected in 1999 from Japan, *M. mustelus* collected from Senegal in 2002, and *M. palumbes* and *M. mustelus* collected in 2010 from the Indian Ocean off the coast of South Africa. Based on previous work on the cestodes of *M. antarcticus, M. californicus, M. canis, M. henlei, M. lenticulatus, M. lunulatus, and M. schmitti*, efforts were focused on the cestode genus *Calliobothrium*. Specimens were examined using light and scanning electron microscopy. This work revealed that the species of *Calliobothrium* hosted by the sharks in the 2 clades differed consistently in a conspicuous morphological feature; whereas the 5 species of *Calliobothrium* known from sharks in the larger clade were found to bear an accessory piece between the bases of their axial hooks, the 5 species hosted by sharks in the smaller clade lacked an accessory piece. Publications of existing species of *Calliobothrium* from *M. antarcticus, M. californicus, M. canis, M. henlei, M. lenticulatus,* and *M. lunulatus* supported this pattern. In order to explore the monophyly of the groups with or without an accessory piece, sequence data were generated for the 16S rDNA gene and D1-D3 region of the 28S rDNA gene for *Calliobothrium* species taken from sharks in each clade. The observed pattern allows predictions of the form of *Calliobothrium* likely to parasitize species of *Mustelus* not yet examined for cestodes.

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MONODB: WORK IN PROGRESS FOR A CENTRALIZED WEB-BASED RESOURCE FOR THE CLASS MONOGENEA

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Yamaguti's *Systema Helminthum,* produced *ca*. 50 yr ago, remains the first point of reference for many helminth researchers. Regarding web-based resources, there are a number of sites specialized in particular genera or regional fauna, but very few synthesize current knowledge concerning the Monogenea. Given the lack of such a synthesis, basic taxonomic and biological information concerning the 700+ known monogenean genera is frequently difficult or impossible to access, often being published in grey literature or inaccessible journals, usually beyond the reach of researchers with limited budgets or informational resources. Even when such data are available, images and descriptions of taxonomically informative traits are of variable quality. This paper describes the development of a web-based resource, the steroid enhanced big sister of "GyroDb". We have started to construct a website, the eponymously named "MonoDb", which will provide access to records for recognized (and retired?) monogenean genera. In addition to overviews of monogenean biology, taxonomy and relevant research techniques written by acknowledged experts, access will be provided to individual species records arranged by family and genus. Each monogenean species record will comprise images and molecular data relevant to their taxonomic identification, original references for descriptions and other key information *e.g*. host and habitat *etc*. For type species and other important species or species groups, the site will contain authored reviews of current biological and systematic knowledge. In the future we intend the site to allow users to submit new data which will be refereed to ensure quality and consistency before upload to the publicly accessible databases. It is intended that the site be accessible for users of all backgrounds and interests including both those with a casual interest in monogeneans and established researchers. Links to relevant sites such as FishBase and researcher and facility homepages will also be provided. A provisional version of MonoDb may be accessed at www.monodb.org.

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SPATIAL LOCALIZATION OF δ-GIARDIN WITHIN THE VENTRAL DISC OF *GIARDIA DUODENALIS* USING LASER SCANNING CONFOCAL MICROSCOPY

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The ventral disc is believed to play a key role in *Giardia duodenalis* virulence by mediating adherence of trophozoites to epithelial cells of the intestine. Previous studies suggested that antibodies against recombinant δ-giardin cytoskeletal protein inhibited trophozoite adherence to glass microscope slides. The functions and interactions of β- and δ-giardins that comprise structural elements of the ventral disk are unknown. This study was conducted to gain insight into the location of δ-giardin in both trophozoite and cyst stages with the aid of laser scanning confocal microscopy and polyclonal antibodies against recombinant δ-giardin and β-giardin. Multiplex immunolocalization of β- and δ-giardin in *Giardia* showed that in free trophozoites and encysted forms δ-giardin is strictly associated with the ventral disc. Optical sectioning of the ventral discs, together with quantitative measurement of the immunofluorescence for δ- and β-giardin, demonstrated that these proteins share a great degree of

colocalization. Delta-giardin, however, is positioned much more ventrally and therefore represents the actual adhesive side of the disc, whereas β-giardin was not found on the ventral proximity of the disc. Immunostaining of the ventral disc for δ-giardin was observed in both methanol- and formaldehyde-fixed trophozoites indicating that δ-giardin is indeed the protein that has intimate contact with the intestinal epithelium of the host, potentially playing an important role in adhesion. These findings provide further support for the crucial role of δ-giardin in *Giardia* adherence and highlight the potential of the giardins as promising targets for immunotherapy of giardiasis.

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CHARACTERIZATION OF A NOVEL PROTEIN KINASE LOCALIZED TO LIPID BODY MEMBRANES OF *TRYPANOSOMA BRUCEI*

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In most organisms membrane-spanning signaling proteins play critical roles in extra- and intracellular sensing, thereby, regulating a variety of cellular processes. The lack of characterized transmembrane signaling proteins in trypanosomatids led us to study several predicted transmembrane protein kinase encoding genes in*T. brucei*. One putative protein kinase, Tb11.01.0670, is expressed at the RNA level in both procyclic and bloodstream forms and encodes a protein kinase, LDK, that localizes to the monolayer lipid membrane of lipid droplet organelles in both procyclic and bloodstream stage parasites. RNAi knockdown of LDK modestly affected growth of mammalian bloodstream stage parasites but did not affect the growth of insect (procyclic) stage parasites. RNA knockdown was, however, accompanied by a dramatic reduction in numbers of lipid droplets. Cell culture conditions which normally induce lipid droplet biogenesis in procyclic cells failed to act as potent lipid body inducers in LDK knockdown cells. While immunoprecipitated LDK protein possesses protein kinase activity, the activity under normal culture conditions is modest, though growth in delipidated serum increased LDK autophosphorylation activity. LDK appears to be required for lipid droplet biogenesis or maintenance, and is one of the few protein kinases specifically and predominantly associated with an intracellular organelle. Hence we propose that LDK activity is regulated by nutrient status, and that it is involved in lipid body biogenesis and/or the mobilization of lipids in response to changing environmental stimuli.

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HAEMOSPORIDIA PREVALENCE IN BREEDING PROTHONOTARY WARBLERS

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The Prothonotary Warbler has shown a range-wide decline in past years due to habitat destruction and degradation as lowland, hardwood forests are logged and converted to agricultural use. They are exposed to parasites in both tropical and temperate regions. The focus of this study is to use molecular techniques to examine the temporal patterns of Haemosporidia prevalence in breeding Prothonotary Warblers. The prevalence (presence or absence) of Haemosporidia was assayed using primer sets for the cytochrome *b* gene of the mitochondrial DNA. Blood samples were obtained from 223 adult Prothonotary Warblers collected at 3 Central Virginia breeding sites. We found that a total of 68.6% of captured Prothonotary Warblers were infected with Haemosporidia, specifically, 60% prevalence in *Haemoproteus* infection and 77% prevalence in *Plasmodium* infection, during the 2008 breeding season. Infection prevalence increased throughout the season. We also found that Haemosporidia prevalence was significantly higher during the second clutch than the first clutch. In addition, infection prevalence in males increased significantly between the first and second clutch. These results indicate that there are differences in

spatial and temporal trends in Haemosporidia infection in *P. citrea* on their breeding grounds in Central Virginia.

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DETERMINATION OF THE FUNCTIONALITY OF THE C2 DOMAIN OF NOVEL *P. FALCIPARUM* EXPORTED PROTEIN, PFEXP-250

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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. We have identified a novel exported protein, PfEXP-250, which we have shown to be associated with membranous structures and interacts with a variety of *Plasmodium* proteins as well as the erythrocyte cytoskeleton. PfEXP-250 is predicted to contain a calcium-lipid binding or C2-domain. C2-domains have been identified in many eukaryotic proteins and have been shown to function in signal transduction events by mediating phosphorylation events, GTPase activation, and membrane trafficking. *Plasmodium falciparum* has five C2-domain containing proteins of which the expression of only PfEXP-250 has been confirmed. In this study we attempt to determine the functionality of PfEXP-250s predicted C2 domain. Analysis of the PfEXP-250 protein sequence suggests that it contains seven of the eight b-sheets found in known structures of C2-domains. Additionally, multiple sequence alignments of PfEXP-250 with other C2-domain containing proteins functioning in vesicle trafficking suggest that PfEXP-250 is of the Type II topology. PfEXP-250s calcium and phospholipid binding properties are currently being assessed. The ability of PfEXP-250 to interact with multiple proteins, its association with membranous structures, and the presence of a C2 domain suggests that it may indeed be important to the parasite's host modulating activities and warrants further characterization of this protein.

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FRACTIONATION OF LIFE CYCLE STAGES OF *NOSEMA BOMBYCIS* (MICROSPORIDIA) FROM *BOMBYX MORI* BY PERCOLL DENSITY GRADIENT

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While various proteomic studies have been performed on some unicellular parasites, very little has been done for *Nosema bombycis*, the pathogen causing silkworm pebrine. This is partially due to problems purifying the early stages of developing *N. bombycis* from their host cells. Due to its small size (mean spore size: 3.1–4.26×1.9–2.6 mm) and fragility, large-scale separation of different *N. bombycis* cell stages from heavily infected silkworm larvae is considered to be a difficult task. Here we present a density gradient-based method to purify the intracellular life cycle stages of *N. bombycis* from infected tissues of the host, as a first effort to analyze differentiation stages of this parasite. The entire procedure can be described as:(1) severe infected silkworm midgut preparation, (2) gently homogenization in PBS buffer and filtration through glass wool columns, (3)centrifugation of the filtrate in a 70% Percoll–0.25 M sucrose gradient, resulting in a reproducible pattern of three layers containing different life cycle stages, (4) further centrifugation of the top fraction (A) in a 30% Percoll–0.25 M sucrose gradient and the middle fraction (B) in a 50% Percoll–0.25 M sucrose gradient respectively, generating empty germinated spore husks (A2) , early sporoblasts (B1) and late sporoblasts (B2). Transmission electron microscopy was used to compare the content and purity of each fraction. Analysis of proteins from main fractions by two-dimensional gel electrophoresis showed a potential use of the described method for proteomic research.

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EFFECT OF NITROSYLATION ON ENCYSTMENT REGULATION IN THE PROTOZOAN *GIARDIA INTESTINALIS*

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The discovery that *Giardia* is able to synthesize nitric oxide (NO) predicts that it could act as a signaling effector perhaps by protein nitrosylation, and that this signaling could be involved in the switch from glycolysis during the trophozoites' growth phase to cyst wall synthesis during encystment. Confocal microscopy, using fluorescent staining, shows the localization of NO in trophozoites. The biotin-switch method, applied to lysates of encysting and non-encysting trophozoites using non-denaturing and denaturing conditions for the proteins, demonstrated that a large number of proteins were labeled under both conditions indicating that the post-translational modification by nitrosylation takes place in *Giardia*. One of these modified proteins, glucosamine 6-phosphate deaminase, the first enzyme unique to the encystment pathway, is induced during encystment and serves as an aminating isomerase in *Giardia* channeling fructose 6-phosphate away from glycolysis and into glucosamine 6-phosphate, the precursor of the cyst wall polysaccharide poly β-(1,3)-N-acetylgalactosamine. In vitro nitrosylation of the recombinant deaminase showed that its K_m changes from about 3.5 mM to 1.5 mM, suggesting that the enzyme's affinity for the substrate increases upon nitrosylation. Screening of five different cysteine residues by in vitro mutation indicated that three of them, position 113, 156, and 230 might be the targeted residues. The activity of a major glycolytic enzyme, glyceraldehyde 3-phosphate dehydrogenase, on the other hand, is significantly decreased following nitrosylation.

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METABOLIC VARIATION BETWEEN HUMAN INFECTIVE *GIARDIA* ASSEMBLAGES

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The protozoan parasite *Giardia duodenalis* demonstrates significant genotypic variation and has been separated into 7 stable and distinct genetic "assemblages". Assemblages A and B can infect human hosts and are capable of causing a range of pathologies from symptomatic to severe diarrheal disease. The link between genotype and pathogenicity and the mechanisms responsible for the broad spectrum of symptoms caused by *Giardia* remain obscure. Limited phenotypic heterogeneity within the human infective genotypes has been shown. However, to date, there have been no comparative studies on the biochemistry of isolates from the two assemblages. Previous work on the metabolism of *Giardia* has focused primarily on specific pathways and metabolic end products. Metabolomics is an approach that can generate a detailed profile of low-molecular-weight metabolites (identity and concentration) in a biological system and uses separation and identification techniques such as LC-MS and NMR spectroscopy. Metabolomics can, therefore, be used to compare similar biological systems, such as two isolates from the same organism. We have been using LC-MS/MS to study the metabolomes of *Giardia* isolates from the 2 human assemblages and have generated some interesting data. These data have generated a number of unexpected observations such as the utilization of galactose and inosine and variations in the ability of these isolates to utilize arginine. Also, the levels of some key intracellular metabolites varied significantly suggesting that metabolic rates differ between isolates and may correlate to factors such as virulence.

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

S.S. Ray, Clemson University

Trypanosoma brucei is one of the major causes of death in some parts of Africa. Transmitted by the Tse Tse fly, these protozoan parasites cause fatal disease in humans (sleeping sickness) and in livestock. Current drugs to treat Human African Trypanosomiasis are toxic and drug resistance is a growing problem. Vaccine development is unlikely because the parasites undergo antigenic variation. GPI-anchored proteins are implicated in antigenic variation, hence lipid synthesis, and specifically, fatty acid synthesis (FAS) could represent novel targets for therapeutic intervention. *T. brucei* can synthesize its own fatty acids by an unconventional FAS pathway. A key substrate for FAS is malonyl-CoA, which is synthesized from Acetyl-CoA by Acetyl-CoA Carboxylase (ACC), and thus, ACC likely serves as one control point for regulating FAS. Specifically, we hypothesize that ACC is negatively regulated by phosphorylation in response to environmental lipids. Bioinformatic phospho-prediction algorithms show multiple high-scoring sites (≥0.95). Quantified ACC protein quantification determined and saw increased levels when the trypanosomes when grown in low lipid media, suggesting some regulation of ACC at the level of mRNA processing, stability, and/or translation. Finally, we assessed whether ACC is phosphorylated by metabolic radiolabeling. We observed a phosphorylated band of with [^{32}P]orthophosphate labeling of ACC-myc cells grown in low, normal, and high lipid media followed by immunoprecipitation of ACC-myc and autoradiography and SA-HRP blotting demonstrated a 500% increase in phosphorylation of ACC-myc in high lipid media and an 80% reduction in phosphorylation in low lipid media. In addition, ACC enzyme activity was higher in cells grown at low lipids than high lipids. Taken together, this data is consistent with our model that *T. brucei* ACC is dynamically phosphorylated in response to the environmental lipid supply. Further, ACC appears to be phosphorylated under conditions when the environmental supply of lipids is abundant and FAS therefore should be down-regulated. Currently, we are examining the direct effect of phosphorylation on ACC activity.

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REGULATORY IMPACTS ON PREVALENCE AND TREATMENT OF FOODBORNE PARASITES

A.M. Adams, US Food and Drug Administration, Kansas City District

The US Food and Drug Administration (FDA) promulgates and enforces regulations to ensure the safety and efficacy of drugs, and the safety of foods. FDA also regulates medical devices, biologics, radiological treatments, and most recently, tobacco. However, FDA only has jurisdiction when interstate commerce is present. Medical devices and drug treatment for parasites must be approved by FDA. For example, FDA approves the manufacture and use of endoscopes which in addition to other uses, are utilized to treat anisakid infections. FDA addresses parasites as a public health or sanitation/wholesomeness issue. Parasitological research performed in FDA has multiple foci in the regulatory arena. Data involving particular foods may be used to establish parameters for regulatory action, or be provided publicly to promote awareness of health risks. Industry often utilizes such information to inactivate or eliminate parasites. Examples include prevalence data for seafood parasites and their hosts, or in processed foods such as sushi and fillets. FDA provides guidance to local governments, industry, and consumers about possible risks. Guidance includes the Food Code and Good Manufacturing Practices. The seafood regulation in 1995 required implementation of Hazard Analysis and Critical Control Points (HACCP) by industry to identify risks in production and to properly address such risks. Most risks posed by seafood parasites and addressed by HACCP generally result in treatment by freezing or heating (including

smoking and microwaving). Guidelines in the Food Code are based on research and scientific literature. FDA's response to outbreaks of foodborne parasites is tempered until jurisdiction and a regulatory basis are established. During outbreaks by *Cyclospora*, research was conducted for the detection and control of the parasite and to support regulatory decisions by the Agency. Ultimately, FDA placed a detention on raspberries from Guatemala to prevent importation of possibly contaminated fruit.

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(54)

THE VIGILANT GENOTYPE

T.V. Rajan, UConn Health Center, Farmington, CT

There has been a gradual increase in the incidence of diseases that share in common a dysregulated immune response to self or environmental antigens. I would like to propose that this is the result of improving standards of hygiene and the resultant lack of exposure to pathogen-derived antigenic stimulation at critical points of ontological development. The analogy would be to a strain of mouse known as NOD/Shi. If mice from this inbred strain are raised in a pathogen-free environment, they develop autoimmune disorders including diabetes at a high rate. If, however, housed in a conventional (dirty) environment, or if exposed to a variety of infectious agents early in life, the mice become relatively resistant to diabetes. In an analogous manner, I propose that the human immune system has been selected through millennia of exposure to multiple pathogens to react expeditiously and aggressively in order to achieve host protection. Appropriately timed exposure to species-appropriate pathogens is critical for proper function of the developing immune system. These interactions between pathogens and the immune system result in a balance of effector and regulatory components. Failure of exposure to species-appropriate pathogens, such as happens in very hygienic environments, results in an immune system that is poised to mediate host- protection in an exaggerated and unregulated manner to otherwise benign immunological stimuli, even if this results in collateral tissue damage. Epidemiological data supportive of this model will be presented.

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THE WILD LIFE OF OUR BODIES-CONSEQUENCE OF HAVING EVOLVED IN THE WILD FOR OUR MODERN, CLEAN, LIVES

R.R. Dunn, Dept. of Biology, North Carolina State University

In the last ten thousand years among the biggest transitions in our ways of life have been in terms of the species we interact with. In this talk I will explore the changes in our interactions with parasites, but also mutualists, predators and commensal species. I will consider the evidence for both costs and benefits of having shed or changed many of these interactions. None of us miss smallpox, but there are ways in which we may miss tapeworms, wild fruits and even a tiger or two.

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EDITORS SYMPOSIUM – 2011

G.W. Esch, Wake Forest University
M. Sukhdeo, Program in Ecology and Evolution, Rutgers University, New Brunswick, NJ

For the fourth year in a row, Associate Editors of the Journal of Parasitology will present talks regarding their personal research activities. Michael Sukhdeo will chair the symposium and lead a Q and A session at the end. Gerald Esch will provide introductory remarks. Dr. Bill Granath of the University of Montana will lead off with a discussion regarding the ecology of whirling disease in salmonid fishes in the western United States. His talk will be followed by two Associate Editors from the University of California at San Francisco. A cell and molecular biologist, Dr. Judy Sakanari at the Sandler Center for Drug Discovery will describe her work on the development of a marofilaricidal drug for *Brugia malayi*. Dr. John Sullivan, who handles invertebrate-parasite relationships for the Journal, will discuss his research on the amebocyte-producing organ of the snail, *Biomphalaria glabrata*. Finally, we will hear from Dr. Al Shostak, University of Alberta. Al was scheduled for this Symposium in Colorado Springs, but due to personal reasons, had to delay his talk until this year. His focus will be on the ecological interactions between larval cestodes and their hosts.

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ECOLOGY OF SALMONID WHIRLING DISEASE IN A WESTERN MONTANA STREAM: A LONG-TERM STUDY (AKA: A TWISTED TAIL)

W.O. Granath, University of Montana

Salmonid whirling disease, caused by the myxozoan parasite *Myxobolus cerebralis*, was introduced into the eastern U.S. in the 1950's and later expanded to many western states. The parasite became "newsworthy" when it was blamed for significant population declines of wild rainbow trout populations in the western inter-mountain states in the late 1980's. When *M. cerebralis* was detected in 1997 in Rock Creek, a blue ribbon trout stream in western Montana, a long-term ecological study was initiated on the parasite in 1998. From 1998 to 2003 the intensity of *M. cerebralis* infections in sentinel rainbow trout increased significantly throughout the drainage and the range of *M. cerebralis* expanded considerably. In addition, the parasite apparently caused a dramatic decline in wild rainbow trout densities but the wild brown trout population numbers increased. Subsequent monitoring indicated that disease intensity may have peaked in 2006 and is on the decline in some areas of the drainage. The decline cannot be directly attributed to a change in the prevalence of *M. cerebralis*-infected *Tubifex tubifex* (the obligatory alternate host of the parasite) as these numbers remained statistically the same from 1998 to 2010. Similarly, changes in water temperature and water flow cannot directly account for the decrease in disease intensity. However, it is possible that wild rainbow trout are developing some resistance to the parasite, a phenomenon recently documented to be occurring in the Willow Creek Reservoir of southwest Montana. Further, it appears that rehabilitation of a severely degraded tributary of Rock Creek, which historically had a high intensity of *M. cerebralis* infections in sentinel fish, is experiencing a decline in disease severity. Continued study will be needed to determine the effects of habitat restoration, the potential development of disease resistance and other factors on the ecology of the parasite in this drainage.

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RESPONSES OF THE AMEBOCYTE-PRODUCING ORGAN OF *BIOMPHALARIA GLABRATA* TO NONSELF

J.T. Sullivan, University of San Francisco

The schistosome-transmitting snail, *Biomphalaria glabrata*, forms hemocytes in a region of the pericardial wall known as the amebocyte-producing organ (APO), which shows increased cell division following infection with larval trematodes. Allografts of the APO (but not other organs) from schistosome-resistant *B. glabrata*confer resistance to infection with *Schistosoma mansoni* in schistosome-susceptible recipients, suggesting a potential role in host defense. Freeze-thaw extracts (FTE) of larval and adult *S. mansoni,* as well as excretory-secretory products of schistosome sporocysts, elicit a mitotic response when injected into snails, and the response to miracidial FTE is much stronger in schistosome-resistant Salvador *B. glabrata* than in susceptible NIH albino snails. Miracidial FTE is also stimulatory in vitro, suggesting a direct effect of parasite components on hematopoietic cells, possibly mediated by protein kinase C. The types of parasite molecules that stimulate the APO have not been identified, and substances known to activate vertebrate immunocytes have no discernable effect on the APO of NIH albino snails. However, the APOs of Salvador snails respond vigorously to injections of crude lipopolysaccharide (LPS) from *Escherichia coli*, and this response is similar to that seen with injections of miracidial FTE. Interestingly, a mitotic response to LPS has not been reported previously in invertebrates. Future efforts will be directed at identifying APO mitogen(s) in crude LPS, as well as elucidating the relationship, if any, between responsiveness to crude LPS and resistance to infection with *S. mansoni*.

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MACROFILARICIDAL DRUG STUDY FOR THE TREATMENT OF HUMAN ONCHOCERCIASIS AND LYMPHATIC FILARIASIS

J. Sakanari, UCSF

The Sandler Center for Drug Discovery at the University of California, San Francisco is a consortium of laboratories that supports discovery and development of new drugs for parasitic diseases that are largely ignored by the pharmaceutical industry. Our research program involves laboratories focused on parasite biochemistry and biology, chemical synthesis, high-throughput screening, genomics and proteomics, drug metabolism and pharmacokinetics, animal models of disease, computer-based drug design, microscopy, and structural biology. In October 2010, the Sandler Center received funding from the Bill & Melinda Gates Foundation to develop macrofilaricides for the treatment of river blindness (*Onchocerca volvulus*) and lymphatic filariasis (*Brugia malayi*). This is a large multi-institutional collaboration with Anacor Pharmaceuticals (Palo Alto, CA), Dr. Sara Lustigman (*Lindsley F. Kimball Research Institute,* NY Blood Center) and Dr. Rahul Singh (Computer Science Dept., San Francisco State Univ.), Dr. John McCall (Trs Labs Inc., Athens, GA), Dr. Andy Moorhead (Filariasis Research Reagent Resource Center, Univ. Georgia, Athens), Dr. Fidelis Cho-Ngwa (Univ. of Buea, Camaroon) and Dr. Daniel Achukwi (Institute for Agricultural Research for Development, Camaroon). The goal of the project is to develop macrofilaricidal drug candidates using Anacor's boron based compounds on the adults of *O. volvulus* and *B. malayi*. Results of this study conducted thus far will be presented at the symposium.

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HYMENOLEPIS AND *TRIBOLIUM* AS A MODEL SYSTEM IN PARASITE ECOLOGY

A.W. Shostak, University of Alberta

The cestode *Hymenolepis diminuta* has been used extensively to study host-parasite interactions in its definitive (rat) and intermediate (insect) hosts. My students and I have been using infections of this cestode in flour beetles *Tribolium confusum* to address behavioral, ecological and evolutionary questions in parasitology for over a decade. There is an extensive literature going back to the 1950s on *Hymenolepis* in its insect hosts. I will argue that while this literature has formed a solid foundation it has not come close to exploiting the potential of this model. The availability of new tools, new questions, and an increasing understanding of host biology recommend this as a model system to address many current problems in parasitology, particularly as researchers begin to cross traditional disciplinary boundaries.

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DAF-16/FOXO TARGET GENE REGULATION DURING EARLY PARASITIC DEVELOPMENT OF HOOKWORMS

X. Gao, **K. Goggin** and **J.M. Hawdon**, The George Washington University Medical Center

The developmentally arrested third stage larva (L3) of hookworms resumes development in response to host-specific signals during infection. Recovery from the analogous arrested dauer stage of *Caenorhabditis elegans* requires insulin/insulin growth factor (IIS) signaling to negatively regulate the forkhead transcription factor DAF-16/FoxO. IIS and DAF-16 are conserved in hookworms, and are postulated to mediate the resumption of development during infection. However, the precise role of DAF-16 in hookworm infection and its downstream effectors are unknown. We used molecular and bioinformatic techniques to identify a group of hookworm DAF-16 target genes. The DNA binding domain of*Ancylostoma caninum* DAF-16 was used to select genomic fragments containing DAF-16 binding elements (DBE) by in vitro genomic selection. The transcript contigs linked to these genomic fragments were identified bioinformatically and defined as candidate direct gene targets of DAF-16. The developmental stage-specific expression patterns of the target genes were examined at 24 hrs, 48 hrs, and 72 hrs post-infection by real-time PCR. Our results show that hookworm DAF-16 is involved in diverse biological processes throughout hookworm development. Further investigation of these target genes will provide insights into the molecular basis by which hookworm DAF-16 regulates its downstream gene network in hookworm infection.

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HOOKWORM TRANSCRIPTION FACTOR DAF-16 WILD-TYPE AND AKT-PHOSPHO-MUTANTS RESTORE DEVELOPMENTAL ARREST IN *C. ELEGANS* MUTANTS

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T. Brodigan and **M. Krause**, LMB, Develomental Biology Section, NIDDK, National Institutes of Health
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The free-living model nematode *Caenorhabtidis elegans* and the parasitic hookworms share a developmental arrested stage, called the dauer stage in *C. elegans* and the infective third-stage larva (L3) in hookworms. One of the key transcription factors that regulate entrance to and exit from developmental arrest is the forkhead transcription factor DAF-16/FoxO. During the dauer stage, DAF-16 is activated and localized in the nucleus. DAF-16 is negatively regulated by phosphorylation by the upstream kinase AKT, which causes DAF-16 to localize out of the nucleus and exit from dauer. DAF-16 is conserved in hookworms, and hypothesized to control recovery from L3 arrest during infection. Lacking reverse genetic techniques for use in hookworms, we used *C. elegans* complementation assays to investigate the function of *Ancylostoma caninum* DAF-16 during entrance and exit from L3 developmental arrest. We performed dauer switching assays and observed the restoration of the dauer phenotype when *Ac*-DAF-16 was expressed in temperature-sensitive dauer defective *C. elegans* mutants. AKT phosphorylation site mutants of *Ac*-DAF-16 were also able to restore the dauer phenotype, but surprisingly allowed dauer exit when temperatures were lowered. We used fluorescence microscopy to localize DAF-16 during dauer and exit from dauer in *C. elegans* DAF-16 mutant worms expressing *Ac*-DAF-16, and found that DAF-16 exited the nucleus during dauer exit. Surprisingly, *Ac*-DAF-16 with mutated AKT phosphorylation sites also exited the nucleus during dauer exit. Our results suggest that another mechanism may regulate DAF-16 nuclear localization during recovery from developmental arrest.

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STRONGYLOIDES STERCORALIS AGE-1: A POTENTIAL REGULATOR OF INFECTIVE LARVAE DEVELOPMENT

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Infective third-stage larvae (L3i) of the human parasite *Strongyloides stercoralis* share many morphological, developmental, and behavioral similarities with *Caenorhabditis elegans* dauer larvae. The 'dauer hypothesis' predicts that the same molecular genetic mechanisms control dauer larval development in *C. elegans* and L3i morphogenesis in *S. stercoralis*. In *C. elegans*, the phosphotidylinositol-3 kinase (PI3K) catalytic subunit AGE-1 functions in the insulin-like signaling (ILS) pathway to regulate dauer larvae formation. Here we report the identification and characterization of *Ss-age-1*, the *S. stercoralis* ortholog of the gene encoding *C. elegans* AGE-1. Analysis of both a 7.2 kb genomic region sequenced by inverse PCR as well as 5' and 3' RACE products from *Ss-age-1* revealed three exons encoding a predicted protein of 1,209 amino acids. FASTA analysis revealed considerable similarity with *C. elegans* AGE-1, including an overall 31% identity and 61% similarity, in addition to conservation of the five PI3K domains. Phylogenetic comparison with other PI3Ks confirmed evolutionary relatedness to PI3Ks from other nematodes. Temporal patterns of expression were examined by RT-qPCR, and *Ss-age-1* transcripts were distinctly up-regulated in the L3i stage of the *S. stercoralis* life-cycle. Spatial patterns

of *Ss-age-1* expression were inferred from observations of post free-living *S. stercoralis* larvae transformed with a construct fusing the *Ss-age1* promoter to the *gfp* coding sequence. These observations revealed strong expression in the anterior intestine, an important site of ILS in *C. elegans*. Application of the PI3K inhibitor LY294002 to post-parasitic first-stage larvae inhibited their development in dose-dependent fashion. These results suggest a crucial developmental function for *S. stercoralis* AGE-1. Studies are currently in progress to determine whether *Ss-age-1* functions as a PI3K in the genetic surrogate *C. elegans*. Together, these data support the hypothesis that *Ss-age-1* regulates the development of *S. stercoralis* via an ILS pathway similar to that of *C. elegans*.

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MOLECULAR AND FUNCTIONAL CHARACTERIZATION OF A UNIQUE DEVELOPMENTALLY EXPRESSED SECRETORY INVERTASE FROM *LEISHMANIA MEXICANA*

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All *Leishmania* are transmitted by phlebotomine sand flies. Within these vector hosts, *Leishmania* parasites multiply and move anteriorly in the digestive tract. During this migration these parasites must obtain host derived nutrients/energy sources to survive and multiply. Sand flies characteristically imbibe plant sugars, including sucrose and other polysaccharides, and store these sugars in their crop. Between blood meal feeds they regurgitate such sugars into their anterior mid-gut. In that regard, recently, we found that *L. mexicana* promastigotes (Pro) secrete/release an invertase/sucrase activity into their culture supernatants during their growth *in vitro*. In contrast, *L. mex* axenic amastigotes (AxAm) do not release any detectable invertase activity. To characterize this invertase activity further, we adopted a molecular approach. Using PCR methods, we identified a gene which encodes a putative *L. mex* invertase (LmxM04.0310; *LmxINV*). Results of RT-PCR demonstrated that mRNA for LmxINV was expressed only by *L. mex* Pro and was not detected in AxAm. The *LmxINV* encodes a 71.5 kDa protein with conserved β-fructofuranosidase domains and a secretion signal peptide. To characterize this enzyme further, we designed two expression constructs containing a C-terminal hemagglutinin tag (*LmxINV:HA*). One of these was ligated into the leishmanial episomal expression vector pKSNEO and the second was ligated into the ribosomal locus-targeted leishamanial expression vector pF4X1.4hyg. Following electroportation, *L. mex* transfectants were selected for growth in increasing concentrations of either G418 or Hygromycin. Results of enzyme assays demonstrated that both transfectants expressed more than 100 fold higher levels of secreted invertase activity than vector-match controls. Such activity was readily immuno-precipitated with anti-HA monoclonal antibody beads. Western blots of such immuno-precipitates showed only a single ~72 kDa band of LmxINV:HA protein. Such transfectants will now allow us to examine the role of LmxINV in the developmental biology of this human pathogen.

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INVOLVEMENT OF THE *LEISHMANIA DONOVANI* VIRULENCE FACTOR A2 IN THE PARASITE STRESS RESPONSE: PROTECTION AGAINST HEAT SHOCK AND OXIDATIVE STRESS

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G. Matlashewski, McGill University, World Health Organization

Leishmaniasis is associated with a broad variety of clinical manifestations, from fatal visceral disease to self-healing cutaneous lesions. A2 proteins are expressed by visceral *Leishmania donovani* but not by cutaneous *Leishmania major,* and A2 has been shown to play a role in visceral infection: *L. donovani* parasites with knocked down A2 expression display decreased virulence. Conversely, introducing A2 into *L. major* increases *L. major* survival in the visceral organs. Here, we examine the molecular basis of these observations, focusing on the involvement of A2 in the *Leishmania* stress response. A2 is expressed in the amastigote stage of *L. donovani,* but it can also be induced in promastigotes by several stress signals, including heat-shock, ethanol and misfolded protein stress. *L. major* promastigotes ectopically expressing A2 survive heat-shock significantly better than control-transfected *L. major*. Conversely, *L. donovani* promastigotes with decreased A2 expression are more sensitive to heat shock than control-transfected cells. A2-deficient *L. donovani* axenic amastigotes are also more sensitive to reactive oxygen and nitrogen species, exhibiting increased internal oxidant levels and decreased survival following treatment with hydrogen peroxide or with a nitric oxide donor, SNAP. These effects are enhanced under heat shock conditions. Finally, A2 is localized to the endoplasmic reticulum (ER) both during macrophage infection and in heat-shocked promastigotes, where it interacts with the ER chaperone BiP but not with other ER-localized proteins, including the chaperone LPG3 or the classically-secreted gp63 and secreted acid phosphatase. These results suggest that A2 may play a role in the parasite stress response and help *L. donovani* survive host defence mechanisms, in particular oxidants and fever. Our results therefore provide valuable insight into the mechanisms of *L. donovani* virulence and into the *L. major-L. donovani* dichotomy.

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HOW DO HABITAT FEATURES AFFECT PARASITE POPULATION CONNECTIVITY?

I. Blasco-Costa, **J.M. Waters** and **R. Poulin**, Department of Zoology, University of Otago.

Gene flow among populations maintains the integrity of a species across its geographical range. To a large extent, the population connectivity of parasite species depends on the mobility or dispersal abilities of their hosts, as well as on landscape features such as the presence of barriers to dispersal. In rivers, for instance, the strong unidirectional dispersal of organisms driven by the current (from upstream to downstream) may only be partially countered by active re-colonization of upstream sites. Using a comparative approach we investigated whether the genetic diversity of parasite populations decreases from downstream to upstream sites. We sampled a native New Zealand fish and collected its trematode species at multiple sites along the 70km long Manuherikia River. We used the mitochondrial cytochrome c oxidase subunit I gene as marker and ran regression analyses between genetic diversity and distance from the river mouth to test our predictions. In addition, we determined the individuals with immigrant ancestry in the context of source-sink directed gene flow along the river course. Our results show a negative correlation between the distance from the river mouth and both haplotype and nucleotide diversity. Fst pairwise comparisons showed upstream sites to be significantly distinct from those downstream. Also, the number of immigrants from downstream to upstream sites was low. In conclusion, there exists a strong effect of unidirectional water flow on the connectivity among parasite populations along the river.

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IDENTIFICATION AND CHARACTERIZATION OF *DIROFILARIA IMMITIS* MICROFIALRIAL CHITINASE

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Dirofilaria immitis is a parasitic filarial roundworm, also referred to as "heartworm", responsible for heartworm disease predominantly in dogs, which is its definitive host. Transmission occurs when a mosquito bites an infected dog, ingesting microfilariae (L1), which undergo a series of molts to the infective third larval stage (L3) and then migrate to the salivary glands of the mosquito, where they wait to infect another host. Heartworms go through several life stages before they become adults infecting the heart of the host animal. Approximately 6.5 to 7 months after infection, the adult worms have mated and the females begin giving birth to microfilariae which can circulate in the bloodstream for as long as two years, waiting for the next stage in their life cycle in the gut of a bloodsucking mosquito. It has been previously reported that chitinase is thought to be important in the exsheathment process of microfilaria of another filarial species, *Brugia malayi*. Exsheathment is required for further development of the microfilaria once ingested by the mosquito vector. In addition, antisera against chitinase was shown to temporarily clear the microfilaria from the bloodstream of infected jirds, suggesting that chitinase may serve as an attractive target for a transmission blocking vaccine strategy. Up till now, no representatives of the chitinase family could be detected in heartworm microfilaria. However, our laboratory recently identified a 1,446 bp DNA sequence encoding for a 481 amino acid chtinase isozyme from *D. immits* microfilaria, with a predicted weight of 54 kDa and pI of 6.77. *D. immitis* chitinase exhibits 82% DNA and 78% amino acid sequence identity with *B. malayi* chitinase (BmCHT1). Sera obtained from naturally *D. immitis* infected dogs reacted positively against recombinant *D. immitis* chitinase on a Western Blot indicating that *D. immitis* chitinase might be a potential target for developing a transmission blocking vaccine strategy against canine heartworm.

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MICRORNAS IN *LEISHMANIA BRAZILIENSIS*

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

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FORWARD GENETICS AS A TOOL TO MAP OXAMNIQUINE RESISTANCE IN *SCHISTOSOMA MANSONI*

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Schistosomes show heritable variation in biomedically important traits such as drug resistance, host specificity, and virulence. Our central aim is to develop forward genetic methods (i.e. linkage mapping) to identify parasite genes that underlie this phenotypic variation. This approach is well suited to *S. mansoni* as the lifecycle can be maintained in the laboratory and clonal propagation of parasites within snails generates large numbers of genetically identical parasites. To demonstrate that this approach is feasible and powerful, we have mapped a genome region that underlies resistance to oxamniquine (OXA). Resistance to OXA has arisen in nature, has a simple recessive basis and results in ~500-fold reduction in drug sensitivity. We crossed resistant and sensitive parasites (parents) and then crossed two F1 individuals to generate multiple F2 progeny, at each stage isolating individual parasite genotypes by infecting snails with single miracidia. We measured OXA-resistance by monitoring death of cultured worms following drug exposure and genotyped parents, F1 and F2 progeny using 64 microsatellite markers distributed at ~20cM intervals across the genome. As expected trait segregation in the cross was consistent with recessive inheritance as F1s were sensitive and ~25% of F2 progeny were resistant. We used the *S. mansoni* linkage map developed by our group to locate quantitative trait loci (QTL) underlying OXA resistance. We found a strong QTL (LOD = 13.5) on the p arm of chromosome 6 where microsatellite markers segregate closely with OXA resistance. By refining the map with microsatellite markers to a 23 Mb supercontig that contains the QTL, we mapped the gene to a 1.5 Mb region with a LOD score of 22. The two parents and F1s of this cross have now been sequenced, simplifying fine mapping, identification of candidate genes and the development of a SNP map. Successful identification of gene(s) that underlie OXA-resistance will provide insights into mode of drug action, allow development of modified compounds that kill resistant parasites and set the stage for forward genetic analyses of a range of biomedically important traits including praziquantel resistance.

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ASSESSING FITNESS CONSEQUENCES OF RESISTANCE ALLELES AT CU/ZN SUPEROXIDE DISMUTASE (SOD1) IN THE *S. MANSONI/B. GLABRATA* MODEL PARASITE SYSTEM

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Schistosomiasis is responsible for approximately 200,000 deaths yearly and 200 million infections worldwide. Examination of the fitness consequences of carrying resistance genes is essential for understanding how resistance to parasites is maintained in vector populations. Allelic variation at Cu/Zn superoxide dismutase (SOD1) in the snail intermediate host, *Biomphalaria glabrata*, has been previously implicated in resistance to the trematode, *Schistosoma mansoni*. The B allele of SOD1, designated by SNPs and indels within the 4th intron, conferred resistance and was associated with increased SOD1 expression in the 13-16-R laboratory strain. This study compared fitness consequences of carrying the B allele of SOD1 with carrying the C allele, which correlates with susceptibility. Three families were generated to compare the fitness effects of carrying the B or C allele within a single genetic background and among different genetic backgrounds. The experimental design enabled us to compare fitness of siblings with different SOD1 genotypes (within a single genetic background) and to compare fitness of

individuals with the same SOD1 genotype from different families (across different genetic backgrounds). The three families were each segregating for the B and C alleles, but varied in overall parasite resistance (80%, 65%, and 40% resistance) owing to unknown loci other than SOD1. We challenged these families with *S. mansoni*, and found a strong interaction effect between genetic background and SOD1 genotype on resistance. The B allele was strongly protective in the most resistant genetic background ($p<0.05$), but negligibly so in the least resistant genetic background. The results of this study also suggest a possible fitness cost associated with egg production and carrying the B allele, while no cost was found when examining growth. Understanding the genetic mechanisms governing resistance and how resistance is maintained in vector populations will be essential for the eventual development of resistant vectors as a means of eradicating vector-borne diseases.

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MOLECULAR CHARACTERIZATION OF *HISTOMONAS MELEAGRIDIS*

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Histomonas meleagridis is the causative agent of histomoniasis, also known as Blackhead disease. Extracted DNA from twenty-eight *H.meleagridis*-infected avian tissue samples from multiple hosts and geographic locations was analyzed for variation in 5.8S rRNA and flanking internal transcribed spacer regions (ITS 1 and ITS 2). Samples were amplified by polymerase chain reaction (PCR), sequenced, and compared with known sequences from GenBank accessions of *H. meleagridis* and other related protozoa. The analyses revealed significant genetic variation within *H. meleagridis* sequences and suggested the possibility of multiple genotypes within the samples or possible misdiagnosis. A phylogenetic analysis using only the 5.8S rRNA sequence grouped all but one *H. meleagridis* sample into one clade, including GenBank accessions submitted from Europe. This analysis suggests that the 5.8S region is a reliable in identifying *H. meleagridis*. To identify sequence components required for the regulation of gene expression in *H. meleagridis* the splinkerette PCR method for the isolation of flanking genomic DNA was modified to identify the entire beta tubulin gene, including promoter and polyadenylation signal sequences. Identification of these DNA elements can be used to design an expression vector system specific for *H. meleagridis* and demonstrates the use of splinkerette PCR to identify upstream and down stream sequences surrounding partial known genes in organisms that lack a sequenced genome.

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IDENTIFICATION OF MAEBL, AN ERYTHROCYTE BINDING PROTEIN, IN *PLASMODIUM GALLINACEUM*

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Malaria is caused by species of *Plasmodium* blood parasites, is found worldwide, and affects many organisms including humans, chimpanzees, reptiles and birds. The extinction of several avian populations in the Hawaiian Islands was due to a newly introduced *Plasmodium* strain that was capable of infecting multiple bird species (a generalist parasite). Host-specific parasites (specialists) can infect only one species. Previous work has shown that specialists may become generalists in host switching events, with associated higher virulence. The molecular basis of host specificity in avian *Plasmodium* parasites is largely unstudied, but our project aims at identifying genes responsible for host specificity. Previous data has implicated the erythrocyte binding-like (*ebl)* genes in human and chimpanzee *Plasmodium* strains as potential host-specific determinants. We have been able to identify at least one ebl gene, MAEBL (merozoite-adthesive erythrocyte-binding ligand), using BLAST analysis and Apollo, a genome annotation tool. We have also been able to identify portions of the MAEBL gene in *Plamodium relictum* and are in the process of testing for MAEBL in *Plasmodium* strains infecting African rainforest birds by using PCR. We will sequence the genes and analyze their DNA and amino acid sequences to

determine whether sequence variability correlates with host specificity. We will also map the distribution of *ebl* gene alleles of African rainforest birds. We expect to identify the *ebl* family of genes in avian malaria and correlate them to host-specificity. The identification of *ebl* genes in avian parasites characterized in this study will allow us to predict potential emerging diseases in avian populations. Predicting potential host-switching events could allow us to slow down the spread of malaria.

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(73)

DESIGNING AND MINING DATABASES: FROM GENES TO DRUGS AND VACCINES

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Biomedical research is increasingly dominated by large-scale datasets: vast quantities of genome sequences and RNA/protein expression results, genetic polymorphisms and epidemiological data, information on protein structure and interactions, metabolic pathways, mutant and clinical phenotypes, *etc*. Parasite 'Omics data is further complicated by the interplay between pathogen, host, and vector species. *Help!!!* How can we effectively collect, store, maintain, integrate, and mine these datasets, so as to advance biological understanding and define targets for investigation in the lab, field and clinic? The Eukaryotic Pathogen Genome Database (http://EuPathDB.org) provides researchers working on a variety of parasites (and other eukaryotic microbes) with convenient access to diverse genomic-scale datasets, facilitating analysis and prioritization of candidates for more detailed study. In addition to providing gene- and genome-centric views, and a forum for capturing expert annotation from the community, a graphical user interface simplifies the formulation and optimization of complex queries. For example, researchers seeking to identify factors likely to modulate host cell interaction might wish to search for parasite genes that are expressed during appropriate life cycle stage(s), secreted from the parasite, harbor domains suggesting interaction with host cell proteins, and exhibit signatures of evolutionary selection. Such queries support systems-level analysis of biologically and clinically relevant problems, and can be shared with colleagues or stored for future review, refinement, or modification. Various queries as will be illustrated using live, on-line demonstrations.

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(74)

GENETIC DISSECTION OF APICOPLAST FUNCTION AND BIOGENESIS

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Apicomplexan parasites are a major threat to human health causing malaria and a variety of AIDS associated opportunistic infections. One of the most promising targets for chemotherapeutic intervention for this group of pathogens is the apicoplast. The apicoplast is a unique parasite organelle that was derived from a red algal endosymbiont. Genomic analyses suggest that the apicoplast is engaged in a variety of anabolic pathways that could be targeted for drug development. Using *Toxoplasma* as a genetic model organism we are dissecting the apicoplast metabolism to identify the most effective choke points. Taking a broader biological view we are interested to understand which of the endosymbiont's functions is most critical and the reason for the continued presence of a plastid long after the loss of photosynthesis. Genetic approaches have also been highly informative to understand the cell biology of this endosymbiotic realationship and we will discuss recent advances.

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THE ROLE OF TRANSLATIONAL REGULATION IN SEXUAL DEVELOPMENT OF MALARIA PARASITE

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Sexual development occupies a central role in the life cycle of the malaria parasite, *Plasmodium falciparum*. Although gametocytes are not directly associated with clinical symptoms, they are responsible for the continued transmission of the parasite through mosquito vectors. In gametocytes, there are a number of genes whose transcripts are stored but not translated into protein until in the subsequent developmental stages. In order to determine the mechanism involved in the regulation of these genes, we have studied the functions of two Puf family translational repressor proteins PfPuf1 and PfPuf2 in gametocytogenesis of *P. falciparum*. Both proteins are expressed preferentially in gametocytes. Genetic knockout of PfPuf1 led to a significant reduction in the number of gametocytes, whereas PfPuf2 disruption resulted in enhanced ability to form gametocytes. Interestingly, PfPuf2 also repressed the formation of male gametocytes and its disruption promoted the formation of male gametocytes. It seems that in the regulation of sexual development in the malaria parasite, PfPuf1 controls the switch of gametocytogenesis, whereas PfPuf2 controls the switch of sex differentiation.

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CONSTRUCTION OF TRANSGENIC *EIMERIA* PARASITES AND STUDY OF THEIR ELICITATION OF MUCOSAL IMMUNITY

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There is a developing consensus that the next generation of promising animal vaccines will be live vector vaccines. While live viral and bacterial vectors have been extensively investigated as potential vaccine delivery systems, we propose that the eukaryotic protozoa *Eimeria* will be promising vaccine vector candidates which can be given orally with a single dose and simultaneously deliver multi-antigens. *Eimeria* parasites belong to the Phylum Apicomplexa together with*Toxoplasma*, *Plasmodium*, and *Cryptosporidium*. *Eimeria* spp. are intracellular protozoa that develop within host epithelial cells, causing coccidiosis of significantly economic importance in the poultry and livestock industries. Fortunately, live attenuated vaccines have long been used for the successful control of coccidiosis in chickens and now also in turkeys. We are endeavoring to develop transgenic attenuated *Eimeria* vaccine strains as a multi-antigen delivery system, through the establishment of a stable transfection platform, studies of immune responses and the mechanisms of protective immunity, and evaluation of the safety using transgenic *Eimeria* as a vaccine vector. In this study we aim to detect mucosal immune responses elicited by transgenic lines which express antigens derived from avian influenza virus in a stage-specific pattern and different localization by the usage of different promoters and signal peptides. We found some transgenic lines of *Eimeria*parasites were attenuated but as expected maintained their immune-protection against *Eimeria* infection. Immunological studies, by the use of ELISA, RT-PCR, ELISPOT and intracellular staining, showed that the same foreign antigen targeted to different compartments in *Eimeria* parasites elicited different levels and/or types of mucosal immunity. Chicken performance trial revealed that immunization with transgenic lines is still an alternative to the use of anticoccidial drugs in term of body weight gain, feed conversion ratio and livability. Findings so far are encouraging our effort to develop transgenic *Eimeria* as a promising antigen delivery system for stimulating at least mucosal immunity. The studies are supported by the National Natural Science Foundation of China (Project

numbers: 30871862, 30671579 and 30471298), the National High Technology Research and Development Program of China (2006AA02Z458), and Chinese Universities Scientific Fund (2009-2-02).

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CRYPTOSPORIDIUM: UNIQUE EVOLUTIONARY POSITION AND METABOLIC FEATURES FOR DRUG DEVELOPMENT

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The *Cryptosporidium* lineage is taxonomically placed under the Suborder Eimeriorina as a Family Cryptosporidiidae that is a sister to the intestinal and cyst-forming coccidia (i.e., Eimeriidae and Sarcosytidae). However, recent molecular evidence suggests that *Cryptosporidium* is in fact a sister lineage to all other apicomplexans. More recently, our genome sequence survey (GSS) data have shown an evolutionary affinity, but metabolic divergence between *Cryptosporidium* and a gregarine at the base of the Apicomplexa. Indeed, *Cryptosporidium* has a number of unique metabolic features that may be explored as potential drug targets. Our laboratory has been working on the molecular and biochemical characterization of a number of enzymes within the energy and fatty acid metabolism, such as lactate dehydrogenase (**LDH**) and alcohol dehydrogenase (**ADH**) in the glycolytic pathway, the type I fatty acid synthase (**FAS**), fatty acid elongase (**ELO**) and fatty acyl-CoA synthetase (**ACS**) in the lipid metabolism. Some of these enzymes have shown to be potential drug targets based on the efficacies of their inhibitors on the growth of *C. parvum* in vitro and in vivo.

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THE AMERICAN SOCIETY OF PARASITOLOGISTS: WHO ARE WE NOW?

ASP PRESIDENTIAL ADDRESS

J. Caira, The University of Connecticut

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COMPLEX INTERACTIONS AMONG A NEMATODE PARASITE (*DAUBAYLIA POTOMACA*), A COMMENSALISTIC ANNELID (*CHAETOGASTER LIMNAEI LIMNAEI*), AND TREMATODE PARASITES IN A SNAIL HOST (*HELISOMA ANCEPS*)

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

Many biotic interactions affect the prevalence and intensity of parasite infections in aquatic snails. Historically, these studies have centered on interactions between trematode parasites or between trematodes and other organisms. The present study focuses on the nematode parasite *Daubaylia potomaca* and its interactions with a commensal, *Chaetogaster limnaei limnae*i, and a variety of trematode species. It was found that the presence of *C. l. limnaei* indirectly increased the mean intensity of *D. potomaca* infections, apparently by acting as a restraint for various trematode parasites, particularly the rediae of *Echinostoma* sp. In turn, *Echinostoma* sp. rediae adversely affected the mean intensity of *D. potomaca*, presumably by their consumption of both juvenile and adult nematodes present in the tissue of

the snail. These organisms not only belong to 3 different phyla, but occupy distinct trophic levels as well. The complex interactions among these 3 organisms in the snail host provide an excellent example of biotic interactions influencing the infection dynamics of parasites in aquatic snails.

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WHEN A TREMATODE SKIPS A HOST: PROGENESIS AS AN ALTERNATIVE LIFE CYCLE STRATEGY

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Most trematodes have a typical three-host life cycle, with sexual reproduction taking place in the vertebrate definitive host. However, selective pressures imposed by a series of improbable transmission events have resulted in some species adopting a shortened life cycle. Facultative truncation of the life cycle can occur via progenesis, i.e precocious maturation in the second-intermediate host. Eggs are then produced through self-fertilization within the metacercarial cyst. Whether the three-host or progenetic life cycle strategy is taken may be a conditional response to different ecological factors related to the probability of transmission to the definitive host. Thus cues associated with life span and density of the second-intermediate host and presence of the definitive host may trigger one of these strategies. Our research investigated how environmental cues influence progenesis in *Stegodexamene anguillae* (Trematoda: Lepocreadiidae). Eels (*Anguilla* spp.) serve as the definitive host, while numerous small fish species are used as second-intermediate hosts by this parasite. We present results from both laboratory and field studies using *Gobiomorphus cotidianus*, common bully, as the second-intermediate host. The results show that cues from hosts under stressful conditions and encystment site within the host may signal transmission opportunities to the parasite so that it may adjust its developmental strategy accordingly. However, presence or abundance of the definitive eel host does not seem to affect the frequency of progenesis in *S. anguillae*. This study is the first to compare life cycle strategies among parasite populations and provide insight into the real plasticity of life cycle abbreviation in nature. These findings highlight the often unrecognised plasticity in parasite developmental and transmission strategies.

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THE IMPACTS OF URBAN WETLANDS ON MOSQUITO POPULATION DYNAMICS AND DISEASE RISK FOR WEST NILE VIRUS

B. Johnson and **M. Sukhdeo**, Department of Ecology and Evolution, Rutgers University

The natural history of urban associated vector-borne diseases like West Nile virus (WNV) becomes increasingly important when over half of the worlds population lives within urban environments. Often overlooked in the surveillance of mosquito-borne diseases are the effects of urban green-spaces on the epidemiology of disease in urban landscapes, especially natural or constructed urban wetlands. Urban wetlands are significant since they bring ornithophilic mosquitoes, migratory birds, and humans in close contact with one another, and this triad can escalate disease risk in these areas. The mosquito communities in these areas also play significant roles in human disease risk as disease vectors move out into the surrounding residential environments. We evaluated mosquito communities over short urban transects at six urban wetlands located in Middlesex and Union counties in New Jersey. Wetland sites had higher measures of diversity, species richness, abundances of mosquitoes, and lower community vector competence values for WNV compared to residential sites. In addition, the highest relative proportions of competent WNV vectors, like *Culex spp.* mosquitoes (*Culex pipiens, Culex restuans*), occurred in residential sites. This gave residential sites higher community competence values for WNV, and consequently, higher measures of disease risk for WNV than urban wetland sites. This finding challenges previous interpretations on the role of urban wetlands in WNV transmission.

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PATTERNS IN THE DISTRIBUTION OF PARASITE BIOMASS IN A RIVERINE FOOD WEB

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The architecture of ecological communities is constrained by fundamental energetic laws. These typically produce pyramidal patterns of trophic biomass, with autotrophs at the base and top predators at the top of the pyramid. Since parasite life cycles are embedded in free-living communities, patterns in parasite distributions should also reflect the energetic constraints acting on the community at large. To examine these patterns, we surveyed a riverine community (Raritan River, NJ) from July of 2009-Spring 2011. On a bimonthly basis, we collected data on the diversity and biomass of bacteria, protozoans, meiofauna, benthic macroinvertebrates, fishes, amphibians, turtles, birds and their respective parasites. Initial analyses revealed that parasite biomass forms a sub-pyramid which mirrors the shape of the free-living pyramid. Converting these data into a highly resolved riverine food web, we consider several mechanisms that might decouple free-living and parasite pyramids. A discrete time dynamic model was used described our food web in terms of energy (biomass) fluxes between linked species, and to determine the oscillation magnitude (dynamism) and the extinction risk for host and non-host species. Our findings support the idea that parasites are not randomly distributed in food webs, but that they exploit species with asymmetric predator-prey interactions, species that are relatively more abundant (by trophic level) and species that are more evolutionarily stable. These factors might act to buffer parasites from variations in the dynamics of energy flow and food web topology.

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WATERBORNE PROTOZOAL REMOVAL BY COASTAL CALIFORNIA WETLANDS

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Fecal pathogen contamination of the near-coastal aquatic ecosystem poses a risk to the health of humans and animals utilizing these resources along the coast. Waterborne zoonotic protozoa including *Cryptosporidium parvum, Giardia lamblia*, and *Toxoplasma gondii* are of particular concern. These parasites can be transported from inland sources of contamination, such as agricultural runoff from livestock operations and storm runoff containing feces of domestic and wild animals, through wetlands to the coast where humans and animals may come in contact with these pathogens. Coastal wetlands play a large role in removal of contaminants from the water, yet anthropogenic activities have decreased the range and extent of these wetlands throughout the United States. Levels of *C. parvum* and *G. lamblia* in wetlands along the central California coast were monitored for over two years. These results indicate that distance from a point source of parasite contamination and rainfall events affect the parasite load recovered from a wetland. To further understand wetland characteristics affecting transport of these parasites, we used re-circulating mesocosm tanks as a model for wetlands, allowing for evaluation of the effect salinity, flow rate, and vegetation parameters have on protozoa removal rates. The mesocosm tank results showed that the presence of vegetation was associated with increased removal of fecal protozoal oocysts from the water when compared to tanks with no vegetation at both fast and slow water flow rates. The important role of vegetation in removal of waterborne protozoa should be considered in wetland reconstruction and management decisions for coastal ecosystems.

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SOCIALITY DRIVES EXPERIMENTAL EPIDEMICS IN GUPPIES

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Infection incidence increases with the average number of contacts between susceptible and infected individuals. Contact rates are normally assumed to increase linearly with host density. However, social species seek out each other at low density and saturate their contact rates at high densities. Although predicting epidemic behaviour requires knowing how contact rates scale with host density, few empirical studies have investigated the effect of host density. Also, most theory assumes hosts have equal chances to transmit parasites, even though individual parasite load can vary. Here, we examine epidemics using a common ectoparasite, *Gyrodactylus turnbulli* infecting its guppy host (*Poecilia reticulata*). Hosts were maintained at different densities (3, 6, 12 and 24 fish in 40L aquaria), and we monitored gyrodactylids both at a population and individual host level. Although parasite population size increased with host density, the probability of an epidemic did not. Epidemics were more likely when the carrier fish had a high mean intensity and duration of infection. Female guppies contracted infections sooner than males, probably because females have a higher propensity for shoaling. These findings suggest that in social hosts like guppies, the frequency of social contact largely governs disease epidemics independent of host density.

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HELMINTH COMMUNITY STRUCTURE IN THREE SPECIES OF COLUMBIDS THAT CO-OCCUR IN EAST TEXAS

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Thirty Rock Pigeons (*Columba livia*), 30 Mourning Doves (*Zenaida macroura*), and 28 Eurasian Collared-doves (*Streptopelia decaocto*) were collected by shooting or bait trapping from east Texas populations in the summer of 2010 and examined for helminths. Two of these columbid species, the Rock Pigeon and Eurasian Collared-dove, were introduced to North America ca. 1600 and 1972 respectively. This study is the first to examine the helminth communities of these three columbids in this geographic region and investigates the effects of exotic hosts and their parasites on native host species and evaluates differences in helminth community structure among columbids with different behavioral, spatial, and temporal habits. These species are confamilials but utilize different ecological habitats. Preliminary results indicate a host infection rate and intensity of infection of (6.6%, 1.5), (57%, 4.8), and (80%, 24.4) for Mourning Doves, Eurasian Collared-doves, and Rock Doves respectively. A total of 667 helminths were recovered including 374 nematodes, 129 cestodes, and 164 trematodes.

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SAFETY IN NUMBERS: SHOALING AS AN ANTI-PARASITE DEFENSE IN FATHEAD MINNOWS EXPOSED TO TREMATODE CERCARIAE

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B.D. Wisenden, Minnesota State Univesity Moorhead

Foraging success and predator avoidance are well-documented benefits associated with group living. Evidence that group living confers protection from parasites comes from studies involving ungulates exposed to biting flies. Whether or not similar benefits accrue to aquatic animals exposed to infective stages of parasites has rarely been evaluated. We tested the anti-parasite benefits of shoaling in fathead minnows exposed to cercariae of their two most common species of trematode (*Ornithodiplostomum ptychocheilus* and *Posthodiplostomum minimum*). In a lab experiment, we evaluated school cohesion in groups of 5 minnows exposed to *O. ptychocheilus* cercariae, non-minnow cercariae, and various other biological, chemical and mechanical stimuli. Results demonstrated that school cohesion increased 15-fold more for groups of minnows exposed to minnow cercariae compared to water controls, and differed significantly from all other groups except those exposed to an alarm cue. In a follow-up lab experiment, we showed that minnows confined within screened cages into a central position with no peripheral fish, and then exposed to cercariae, had 3 times the number of metacercariae than those caged with minnows in peripheral locations. Finally, we added infected snails directly into replicated outdoor mesocosms that contained screened containers with one or 5 minnows. In this case, minnows fed and behaved normally for a 5-day period of cercarial exposure. Results demonstrated that metacercariae intensity was significantly higher (3-fold) in the single containers. Overall, these results indicate that minnows detect and distinguish various threats present within the water column, and respond via a generalized shoaling response. Further, living in a shoal, particularly in its centre, reduces risk of exposure to cercariae.

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RESISTANCE TO TREMATODE PARASITES CARRIES A DEVELOPMENTAL COST IN ANURAN TADPOLES

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Anuran tadpoles frequently exhibit behavioral resistance to trematode cercariae, in which vigorous bursts of swimming prevent infection. Little is known about how this anti-parasite behavior varies across host species or whether it carries a usage cost, as do many mechanisms of immunological resistance. We hypothesized that behavioral resistance 1) is exhibited more strongly by rapidly-developing than slowly-developing tadpole species, and 2) carries a cost to the host in the form of slowed growth. To test these hypotheses, we compared investment in behavioral and immunological resistance, as well as mass change, among seven anuran species that differ considerably in their rates of development (from fast to slow: *Scaphiopus holbrookii, Osteopilus septentrionalis, Gastrophryne carolinensis, Pseudacris* sp., *Hyla femoralis, Hyla gratiosa,* and *Rana catesbeiana*). Tadpoles were benzocaine-anesthetized to experimentally remove behavioral resistance or un-anesthetized (control) and then were exposed to a range of 0-30 plagiorchiid cercariae for 10 minutes. Rapidly-developing species demonstrated a significantly higher rate of anti-parasite behavior than slowly-developing species. However, slowly-developing species were better at maintaining mass post-exposure, thereby demonstrating a reduced cost of parasite exposure. Strikingly, these differences were observed across all seven host species, despite only three species (*O. septentrionalis, H. femoralis,* and *H. gratiosa*) being successfully infected by trematodes after the 10 minute exposure. This pattern may indicate that resistance to cercariae during and after

exposure, not the parasites themselves, comprise the major costs of parasite exposure in this host-parasite system.

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USING TROPHICALLY TRANSMITTED PARASITES TO ESTABLISH LINKS BETWEEN PACIFIC SALMON AND VARIABILITY IN OCEAN CONDITIONS

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K.C. Jacobson, NOAA/NMFS

Trophically transmitted parasites have been used to help clarify food web processes of their host. Currently, we are examining the macroparasite communities of Chinook salmon (*Oncorhynchus tshawytscha*) and coho salmon (*O. kisutch*) in the Northern California Current to better understand how interannual variability in food web processes affects salmonids as they enter and move through the Northern California Current. Salmon in this study were caught off the Oregon and Washington coast during a 10-year period (2000 to 2010) of variable ocean conditions, measured through the Pacific Decadal Oscillation(PDO). A total of 9 marine-origin macroparasite species were recovered from the stomachs, intestines and body cavities of 920 juvenile salmon. The acanthocephalan, *Rhadinorhynchus trachuri* and a tetraphyllid cestode were more abundant in "warm" ocean years (positive PDO) associated with subtropical copepod communites and poor salmon returns while *Anisakis simplex* and *Lecithaster gibbosus* were more abundant in "cold" ocean years (negative PDO) associated with lipid rich, neritic copepod species and favorable salmon survival. These findings suggest interannual variability in salmon trophic interactions associated with ocean processes.

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SEASONAL AND SPATIAL DISTRIBUTIONS OF AN INVASIVE SNAIL (*BITHYNIA TENTACULATA*) AND ITS PARASITIC HITCHHIKERS IN THE UPPER MISSISSIPPI RIVER NATIONAL WILDLIFE AND FISH REFUGE (UMRWFR)

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J. Nissen, United States Fish and Wildlife Service

Bithynia tentaculata is an invasive aquatic snail that first appeared in the Upper Mississippi National Wildlife and Fish Refuge (UMNWFR) in 2002. Since that time the species has become a major concern in the region because it harbors a number of trematode species that cause large annual waterfowl die-offs when birds consume infected snails. Although *B. tentaculata* and its parasites are having significant biotic and economic impacts in the region, little is known about the spatial and temporal distribution of these snails and their trematodes in the UMNWFR. The objective of this study was to investigate *B. tentaculata* densities and the intensities of its parasites at offshore sites at three time points: prior to fall bird migration, during migration, and after migration (iceon). Three replicate samples were taken using a ponar grab at each of 10 sites prior to and during migration; a single replicate was acquired per site during the winter. Snails were enumerated per sample and then necropsied to assess infection. Results suggest that substrate shifts, vegetation presence and water velocity are important for predicting snail densities across sites and time points. In terms of parasitism, both primary (rediae/cercariae) and secondary (metacercariae) infections decreased during the year, which could be attributed to mortality of older, infected snails and/or predation of larger snails by migrating waterfowl. The ecological implications of these results will be discussed.

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A COMMON SCALING RULE FOR THE ABUNDANCE AND ENERGETICS OF PARASITIC AND FREE-LIVING SPECIES

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A. Dobson, Princeton University
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The metabolic theory of ecology uses the scaling of metabolism with body-size and temperature to explain variation in species abundance. However, the theory and its empirical tests have never simultaneously examined parasites alongside coexisting free-living species. This is unfortunate because parasites account for at least half of biodiversity. We show that metabolic scaling theory could not account for the abundance of parasitic or free-living species in three estuarine food webs until we included a simple extension. After incorporating trophic dynamics in a way that works for parasitic and free-living species, all species clustered closely around a single allometric relationship, where abundance scaled with body mass to the -¾ power. This result indicates "production equivalence" within trophic-levels, the invariant production of biomass across all body-sizes for all species: invertebrate or vertebrate, ectothermic or endothermic, and parasitic or free-living. Consideration of parasites encouraged the simple, yet general, addition of trophic dynamics to the metabolic theory of ecology that appears to perform well for all species, and may be broadly applicable for any organisms in any ecosystem.

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PARASITE ASSEMBLAGES AND JUVENILE CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) HABITAT USE IN THE COLUMBIA RIVER ESTUARY IN 2004 AND 2005

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The Columbia River and estuary has undergone extensive simplification which has reduced habitat diversity and rearing opportunities for anadromous salmon. We examined community structure of trophically-transmitted parasites in juvenile Chinook salmon (*Oncorhynchus tshawytscha*) collected in the lower Columbia River to better understand salmon habitat use in the estuary. Salmon were collected in May and July of 2004 (n=376) and 2005 (n=476) at 12 sites: four in the marine mixing zone, five from a matrix of freshwater tidal wetlands in the mid-estuary, and three in tidal freshwater areas 53km upstream. Genetic stock of origin for each salmon was determined by identification of microsatellite DNA markers. Differences in parasite assemblages were identified by two-way ANOSIM of infected individuals after square root transformations of parasite abundance. Factors controlled for when comparing habitats were month and year of collection and stock of origin. In 2004, there were no differences between sites within the mixing zone or tidal freshwater habitats. There were two distinct parasite assemblages in the wetlands (Global R=0.357; P=0.1%) with one assemblage in the upper sites and another in the lower wetlands 20km downstream. The parasite assemblages from all four areas: mixing zone, tidal freshwater, and the upper and lower wetlands were significantly different from each other (ANOSIM Global R=0.208; P =0.1%) suggesting differences in parasite community structure between areas based on habitat usage. In 2005, parasite assemblages throughout wetlands sites were not distinct as in 2004. Parasite communities were not different between tidal freshwater and wetlands habitats in 2005; however, both were distinct from assemblages from the mixing zone. In conclusion, parasite assemblages result from successful

foraging on infected prey items. In this study, variation in parasite communities between habitats suggests that many areas in the estuary provide different feeding opportunities for salmon growth and rearing.

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DESCRIPTION OF A NEW STRAIN OF *GYRODACTYLUS SALMONIS* (PLATYHELMINTHES, MONOGENEA) COLLECTED IN MEXICO FROM RAINBOW TROUT (*ONCORHYNCHUS MYKISS WALBAUM*): MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION

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The native distribution range of rainbow trout, *Oncorhynchus mykiss*, in North America spans from the Aleutian Islands in Alaska to near the USA–Mexico border in Baja California. Rainbow trout were first introduced to Mexico for aquacultural purposes in the 1880s, with different varieties of *O. mykiss* and other salmonids being subsequently introduced in the 20th century. Monogenean flatworms of the genus *Gyrodactylus* include important fish pathogens that affect aquaculture and potentially endanger the survival of wild fish stocks; examples include *Gyrodactylus salaris* infecting salmonids and *Gyrodactylus cichlidarum* infecting cichlids. Salmonid fish in North America are parasitized by at least 5 species of *Gyrodactylus*: *G. avalonia*; *G. brevis*; *G. colemanensis*; *G. nerkae*; and *G. salmonis*. Of these 5 species, *G. colemanensis* and *G. salmonis* are the most geographically widespread in North America, occurring at fish farms across the USA and Canada. In the current study a new strain of *G. salmonis* collected from feral rainbow trout captured in Veracruz, central Mexico, is described. Morphologically, the new strain's marginal hooks, while closely resembling those of *G. salmonis*, have features that permit their separation. Given the morphological similarity, we sequenced its ribosomal genes 18s and ITS, and the mitochondrial gene Cox1. Molecularly, this Mexican parasite is 98% identical to *G. salmonis*; we thus consider it as a *G. salmonis* strain. Given the geographical separation between Mexican rainbow trout populations (both farmed and feral) and the native *O. mykiss* distribution range, it is conceivable that this *G. salmonis* strain has a limited gene pool and could eventually diverge from the known *G. salmonis*. We discuss the natural and anthropogenic scenarios that may have led to the isolation of this gyrodactylid population in central Mexico. This first record of *G. salmonis*in Mexico extends its known distribution range in North America.

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NEW SPECIES OF GORDIONUS (NEMATOMORPHA: GORDIIDA) FROM THE SOUTHERN ROCKY MOUNTAINS

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The phylum Nematomorpha contains approximately 350 species in twenty genera. The genus *Gordionus* contains 56 species, four of which occur in the contiguous United States. Here we describe two new *Gordionus* species from the southern Rocky Mountains. Worms were collected at two sites in the Santa Fe National Forest in northern New Mexico during the summer months of 2005 to 2010. Sites consisted of first order streams above 3120 meters. The first new species measures 163 (57-220) cm long has flat, roundish, and sometimes fused areoles covering all parts of the body, with indistinct interareolar furrows and short interareolar structures. Tubercles between areoles are present in fair quantity. Males contain precloacal rows of bristles and postcloacal spines immediately posterior of the cloacal opening and extending onto the inner side of the tail lobes. The cloacal opening is surrounded by broad bristles with stout apexes. At the anterior of the cloacal opening, raised, narrow adhesive warts are present on the ventral side. The second species measures 98.5 (87-107) cm long, and has many similarities to the first, but shows unique circumcloacal spines and a cuticular pattern resembling *G. violaceus* from Europe, which has not yet been described for Nearctic species. The limitations of morphological characters and the utility of molecular data in determining species within this genus will be discussed.

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HIDDEN DIVERSITY IN *GORDIUS ROBUSTUS* (NEMATOMORPHA: GORDIIDA); HOW MOLECULAR DATA IS SHEDDING LIGHT ON A CRYPTIC SPECIES COMPLEX

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Morphological systematic treatment of hairworms or gordiids, (Phylum Nematomorpha), has been hampered by a paucity of informative diagnostic characters. One of the more useful characters is the shape, arrangement, and ornamentation of cuticle areoles, which are polygonal, flat or elevated structures rising from the underlying cuticle. However, some hairworms within the genus *Gordius* lack areoles, including *Gordius robustus*, which is one of the most widely distributed hairworm species in the New World, ranging from Canada and Hawaii to Argentina. Specimens have been described to contain a wide range of sizes and colors, and have been described with and without spots, a collar, and midline coloration. To determine the presence of cryptic species within what we refer to as *G. robustus*, we examined morphological characters, and 3 genetic markers of specimens collected from 20 localities throughout the contiguous United States. Scanning electron microscopy showed inconsistent characters within and between populations and revealed only a few reliable synapomorphies. Genetic distances among the populations were considerable, ranging from 10 to 26% for 720 bp of the mitochondrial *cox*1 gene, suggesting that *G. robustus* is a species complex of as many as 6 species. Many of these species are separated by major river drainages and in some cases mountain ranges, suggesting allopatric speciation. Finally, this study demonstrates not only the importance of genetic data and limitations of

morphological characters in determining some gordiids species but also the feasibility of using the mitochondrial *cox*1 gene as a taxonomic marker for 'barcoding' and species identification.

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RHINEBOTHRIIDEAN CESTODES FROM RAYS (ELASMOBRANCHII: BATOIDEA) IN VIETNAM AND A COMPARISON OF PARASITE FAUNAS FROM THREE LOCALITIES ACROSS THE INDO-WEST PACIFIC: VIETNAM, BORNEO AND AUSTRALIA

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Adult rhinebothriidean cestodes are exclusively parasitic in batoid fishes, and these cestodes are found in batoids worldwide. Although the global diversity of these cestodes is unclear because numerous geographic regions and batoid species remain to be sampled for these cestodes, the Indo-West Pacific seems to be a region of marked species richness for some rhinebothriidean taxa, including the relatively speciose *Rhinebothrium* and several newly recognized, but not yet described, new genera. The geographically complex Indo-West Pacific has been sparsely sampled for these cestodes, with a few records from coastal Thailand, China, and Japan, and most of the available data deriving from extensive surveys of parasites of elasmobranchs in Australia and Borneo. In order to complement these data, a collaborative survey of cestodes from elasmobranchs of Vietnam was undertaken last year. Prior to this survey, no records of cestodes of elasmobranchs existed for the waters of Vietnam. Rhinebothriideans were obtained from 8 batoid species in Vietnam, including 1 rhynchobatid and 7 dasyatid ray species. Several new rhinebothriidean species were present in the material, which included members of *Rhinebothrium*, *Anthocephalum*, and 2 recently recognized, new rhinebothriidean genera. The fact that at least some data exist on the rhinebothriidean fauna of each of the 8 host species from elsewhere in their geographic ranges made it possible to compare the rhinebothriidean faunas of these batoid fishes within this region.

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PHYLOGENY OF THE LEECH FAMILY GLOSSIPHONIIDAE (ANNELIDA: RHYNCHOBDELLIDA) BASED ON MOLECULAR DATA

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Glossiphoniidae (Vaillant, 1890) is the most diverse family of leeches in terms of number of species, which are distributed in all continents with the exception of the Antarctica. Glossiphoniidae includes leeches with a dorsoventrally flattened body, an eversible and large proboscis and yolky eggs. Previous classifications of the group were based on the number of eyespots, annulation patterns and on the form of parental care. Of the three subfamilies recognized by Sawyer (1986), only the monogeneric subfamily Theromyzinae, was found to be monophyletic in previous phylogenetic analyses. Including recently collected material representing 15 of the 23 genera recognized by Sawyer (1986) here we reevaluate their phylogenetic relationships based on DNA sequences of 6 genes (18S, 28S, ITS, 12S, ND1 and COI) and parsimony and Maximum Likelihood methods. Based on the results obtained from the analyses, a variety of taxonomic rearrangements and re-definition of several groups are discused in order to name only monophyletic groups. In addition, the phylogenetic position of the family Glossiphoniidae within the paraphyletic Rhynchobdellida is reevaluated. Rhyncobdellida and Arhynchobdellida are the two major groups of leeches, defined by the presence or absence of proboscis respectively. Surprisingly, the presence of proboscis is not a synapomorphy but its absence defines the group of Arhynchobdellida. Additionally, the phylogenetic relationships of two haematophagous clades (Haementeria and Placobdella) will be presented and discussed in relationship of their symbiotic proteobacteria.

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HELMINTH PARASITES OF THE ALLIGATOR SNAPPING TURTLE (*MACROCLEMYS TEMMINCKII* HARLAN, 1835) FROM THE PASCAGOULA RIVER

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The alligator snapping turtle is the largest freshwater turtle in North America and is confined to the northern Gulf of Mexico drainages. Compared with its closest relative, the common snapping turtle (*Chelydra serpentina*), with which it shares its entire range, *Macroclemys temminckii* reveals few published reports on its helminth fauna, and few species are reported. Turtle helminths are not often host specific, so the paucity of species reported from *M. temminckii* may indicate that either not enough turtles have been examined for parasites or that the helminth fauna of this turtle species is truly depauperate. During 2009 and 2010, we have examined exhaustively four adult *M. temminckii* for helminth parasites. Previously only 3 acanthocephalan, 6 nematode, and 2 trematode species had been reported from *M. temminckii*. In addition to the previously reported *Lophotaspis interiora*, *Proctocaecum macroclemidis,* and *Falcaustra chelydrae,* we also found intestinal digeneans *Auridistomum chelydrae* and three species of blood flukes including two species of *Spirochis* (one representing a new species currently being described) and *Hapalorhynchus brooksi*. Also, 2 species of polystomatid monogeneans and *Capillaria* sp. (Nematoda) were found and represent new host records. The majority of the helminths found in *M. temminckii* are also known from other turtle species. Only *Lophotaspis interiora* and *P. macroclemidis* seem to be specific to *M. temminckii*. In the future, we plan to study helminths of *C. serpentina* from the same areas to determine actual overlap in parasite communities and level of specificity among parasites of these two related turtle species. Funded by NSF awards 0529684, 0515492 and NOAA NA08NOS4730322.

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A TWO-YEAR SURVEY OF THE FISH PARASITES OF OTSEGO LAKE, NEW YORK

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Results of a two-year fish parasite survey of Otsego Lake, New York are presented. 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 from 2008 until 2010. Over five hundred individual fish representing 15 species were necropsied for parasites in conjunction with undergraduate students from the State University of New York College at Oneonta. Fish species examined included: *Micropterus salmoides* (Largemouth bass); *Micropterus dolomieu* (Smallmouth bass); *Ambloplites rupestris* (Rock bass); *Lepomis macrochirus* (Bluegill); *Lepomis gibbosus* (Pumpkinseed); *Lepomis auritus* (Redbreast sunfish); *Perca flavescens* (Yellow perch); *Sander vitreus* (Walleye); *Etheostoma olmstedi* (Tesselated darter); *Esox niger* (Chain pickerel); *Catostomus commersoni* (Common White sucker); *Cyprinus carpio* (Common carp); *Alosa pseudoharengus* (Alewife); *Rhinichthys atratulus* (Blacknose dace); and *Salvelinus namaycush* (Lake trout). Multiple species of arthropods, nematodes, monogeneans, digeneans, cestodes, and acanthocephalans were encountered in or on the fish examined. Among these, the acanthocephalan *Leptorhynchoides thecatus* was the most common in terms of prevalence, and it was the least host specific. Adult *L. thecatus* were encountered in nine of the 15 fish species examined, and gravid *L. thecatus* were found in four fish species. Taxonomic issues encountered during attempts to identify parasite species are addressed.

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NEW *DRACOVERMIS* (DIGENEA, LIOLOPIDAE) FROM AUSTRALIAN CROCODILES AND ITS PHYLOGENETIC AFFINITIES

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Crocodilians are characterized by a highly specific and ancient helminth fauna. Some of the helminth genera are shared by crocodilians inhabiting different continents. *Dracovermis* (Liolopidae) is one of such broadly distributed genera, with four previously known species described from the United States, Congo, India and Philippines. In the course of a parasitological study of freshwater crocodiles in Northern Territory, Australia, we have collected several digenean species including a new species of *Dracovermis*. This is the first record of the genus in Australia. The new species is clearly distinct from previously described species, being morphologically closest to *D. nicolli* from India rather than to geographically closest *D. rudolphii* from Philippines. Discovery of *Dracovermis* in Australia is interesting from the phylogeographic viewpoint and allows us to predict that representatives of the genus may be found in crocodilians elsewhere in the region, e.g., in the New Guinea crocodile. The Liolopidae is a small family of digeneans parasitic primarily in amphibians and reptiles, although one species is found in duck-billed platypus. Systematic position of the Liolopidae is uncertain; in the most recent taxonomic treatment of the group it was placed in the superfamily Clinostomoidea together with the Clinostomidae which was conspicuously nested among blood fluke lineages in all recent molecular phylogenetic studies. This association is fascinating from the evolutionary viewpoint because the Clinostomidae have 3-host life cycles while blood flukes have 2-host life cycles. Our molecular phylogenetic analysis based on partial sequences of nuclear lsrDNA has revealed that *Dracovermis* (and the Liolopidae) most probably belong to the Diplostomoidea as a sister group to the Strigeidae+Diplostomidae. This finding suggests a three-host life cycle in *Dracovermis* and provides an additional insight into the evolution of digenean life cycles and host associations. This study was supported by the NSF grants 0515492 and 0515460.

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EVOLUTIONARY RELATIONSHIPS OF NEMATODES IN THE FAMILY VIANNAIIDAE (NEMATODA: TRICHOSTRONGYLINA) BASED ON THE FIRST MOLECULAR PHYLOGENY

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No phylogeny exists for Viannaiidae, a family in the diverse and cosmopolitan suborder Trichostrongylina. Reliance on a small set of morphological characters has cast uncertainty over the relatedness and phylogenetic history of certain trichostrongyles, especially at higher levels of taxonomical hierarchy (i.e., family). Nematodes in Viannaiidae are distributed mainly in Central and South America, primarily infecting opossums and hystricognath rodents and can even be found in lagomorphs and Neotropical primates. In this study, fragments of the ribosomal large subunit (16S) and cytochrome B (CytB) from several species of Viannaiidae were amplified and sequenced. Resulting sequences were used to reconstruct phylogenetic trees. The family appears to be nested in Heligmosomoidea. Both datasets support the monophyly of Viannaiidae, in which three clades are apparent. The basal clade includes species of *Travassostrongylus* Orloff, 1933 that are characterized by a synlophe with multiple ridges on each side and are didelphic. The other marsupial trichostrongyles, which have three ventral ridges on the synlophe and are monodelphic, are shown in the additional clades. They include *Hoineffia* Diaw, 1976 and *Viannaia* Travassos, 1914 collected from multiple localities. This study clarifies the relationships of the family with other groups, proposes classifications within the family, and makes inferences on the evolution of the group.

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UNRAVELING A GORDIAN KNOT: BIODIVERSITY OF GORDIAN WORMS, PHYLUM NEMATOMORPHA

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Hairworms are one of the most poorly studied groups in the animal kingdom and their relationships and diversity are currently unknown. Freshwater hairworms, commonly called Gordian worms, can be over two meters long and seem to appear suddenly in domestic sources of water (swimming pools, toilets, pet bowls, etc.), thus making human interactions with them quite common. These encounters have led to unnecessary panic and numerous trips to doctors and veterinarians. Hairworms, are parasites of terrestrial arthropods, but are free-living in aquatic environments as adults. Terrestrial arthropods become infected with nematomorphs when they ingest cysts that infect most aquatic invertebrates. Previous studies on the relationships and biodiversity of this group of parasites have been hindered by the lack of reliable ways to collect and differentiate adult free-living hairworms. The Nematomorpha is a small phylum, with five marine and about 350 freshwater species. The 350 freshwater species are divided into 19 extant and two extinct genera, and are distributed globally. However, recent estimates suggest that only 15% of hairworm species have been described worldwide; of these, many descriptions are inadequate, lack type specimens, and/or were based on single worms. The taxonomy is in such disarray, that the order Gordiida contains only two named families (considered orders by some), no orders, and the validity of some of the 19 extant genera is uncertain. We discuss recent advances in the use of non-adult cyst stages, the most common life stage of horsehair worms in the environment, and the use of modern DNA techniques to match cysts and adult worms in future studies of nematomorph systematics and biodiversity.

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FRONTEIRS IN PARASITE PHYLOGENOMICS - EXPRESSED SEQUENCE TAGS AND THE NEXT 5 YEARS

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Great strides have been made in understanding the evolutionary relationships of most parasite groups in the last 10 to 20 years. The advent and eventual simplicity of DNA isolation, PCR amplification and sequencing has allowed for taxonomically large datasets of molecular sequence data combined with carefully thought out morphological character information. However, in most cases, the relationships of various groups of metazoan or protozoan parasites are still, even now, being inferred on the basis of rather few loci – sometimes only one, often in isolation. While expressed sequence tag libraries typically are employed to differentiate mRNA cell content relative to stimuli, life-history stage or varying conditions, they can also provide a wealth of information for new phylogenetically informative loci. As well, several such libraries being available for related taxa opens the possibility of truly comparative functional genomics. An effort to rapidly explore expressed genes on a broader parasitological basis is argued.

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HOST USE AND GEOGRAPHIC DISTRIBUTION OF TWO SPECIES OF PINWORMS (*SYPHACIA*: OXYURIDAE) IN SOUTH AMERICA

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The cosmopolitan genus *Syphacia* includes monoxenous nematodes considered to be species specific to muroid rodents. In the New World they occur in arvicoline, neotomine and sigmodontine rodents. Twelve species are known to infect the latter group in South America; from these, *Syphacia carlitosi* and *Syphacia alata* have been recorded from sigmodontine rodents. *Syphacia carlitosi* is known from rodents of the genus *Akodon* in the Atlantic forest and Pampean region of Argentina. *Syphacia alata* is known from akodontine and oryzomine rodents from central Argentina to northern Colombia. We have found that haplotypes matching the morphotype of *S. carlitosi* appear to be restricted to mice of the genus *Akodon* (*A. montensis*, *A. azarae*, *A. serrensis* and *A. phylipmayersi*) in eastern Argentina. In contrast, morphotypes of *S. alata* appear to have a wide geographic distribution and be able to use different species of mice in a single locality. These mice may belong to the tribes Oryzomini and Akodontini. Genetic diversity for specimens collected from the same geographic area show less genetic diversity that across distantly geographic areas (Atlantic forest vs Andes).

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DISTRIBUTION OF *NEORICKETTSIA* AMONG DIGENEANS: EVOLUTIONARY AND ECOLOGICAL CONSIDERATIONS

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The genus *Neorickettsia* is comprised of a small group of bacteria within the family Anaplasmataceae. They are endosymbionts in representatives of several lineages of the Digenea and may be passed from digeneans to vertebrate animals and humans. Neorickettsiae infect their vertebrate hosts' leucocytes and may cause diseases, among them salmon dog poisoning in canids, Potomac horse fever, Elokomin fluke fever in various carnivores and Sennetsu fever in humans. So far, neorickettsiae have been found in a small number of digenean groups with relatively limited spectrum of life cycles involving an aquatic mollusk and mainly lotic ecosystems. The goal of our study was to investigate the natural occurrence of neorickettsiae by screening digenean DNA samples with PCR/sequencing techniques and to summarize the existing knowledge on distribution of the *Neorickettsia* among digeneans. PCRs were performed using primers specific to the 16S rRNA gene of Anaplasmataceae and DNA extracts from a broad diversity of digenean species belonging to numerous families and collected from different continents, primarily North America and Europe. Positive PCR products have been sequenced and compared with sequences available in the GenBank. Newly obtained and previously published sequences were used in phylogenetic analysis. All available *Neorickettsia* records were mapped onto phylogenetic tree of the Digenea published by Olson et al (2003). The major findings of our study were: 1) the transmission cycles of *N. risticii* (agent of Potomac horse fever) may occur in lentic and fully terrestrial ecosystems; 2) two new genotypes of neorickettsiae were discovered in different digenean species parasitizing freshwater fish; 3) we have expanded the list of digenean families known to harbor Neorickettsia. To-date, neorickettsial DNA has been recovered from representatives of 13 families of Digenea. The wide phylogenetic range of their occurrence among Digenea indicate that neorickettsiae have had a long evolutionary history with digeneans and thus may be more common in nature than presently realized.

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INFECTION-INDUCED HEMOCYTE AGGREGATION ON THE SURFACE OF THE MOSQUITO HEART

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Mosquitoes respond to infection by mounting cellular and humoral immune responses. The cellular immune response is mediated by hemocytes that sequester pathogens by phagocytosis and produce humoral factors that kill pathogens via lytic and melanization pathways. To date, studies on the function of mosquito hemocytes have focused on visualizing discrete events in which the hemolymph of an infected mosquito is extracted at a specific point in time following an infection, and the cells visualized or gene expression assayed. Here we present data detailing our efforts to understand the dynamics of mosquito-pathogen interactions in the hemocoel. To accomplish this we first developed a novel fluorescence-based method for the in vivo staining of circulating hemocytes in the mosquito, *Anopheles gambiae*. This method does not interfere with the natural function of hemocytes, and perfusion-based experiments revealed that it is 95% effective in staining these cells. Then, using this technique we found that mosquito hemocytes occur in two forms: as cells that flow with the hemolymph and as cells attached to tissues. Of particular importance is the finding that, upon an infection, flowing hemocytes remove themselves from circulation and bind the periostial regions of the heart (regions adjacent to the heart valves), where they engage in the intense phagocytosis of invading pathogens. Quantitative data showed that hemocyte recruitment to the periostial regions occurs in a time-dependent and dose-dependent manner, with higher doses of bacteria eliciting the aggregation of higher numbers of hemocytes. Taken altogether, these data conclusively show a physiological interaction between the mosquito circulatory and immune systems, where infection induces the migration of circulating hemocytes to the heart, which is an ideal location for pathogen sequestration as it places immune cells in areas of highest hemolymph flow.

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EVALUATION OF WEST NILE VIRUS VECTORS IN BERNALILLO COUNTY, NEW MEXICO, USA: IMPLICATIONS FOR DISEASE TRANSMISSION

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Culex quinquefasciatus (Say), *Cx. tarsalis* (Coquillett), and *Aedes vexans* (Meigen), have tested positive for West Nile Virus (WNV) in Bernalillo County, New Mexico. All three mosquito species are considered to be competent WNV vectors. We have formulated a model utilizing relative abundance, rate of WNV infection and blood meal preference to assess the relative importance of these potential WNV vectors in both the enzootic WNV cycle and as bridge vectors to mammals. Our results suggest that *Cx. quinquefasciatus* is especially important in the enzootic WNV cycle, and consequently in viral amplification. Although both*Culex* species probably transmit WNV to mammals, *Cx. tarsalis*may be especially important in this regard. It is unlikely that *Ae. vexans* is an enzootic vector, but it may occasionally be involved in bridge transmission. Should our model be validated through additional testing, it may have practical value as a means to anticipate WNV outbreaks, and thereby implement protective measures.

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KAZAL-TYPE SERINE PROTEASE INHIBITORS IN *PHLEBOTOMUS PAPATASI* MIDGUT

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Sand flies (Diptera: Psychodidae) are vectors of parasites of the genus *Leishmania* transmitted to suitable vertebrate host during blood feeding. For blood feeding arthropods, including sand flies, preventing the blood from coagulating within the mouth parts or the midgut requires the secretion of inhibitory molecules, such as kazal-type serine proteases that can block thrombin and prevent coagulation. Previous studies have identified such molecules in the saliva of *Anopheles albimanus*, and in the midgut of triatomine bugs. Following studies of the midgut transcriptome of *Phlebotomus papatasi,* the principal vector of *Leishmania major*, two Kazal-type serine protease inhibitors were identified (PpKzl1and PpKzl2). We are interested in the role of these proteins as inhibitors of thrombin, in addition to their potential effects on blood digestion in *P. papatasi*. We are currently characterizing PpKzl1 and PpKzl2 molecularly and biochemically. We have expressed recombinant forms of these proteins and are in the process of testing their specific activity on thrombin. In addition, expression profiles suggest that both transcripts are constitutively expressed in the midgut of *P. papatasi*. RNAi knock-down of each transcript is also being used to assess the role of each protein in blood digestion within the fly. Moreover, as *Leishmania* development is restricted to the sand fly midgut, and parasite escape from the endoperitrophic space is required, targeting PpKzl1 and PpKzl2 may provide a new strategy to prevent transmission. Therefore, future experiments will assess differences of parasite prevalence and load in RNAi silenced flies.

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EFFECTS OF CO-INFECTION WITH AVIPOXVIRUS ON DIVERSITY OF PLASMODIUM RELICTUM IN NATIVE HAWAIIAN FOREST BIRDS

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The introduced diseases avian malaria (*Plasmodium relictum*) and avian pox (*Avipoxvirus* sp.) are recognized today as major contributing factors in the population decline and limited recovery of native Hawaiian forest birds. Prevalence of *Avipoxvirus* (based only on records of pox-like lesions) is generally lower than malaria, ranging from 5-15% in native species and generally <5% in non-native passerines while prevalence of *P. relictum* can exceed 80% in some low elevation populations. Our data documents the presence of both mixed genotype infections of single pathogen species, and also co-infection with both pathogens infecting a single host. Co-infection with *Avipoxvirus* and chronic malarial infection occurs more frequently than expected by chance, suggesting that the two diseases interact with each other. A modified single base extension method was used to explore distribution patterns of single nucleotide polymorphisms (SNPs) in the thrombospondin-related anonymous protein (*trap*) gene of *P. relictum* infecting 241 forest birds on the east side of Hawaii Island. We analyzed the prevalence of mixed *Plasmodium* infections and average *trap* complexity of groups of birds either co-infected with *P. relictum* and *Avipoxvirus* or infected with *P. relictum* alone. Overall, *Plasmodium* diversity appears greater in hosts co-infected with both *Avipoxvirus* and *Plasmodium* than in those infected only with *Plasmodium*. Differences in *Plasmodium* diversity due to co-infection appear to be related to species, age, and level of mosquito transmission (site). Increased diversity could be related to the potential immunosuppresive effect of *Avipoxvirus* on the host immune system, but the roles of differential mortality, transmission and recovery rates of the two diseases in this interaction have yet to be determined.

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ROLE OF MOSQUITO EGF-REPEAT CONTAINING PROTEINS IN THE ANTIBACTERIAL IMMUNE RESPONSE IN THE HEMOCOEL

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Mosquitoes mount robust immune responses against invading pathogens. These immune responses range from cellular processes such as phagocytosis to humoral processes such as melanization and lysis. In the fruit fly, *Drosophila melanogaster*, it has been shown that members of a protein family characterized by the prominence of EGF-like repeats (EGFs) serve various roles in immunity. Three such members, Eater, Nimrod and Draper, have been implicated as positive regulators of phagocytosis. A fourth member, Hemese, has been shown to act as a negative regulator of cellular immune responses. While much work has been directed toward characterizing this gene family in *D. melanogaster*, little is known about EGFs in mosquitoes. Here we will bioinformatically identify the members of the EGF gene family in the mosquito, *Anopheles gambiae*, and will show that two such members respond to systemic bacterial infections. Specifically, *A. gambiae* genes AGAP012386 and AGAP009762 are transcriptionally and translationally upregulated following infection with *Escherichia coli* and *Micrococcus luteus*. Both genes are expressed primarily in hemocytes and fat body (the two primary immune tissues in mosquitoes) and RNA interference-based transcriptional knockdown of AGAP012386, but not AGAP009762, renders mosquitoes with an impaired ability to kill intrathoracically injected *E. coli*. Interestingly, transcriptional knockdown of either gene does not result in reduced mosquito survival following bacterial infection, suggesting that while AGAP012386 is required for efficient bacterial clearance, other immune mechanisms can compensate for its absence.

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DIVERGING IMMUNE RESPONSES IN BALB/C MICE TO INFECTION WITH DISTINCT *TRYPANOSOMA CRUZI* STRAINS FROM THE UNITED STATES AND SOUTH AMERICA

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Trypanosoma cruzi, the causative agent of Chagas disease, is divided into six groups (Type I-VI), with only TcI and TcIV being found in the United States (US). Infection and virulence of different *T. cruzi* isolates is dependent on numerous factors including parasite and host genetics. Murine models are frequently used to increase knowledge of the virulence, pathogenicity, and immune response of different *T. cruzi* strains. Previous studies have indicated that a prolonged and exaggerated pro-inflammatory response to *T. cruzi* results in successful establishment and replication of the parasite which can result in morbidity or mortality of the host. The aim of the current study was to evaluate the immune response of Balb/c mice during the acute phase of infection with four genetically distinct isolates from the US and South America (SA). The US strains were from a Virginia opossum (*Didelphis virginiana)* (TcI) and a striped skunk (*Mephitis mephitis)* (TcIV). Similar genotypes from SA were also included, Brazil (TcI) and CANIII (TcIV), both isolates from humans. A previous pilot study indicated that US isolates are less virulent than SA *T. cruzi* isolates for mice. Therefore, we hypothesized that the SA isolates would elicit higher levels of pro-inflammatory cytokines in response to infection than the United States isolates. Groups of 21 mice were intraperitoneally inoculated with 5 x 10^6 culture-derived *T. cruzi* trypomastigotes of each isolate. Mice were sacrificed at 6 and 24 hours and at 2, 3, 5, 7, and 10 days post infection. Levels of seven cytokines were determined by analysis of serum using a cytometric bead assay. Additionally, splenocytes were cultured, stimulated, and stained for intracellular cytokines to identify the number of cells producing interferon gamma (IFN-γ). Analysis is ongoing, but preliminary data show that IFN-γ levels in response to infection with the Brazil strain were 5-fold higher than in response to infection with

US strains. These results suggest that infection with different *T. cruzi* strains elicit diverging immune responses in mice.

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ALTERNATIVE APPROACHES TO EVALUATE THE EFFECTS OF CHEMICAL AND PHYSICAL DISINFECTANTS ON WATERBORNE PROTOZOA

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Cryptosporidium spp., Giardia duodenalis (syn: G. intestinalis, G. lamblia), and *Toxoplasma gondii* are important waterborne pathogens that cause disease worldwide. The environmental forms of these parasites are resistant to many common disinfectants and survive outside the host for months. Animal models of infection have been the gold standard to determine susceptibility of these parasites to disinfection, but they are expensive and labor intensive. In this study, we evaluated three alternative approaches to quantitfy parasite viability on one or more protozoa including, 1) quantitative reverse-transcriptase real-time PCR (RT-qPCR), 2) propidium monoazide-quantitative polymerase chain reaction (PMA-qPCR), and 3) *in vitro* cell culture. Results revealed that, while the mRNA-based RT-qPCR assay was found to be a rapid technique for detecting the presence of *T. gondii* in water, it can only reliably measure disinfection efficacies of strong oxidizing and fixative chemicals like bleach and formalin. Likewise, while the PMA-qPCR technique is a rapid and quantitative approach for determining *C. parvum* and *G. duodenalis* viability, its application is limited to certain disinfectants that perturb cyst and oocyst membrane integrity. By contrast, the cell culture assay was found to more accurately quantify *T. gondii* viability for many of the treatment conditions evaluated. Our results illustrate the advantages and limitations on the use molecular-based and cell culture assays to assess the viability of these organisms. The results also emphasize that great care must be used in the selection of the type of assay used for measuring disinfection efficacy.

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MOMORDICATIN IS A NOVEL AND EFFECTIVE CHEMOTHERAPEUTIC AGENT TO TREAT VISCERAL LEISHMANIASIS

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Visceral leishmaniasis (commonly known as kala-azar) is a chronic and deadly parasitic disease of the viscera caused by the protozoa *Leishmania donovani*. The internal organs, particularly the liver, spleen, bone marrow and lymph nodes are severely affected due to infection by the parasite. Treatment of this parasitic disease is being conducted with various antileishmania agents. However, available drugs are toxic, nonspecific and costly. At the same time, no definite drug is available for a complete cure of the disease having no side effect. Cases of drug resistance have also been reported to hamper the treatment of this parasitic disease with available drugs including miltafosine. Again, there is a possibility to develop post kala-azar syndrome usually known as Post Kala-azar Dermal Leishmaniasis (PKDL). We have recently envisioned that normal properties of the host peroxisomes are impaired due to infection by the pathogen and can not be restored after treatment with existing chemotherapeutics. It is already known that peroxisomal damage is responsible to promote various diseases including genetic disorders. Thus it is necessary to search for potent and effective antileishmania agents to treat kala-azar for the benefit of mankind. We have established that crude extract of the fruits of *Momordica charantia* (Karela) can act as an anti-kaka-azar agent. A novel compound Momordicatin has been purified from the fruit extract and proved to be a potential candidate for an effective chemotherapy against this disease. The newly found

purified compound is non toxic to the hosts and its mode of action deals with the oxidative burst system of the parasite without affecting its host counterpart. It is proposed that Momordicatin may be considered as a definite contender for a safe and low cost therapy of kala-azar and thereby establish its efficacy as the future drug of choice.

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MAJOR CHANGES IN PARASITE COMMUNITY STRUCTURE IN TROUT-PERCH (*PERCOPSIS OMISCOMAYCUS*) ON THE ATHABASCA RIVER: EFFECTS OF OIL SANDS OPERATIONS?

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To assess the effects of Athabascan oil sands installations on parasite community structure in small-bodied fish, 150 trout-perch (*Percopsis omiscomaycus*) were collected from five sites in October 2009. These included a reference site upstream, two sites adjacent to oil sands installations, and two sites located further downstream. Information was collected on abundance of individual macroparasite species, as well as macroparasite infra- and component community composition and richness. We also collected data on fish length, weight, condition, and organosomatic indices for spleen and gonads. Athabasca trout-perch parasite communities included seven species: *Urocleidus baldwini*, two species of *Diplostomum*, *Crepidostomum percopsisi*, *Triaenophorus stizostedionis*, *Ichthyobronemaham ulatum*, *Raphidascaris acus*, and *Contracaecum* sp. We did not note any among-site differences in infracommunity richness, nor did we find any significant differences in host morphometrics or organosomatic indices. However, multivariate Analysis of Similarity (on a Bray-Curtis similarity matrix based on untransformed data) found significant among-site differences in parasite community structure (ANOSIM $R=0.227$, $p<0.01$). SIMPER analysis indicated that these differences were primarily driven by changes in the abundance of *Diplostomum* spp. and *U. baldwini*. Whereas *Diplostomum* spp. dominated parasite communities at upstream and downstream sites, their abundance was drastically reduced at sites adjacent to oil sands installations. Oil sands communities were instead dominated by *U. baldwini*. This represents a significant shift in community structure, as *Diplostomum* spp. are larval digeneans with complex life cycles requiring snails and fish-eating birds, whereas *U. baldwini* is a monogenean with a simple life cycle requiring only fish. The observed shift from communities dominated by parasites with complex life cycles to those with simple life cycles suggests that trophic relationships are being disrupted at sites near oil sands operations.

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A NEW METHOD TO DIAGNOSE DEER KED (*LIPOPTENA CERVI*) INFECTION IN CERVIDS DURING WINTER TIME

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The deer ked (*Lipoptena cervi*) is an obligatory haematophagous ectoparasite of cervids. In eastern Fennoscandia the main host is the moose (*Alces alces*). One single moose can serve as a breeding host for several thousands of deer keds. The life cycle of the deer ked includes host dependent (adult) and off-host (pupae) stages. Adult deer keds emerge from pupal stage on the ground layer and colonize their hosts in late summer and early autumn. The adult generation reproduces and feeds on blood regularly on the host

throughout the winter, females giving birth to one individual pupa at a time. Deer ked pupae then drop off the host, mostly onto the cervid bedding sites. Invasion of this fly has been relatively rapid in Finland during the last five decades. As the distribution area of the species has expanded towards the northern latitudes, related problems have become more apparent. The deer ked can be a nuisance for domestic animals and in certain areas, the deer ked causes major inconveniences and allergic reactions in humans, potentially limiting outdoor activities in forests during the flight period of emerged, host seeking adults. The principal aim of our study was to explore whether the deer ked parasitism and intensity of the infection could be diagnosed in winter time by using visual snow examination on cervid bedding sites and by analyzing biotic samples found from the bedding sites. Our results demonstrate that chronic deer ked infection causes reddish-brown snow discolouration (due to host tissue fluid and deer ked faeces) on the bedding sites to the extent that parasitism can be diagnosed visually. This method is practical and can potentially be used in the future in predicting and perhaps preventing the socio-economic negative effects of the deer ked.

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INFECTIOUS PERSONALITIES: LARVAL AMPHIBIAN BEHAVIOURS AND RISK OF PARASITISM

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Consistent and predictable correlations among behaviours through time, forming syndromes or personality types, likely have substantial influences on animal life histories and fitness. Various host behaviours have been separately linked with susceptibility to parasitism, likely playing a role in observed macroparasite aggregation within host populations; however, the role of pre-existing personality types in acquiring parasitic infections has not been investigated experimentally. Here we use a model system involving larval amphibians (wood frogs –*Lithobates sylvatica*) and a trematode parasite (*Echinoparyphium* sp.) to show that individuals can exhibit behavioural syndromes through similar responses to both novel stimuli and the threat of parasitism and report strong correlations in activity level and refuge use across these different contexts, as well as between these two behaviours. Additionally, while individual activity level and refuge use under parasite threat were significant predictors of host parasite load, these same behaviours in response to a novel stimulus were also significant, indicating that personality type is important for disease risk. We suggest that this system illustrates how multiple benefits could drive selection for behavioural consistency if wood frog larvae reliably exhibit high levels of activity and boldness in different contexts to maximize both their energy acquisition and resistance to trematode parasites due to the particulars of their life histories.

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EFFECTS OF HABITAT CHANGE ON AVIAN BLOOD-PARASITES

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The effects of deforestation on health are diverse and are becoming increasingly apparent with the highly publicized recent outbreaks of several diseases spread to humans by animals. Here we conduct a study of the effects of deforestation and habitat type on the prevalence and diversity of blood parasites in African rainforest birds. Over the past 18 years, we have collected more than 10,000 individual blood samples from over 200 rainforest bird species in a variety of habitats across Africa. Significantly, the samples were collected from sites pristine and degraded sites, permitting a unique examination of the direct effects of

human-induced habitat alterations. Using complementary techniques of blood smear analysis and molecular biology, samples are assayed for *Plasmodium*, *Haemoproteus*, *Leucocytozoon* and *Trypanosoma*. We have obtained results regarding the host-specificity, prevalence and lineage diversity of these parasites in rainforest birds. As part of the larger project, we collected blood samples from two bird species from eight paired disturbed and undisturbed sites in Southern Cameroon. We describe the parasite lineages in 2 common bird species. Linking these DNA sequence lineages with identified parasite morphospecies, we describe significant differences in prevalence between habitat types in the haemosporidian parasites. We also present recent data on the evolution of specialist vs. generalist strategies in avian malaria. Our work incorporates satellite imagery data to quantify differences among the sites, and predict how changes in forest composition may affect the spread of diseases. With the combined information we have developed models to help predict how deforestation will influence future disease outbreaks.

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BIOMPHALARIA GLABRATA IN PUERTO RICO: WHERE AND HOW THEY SURVIVE TODAY

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The Caribbean island of Puerto Rico (PR) is the only places under the United States flag where *Biomphalaria glabrata*, the intermediate host of *Schistosoma mansoni*, is native. Clinically, few active cases of *S. mansoni* are detected in PR at present; however, continued presence of the intermediate host is of interest if only because most laboratory strains of the snail derive from a hybrid of the PR strain. Over the last 25 years I studied populations of the snail and will report my observations here. *B. glabrata* is present and can be found mainly in swampy pastures and drainage ditches, rather than permanent rivers or lakes; in sites that dry up for months during the year. They survive by aestivating under mud and organic matter. While most (85%) survive aestivation in the lab, few survive in the field. However, when the conditions are right they emerge and produce large numbers of eggs very fast and the young grow rapidly into adults. The F1 from wild stock is susceptible to *S mansoni* from humans infected in PR, but not as susceptible to laboratory strains of the parasite. A significant number of field collected snails are parasitized by one of at least 9 species of larval trematode, excluding, *S. mansoni*. Sites where this snail persists, and the trematode parasites it propagates in nature will be presented and illustrated.

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TAPEWORMS IN ELASMOBRANCH FISHES: RICHNESS CORRELATES AND SPECIES DISCOVERY

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Parasite richness is a fundamental characteristic of host species and varies substantially among host communities. In this study, we use tapeworms of elasmobranch fishes to examine the environmental and phylogenetic influences on the variation in species richness. This is an ideal model system in which to examine global patterns in species diversity. First, tapeworms are the most diverse group of helminths to infect elasmobranchs and show a wide range in sizes. Second, the hosts are cosmopolitan in their distribution and also vary greatly in size. Third, different tapeworm orders infecting elasmobranchs exhibit varying degrees of host specificity. Here: (1) using general linear models, we identify the host features correlated with tapeworm richness; (2) using phylogenetic independent contrasts, we examine the phylogenetic influences of hosts on tapeworm richness; (3) using Species Area Relationships (SAR), we detect potential “hotspots” and “coldspots” for tapeworm biodiversity; and (4) using principal component analyses, we identify factors influencing the discovery of these tapeworms. Currently, we are

facing a biodiversity crisis and many elasmobranchs are on the verge of extinction or local extirpation. Understanding the ecological roles played by these hosts and the biodiversity of parasites they support are critical to the conservation of marine ecosystems.

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NUTRIENT RESTRICTION ALTERS THE INTERACTION BETWEEN AN AQUATIC SNAIL, *BIOMPHALARIA GLABRATA*, AND ITS TREMATODE PARASITE, *SCHISTOSOMA MANSONI*

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Interactions between infection and host nutrition have rarely been examined from both host and parasite perspectives. The primary objective of this study was to investigate the roles that both host nutrient availability and infection play in the expression of host and parasite life-history traits. In addition, we investigated assimilation/allocation patterns in control and infected hosts under different resource treatments. *Biomphalaria glabrata* snails were initially either exposed or sham-exposed to 10 miracidia of *Schistosoma mansoni* and then maintained on a diet composed of dried lettuce, agar and water. Shortly after the onset of patency cercariae were collected, counted, and measured every two days. After one week, both control and infected snails were then randomly allocated to either fed or starved treatments; cercariae continued to be collected every 2-3 days. Approximately 4 weeks after nutrient restriction, all hosts were necropsied and their tissues were separated for carbon:nitrogen (C:N) analyses. Not surprisingly, cercarial output was influenced by host resource availability; however, these differences did not appear until approximately 3 weeks after starvation. Preliminary analysis revealed little difference in cercariae sizes based on whether hosts were starved or fed. Conversely, elemental (C:N) ratios in host tissues varied dramatically based on tissue type (somatic vs reproductive; parasite vs host) and whether snails were starved or fed. The implications of these results for life-history evolution and disease transmission will be discussed.

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PLEUROCERCOIDS OF THE TRYPANORHYNCH CESTODE *NYBELINIA SURMENICOLA* IN PACIFIC HAKE (*MERLUCCIUS PRODUCTUS*) CAUGHT OFF OREGON AND WASHINGTON

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The trypanorhynch cestode *Nybelinia surmenicola* uses a broad spectrum of marine fishes as paratenic hosts prior to maturing in salmon sharks (*Lamna ditropsis*). A total of 834 Pacific hake (*Merluccius productus)* stomachs collected from 341 trawl stations along the United States west coast during the summers of 2008 and 2009 were examined for pleurocercoids of this marine cestode. Pleurocercoids were recovered from 75.2% of Pacific hake in 2008 and in 88.0% in 2009. In an examination of 131 Pacific hake stomachs collected along the United States west coast in 1999, *N. surmenicola* prevalence was 35.1%. The results from a general linear model suggested that prevalence is influenced by year and latitude of collection site, Pacific hake length and sex. Mean intensity of *N. surmenicola* 2008-2009 was 20.22 (± 1.13 SE) and was positively related to Pacific hake length and the latitude of collection site. Year one Pacific hake (< 27 cm length) had significantly lower prevalence and intensity of *N. surmenicola* compared to older and larger fish. Pacific hake collected south of Point Conception, California (32.5º N to 35º N) had lower prevalence and intensity of *N. surmenicola* compared to those collected in northern latitudes (35.1º N to 48.4º N). Higher *N. surmenicola* prevalence in Pacific hake in

recent years suggests a dynamic food web in the Northern California Current ecosystem potentially caused by changes in ocean transport of zooplankton or distributions of pelagic fishes. The observed increase in the abundance of this larval cestode warrants future monitoring in Pacific hake.

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ECOLOGICAL CONSEQUENCES OF TREMATODE-SNAIL ELEMENTAL MISMATCHES: STOICHIOMETRY FOR PARASITOLOGISTS

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Parasites are ubiquitous members of ecological communities, but have only recently been recognized as key players in broad ecological interactions and ecosystem dynamics. We explored the effects of trematodes on gastropod body elemental content, excretion N:P ratios, and egestion N:P ratios using field collections, experimental infections, and laboratory experiments. The consequences of trematode-altered snail elemental ratios on snail-resource interactions were then investigated using a field survey of 50 sites in east-central Indiana and in outdoor mesocosms containing *Physa acuta* and periphyton. Infection rates of trematodes on field-collected freshwater snails ranged from 2 to 36%. Infected snails had significantly higher body N:P than uninfected snails. Trematode body N:P ratios were lower than snail N:P ratios but did not differ among trematode taxa. Additionally, periphyton N:P ratios were positively related to snail infection rates. In outdoor mesocosms, experimentally-infected *Physa* excreted higher N:P ratios than uninfected snails, resulting in lower primary productivity, but higher periphtyon N:P ratios in mesocosms with greater infection rates. Thus, trematodes indirectly affected periphyton production and N:P by altering host snail stoichiometry. Overall, these results indicate that trematodes modify snail-periphtyon interactions through a nutrient pathway and suggest that stoichiometrically accounting for parasites may provide insight into their role in ecosystems.

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MIGRATION PATTERNS AND STOCK STRUCTURE OF PACIFIC SARDINES (*SARDINOPS SAGAX*) USING PARASITE COMMUNITY AND POPULATION GENETICS

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Pacific sardines (*Sardinops sagax*) are an economically and ecologically important forage fish, transferring energy from planktonic primary producers and secondary consumers to upper trophic predators. Our research applied parasite community analyses and population genetics techniques to assess migration patterns and stock structure of Pacific sardine in the California Current from Vancouver Island, British Columbia, Canada to San Diego, California, USA. Approximately 1500 sardines were collected from 2005 through 2008. Twelve parasite species were recovered, and two parasite species show strong potential as biological tags. The geographical distribution of *Myosaccium ecaude* (Trematoda) supported a previously described coastwide migration for sardines, and the geographical distribution of *Lecithaster gibbosus* (Trematoda) identified a second migration pattern limited to the Pacific Northwest. Population genetics studies identified a panmictic distribution for: 1) the trematode *M. ecaude*using a 283bp portion of the NADH-dehydrogenase subunit 1 (ND1) mitochondrial DNA (mtDNA) gene; and 2) three species of *Anisakis* nematodes (*A. simplex s.s., A. pegreffii*, and *A. simplex*‘C’) using a 524bp portion

of the cytochrome c oxidase 2 (*cox2*) mtDNA gene. These results suggest that the extensive movement of all of the potential hosts utilized by these parasites, limited oceanographic barriers, and complexity in the California Current may enable large geographically distributed populations of these parasite species. In summary, the panmictic distribution of four parasite species did not suggest population subdivision of Pacific sardines in the California Current system, however, two different migration patterns that overlap off of Oregon and Washington suggest little migration between southern California and British Columbia during years examined.

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ECOLOGICAL DRIFT IN PARASITE INFRACOMMUNITIES

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Ecological drift, a key component of the unified neutral theory of biodiversity and biogeography, is an extension of the assumption of species equivalence proposed as part of the equilibrium theory of island biogeography. Many parasite infracommunities have been characterized as colonization-dominated systems, suggesting that stochastic processes might play a large role in infracommunity structure. In addition to species equivalence and stochastic structuring, ecological drift requires zero-sum dynamics, such that colonization only can occur when habitat has been made available through the loss of individuals. Examination of the relationship between variation in local abundance and metacommunity relative abundance for a quadratic signature provides a facile test of the assumption of zero-sum dynamics. The test is of limited utility in free-living communities because metacommunity relative abundances tend to be lower than 0.5, the predicted point of peak variation, but high relative abundances are not as uncommon in parasite component communities. The relationship between the variance in infrapopulation abundances as a function of component community relative abundance is examined for component communities of fishes, frogs, and turtles, revealing no evidence of a quadratic signature.

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STATIC AND ONTOGENETIC ALLOMETRY OF TRUNK SPINES IN TWO SPECIES OF *CORYNOSOMA* (ACANTHOCEPHALA: POLYMORPHIDAE): ATTACHMENT STRATEGIES TO THE DEFINITIVE HOST MAY DIFFER BETWEEN SPECIES AND SEXES

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It is generally assumed that the holdfast of acanthocephalans is fully developed at the cystacanth stage as an adaptation to maximize the likelihood of successful attachment after recruitment to the definitive host. However, some acanthocephalan species are known to generate new holdfast devices (e.g., an inflation of the proboscis, neck or foretrunk) in the definitive host. Accordingly, less dramatic changes may also occur in typical holdfast features (e.g., the size of proboscis, hooks, or trunk spines). We tested this hypothesis by investigating patterns of static and ontogenetic allometry of trunk spines using cystacanths and adults of *Corynosoma cetaceum* and *C. australe* that were collected from fish and marine mammals from Argentina. Spines were measured at the disk border, and the anterior and posterior hindtrunk. In males of both species, the size of spines did not differ between cystacanths and adults, nor was there a significant correlation between spine size and trunk size within each development stage. In females of *C. cetaceum*, spine size of cystacanths did not differ from that of males. However, spines from adult females were significantly larger than that of female cystacanths and adult males, and spine size was correlated with body size. In females of *C. australe*, only spines at the disk border were larger in adults than in

cystacanths, and hidtrunk spines were significantly larger than that of males regardless of development stage. Sexual dimorphism in spine size did not result from body size differences between sexes. In summary, the final size of the trunk armature of males, but not of females, is reached at the cystacanth stage. Females of *Corynosoma* live longer than males and carry the offspring; larger spines could thus improve attachment efficiency. Females of each species apparently use different ways to adjust trunk spine size to the microhabitat conditions they encounter during adult development (the stomach of dolphins in *C. cetaceum* and the intestine of pinnipeds in *C. australe*).

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TEMPORAL VARIATION IN THE INFECTION PARAMETERS OF *MEXICONEMA CICHLASOMAE* (NEMATODA: DANICONEMATIDAE) IN THE MAYAN CICHLID *CICHLASOMA UROPHTHALMUS* FROM YUCATAN, MEXICO

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Understanding the variability of infection parameters of parasites of aquatic hosts through time, together with the biotic and abiotic factors affecting them, has become an important issue due to the potential effect of Global Climate Change (GCC). For temperate latitudes, parasite abundance in hosts varies seasonally and is driven mainly by temperature, but for tropical latitudes, there is a lack of information on key environmental factors affecting parasite abundance through time. However, rainfall has been recently suggested as a key factor because both aquatic hosts and their parasites experience numerical oscillations due to annual patterns of precipitation and hydrodynamic disturbances such as tropical storms and hurricanes. A further complication in the tropics is that natural disturbances occur at time scales longer than a year (e.g. El Niño 3-5 years), for which it is necessary to carry out long-term observations. The aim of this study is to determine whether temporal rainfall patterns influence long-term fluctuations in the prevalence and mean abundance of the nematode *Mexiconema cichlasomae* in its intermediate (*Argulus* sp.) and definitive hosts *(Cichlasoma urophthalmus*) from a coastal lagoon in Yucatan over a period of 8 years. Variability in rainfall and monthly infection parameters for both hosts were analyzed using time series and cross-correlations to detect possible recurrent patterns. Infection parameters of *M. cichlasomae* in *Argulus* sp. showed six monthly peaks, while in *C. urophthalmus* the peaks were bi-annual. The latter peaks appear to be related to the accumulation of several generations of this nematode in *C. urophthalmus*. The present results therefore suggest that rainfall is a key factor affecting this host parasite system. In addition, the temporal variability of infection parameters of *M. cichlasomae* expanded over periods longer than a year, suggesting the need for long term data sets in studying temporal variability in infection levels in the context of GCC.

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STANDARDIZED METHOD FOR AMPHIBIAN METAMORPH NECROPSIES

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Amphibian populations are declining due to parasite-induced malformations associated with *Ribeiroia ondatrae*. This has led to an increase in necropsies of amphibian metamorphs to assess *R. ondatrae* prevalence. Historical amphibian parasitology literature focuses on adult parasites inhabiting the gastrointestinal tract, lungs, mouth, and blood; in contrast, *R. ondatrae* encysts within muscle, gills, and skin. Previous methodologies for necropsying amphibians failed to thoroughly examine localities for juvenile parasites in metamorphic amphibians. Successfully identifying parasites in earlier life stages, such as metacercariae, requires a shift in methodologies to properly access encystment areas of early stage parasites. After over 15,000 necropsies of amphibians throughout North America, we were able to create a standardized method for a simple technique to necropsy amphibian metamorphs. Furthermore, we discovered most metacercariae encysted in skin tissues, reabsorbed gill tissues, and reabsorbed tail tissues. We used this data to generate a map of common locations of parasites as well as better techniques for identification of immature parasites. We concluded that there are twelve commonly reoccurring species of metacercariae, including *R. ondatrae,* and we produced a quick reference key for easy identification these parasites. This key and standard procedure will allow for more uniform results by providing parasitologists and non-parasitologists with a simple tool to assess parasites of juvenile amphibians.

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INSECT IMMUNE RESPONSES TO ENTOMOPATHOGENIC NEMATODES AND THEIR SYMBIOTIC BACTERIA

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The bacteria *Photorhabdus* and *Xenorhabdus* live in a ‘symbiosis of pathogens’ with the entomopathogenic nematodes, *Heterorhabditis* and *Steinernema*, respectively, which invade and kill insects. However, little is known about the roles of entomopathogenic nematodes in natural infections. Unlike other animals associated with bacterial symbionts, these nematodes are viable in the absence of their symbiotic bacteria. Consequently, each partner of this symbiotic/pathogenic relationship can be separated and studied in isolation or in combination, thus enabling pathogenesis and symbiosis to be investigated separately or together. We have investigated the respective contributions of nematodes and bacteria by examining humoral and cellular immune reactions of the lepidopteran insect *Manduca sexta* against *Heterorhabditis* carrying *Photorhabdus*, nematodes free of bacteria (axenic nematodes) and bacteria alone. Insect mortality was slower following infection with axenic nematodes than when insects were infected with nematodes containing *Photorhabdus*, or the bacteria alone. Nematodes elicited host immune responses to a lesser extent than bacteria. Transcription of certain recognition and antibacterial genes was lower when insects were naturally infected with nematodes carrying no bacteria compared to insects that received bacteria, either with or without nematodes. These results imply that both bacteria and nematodes contribute separately to the pathogenic modulation of host immune responses during natural infections by the mutualistic *Heterorhabdus-Photorhabdus* complex. We recently began to use the powerful genetics of the model insect *Drosophila melanogaster* to dissect the molecular and evolutionary basis of insect immunity, bacterial symbiosis/pathogenicity and nematode parasitism, and to understand the basic principles of the complex interactions between these important biological processes.

Finally, such studies set the scene for revealing not only how pathogens evolve virulence but also how two pathogens can come together to exploit a common host.

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FREP3 (FIBRINOGEN-RELATED PROTEIN 3) IS AN IMPORTANT COMPONENT OF SNAIL RESISTANCE TO DIGENTIC TREMATODE INFECTION

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The size, strain and prior trematode exposure profile are all factors that influence resistance of the planorbid snail *Biomphalaria glabrata* to digentic trematode infection. Transcriptional analysis of *B. glabrata* snails following challenge with *Schistosoma mansoni* and *Echinostoma paraensei* revealed a number of transcripts associated with snail resistance to infection. Comparison of the transcriptional profiles of resistant snails to those that were successfully infected yielded a small group of resistance-associated transcripts that were commonly up regulated in all three resistance models (size, strain, acquired resistance). Fibrinogen related protein 3 (FREP3) was identified as one such transcript, demonstrating an increased expression beginning as early as 12 hours post exposure, and continuing until 8 days. 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 rate of point mutation and gene conversion events made FREP3 a high priority for further functional analysis. *In situ* hybridization studies suggested that newly developed hemocytes are major producers of secreted FREP3, and by using an anti-FREP3 antibody we were able to purify native FREP3 from *B. glabrata* plasma to develop assays to asses FREP3 function. We identified that FREP3 is involved in the binding and recognition of galactose sugars, and that it can act as an opsonin to enhance phagocytosis of bound targets. Injection of FREP3-specific small interfering RNA into size or strain resistant snails and then challenging them with *E. paraensei* or *S. mansoni* respectively resulted in a partial loss of the resistance phenotype, suggesting that FREP3 is an important component of snail resistance to trematode infection.

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PARASITES AND PRESPAWNING MORTALITY IN CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) IN THE WILLAMETTE RIVER, OREGON

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Prespawning mortality in Chinook salmon in the Willamette River system in Oregon has become a serious concern, as in some years the mortality exceeds 50%. We are investigating the cause of this mortality through histopathological and parasitological examinations. In the summer and fall of 2009 and 2010, we examined a total of about 200 adult salmon from this watershed representing three categories: 1) prespawning mortalities, 2) healthy salmon collected during the summer, and 3) post spawn survivors from both the rivers and Willamette Hatchery. Some of the most noteworthy parasite infections included *Parvicapsula minibicornis* in the kidney causing severe glomerular nephritis, systemic or gastrointestinal infections caused by *Ceratomyxa shasta*, severe *Myxobolus* sp. infection in the brain and spinal cord, heavy infections of metacercariae of *Nanophyetus salmincola* in the kidney and heart, and

metacercariae of *Apophallus* sp. and *Echinochasmus milvi* in the gills associated with prominent cartilage hyperplasia. In general, most prespawning mortalities had heavier infections than presumably healthy fish collected at the same time in the summer. However, parasite burdens increased with time, and fish surviving to spawn in September often had heavy parasite burdens. We applied traditional parasitology methods used to assess the parasite associated mortality in wild animals. For example, using Crofton's negative binomial truncation method, we found that a threshold for parasite induced mortality with *N. salmincola* was at 2,500 parasites/g kidney. Most of the fish, including prespawning mortalities, were below this threshold. Regardless if the salmon survive to spawn, heavy infections by multiple parasites are common in adult Pacific salmon after they return to freshwater. Presumably this is because they are immune compromised and destined to die after spawning. This presents a challenge when determining which pathogens contribute to early mortality, and at this point, it is still not clear which parasites are the most strongly linked to premature death.

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THE PROTEOMIC INTERFACE OF STRESS, PARASITES, AND HOSTS: LESSONS FROM SALMON AND COD

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Stress in fish leads to physiological changes that can be identified using molecular and proteomic techniques. These methods can provide information on what is happening at the cellular level during a host' stress response. Genetics will identify novel genes while a proteomic approach will identify proteins and changes in these proteins through post-translational modifications. Interactions between the stressor and the host are at the protein level thus changes in protein complement can indicate an alteration in the homeostatic state of the animal. Fish were subjected to stressors including sea lice and chemicals used in bath treatment of ectoparasitic infection. Mass spectrometry data showed transferrin and apolipoproteins in epidermal mucus from both salmon and cod. Protein profiles of mucus from cod have been illustrated using SDS-PAGE and preliminary results show similar patterns given the treatment. Ongoing studies include identification of genes and measurement of expression during treatment and infection stress. Characterization of molecules and mechanisms involved in disease susceptibility with a particular interest in the interplay between stress and immunity is suggested.

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EXPRESSION AND LOCALIZATION OF *PLASMODIUM*-EXPORTED PROTEINS IN THE LIVER STAGES

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After invading a host erythrocyte, *Plasmodium falciparum* induces extensive modification of the host erythrocyte. Thus far, the expression and localization of Plasmodium-exported has only been studied in the erythrocytic stage. Very little is known about the *Plasmodium* proteins exported during the liver stage. We have previously characterized PfEXP-250, a unique *P. falciparum*-exported protein containing a PEXEL motif located at the carboxy terminus of the protein. PfEXP-250 is highly conserved and has paralogues in *P. vivax*, *P. yoelii* and *P. berghei*. We have also found EXP-250 to be expressed in sporozoites and in the exo-erythrocytic forms of *P. berghei*. However, EXP-250 does not appear to be exported in the sporozoite and exo-erythrocytic forms. We have examined the expression of skeleton-binding protein 1 (SBP-1) and ring-exported protein 1 (REX-1) in *P. berghei* and found both to be expressed in the liver stage. However, REX-1 and SBP-1 were not exported in the liver stage, suggesting that protein export occur at specific stages of the parasite life cycle.

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MOLECULAR CHARACTERIZATION OF THE SCHISTOSOME SURFACE

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Intravascular schistosome parasites are covered by an unusual double lipid bilayer. This surface constitutes a major site of interaction with the host. In recent years proteomic analysis has been used to assess the protein composition of the tegumental surface bilayers. The precise functions played by many of the molecules found in the tegumental surface membranes, and how they avoid being targeted by effective host immunity, are largely unknown. We are using RNA interference (RNAi) to suppress the expression of genes whose products are found in the host-exposed tegumental membranes. In this way, we have begun a functional characterization of the schistosome surface. It has been found that suppressing the expression of genes encoding tegumental glucose importing proteins (SGTP1 and SGTP4) impairs parasite feeding and severely decreases their viability. In work that expands the known functions of the tegument, we observe that suppressing the tegumental aquaporin gene (SmAQP1) makes the parasites less able to osmoregulate and impairs their ability to excrete lactate. Finally, selective suppression of genes encoding tegumental phosphatases has allowed us to delineate a pathway whereby schistosomes could degrade host pro-inflammatory and pro-thrombotic signaling molecules. Our experiments are designed to generate a comprehensive understanding of the role of the schistosome tegumental surface in promoting parasite survival through immune modulation and by controlling the movement of metabolites into and out of the tegument.

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SITE FIDELITY OF AMPHIBIAN HEMIURID TREMATODES IN THE GENUS *HALIPEGUS*: DOES AMPHIBIAN HOST MATTER?

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Species of *Halipegus* infect the intestine, stomach, esophagus, buccal cavity, or eustachian tubes of amphibians and exhibit incredible site fidelity in their anuran hosts. Two species of *Halipegus* have been reported from North American anurans. *Halipegus eccentricus* resides in the eustachian tubes of frogs, whereas *H. occidualis* resides on the lingual veins under the tongue of frogs. However, surveys of anurans in North America indicate that populations of *H. occidualis* from eastern North America reside under the tongue of frogs, whereas populations of *H. occidualis* from western North America reside in the stomach of frogs. Our surveys of anurans of 12 species from Nebraska and Oklahoma revealed gravid *Halipegus* sp. from the stomach of bullfrogs morphologically indistinguishable from *H. occidualis*. In order to investigate this site fidelity, we established this life cycle in the laboratory. Three species of laboratory reared snails (*Physa gyrina*, *Planorbella trivolvis* and *Biomphilaria glabrata*) were exposed to eggs from worms recovered from the stomach of naturally infected bullfrogs. Sixty DPI *P. trivolvis* shed cercariae morphologically indistinguishable from the cercariae of *H. occidualis*. Next we exposed laboratory reared ostrocods (*Cypridopsis* sp.), harpacticoid copepods (*Phyllognathopus* sp.), and cyclopoid copepods (*Thermocyclops* sp.) to laboratory reared cercariae. Cercariae developed to infective metacercariae within 15-20 DPI in all 3 species of microcrustaceans. Infected microcrustaceans were then fed to Woodhouse's toads and adult gravid worms appeared on the lingual veins under the tongue of toads 50-75 DPI. Our data suggest that site fidelity of *H. occidualis* differs in different amphibian hosts and depends on the species of amphibian these worms infect. These findings have implications for speciation in the genus *Halipegus,* particularly when considering amphibian biogeography and their overlap with their hemiurid trematodes.

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LONGTERM *BIOMPHALARIA GLABRATA/SCHISTOSOMA MANSONI* INFECTIONS STUDIED BY RNA-SEQ

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The penetration by a *Schistosoma mansoni* miracidium into a susceptible *Biomphalaria glabrata* snail initiates a long term parasitic infection with dramatic impact on the snail host. As consecutive stages of intramolluscan schistosome larvae develop, asexual multiplication increases the parasite-contributed biomass within the snail. For survival, growth and progression of the life cycle, schistosomes modify neurophysiology, immunology, metabolism and reproductive output of the snail host. It is currently not known how these complex interactions contribute to host-parasite compatibility, parasite development, survival of infected hosts and parasite transmission. A 454 RNA-seq approach (pyrosequencing) was used to study the interactions between snail and intramolluscan larvae. Total RNA was extracted from M line *B. glabrata* snails, harboring *S. mansoni* at 3 weeks post infection (wpi; sporocysts present), 5 wpi (sporocysts, starting to shed cercariae) and 8 wpi (prolonged shedding of cercariae). Purified mRNA was used to generate a cDNA library for one infected snail per time point each. Massively parallel 454 sequencing of random transcripts yielded 668,534 reads (5wpi sample) and 799,434 reads (8wpi). The ratios of *B. glabrata* versus *S. mansoni* contributed transcripts were 56.3%/41.9% at 5 wpi and 61.7%/37.1% at 8wpi. Comparison against the *S. mansoni* unigene data and preliminary assemblies of *B. glabrata* genome and transcriptome indicate that the sequence data represent transcripts of some 7000 *S. mansoni* genes and over 12000 *B. glabrata* genes, with many expressed differentially between time points. Comparative analysis (including data forthcoming for 3wpi) is performed to reveal differentially expressed sequences and the pathways involved.

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DOES PARASITE IMMUNE FUNCTION CONTRIBUTE TO SURVIVAL OF LONG-TERM *SCHISTOSOMA MANSONI*-INFECTED *BIOMPHALARIA* SNAILS?

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The successful long term establishment of *Schistosoma mansoni* infection in B*iomphalaria glabrata* relies on suppression by the parasite of immune function of the snail intermediate host. How then does the parasite/host combination survive in an environment full of opportunistic pathogens (bacteria, fungi, viruses) to assure release of cercariae as needed for completion of the life cycle of *S. mansoni*? Especially snails with patent infections that are continuously "wounded from within" by emerging cercariae may frequently be exposed to secondary infection. Is the immune capability of parasitized *B. glabrata* adequate or does *S. mansoni* contribute to immune function? Publicly available transcribed sequence data for *B. glabrata* were used to design a snail microarray containing over 30,000 unique 60-mer oligos for commercial production by Agilent (ID:030447). This snail array and another schistosome- specific array (designed Gobert et alm ID: 016061) were used to record transcription profiles from host snail and schistosome parasite using RNA samples extracted from whole bodies of *B. glabrata* snails with *S. mansoni* infections. Host and parasite were analyzed at a) 3 weeks post infection (wpi), before cercariae production; b) ~5 wpi at the first appearance of cercarial shedding; and c) 8 wpi with prolonged cercariae shedding. Samples were also taken at these time points for schistosome-infected snails that were exposed for 1 day or 1 week to bacteria by seeding the snail tanks with *Escherichia coli* and *Micrococcus luteus*. Microarrays were hybridized with labeled probes generated from RNA pooled from 5 schistosome-

harboring snails (3 replicates). Analysis of snail responses is pending, but sixty transcripts, including ferritin, cystatin and an immunophilin-binding protein, were differentially expressed by the parasite (5wpi) when bacteria were added to the snail tanks. These results may provide insight in survival and persistence of cercariae-shedding *Biomphalaria* snails in the field.

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MICROARRAY TRANSCRIPTION PROFILES OF *BIOMPHALARIA GLABRATA* RESISTANT AND SUSCEPTIBLE FOR *SCHISTOSOMA MANSONI*

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Immunological compatibility between *Schistosoma mansoni* and a *Biomphalaria glabrata* snail is determined genetically and becomes evident only after the parasite penetrates into a potential snail host. Analysis of the responses of predictably resistant or susceptible snail strains to invading schistosomes, and other immune challenges, may show which components of the internal defenses of *B. glabrata* contribute to immuno-elimination of larval schistosomes. Additionally, this approach may potentially identify particular (patterns of) expressed genes that serve as early predictors of susceptibility or resistance in the snail for schistosome infection. Such markers could in turn help to estimate host competency of *Biomphalaria* in endemic areas to help interpret patterns of transmission of schistosomiasis. Initial analyses of microarray data revealed differentially expressed transcripts representing novel or unknown sequences, 53 from resistant snails and 25 in susceptible snails, within 12 to 48 hours following exposure to *S. mansoni*. A new 60-mer oligo-based microarray incorporating 30,000 sequence features from *B. glabrata* (design made commercially available as Agilent ID:030447), was used to monitor differences in the (immune) responses of BB02 snails, susceptible to *S. mansoni* and of resistant BS90 snails. These snails are subjected to wounding, bacterial challenge and schistosome exposure. RNA was extracted and pooled from 5 snails at 12h, 24h and 120h post treatment to generate probes for querying of the array, relative to controls. Analysis is performed to reveal differentially expressed sequences of *B. glabrata* and the pathways involved, in relation to resistance or susceptibility for *S. mansoni*.

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BIOMPHALARIA GLABRATA SNAIL HOSTS OF *SCHISTOSOMA MANSONI* ARE IMMUNOLOGICALLY DIVERSE

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For interpretation of host-parasite interactions and transmission of parasites by invertebrates, it is important to consider the mounting evidence that reveals considerable sophistication of anti-pathogen defenses in invertebrates. Diversification of innate immune factors broadens both the potential specificity of defense responses and the range of non-self recognition in ways that dynamically affect the immuno-compatibility between parasites and invertebrate hosts. *Biomphalaria glabrata*, a snail intermediate host that transmits *Schistosoma mansoni* (digenetic trematode that causes human schistosomiasis) reacts to infection with a complex set of soluble parasite-reactive lectins, including fibrinogen-related proteins (FREPs). FREP genes undergo somatic diversification and may function to counter the antigenic variation capabilities of *S. mansoni* that result in individually diverse antigen repertoires of *S. mansoni* polymorphic mucins (SmPoMucs). It was investigated whether the occurrence of diversification of immune factors in *B. glabrata* is more common than previously assumed. To expand insights into immunity of *B. glabrata*, FREPs and other putative non-self recognition factors, identified by

transcriptomic approaches, were investigated for sequence diversity using bioinformatics (preliminary Genome Assembly v2.1), as well as single strand conformation polymorphism (SSCP) analysis and sequencing of multiple cloned PCR amplicons derived from subsets of hemocytes from individual snails (M line lab-strain and a recent field isolate from Brazil). Sequence diversity of FREP4 was detected by SSCP and confirmed by sequencing. Lab strain and a field isolate share common FREP4 sequences, and each has unique variants. SSCP indicates diverse sequences for multiple defense factors and as well as genomic level sequence diversity of additional immune factors of *B. glabrata*.

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HOW DOES THE BOPYRID PARASITE *PROBOPYRUS PANDALICOLA* AFFECT THE DAGGERBLADE GRASS SHRIMP *PALAEMONETES PUGIO*: A CLOSER LOOK AT ABUNDANCE, GROWTH RATES, BEHAVIOR, AND PREDATION

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The daggerblade grass shrimp *Palaemonetes pugio* is host to a variety of parasites including the bopyrid *Probopyrus pandalicola*. This parasite has the potential to reduce shrimp densities because hosts no longer reproduce while infected. Mean parasite prevalence ranged from approximately 1-3% in South Carolina and Georgia estuaries. We have found that there is no effect of the parasite on shrimp behavior or swimming endurance. Instead, shrimp activity was affected by size, tidal stage, and time of day. Furthermore, there was no effect of the parasite on the likelihood of shrimp being eaten by the mummichog *Fundulus heteroclitus*. Fish ate more active individuals regardless of parasite presence. Recently our research is focusing on the effect of multistressors (shrimp with parasites plus insecticides or coded wire tags) and we have found differences in predation rates, growth, and LC_{50} values when shrimp are parasitized.

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PROCESSES INFLUENCING THE DURATION AND DECLINE OF EPIZOOTICS IN *SCHISTOCEPHALUS SOLIDUS* INFECTING THREESPINE STICKLEBACKS

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The interplay of intermediate host fish and plerocercoids of diphyllobothriidean cestodes results in epizootics which are deceptively simple, but which conceal complex biotic and abiotic interactions shaping each event independently. Although general descriptions of epizootics and some details of biotic interactions between enemies are known, much remains to be discovered about the abiotic and biotic forces and their interactions driving epizootics. This study shows that the duration of an epizootic of *Schistocephalus solidus* was sustained by high prevalence, mean intensity, and PI levels among young-of-the-year and 1-year-old threespine sticklebacks. Many infections and most parasite growth in young-of-the-year fish apparently occurred under the ice during the winter. Few new infections appear to have occurred among 1-year-old fish, which may live 2 years and sometimes 3 years. The decline of the epizootic occurred as the recruitment of 1-year-old to 2-year-old hosts decreased significantly, followed by

reduced infections of young-of-the-year fish. Thus, a major factor influencing parasite population dynamics was reduced transmission (probability of infection) as a result of over-winter host mortality among 1-year-old fish. Mega-epizootics, named and described here, appear to represent a 'perfect storm' phenomenon dependent on a particular and rare combination of circumstances. Less extreme and more gradual epizootics may be more common and play out in myriad ways due to complex abiotic and biotic factors influencing both parasite and host populations. The interplay of parasite and host resulting in reciprocal effects upon one another occurs during both the emergence and decline phases of an epizootic.

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APODEMUS AND *EIMERIA*: POPULATION STRUCTURE, HOST SPECIFICITY AND BIOGEOGRAPHY

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The question of host-parasite coevolution belongs to the most intriguing issues in parasitology. In the species-rich genus *Eimeria*, this question has been mainly studied on the phylogenetic level, using mostly the conserved sequences of 18S rDNA. In this study, we present a pilot analysis on the population structure of *Eimeria* in three closely related host species based on the mitochondrial cytochrome c oxidase subunit I (COI) gene. We chose the field mice *Apodemus agrarius*, *A. flavicollis* and *A. sylvaticus* as the model hosts, since they represent the most common rodent species in the Czech Republic that live in sympatry. This feature is an important basis for disentangling the influence of host-specificity and biogeography on the population structure and speciation of *Eimeria*. Moreover, several population-genetic studies show that even phylogenetically and ecologically closely related species, such as *A. sylvaticus* and *A. flavicollis*, differ in many aspects of their evolutionary histories and phylogeography. We sequenced ~700 bp of eimerian COI from 50 *Eimeria*-positive samples from 6 European countries (Czech Republic, Slovakia, Germany, Italy, Macedonia and England) and analyzed the sequences by phylogenetic and population-genetics methods. Preliminary results indicate that *Eimeria* species divide into five clades whose arrangement is not dependent on the host species and/or geographic origin.

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BISTABILITY IN *GIARDIA LAMBLIA* ENCYSTMENT

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The protozoan parasite *Giardia lamblia* exists as either a vegetative trophozoite or an infective cyst. Differentiation of *Giardia* trophozoites into dormant forms (encystment) in response to physiologic stimuli is crucial for its pathogenesis. In vitro, *Giardia* encysts when bile sequesters lipids necessary for this lipid auxotroph, and in vivo they encyst to infect new hosts. During encystment, *Giardia* trophozoites elicit a unique pattern of gene expression that results in the synthesis and transport of cyst wall components and ultimately, formation of the protective cyst wall. Initiation of this developmental program appears to be a regulatory process with a bistable outcome; when trophozoites are induced to encyst, a significant proportion of the population remains undifferentiated after 72 hours in encysting conditions. Using a single cell approach, we show that trophozoites induced to form cyst respond heterogeneously to encystment; encystment specific proteins (cyst wall protein 1 and cyst wall protein 2) are expressed in a non-uniform manner across the population. The signaling pathways that regulate encystment also exhibit bistable properties; trophozoites induced to form cyst become committed after a short period of time and the production of encystment specific proteins is stably maintained. After 6 hrs

in inducing conditions, encysting trophozoites continue to encyst regardless of whether the inducing stimulus remains, and transfer of encysting cells into non-inducing conditions does not result in disruption of the production of encystment specific proteins, this suggests the involvement of bistable signaling pathways during encystment.

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PHENOTYPIC AND GENETIC VARIATION OF CERCARIAE: CONSTRAINTS OF HOST SPECIFICITY?

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The constraints of host specificity are important to the understanding of the ecology of specialization and the evolution of parasitic diseases. Genotypic and phenotypic variance of parasites may constrain the range of hosts that a given parasite can infect. Phenotypic variability (developmental noise) is the variation observed among individuals once environmental and genotypic effects are removed. To test how phenotypic variability constrains host range it is necessary to control for genotypic variability. Using clonal organisms provides such a control. Parasitic trematodes, with their clonal dispersal stage (cercariae), are ideal for testing the constraints of host specificity: each genotype comes in replicates, and phenotypic variability among individuals of the same genotype can be assessed free of genetic influences. There have been no studies to date examining how genetic or phenotypic variability can provide a means for parasites to expand their host range, i.e. to succeed on a wider range of host species. In the present study we test whether organisms possessing higher genetic and phenotypic variability have higher fitness levels. Measurements of intraclonal morphological and behavioural variation among cercariae of the trematode *Maritrema novaezealandensis* were related with parasite fitness in the host following experimental infections. Additionally, heterozygosity of each clone, determined from microsatellite loci, was also related with parasite fitness. These tests were repeated in a range of host species to see if the responses are host specific. The results provide new insights into what constrains parasite performance in different host species.

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THE EFFECT OF TEMPERATURE ON SHEDDING RATE OF *EUHAPLORCHIS CALIFORNIENSIS* CERCARIAE

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Global climate change is predicted to increase the transmission rate of parasitic trematodes and other infectious diseases. Previous research has shown that cercarial production increases with temperature. This increased rate cannot continue indefinitely due to physiological limitations in both parasites and snail hosts. To better understand the role temperature plays in the transmission efficiency of dispersal stages of parasitic trematodes, we used the host-parasite system of the California Horn Snail (*Cerithidea californica*) and the digenetic trematode (*Euhaplorchis californiensis*) to investigate the effect of temperature on cercarial shedding rate. Shedding rate was measured on a total of 100 California Horn Snails collected from Carpinteria Salt Marsh Reserve in Santa Barbara County, California. The snails were placed on a temperature gradient platform to test the effect of temperatures ranging from 10 to 45°C on cercarial emergence. We found that the rate of cercarial emergence continued to increase with temperature, even as the thermal limit of *C. californica* was exceeded. This suggests that the upper temperature threshold of *E. californiensis* might be higher than that of the snail host.

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COMBINED EFFECT OF PARASITES AND VIRAL DISEASES ON SURVIVAL OF EUROPEAN WILD RABBITS

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The European rabbit is an important native species for maintaining ecosystem function in the Iberian Peninsula. Rabbits are the staple prey of at least 29 predator species. Over the last 50 years, rabbit populations have declined dramatically, mainly due to the arrival of myxomatosis in the 1950s, followed by rabbit haemorrhagic disease (RHD) in the late 1980s. There is little information on how rabbit populations are currently responding to repeated annual outbreaks of these diseases. Most studies have failed to consider the importance of co-infecting parasites on the epidemiology of these viral diseases. The prevalence and intensity of animal parasites can vary with season, year, host age, sex, immune status, the presence of other parasitic organisms, and intra-specific competition. Recent studies have shown that co-infection can be an important factor in the epidemiology of common diseases. We conducted a disease surveillance and rabbit survival study in 2009 and 2010 in southern Spain. We monitored the coccidian and gastro-intestinal nematode loads, and the prevalence of myxomatosis and RHD, in three populations of wild rabbits, bred in semi-natural conditions. Survival of both adult and juvenile rabbits was reduced by prevalence of myxomatosis and RHD, but juvenile survival was further reduced by increasing loads of parasites, with a 6-month time lag. Coccidian and helminth parasites may therefore play a role in how rabbit populations respond to viral diseases.

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HELMINTH COMMUNITIES OF THE GOLDEN GREY MULLET *LIZA AURATA* (ACTINOPTERYGII: MUGILIDAE) IN TWO WESTERN MEDITERRANEAN LOCALITIES: WHY CARE ABOUT TRANSMISSION?

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Liza aurata harbors a highly diversified helminth fauna dominated by species specific of mullets. This study provides a description of its helminth communities and investigates the role of spatial, temporal and host variables, and parasite transmission modes in determining their structure. Fish came from two Mediterranean localities ca. 290 km apart. Fish were collected from each locality in spring and fall in 2004 and 2005. To visualize a spatial ordination of the infracommunities, a self-organizing map (SOM) was built using species abundances, and subgroups based on infracommunity similarities were established by a k-means clustering method. The relationship between infracommunity composition and explanatory variables (host size, locality, and year and season of harvest) was studied by Redundancy Analysis (RDA) applied to species abundances. In order to test the influence of long-lived metacercariae in infracommunity structure, species were grouped into guilds according to transmission mode, and two additional RDAs were run including and excluding the guild formed by metacercariae. A total of 33,241

helminth parasites belonging to 18 species were collected: 12 species of adult digeneans (23% of the parasite specimens), 3 digenean as metacercariae (68%), 1 acanthocephalan (2.1%) and 2 monogenean (6.5%). The optimal number of SOM clusters did not unequivocally correspond to natural subgroups (based on localities, years or seasons), which probably resulted from high similarity between the infracommunities. However, most differences at both component and infracommunity level were related to geographical locality. In fact, the RDAs based on abundances and guild composition showed that sampling locality accounted for most variation. However, when the metacercaria guild was omitted in the analysis, time variables accounted for a higher share of variation. The total variation accounted by the explanatory variables was relatively low (~10%), which may indicate that transmission and small local and time scales can play a crucial role in helminth transmission.

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INTESTINAL HELMINTH FAUNA FROM MEDITERRANEAN BOTTLENOSED DOLPHIN (*TURSIOPS TRUNCATUS*) AND COMMON DOLPHIN (*DELPHINUS DELPHIS*)

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Information about of the helminth fauna of the bottlenosed dolphin, *Tursiops truncatus*, and the common dolphin, *Delphinus delphis*, is very scarce in the Mediterranean Sea. In this study, we provide new data on the intestinal helminth parasites of these hosts. Fifteen bottlenose dolphins and 7 common dolphins from Western Mediterranean were analyzed. A total of 8 helminth species were collected from the bottlenosed dolphin: *Synthesium tursionis*, *Brachycladium atlanticum* and *Pholeter gastrophilus* (Digenea); *Tetrabothrius forsteri, Strobilocephalus triangularis*, *Diphyllobothrium sp*. and *Trigonocotyle* sp. (Cestoda); and *Anisakis simplex*(Nematoda). In addition, 2 morphotypes of tetraphyllidean plerocercoids were identified. *S. tursionis* and *T. forsteri* showed the highest prevalence (73.3% and 40%, respectively), the latter showing the highest mean abundance and intensity. The remaining species appeared with a very low intensity and prevalence. *B. atlanticum, S. triangularis* and *Trigonocotyle sp*. represented new host records in the Mediterranean Sea.
Four helminth species were collected from the common dolphin: *Synthesium delamurei*, *Trigonocotyle sp*. and 2 morphotypes of tetraphyllidean plerocercoids. *Trigonocotyle sp*. was the most prevalent and abundant species, showing also the highest intensity of infection. The intestinal helminth communities of the bottlenosed and common dolphins in the Mediterranean are species–poor, as it is generally expected for cetaceans. Both host species have similar distribution ranges in the Mediterranean and possibly share some food resources which results in similar parasite communities. Supported by grant CGL 2009-07465 (MICINN).

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ROLE OF TEMPERATURE ON THE TRANSMISSION AND IMPACT OF A PARASITE TO ITS HOST

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It has been suggested that climate change might influence parasite-mediated impacts on local host populations. To test this idea, we conducted a series of laboratory experiments using the digenean *Ganaecotyla adunca* and its first intermediate host, the intertidal amphipod *Corophium volutator*. Specifically, we were interested in the effects an increase in temperature might have on the transmission of the parasite to its second intermediate host. We measured, under different temperatures, the output of *G. adunca* cercariae from its snail host, the survivorship and swimming activity of the cercariae, the infectivity (penetration success) of the parasite to the amphipod host, and also the survivorship of infected

hosts. The parasite output was significantly higher at 22°C than at 17°C and 12°C; however, the cercariae survived significantly shorter periods of time at 22°C than at 17°C and the numbers swimming was less at higher temperatures. The infectivity was not different between 22°C and 17°C, while the survivorship of infected hosts was only significantly shorter compared to the (non-infected) controls at 12°C and not different at the higher temperature (17°C and 22°C) treatments. Thus, the only impact higher temperature has on the parasitism of host populations, at least for this host-parasite system, is the higher numbers of infective cercariae stages exiting from snails at a higher temperature that directly penetrate their hosts, causing direct injury and death.

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INTESTINAL HELMINTHS FROM THE SOUTH AMERICAN SEA LION, *OTARIA FLAVESCENS*, FROM NORTH PATAGONIA, ARGENTINA

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In this study we report on the intestinal helminth fauna of 56 South American sea lions, *Otaria flavescens* (27 females and 29 males) stranded along the North Patagonian coast (Argentina). A total of 12 species was found. The following species had gravid individuals: the cestode, *Diphyllobothrium scoticum* (prevalence [95% C.I.]: 28.6% [17.2-42.2]; mean intensity [95% C.I.]: 3.4 [1.8-7.9]); the acanthocephalan, *Corynosoma australe* (98.2% [90.4-99.9]; 1562.8 [1153.8-2207.3]); the nematodes, *Uncinaria hamiltoni* (5.4% [1.1-14.9]; 25.7 [1.0-46.0]), *Contracaecum ogmorhini* (62.5% [48.5-75.0]; 13.3 [9.4-19.7]) and *Pseudoterranova cattani* (64.3% [50.3-76.7]; 15.2 [5.6-51.3]) and the digeneans, *Synthesium* sp. (n=1) and *Ascocotyle* (*Phagicola*) sp. (from 2 hosts; infection parameters could not be determined reliably). We also found immature specimens of the acanthocephalans *Corynosoma cetaceum* (n=7), *Profillicollis* sp. (n=1) and *Andracantha* sp. (n=1); L3 larvae of the nematodes *Anisakis* sp. (26% [15.8-40.3]; 2.4 [1.5-3.9]) and *Contracaecum* sp. (67.9% [54.0-79.7]; 67.1 [33.0-172.5]). These results suggest that South American sea lions harbour the intestinal helminth fauna that could be predicted for a pinniped (i.e., the combination of species of *Corynosoma*, *Diphyllobothrium* and Heterophyidae), except for the presence of *Synthesium* sp., which is presumably a typical parasite from cetaceans. In addition, sea lions would act as an ecological 'sink' for as many as 5 parasite species from sympatric fish-eating cetaceans (*C. cetaceum* and *Anisakis* sp.) and birds (*Profillicollis* sp., *Andracantha* sp. and *Contracaecum* sp.).

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BIOMASS INEQUALITIES IN THE ACANTHOCEPHALAN *CORYNOSOMA CETACEUM*: POPULATION SIZE AND HABITAT VARIABILITY INCREASE INEQUALITIES IN REPRODUCTIVE FEMALES

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Reproductive inequalities may have a profound impact on the population dynamics, genetics, and evolution of parasites. In this study we quantified the inequalities in biomass in females of the acanthocephalan *Corynosoma cetaceum*, a parasite from the stomach and upper duodenum of the franciscana dolphin, *Pontoporia blainvillei*. We also investigated the effects of population size and habitat variability on inequality levels. Individual worms from 10 dolphins were collected (total n = 10262) from

three sites (main stomach, pyloric stomach and duodenal ampulla) and sexed. All females (n = 5368) were then individually weighed to the nearest 0.0001 g and their reproductive status was determined: stage 1 (ovarian balls only), stage 2 (also with developing acanthors), or stage 3 (also with fully developed acanthors). Based on a sample of 15 females of stage 3 from each of 15 additional dolphins, we found that biomass was a modest but highly significant predictor of fecundity ($r^2 = 0.176$, n = 225, $p < 0.0001$). Gini values of biomass per dolphin ranged from 0.19 to 0.33, and a significant positive correlation with intensity was found ($r = 0.756$, $p = 0.011$, n= 10). When the sample was stratified by reproductive status, the relationship between Gini values and total intensity was significant only for females of stages 2 and 3 ($r = 0.755$, $p < 0.012$ in both cases), and was even stronger when total intensity was substituted by the intensity of stage 3 females ($r > 0.80$, $p < 0.005$ in both stages). Also, Gini values in stage 3 females had a significant positive relationship with the standard deviation of the mean worm (a measure of habitat variability) ($r = 0.745$, $p = 0.007$). No crowding effects were detected for any stage. Gini values for biomass in the *C. cetaceum* population are the lowest reported for any helminth species infecting vertebrates. However, increases in both population size and microhabitat variability might contribute to a modest reduction of effective size of the reproductive population.

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AN INTEGRATIVE ASSESSMENT OF SNAKE PARASITISM IN AN URBAN ENVIRONMENT

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Parasites are ecologically significant and may influence community structure through a variety of interactions. Notably, the ecological interactions of parasites in snakes are largely unknown. We integrated histology, molecular techniques, and geographic information science (GIS) to characterize parasitism of snakes in an urban park. We identified snake species and sex, measured mass and length, and collected GPS coordinates, ectoparasites, and blood and fecal samples from 34 individuals. We confirmed parasite species by amplifying the parasite's mitochrondrial cytochrome B gene or the 18S ribosomal gene, and then sequenced the isolate. We analyzed stained blood smears by microscopy and quantified immature:mature erythrocyte and heterophil:lymphocyte ratios and parasite prevalence and load. We used fecal floats to extract parasites and their ova from samples and determined parasite prevalence by microscopy. Finally, we used GIS to assess land cover surrounding each study site, determined the distance of each snake to sources of disturbance (e.g., forest edge, paved roads), and performed nearest neighbor analysis to determine spatial patterns in parasite loads. We determined that snakes in our study population host one ectoparasite, mites (*Acariasis* spp.), three types of fecal parasites, roundworms (*Ophiascaris* spp.), hookworms (*Kalicephalus* spp.), and pinworms (*Enterobius* spp.), and two blood parasites*, Hepatazoon* spp. and *Plasmodium* spp. For all snakes, we determined that ectoparasite prevalence was 0.26, fecal parasite prevalence was 0.78, and *Hepatazoon* sp. and *Plasmodium* sp. prevalence were 0.35 and 0.18, respectively. Of snakes infected with blood parasites, *Hepatazoon* sp. load was 11.1 parasites per 1,000 erythrocytes and *Plasmodium* sp. was 35.3 per 1,000 erythrocytes. Snake sex, age, and body condition were not correlated with parasitism. Using an integrative approach our results provide an assessment of snake-hosted parasite ecology that will be useful when evaluating the utility of these parasites as bio-indicators of environmental impact on snakes.

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HABITAT SELECTION AND POPULATION STRUCTURE OF *CORYNOSOMA STRUMOSUM* (ACANTHOCEPHALA) IN COMMON SEALS (*PHOCA VITULINA*) FROM THE NETHERLANDS

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We investigated population structure and habitat selection by the acanthocephalan *Corynosoma strumosum* in 96 common seals (*Phoca vitulina)* collected in August-September, 2002, along the coast of the Netherlands during a viral epidemic. *Corynosoma strumosum* has been reported as a generalist dweller of the small intestine of pinnipeds. Therefore, we firstly investigated whether there were finer microhabitat preferences in this species. In addition, we analyzed the influence of the polyginic reproductive system of this species (with males competing for access to females) on potential sexual differences in habitat selection behavior. A total of 3,458 individuals of *C. strumosum* was found. The sex and trunk length of each individual and, in the case of females, the reproductive status (mated, non-mated) was determined. Individuals of *C. strumosum*, including gravid females, were found throughout the whole intestine, although worms concentrated significantly in the posterior half of the small intestine, with only a few worms being collected in the anterior duodenum and the large intestine. Males and non-mated females exhibited a more anteriad distribution than females and mated females respectively. Males from the first third of the intestine were significantly smaller than those from the remaining sections. Females, however, tended to increase their length along the small intestine. Overall, these patterns suggest that, after excystment in the stomach, worms would reach sexual maturity in the duodenum and would copulate in the anterior half of the intestine. Mated females would then migrate into the ileum and the jejunum where conditions would be optimal for egg production. In contrast, males would tend to remain in more anteriad positions, thus increasing contacts with non-mated females, and would become less frequent in the posterior intestine, where most females would have already mated and, presumably, could not be re-inseminated.

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MOLECULAR CLONING AND CHARACTERIZATION OF A CDNA ENCODING A YOLK FERRITIN PROTEIN OF *FASCIOLA HEPATICA*

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Fascioliasis, caused mainly by *Fasciola hepatica,* is an important parasitic disease of livestock and an emerging human pathogen that merits international attention. Growing resistance to the drug of choice, Triclabendazole, is compromising control options and underscores the need to discover novel chemo- and/or immunotherapeutics. Proteins released by *F. hepatica* are key players in the host-parasite interaction and offer appealing targets for chemo/immunotherapy. Ferritins are proteins that play a central role in the maintenance of the delicate intracellular iron balance. A cDNA clone of *Fasciola hepatica* (FhYF-1), 606bp long, encoding a putative 176 amino acids polypeptide was identified. FhYF-1 polypeptide shows secondary and tertiary structure highly similar to those from ferritins of vertebrates and invertebrates. Phylogenetic tree analysis showed that FhYF-1 clustered with the ferritins of *Paragonimus westermani*, which suggest a common ancestry for ferritins of these two trematodes.

Recombinant FhYF-1 protein was expressed and purified from an *Escherichia coli* system as a GST fusion protein. FhYF-1 mRNA was upregulated in eggs and adult compared to NEJ and miracidium stages. Based on these results, FhYF-1 cDNA is considered to encode a *F. hepatica* yolk ferritin. Moreover, FhYF-1 showed strong reactivity with sera from rabbits with 4 and 12 wk of *F. hepatica* infection, which suggest that this protein could be a potential antigen for immunodiagnosis of fascioliasis.

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LEISHMANIA VIRUS 1 MICRORNA IN *LEISHMANIA GUYANENSIS*

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Leishmania Virus 1 (LV1) is a viral like particle found only in *Leishmania* species of the Amazon basin. Whether the viral like particle regulates gene expression in *Leishmania* is unknown. MicroRNAs have been described in most organisms from worms to human and recently in protozoans. MicroRNAs are a group of small RNAs that regulate gene expression posttranscriptionally in a complex process of binding to mRNA in a perfect complement or almost perfect complement that cleave mRNAs or inhibit their translation. Our hypothesis is that viral microRNAs regulate gene expression in *Leishmania*. Here we show our preliminary data using computational data analysis describing viral microRNAs in *Leishmania guyanensis*.

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GENOTYPING OF *TOXOPLASMA GONDII* FROM DOMESTIC CATS OF THREE REGIONS OF MEXICO

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The genetic variability of *Toxoplasma gondii* has been classified in recent studies, in 11 major haplogroups demonstrating a large variability, which depends on the host and geographical location.There are very few studies on *T. gondii* genotyping in animals in Mexico, and the results from other groups and ours suggest that the strains circulating in the country may be different from those found in other parts of the world. The aim of this study was to genetically characterize *T. gondii* strains found in domestic cats of the Valley of Mexico (Center) and Colima (occidental Coast). To achieve this, DNA was extracted from the heart, tongue, spleen, liver and brain of seropositive animals, and analyzed by PCR-RFLP for the *SAG2, SAG3, GRA6* and *β-TUB* genes. To attempt isolation, bioassays were simultaneously carried out in Balb/c mice. Genotyping was achieved in two cases by RFLP of the *SAG3* gene: one from the Valley of Mexico which corresponding with type I, and one of Colima corresponding to type III. One strain was isolated from a second case of Colima, which resulted to be type I for all genes studied. This work is the first in this country that reports direct genetic characterization of *T. gondii* in cat tissues and the second by bioassay.

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ACUTE TOXOPLASMOSIS IN SQUIRREL MONKEYS (*SAIMIRI SCIUREUS*) IN MéXICO

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In New World primates, *Toxoplasma gondii* is a cause of fatal multisystemic disease with development of respiratory disease and multifocal necrotic lesions. In the scientific literature, cases and outbreaks of toxoplasmosis in these species have been described; however, there are few genotyping studies. In this study, we describe a case of acute toxoplasmosis in two squirrel monkeys (*Saimiri sciureus*) in Mexico City confirmed by different techniques and characterization of *T. gondii* genotype involved by RFLP. The postmortem study of two squirrel monkeys with clinical history of anorexia, depression and sudden death, was conducted. The main macroscopic and histopathological findings included pulmonaryoedema, interstitial pneumonia, necrotic hepatitis and lymphadenitis, with presence of parasitic structures suggestive of *T. gondii* tachyzoites, which were confirmed by immunohistochemistry, transmission electron microscopy and PCR. Digestion of the *SAG3*amplicon showed similar bands to type I reference strain RH, this genotype was virulent for the primates studied which is the first described in our country and differs from those recently reported in other regions of the world and other species in Mexico.

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MOLECULAR DIAGNOSIS AND GENOTYPING OF HUMAN CASES OF PERINATAL TOXOPLASMOSIS

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Congenital transmission of *Toxoplasma gondii* occurs depending on various factors such as the trimester in which the mother is infected, the immune response, parasite load and genotype. The strains of *T. gondii* are classified in 11 haplogroups present in variable frequency along the world. In Mexico there are no studies on the genetic variability of *T. gondii* infecting humans. The aim of this study was to describe the parasite genotype in perinatal cases of toxoplasmosis. DNA samples from different biological tissues of mother/newborn pairs with perinatal or congenital toxoplasmosis (without or with clinical problems [i.e. abortion, hydrocephalus products] were analyzed by end-point PCR and real-time PCR for the *B1* gene. Genotyping was performed by PCR-RFLP of the *SAG2*, *SAG3*, *GRA6* and *β-TUB* genes. The four pairs (either the mother or the child) were positive by end-point or real-time PCR. In two mother-son pairs *β-TUB* and *SAG2* alleles were different from but related to type I strains, since they contained unique alleles. The parasite was vertically transmitted in one of these cases only, alhtough the newborn was asymptomatic. In a third case, the pattern of alleles in the mother and her son was type I for the SAG3 gene, and the infant had severe problems, and cerebral calcifications. The fourth case was a premature girl with severe clinical problems at birth who died two months later; the parasite was also type I for *SAG3* and *SAG2*. We conclude that type I and type I-related strains of *T. gondii* are infecting and affecting newborns in Mexico, although they are not always related to a bad clinical outcome.

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LONG-TERM EPIDEMIOLOGICAL TRENDS IN *ICHTHYOPHONUS* SP.-INFECTED CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) IN THE YUKON RIVER, ALASKA; 1999–2010

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Ichthyophoniasis is an emerging lethal disease of Chinook salmon (*Oncorhynchus tshawytscha*) in the Yukon River, Alaska, caused by the Mesomycetozoan parasite, *Ichthyophonus* sp. Previous studies demonstrated that ~60% of infected individuals died, reducing the overall population > 20% prior to spawning. Epidemiological sampling consisted of visual examination of heart muscle for the presence of clinical lesions, as well as *in vitro* explant culture and histopathological evaluation of tissues to detect both clinical and subclinical cases. Data collected from 2004-2010 were appended to data from a previous 5-year study (Kocan et al. 2004) to give a 12-year picture of disease trends within the host population. Mean clinical *Ichthyophonus* prevalence in male and female Chinook from 2004-2010 was 21% and 8% respectively; significantly lower than the previous 5 years. Prevalence in females declined from 45% to 9% between 2004 and 2010, paralleling a 57% decline in the number of Chinook returning to the Yukon River over the same period (Joint Technical Committee 2010). There was a positive correlation between clinical disease and fish size. Clinically diseased males increased from 5% in fish < 50 cm to 14% in fish > 91cm, while female prevalence increased from 17% in fish 65-70 cm to 21% in fish > 91cm; females less than 65 cm were rarely encountered. Clinical disease in males increased from 6% to 24% between week-1 and week-6 of their upriver migration, while female disease prevalence increased from 11% to 50% during the same period. Data collected from 1999 to 2010 showed that *Ichthyophonus* prevalence and host population numbers rose and fell synchronously 91% of the time, being out of phase only once in 11 years. Since Chinook are infected prior to entering the Yukon River, this suggests that a third factor may be affecting both fish numbers and transmission of *Ichthyophonus* prior to entering the Yukon River.

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TETRAMERES PATTERSONI IN A NORTHERN BOBWHITE POPULATION FROM TEXAS

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Tetrameres americana and *T. pattersoni* have been reported in the proventriculus of northern bobwhites (*Colinus virginianus*) from North America. However, it is unclear which species occurs in northern bobwhites in Texas. Of the two species, *T. pattersoni* is thought to be more pathogenic to northern bobwhites. Thirty-seven northern bobwhites from the Rolling Plains Ecoregion of Texas were collected in February-March 2010 and examined for *Tetrameres* spp. Sixteen (43%) were infected with 46 *T. pattersoni* (identification based on examination of all 32 male specimens), whereas no specimens of *T. americana* were found. Of the 14 female specimens, all co-occurred with males and were found in five hosts. Overall mean intensity was 2.9 + 0.6 (SE) and ranged from 1-8, whereas abundance was 1.2 + 0.3. No differences were found in prevalence between host age ($P = 0.12$) or sex ($P = 0.42$). Based on ANOVA of the ranked abundance values, adult bobwhites averaged more *T. pattersoni* than juveniles ($P = 0.05$), whereas no differences were found between host sex ($P= 0.42$) or the age by sex interaction ($P = 0.24$). This study represents the first confirmation of *T. pattersoni* occurring in northern bobwhites in Texas and points to a need for further research within the bobwhite population in Texas.

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SNAIL HOST FINDING BY MIRACIDIA OF *FASCIOLOIDES MAGNA*

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The liver fluke *Fascioloides magna*, is a digenetic trematode infecting deer, primarily in North America. Miracidia hatch from eggs passed in deer feces, then seek out and infect a snail. A limited number of Lymnaeids (*Lymnaea caperata, L. elodes, Fossaria parva, F. modicella*) have been found naturally infected by *F. magna*, but several species, including *L. catascopium* in this study, have proven susceptible to experimental infection. Susceptible snail hosts share habitats with non-susceptible snails, both Lymnaeids and other genera, and snail density and diversity should affect a miracidium's ability to find and infect appropriate intermediate hosts. We tested geotaxis and phototaxis of the miracidia and two snail hosts (*L. caperata* and *L. catascopium*); chemotaxis and host-recognition capabilities of miracidia; and minimum snail density, with or without decoy snails, to examine strategies and limitations of snail host finding by *F. magna* miracidia. Snails and miracidia were positively phototaxic, but did not display clear geotaxis. Miracidia were positively chemotaxic toward intact snail hosts, but phototaxis could override the chemotaxic response. We saw no difference in infection rates when individual snails were exposed to a single miracidium in 10, 100, or 1000 ml, but infection rates decreased at a density of 1 snail per 10 liters. There was a trend for decoy snails, especially snails in the same genus, to decrease infection rates in the natural intermediate host, *L. caperata*. In competition assays with single miracidia, *L. caperata* and *L. catascopium* were infected at equivalent rates. Infection rates for *L. caperata* were slightly reduced with a non-susceptible decoy snail (*Gyraulus* spp.) as well, but it is unknown whether miracidia attacked these snails and failed or the decoys simply decreased the ability of miracidia to find appropriate hosts.

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PRESENCE OF *LEISHMANIA* AMASTIGOTES IN INTESTINE OF DOGS

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Canine visceral leishmaniasis (CVL) is caused by a protozoa parasite of the specie *Leishmania* (*L.*) *chagasi,* endemic in humans and dogs in many regions of Brazil. The purpose of the present study was to evaluate by histochemistry as well as by immunohistochemistry the presence of *Leishmania* amastigotes in intestines from a group of *Leishmania*-infected dogs. For this study, intestinal tissue samples, including small and large intestines were harvested from 10 polysymptomatic *Leishmania*-infected dogs euthanized by the Zoonotic Disease Control Center from Ilha Solteira, SP, Brazil. This study demonstrated the presence of amastigote parasites in the lamina propria (villus and cripts), submucosa and muscular layers (circular and longitudinal smooth muscles) of the small intestines (duodenum, jejunum and ileum) and in the lamina propria and submucosa of the colon (large intestine) in two dogs. The amastigote forms were particularly seen inside mononuclear cells. In smooth muscle layers, the parasites were seen between the muscle fibers associated with inflammatory cells. Nodular inflammatory reaction was observed also in the submucosa. The presence of amastigote forms of *L.* (*L.) chagasi* in the intestine of dogs suggests the importance of these organs in CVL disease and needs further investigation.

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SERUM PROTEOME OF EIMERIA-INFECTED BROILER CHICKENS

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Poultry coccidiosis is an intestinal disease caused by protozoal parasites of the genus *Eimeria* and continues to result in substantial economic losses to the industry. Much is still unknown about the host response to infection with no reports of protein profiles in the blood of *Eimeria*-infected birds. This study evaluated the serum proteome of two genetic lines of broiler chickens after infection with one of three species of *Eimeria*. Birds from lines A and B were either not infected or inoculated with sporulated oocysts from one of the three *Eimeria* strains at 15 d post-hatch. At 21 d (6 d post-infection), whole blood was collected and lesion scoring was performed. Serum was harvested and used for 2-D gel electrophoresis. A total of 1,266 spots were quantitatively assessed by densitometry. Protein spots showing a significant effect of coccidia strain and/or broiler genetic line on density at P<0.0520.01 (250 spots), P<0.0120.001 (248 spots), and P<0.001 (314 spots) were excised and analyzed by matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry. Proteins were identified in 172 spots. A total of 46 different proteins were identified. Of the spots with a corresponding protein identification, 57 showed a main effect of coccidia infection and/or 2-way interaction of coccidia infection x broiler genetic line at P<0.001. Several of the metabolic enzymes identified are potential candidates for early diagnostic markers of *E. acervulina* infection including malate dehydrogenase 2, NADH dehydrogenase 1 alpha subcomplex 9, and an ATP synthase. These proteins were detected only in Line A birds that were inoculated with *E. acervulina*. Results from this study provide a basic framework for future research aimed at uncovering the complex biochemical mechanisms involved in host response to *Eimeria* infection, and in identifying molecular targets for diagnostic screening and development of alternative preventative and therapeutic methods.

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GLYCOTOPE SHARING BETWEEN LARVAL *SCHISTOSOMA MANSONI* AND HEMOLYMPH OF SUSCEPTIBLE AND RESISTANT *BIOMPHALARIA GLABRATA* SNAILS

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The sharing of molecular structures at the parasite-host interface has been hypothesized as a possible mechanism (termed “molecular mimicry”; Damian, 1964) by which the parasite may avoid or escape detection by the host’s immune system. Because of the widely accepted notion that lectins (nonenzymatic carbohydrate-binding proteins) function as pattern recognition receptors in innate immunity, and the fact that lectins are present in the hemolymph of the snail *B. glabrata*, it also has been suggested that glycans presented by invading larvae may represent important ligands mediating host immune recognition/reactivity. Given this scenario, as protection against a lectin-based internal defense system, selection may have favored schistosome larvae that exhibited similar glycan structures as the snail host, thereby reducing host immunoreactivity. In the present study, using a panel of schistosome glycan-specific monoclonal antibodies, cross reactivity with plasma and hemocyte glycoproteins was evaluated by Western blot analyses in inbred susceptible (NMRI) and resistant (BS-90)*B. glabrata* strains. Results revealed both qualitative and quantitative differences in glycan expression on plasma and hemocyte proteins, with NMRI snails exhibiting higher levels of protein-associated shared glycans than those of the BS-90 strain. Overall, it appears that early *S. mansoni* larval stages exhibit a greater degree of glycotope

sharing with hemolymph proteins of susceptible NMRI snails than those of the BS-90 strain. However, treatment of blotted hemolymph components with transformation proteins released by *in vitro* cultured miracidia/sporocysts (LTPs) partially blocked anti-glycan reactivity indicating a complex interaction between host proteins, shared glycans and LTPs released during initial larval infections.

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PERFORMANCE, INTESTINAL MORPHOLOGY, AND AMINO ACID DIGESTIBILITY OF BROILERS ADMINISTERED A LIVE COCCIDIA VACCINATION AND FED DIETARY PHYTIC ACID

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A study evaluated if the reduced nutrient availability from phytate combined with the hindered absorption from coccidia will synergistically diminish bird performance, as it has been suggested that the antinutritive effects of PA may be more severe when intestinal absorptive capacity is limited. Day old broilers were obtained from a commercial hatchery, weighed, and half were spray-vaccinated with a live coccidia vaccine before placement into pens with clean pine shavings. Vaccinated and non-vaccinated birds were given one of three diets with different phytic acid (PA) levels (low = 0.20% phytate-P; medium = 0.28% phytate-P; high = 0.36% phytate-P) for a total of 6 vaccination X diet treatments (12 replications/treatment). Performance data were measured on days 18 and 30. On day 21, ileal digesta was collected for amino acid (AA) digestibility, and duodenal, jejunal, and ileal tissue samples were collected for histological examination. Vaccinated birds given diets with added PA had lower feed intake ($P \leq 0.0089$ to 0.0003) and body weight gain ($P \leq 0.0145$ to 0.0003) compared to the non-vaccinated birds given the same diets. Feed conversion was worsened ($P = 0.0120$) from d 18 to 30 by vaccination, but birds given the medium PA diet generally had improved FC ($P \leq 0.0158$ to 0.0001) compared to birds given the low or high PA diets. Vaccinated birds given the medium PA diet had higher mortality ($P \leq 0.0009$ to 0.0001) than all other treatments. Phytic acid alone generally resulted in longer villi while vaccination alone tended to increased crypt depth. Vaccination and PA both had main effects on apparent ileal amino acid digestibility where vaccination decreased ($P < 0.0001$ to 0.0047) apparent IAAD of most amino acids on d 21 and addition of PA improved ($P = 0.0001$ and 0.0011) total IAAD. These results suggest that phytic acid in the diets of broilers vaccinated with a live coccidia oocyst vaccine could elicit negative consequences on FI, BWG, and mortality, while combined effects on intestinal morphology and apparent IAAD are less conclusive.

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TOXOPLASMOSIS IN CAPTIVE AUSTRALIAN MARSUPIALS IN MéXICO

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Australian marsupials are considered susceptible to infection by *Toxoplasma gondii*: clinical cases and outbreaks of acute and chronic infections, in both free-living and captive animals have been described. The most common histopathological findings include degenerative changes, inflammation and necrosis in several organs with the presence of parasitic structures. To date, few studies relating the pattern of injury by *T. gondii* with the genotype involved have been done. The aim of this study is to describe the pathological findings of toxoplasmosis in Australian captive marsupials living in two zoos of Mexico, and the parasite genotypes involved. Formaldehyde-fixed and and fresh tissues were recovered from different

samples from 15 animals suspected of toxoplasmosis, and processed with routine methods for histopathology, immunohistochemistry (IHC), PCR and PCR-RFLP. Microscopically, degenerative, inflammatory and/or necrotic lesions were observed in lungs, livers, spleens, lymph nodes, stomachs, myocardia and brains. The presence of parasitic structures compatible with tachyzoites or tissue cysts of *T. gondii* was confirmed by IHC in all cases and in 11 of 15 cases by PCR for at least one of the *B1*, *SAG2*, *SAG3* or *GRA6* genes. PCR-RFLP analysis demonstrated type I alleles of the *GRA6* and *SAG3* loci. The results differ from those of other regions, which have been reported to be type III in wallabies with blindness and neurological signs (U.S.), genotypes II and III in disseminated toxoplasmosis of kangaroos (in Argentina), and atypical genotypes in kangaroos of Australia, with neurological signs and sudden death.

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INVASION KINETICS OF *TOXOPLASMA GONDII* RH AND ME49 STRAINS TO HUMAN ENDOTHELIAL CELLS

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Toxoplasma gondii can cause congenital infection in the developing foetus. Endothelial cells will become infected during the dissemination of the parasite and the invasion of the cells lining the villous blood vessels is potentially one of the major transmission routes to the foetus. The invasion of epithelial barriers has been claimed to be at least partially due to the parasite virulence. Thus, the aim of this work was to compare the invasion kinetics of the RH (virulent) and ME49 (non-virulent) strains in a semi-immortalized human microvascular endothelial cell line (HMEC-1). The cells were grown in 24-well culture dishes at 100,000 cells/well for three days and the tachyzoites of the RH and ME49 strains were added at a 10:1 (parasite:cell) ratio and incubated with or without antibiotics (penicillin G, streptomycin, amphotericin B) at different times (0.5, 1, 2, 3, 4h). The supernatants were collected to count free parasites and the cells on slides were fixed, stained with Wright to determine the proportion of infected cells and the number of vacuoles per cell. The percentage of infected cells was positively related to the time for both strains; however, in those experiments with antibiotics the invasion degree was lower in comparison to those without. The ME49 strain entered much faster to the cells than the RH in antibiotic-free cultures, although both strains infected around 60% of cells after 4h. The number of parasites/cell increased with time, being faster and larger for the ME49 strain, but at all times ~50% cells beared 1 parasite only. We found differences between these strains in their capacity to infect HMEC-1 cells, but opposite to what it was expected on the basis of their virulence in mice.

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WINNER TAKES ALL: INTERSPECIFIC AND INTRASPECIFIC COMPETITION AMONG AUSTRALIAN PARASITOIDS FOR THEIR HOST, THE LIGHT BROWN APPLE MOTH.

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Many parasite species compete in the same host and thus allocate nutrients and space differentially allowing them to coexist. This is in stark contrast to competition among parasitoids however. When different female parasitoids oviposit on the same host, the offspring that win the ensuing competition take everything, subjecting the loser to death. I investigated this competition among and between two species of Australian parasitoid wasps that utilize the Light Brown Apple Moth, *Epiphyas postvittana*, as their host. One Australian species, *Dolichogenidea tasmanica* (Braconidae) is a solitary endoparasitoid and the second species*; Goniozus jacintae* (Bethylidae) is a gregarious late larval ectoparasitoid. I compared clutch size (number of offspring placed on/in a host), development time, survival rates, size and sex-ratio

between offspring from hosts parasitized by one female, and those from hosts subjected to either intraspecific or interspecific competition. I compared these factors on hosts ranging in age and freshweight. Clutch size was significantly higher on larger and older hosts. Survival and clutch size was greater on hosts that had been previously parasitized by another female. In addition offspring size was influenced by host size and the clutch size on that host. It is important to acknowledge any antagonistic behavior among these parasitoids, as they are being investigated for potential as biological control agents for the Light Brown Apple Moth invasive in California. Differences between parasitoids and parasites with regards to competition for hosts and the outcome are important contributions to the discipline of parasitology.

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COMPARATIVE EVOLUTION OF PARASITIC SCABIES MITES AND FREE-LIVING HOUSE DUST MITES

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The ectoparasitic mite, *Sarcoptes scabiei*, has co-evolved with its mammalian host over evolutionary time. The co-evolution has favored selection of parasite adaptations that allow it to down-regulate aspects of the host's innate and immune responses. Hosts are initially infested with very few parasites so these adaptations favor the parasite's survival and its ability to establish a population on the host. In contrast, ancestral mites of the related family Pyroglyphidae were skin/feather parasites of birds and mammals. It is theorized that some of the species in this family (house dust mites) became free-living in the host's nest and fed on shed skin flakes. However, their parasitic ancestors likely could also modulate the host's immune responses. Because these adaptations were no longer needed, some or all of these unnecessary modulating factors could be lost over evolutionary time without detriment to the organism. Thus, we have compared the immune modulating properties of the scabies mite, *S. scabiei*, and the common allergy-causing house dust mites, *Dermatophagoides farinae*, *D. pteronyssinus*, and *Euroglyphus maynei* on effector cells of human skin. We have done this by stimulating skin cells with mite extracts or live mites and measuring cytokine secretion and adhesion molecule expression using ELISA. We have found that scabies mites can down-regulate expression of many cytokines and adhesion molecules of skin epidermal keratinocytes, dermal fibroblasts and dermal microvascular endothelial cells. In contrast, house dust mites down-regulated secretion of some cytokines, but many fewer than did scabies mites, and they did not down-regulate expression of adhesion molecules.

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IMMUNODIAGNOSIS OF HUMAN FASCIOLIASIS USING A TEGUMENTAL SOLUBLE EXTRACT AS ANTIGEN

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Fascioliasis, caused by the common liver fluke *Fasciola hepatica* affects primarily sheep and cattle. Recently, it is has also been considered as an emerging human pathogen, with about 17 million people infected. The outer membrane of the parasite, the tegument, is a complex antigenic structure that plays a key role in the host-parasite relationship. Tegument is the interphase between the parasite and immune system and is widely believed that the tegument plays an essential role in the stimulation of immune responses against parasite. The potential of tegumental antigens for immunodiagnosis of fascioliasis remain unexplored. In the current study we prepared a tegumental *F. hepatica* extract that was used as

antigen in an enzyme-linked immunosorbent assay (ELISA) to detect antibodies in sera of patients with chronic fascioliasis. The results of this assay were compared with those obtained with the ELISA assay that use *F. hepatica* excretory-secretory (ES) antigen, which is traditionally used for serodiagnosis of fascioliasis. A total of 119 serum samples were analyzed. It included 51 sera from persons infected with *Fasciola hepatica,* 12 sera from persons infected with *Schistosoma mansoni,* and 56 sera from healthy humans. Coprologic examination was taken as a gold standard for the evaluation of the assays. The diagnostic sensitivity, specificity, predictive values of ELISA was determined for each antigen. The Tegument-ELISA assay showed sensitivity of 92.7%, specificity of 100% and positive and negative predictive values of 92.9% and 100% respectively. The diagnostic sensitivity and negative predictive values of the ELISA using ES antigen were 100% whereas the specificity and positive predictive values were 93.5% and 88.1% respectively. Using immune blotting techniques, we identified immunodominant antigens using immune blotting, we identified immunodominant antigens of 52, 38 and <10KDa recognized by most of the sera from fascioliasis patients. Our results demonstrate that the ELISA assay using Tegument antigen is comparable, if not superior, to the ELISA using ES-antigen for serodiagnosis of human fascioliasis.

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ROLE OF THE *FASCIOLA HEPATICA* ES PRODUCTS IN TLR INTERACTION

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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. 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 is possible to hypothesize that the *F. hepatica* ES products (FhES) interact with the cells of the innate system resulting in a favorable immunological response that facilitates parasite survival in the host. In the current study, we present data examining the interaction of total and molecular mass-fractioned ES antigens on human monocytes cell lines (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 conclude that ES antigens stimulate positively the TLR-4 and TLR-8 and possibly also interact with the TLR-2 and TLR-5. We also observed 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 their influence on the adaptive immune response.

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IMMUNODIAGNOSIS OF BUFFALO AMPHISTOMOSIS BY COPROANTIGEN DETECTION

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The infection of gastrointestinal helminthes in livestock is routinely diagnosed by microscopical examination of faecal samples for the presence of ova/eggs but this approach becomes ineffective for the seasonally egg producing trematodes. Therefore, an alternative approach to detect the coproantigens of liver and rumen amphistomes, *Gigantocotyle explanatum* and *Gastrothylax crumenifer* respectively, infecting Indian water buufalo *Bubalus bubalis*, was undertaken using ELISA, Immunodot and

Countercurrent immunoelectrophoresis (CCIEP). The hyperimmune polyclonal antisera were separately raised in rabbits against excretory/secretory (ES) antigens of both the flukes under study. An overall 75% buffalo faecal samples were tested positive for *G. crumenifer* and *G. explanatum* in Aligarh region. The ELISA results reflected raised infection intensity among individual buffaloes that was also observed at necropsy. Using the respective homologous hyperimmune antiserum, 80% of buffaloes tested positive for *G. crumenifer* and 65% were positive for *G. explanatum* in immunodot assay. Further, the faecal samples with high absorbance values in ELISA and strong immunodot reaction tested positive in CCIEP. The analysis of CCIEP result revealed two and one precipitin arc in *G. crumenifer* and *G. explanatum* respectively, indicating prominent antigenic differences in the coproantigens of these two parasites. Taken together, it is suggested that polyclonal antibodies could be conveniently used for the detection of coproantigens by ELISA and immunodot methods, particularly during the non-egg producing phase of the rumen amphistome *G. crumenifer*. It is concluded that the coproantigen detection is a good alternative over conventional method. Since previous reports are not available on coproantigen detection, further studies on a larger sample of field buffaloes are required to augment the reproducibility of the present results on amphistomes.

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PREVALENCE OF ANTIBODIES ANTI-*TOXOPLASMA GONDII* IN DOGS FROM THE TAPIRAPE INDIGENOUS COMMUNITY IN THE STATE OF MATO GROSSO, AMAZON REGION OF BRAZIL

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A study was conducted to determine the prevalence of anti-*Toxoplasma gondii* antibodies in dogs from 7 villages from the Tapirapé indigenous community, located in the state of Mato Grosso, Brazilian Amazon region. For this purpose, 110 blood samples were collected from all dogs, of different ages and gender, presented in the villages at the time of the visits, in September 2010. An indirect fluorescent antibody test (IFAT) was used for the detection of anti-*T. gondii* antibodies, with a cutoff value of 1:16 . Tachyzoites of the *T. gondii* RH strain were used as antigen. The effects of gender, age and hunting activities were analyzed using Chi-square or Fisher's exact test and $P \leq 0.05$ were considered significant. Antibodies anti-*T. gondii* were found in 45 (40.9%) out of the 110 dogs, and seropositive dogs were found in all villages. The IFAT titers were 1:16 in 6 dogs, 1:32 in 15 dogs, 1:64 in 12 dogs, 1:128 in 9 dogs, 1:256 in 1 dog, 1:512 in 1 dog and 1:4096 in 1 dog. No association ($P > 0.05$) was found between the presence of *T. gondii* antibodies and gender with seroprevalence values of 40.78% in male (31 out of 76) and 41.2% (14 out of 34) in female dogs. Seroprevalence observed in young (<1-yr-old) and adult (≥1-yr-old) dogs, respectively 10.5% (2/19) and 47.2% (43/91) was statistically difference ($P < 0.05$), suggesting postnatal exposure to *T. gondii* infection. Dogs used for hunting (37 in 69 dogs) presented a higher prevalence (53.6%) than dogs that never hunted (8 in 40 dogs - 20%) and this difference was significant ($P < 0.05$).

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PREVALENCE OF ANTIBODIES ANTI-*NEOSPORA CANINUM* IN DOGS FROM THE TAPIRAPé INDIGENOUS COMMUNITY IN BRAZILIAN AMAZON REGION

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A total of 110 dogs that live in 7 villages from the Tapirapé indigenous community, located in the state of Mato Grosso, Brazilian Amazon region, were used in this study. In September 2010, all the dogs

presenting on the villages during the visits had blood collected and serum was obtained. Sera were tested for antibodies anti-*Neospora caninum* by an indirect fluorescence antibody test (IFAT) using cultured derived tachyzoites of the NC-1 isolate. Sera were tested by IFAT at 2-fold serial dilutions beginning at a 1:50 dilution. The effects of sex, age and the use of the dog for hunting were analyzed using Chi-square or Fisher's exact test and P ≤0.05 were considered significant. Antibodies anti-*N. caninum* were found in 12 (10.9%) out of the 110 dogs, with at least 1 seropositive dog found in 6 of the 7 villages. The IFAT titers were 1:50 in 2 dogs, 1:100 in 5 dogs, 1:200 in 1 dog, 1:400 in 2 dogs, 1:800 in 1 dog and 1:1600 in 1 dog. The 13.1% seroprevalence of *N. caninum* in male dogs (10 out of 76) was statistically similar (P >0.05) to 5.88% (2 out of 34) observed in the female dogs. All 19 dogs with less than 1 year old were negative and 12 (13.2%) out of 91 adult dogs (≥1-yr-old) were positive to antibodies anti-*N. caninum* (P >0.05), indicating postnatal exposure to *N. caninum*. From the 69 dogs used for hunting, 11 (15.9%) presented antibodies against the parasite and from the 40 dogs that were not used in hunting activities only 1 (2.5%) were positive (P <0.05).

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EVALUATION OF ELISA AND WESTERN BLOT FOR ANTI-*TOXOPLASMA GONDII* IGG ANTIBODIES IN HUMAN SERUM SAMPLES FROM THE WHOLE POPULATION OF MEXICO

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Different serological tests have been used to detect IgG specific antibodies against *Toxoplasma gondii*. In order to have low cost immunoassays for epidemiological and clinical purposes, we evaluated two anti–*T. gondii* IgG antibody detection systems: an indirect ELISA and western blot (WB). Serum samples from the 2000 and 2006 National Survey Banks were used. Three hundred six sera from a stratified random sample of children (1 to 9 years old), adolescents (10 to 19 years) and adults (20 to 39 years) from all zones of Mexico (north, central and coast) and both genders, were tested by three enzyme immunoassays. Indirect ELISA and western blot were developed and standardized in our laboratory and preliminarily evaluated for diagnosis in pregnant women´s samples. The third test was a commercial ELISA kit. After the immunoassays were carried out, a final result was built considering three of five possible results (ELISA with a 3 standard deviation–based cut off [SD], ELISA with 4 SD, WB read by observer A, WB read by observer B and kit) and each assay was compared with it. The ELISA evaluated here identified the presence of anti–*T. gondii* with al least 93.5% sensitivity (CI_{95} = 87.7-96.7), 69.9% specificity (CI_{95} = 62.9-76.1), a ppv of 67.6% (CI_{95} = 60.3-74.2) and a npv of 94.1% (CI_{95} = 88.8-97.0). This assay can be used as a screening test for serum samples of male and female Mexican people under 40 years and from any place in the country. The western blot had 87.8% sensitivity (CI_{95} = 80.9-92.5), 93.4% specificity (CI_{95}= 88.9-96.2), a ppv of 90.0% (CI_{95} = 83.3-94.2) and a npv of 91.9% (CI_{95} = 87.1-95.1). Thus, it presented the highest diagnostic performance, but because it is relatively more expensive it will be used as a confirmatory test.

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SEROPREVALENCE AND NATIONAL DISTRIBUTION OF HUMAN TOXOPLASMOSIS IN MEXICO: ANALYSIS OF THE 2000 AND 2006 NATIONAL HEALTH SURVEYS

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Toxoplasmosis is a common parasitic disease caused by *Toxoplasma gondii*, a remarkably successful parasite found in many species of the world. In humans, *T. gondii* infections are widespread but its prevalence varies from place to place. Even though this zoonosis has been found in people from Mexico since the 50's, there is scarce information about this in recent years. A study performed during 1987 in persons of all 32 states of Mexico showed a prevalence of anti-*T. gondii* IgG antibodies between 19 and 32% by indirect immunofluorescence. Global warming has had serious implications in many aspects of human life, including infectious diseases. Since the frequency of *T. gondii* largely depends on climatic conditions, we studied the seroprevalence of toxoplasmosis using 3599 samples of the National Health Survey (ENSA 2000) and 2916 of the National Health and Nutrition Survey (ENSANUT 2006) serum banks. Sera were from one to 98 year-old subjects of both genders. They were used to search for anti-*T. gondii* IgG antibodies by indirect ELISA. Five percent of randomly selected samples and all with border-line results were confirmed by western blot. IgG antibodies to *T. gondii* were detected in 60.1% (CI_{95} = 58.5-61.7) of the ENSA 2000 and 62.1% (CI_{95} = 60.3-63.9) of the ENSANUT 2006. Coastal states had the highest prevalence and seropositivity increased with age. No significant differences were found regarding gender. A significant higher prevalence of *T. gondii* infection was observed in both surveys compared to that performed in 1987, probably due to the higher sensitivity of the immunoassay employed, to the climatic change over these 13-19 years, or both.

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UNDERSTANDING THE ROLE OF SQUID IN THE TRANSMISSION OF CESTODES IN FALKLAND ISLANDS' SHELF WATERS USING A PHYLOGENETIC APPROACH

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Globally, cephalopods are known to harbour various larval stages of rhinebothriidean, tetraphyllidean and trypanorhynch cestodes. However, the absence of distinct morphological features necessary to accurately assign them to species, or even genus, hinders our efforts to understand the ecological role(s) they play in the transmission to their elasmobranch definitive hosts. Here, we attempt to identify the various cestode larvae to species-level using a phylogenetic approach. Gene-sequence data for the D2 region of the large subunit ribosomal DNA were obtained for 160 cestode larvae recovered from two squid species from waters off the Falkland Islands: *Onykia ingens* and *Illex argentinus*. Sequence data indicate that *O. ingens* is host to one rhinebothriidean (Rhinebothriidea gen. sp.), three tetraphyllideans (*Clistobothrium* cf. *montaukensis*, *Dinobothrium* sp. and Phyllobothriidae gen. sp.) and one trypanorhynch (*Grillotia dollfusi*), whereas *I. argentinus* hosts *C.* cf. *montaukensis*, *Dinobothrium* sp., Phyllobothriidae gen. sp. and *G. dollfusi*. The sequence divergence between these larvae and respective adult worms in waters surrounding the Falkland Islands was 0%. *Clistobothrium* cf. *montaukensis* and *Dinobothrium* sp. both use the porbeagle shark as a definitive host, whereas the other three species are known parasites of

skates. More precisely, adult Phyllobothriidae gen. sp. and *G. dollfusi* are found in 12 and 13, of 13 species, respectively. Conversely, adult Rhinebothriidea gen. sp. are restricted to the inshore Magellanic skate (*Bathyraja magellanica*) and the inshore sand skates of the genus *Psammobatis*. The modes of transmission of these five tapeworms are discussed given differences in the bathymetric and/or geographic distributions of the intermediate and definitive hosts in this study.

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URINARY SCHISTOSOMIASIS AND BACTERIAL CO-INFECTION AMONG SCHOOL CHILDREN IN NDONI LOCAL GOVERNMENT AREA OF RIVERS STATE, NIGERIA

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Urinary schistosomiasis usually interferes with the capacity for work and healthy development of children. Co-infection with bacteria causes complication in the management of the disease. A study of urinary schistosomiasis and bacteria co-infection among school children in Ndoni Local Government Area (LGA) of Rivers State, Nigeria was conducted between October and December of 2010. One hundred and twenty school children, made up of 70 males and 50 females and aged 5-16 years were tested. Units of 10ml urine samples were collected from subjects and tested for presence of eggs of Schistosoma haematobium. For bacterial infection, 0.002ml of samples were inocculated onto cystein-Lactose-electrolyte deficient medium (CLED-BIOTEC, UK) and Blood agar Medium (Blood Agar base-Biotec, Uk) and incubated at 37 C for 24 hrs. Bacteria isolated were identified and characterized. The collected data were analyzed. Of the 120 pupils tested, 41 (34%) had eggs of *S. haematobium* in their urine. Males were more infected, 26 of 70 (37%) with *S. haematobium,* than females, 15 of 50 (30%). Of the pupils with ova of *S. haematobium* in their urine, 18 (43.9%) yielded bacterial growth. Of the 79 urine samples without ova, only 21 (26.5%) had bacteria. There exists a direct correlation between the distribution of urinary schistosomiasis and bacteria among school pupils in the study area. Of the 15 females with ova of *S. haematobium* in urine, 11 (73%) had concomitant bacteuria while 18 of 26 males (69.2%) had similar concomitant bacteuria. Among those aged 5-7 years, there were no bacteria in males while 1 of 15 (6.6%) females harbored bacteria. The highest yield of bacterial isolates was among those aged 14-16 years. There was a significant difference in the distribution of schistosomiasis and bacteria among various age groups ($P<0.05$). The bacteria isolates include *Escherichia coli*, *Staphylococcus aureus, S. saprophyticus and Pseudomonas* sp. with *E. coli* having the highest frequency (65.7%). Health education and treatment are recommended for speedy control of infection and reinfection.

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THE DEVELOPMENT OF *LEPEOHTHEIRUS NORDMANNI* (H. MILNE-EDWARDS, 1840) (COPEPODA: CALIGIDAE) ON THE SKIN AND MOUTH OF THE SUNFISH (*MOLA MOLA* L.)

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Lepeohtheirus nordmanni (H. Milne-Edwards, 1840) is a parasitic copepod that has been recorded in *Mola mola* (L.) and *M. ramsayi* (Giglioli, 1883). These parasites are located on the skin and the oral cavity. The adult stages of this parasite were described in detail by Hewitt in 1971, but the larval stages and biology are unknown. In the parasitological analysis of 108 sunfish sampled from Puerto de Mazarrón, Murcia, Spain, in May (2005 to 2008), copepodid, chalimus and preadult stages of *L. nordmanni* were collected and described. Furthermore, some morphological traits of the adult stages,

different from previous descriptions. Some males were observed guarding young females (first and second preadult female) to guarantee the copula, what is known as *Mate guarding*. This kind of behaviour has been reported in other species of *Lepeophtheirus*, guarding mainly second preadult females. Surprisingly, in this case, mate guarding was also observed with very early stages: copepodid and all chalimus stages. And with first and second preadult females too. Although most of the parasite stages did not show a specific location on the fish, the ovigerous females were found mainly in the oral cavity of the fishes. Despite the fact that sunfish are not fast swimmers, the low hydrodynamism of gravid females seem to oblige them to look for a refuge within the mouth. Moreover, the energetic requirements of adult females to produce the egg sacs could be more easily be attained in the oral cavity as they can feed on blood while on the thick sunfish skin they can only feed on skin and mucus. N.S.G. funded by a University of Valencia *V Segles* PhD student grant.

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DEVELOPMENT OF THE HAPTOR AND THE COPULATORY ORGAN OF TWO SPECIES OF *LAMELLODISCUS* (DIPLECTANIDAE, MONOGENEA)

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The present study characterizes the developmental stages of two species of the genus *Lamellodiscus, L. theroni* and *L. falcus,* parasiting the gills of cultured and wild sharp snout seabream (*Diplodus puntazzo*) in the Mediterranean Sea. The haptor and the copulatory organ were studied morphologically and mophometrically. The haptor of *Lamellodiscus* sp. is formed by different sclerotized structures, 14 hooklets, one pair of dorsal and ventral anchors, a single ventral bar, a pair of dorsal bars and 2 squamodiscs formed by plates. The copulatory organ is formed by two sclerites. Thirty naïve fishes were infected by cohabitation with natural infected fishes. From the first day after the infection (a. i.), four fishes were sacrificed daily during 20 days. Gills were checked under stereomicroscope and parasites collected. Specimens were examined under light microscope on semi-permanent preparations in glycerol gelatin. Six developmental stages could be distinguished, according to the first findings of the sclerotized structures: phase I (from first day a.i.), oncomiracidia with 14 hooklets; phase II (from fith day a.i.), the dorsal and ventral anchors appear; phase III (from seventh day a.i.), the ventral bar appears; phase IV (from eighth day a.i.), the dorsal bar emerges; phase V (from ninth day a.i.), squamodiscs development, and phase VI (from fourteenth day a.i.), the male copulatory organ appears. The detailed study of the changes of sclerotized pieces showed that parasite attach in different ways during the development, parasitizing different parts of the first and secondary lamellae. The sequence of appearance of the different sclerites corresponds to anterior studies that described the development of other species of *Lamellodiscus* (Bychowsky, 1957). N.S.G. funded by a University of Valencia "V Segles " PhD student grant.

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ITCHY KIWIS. RESEARCH ACCOMPLISHED IN NEW ZEALAND FROM 1990 THROUGH THE PRESENT. WHERE TO FROM HERE?

N.E. Davis, New Zealand

Cercarial dermatitis is a disease caused by schistosomes world wide. In New Zealand, avian schistosomes cycling between *Lymnaea tomentosa* snails and the protected NZ Scaup *Aythya novaeseelandia* cause cercarial dermatitis in humans. The result of this infection is a distressing fiery itch which appears within 30 minutes of exposure and can last for ten days or more. Following earlier research into chemical control

which proved effective but prohibitively expensive, research to discover a method of biological control using endemic echinostomes parasitic in waterfowl commenced in 1990. This poster illustrates chronologically the steps taken since 1990 to study snail/parasite population dynamics, establish control parasites in the laboratory, investigate methods for control and suggests such methods be applied in selected recreational areas of the lake. Recent discovery of a second neuropathogenic avian schistosome parasitic in *L. tomentosa* and *A. novaeseelandia* with unknown but potentially serious medical consequences to mammals is also described. Recommendations for continuing research are made to include aggressive methods for control and medical research into neurological consequences of the newly discovered neuropathogenic schistosome.

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GENETIC VARIATION OF *NEOECHINORHYNCHUS BRENTNICKOLI* (ACANTHOCEPHALA: NEOECHINORHYNCHIDAE) AN ENDOPARASITE OF *DORMITATOR LATIFRONS* FROM PACIFIC SEA SLOPES OF MEXICO, INFERRED FROM NUCLEAR AND MITOCHONDRIAL GENE SEQUENCES

C.D. Pinacho-Pinacho, **R. Rosas-Valdez, D.I. Hernández-Mena** and **M. Garcia-Varela,** Dept. Zoologia, Instituto de Biología, Universidad Nacional Autonoma de México.

Neoechinorhynchus brentnickoli is an endoparasite of the Pacific fat sleeper fish (*Dormitator latifrons*) that inhabit the Pacific Sea slopes. Nuclear (domain D2-D3 from 28S RNA Ribosomal) and mitochondrial (cytochrome c oxidase) DNA sequences were obtained for 60 acanthocephalans of 11 populations from south, central and north of Mexico. The length of the LSU and cox 1 were of 810 bp and 490 bp, respectively. The genetic divergence estimated among the populations from north, central and south of Mexico ranged from 9 to 10% for LSU and from 20 to 22 % for cox 1. The maximum likelihood and maximum parsimony analyses were performed for each data set and the combined of both data sets (LSU + cox 1). The individual and combined analyses yielded identical topologies with high bootstrap values ranged from 68 to 100%. All the phylogenetic trees suggested that *N. brentnickoli* is composed at least 2 lineages with evolutionary independence, particularly when considering that the populations are fragmented. The first lineage (sensu stricto), contained 45 specimens of 9 localities from central to north of the Pacific Sea slopes of Mexico. The second lineage included 15 specimens of 3 localities from south of Mexico. Both lineages share the same definitive host, however, the intermediate host (ostracods) could be playing a principal role in the diversification of both lineages.

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MOLECULAR AND MORPHOLOGICAL DIFFERENTIATION OF TWO SPECIES OF *PARASTRIGEA* SZIDAT, 1928 (DIGENEA, STRIGEIDAE) PARASITES OF THE WHITE IBIS (*EUDOCIMUS ALBUS*)

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Parastrigea Szidat, 1928 (Strigeidae) is a worldwide, endoparasitic genus found in wading birds. The genus is characterized by possessing two lateral and symmetrical bands of vitelline follicles at the anterior segment. In the current study the species *P. cincta* and *P. diovadena* were found in the mid and posterior intestine of white ibis (*Eudocimus albus*), respectively. DNA sequences from Internal transcribed spacers (ITS-1, 5.8S and ITS-2) for *P. cincta* and *P. diovadena* were generated. The genetic divergence estimate between both species ranged from 0.6 to 0.8%. This range of genetic divergence is low compared with

other species of digeneans and particularly among strigeids. Based on the genetic evidence inferred with ITS, both species should be synonym. However mitochondrial sequences of the cytochrome c oxidase subunit I (cox1) generated for both species reveal a genetic divergence from 15.9 to 18.9%. Maximum parsimony, maximum likelihood and Bayesian analyses of each data set and the combined of both data set (ITS + cox 1), indicated that *P. cincta* and *P. diovadena* represent two independent lineages. Our data suggest that a combination of nuclear and mitochondrial DNA sequences are necessary to separate congeneric species of strigeids.

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PHYLOGENETIC RELATIONSHIPS OF *EIMERIA* (APICOMPLEXA: EIMERIIDAE) PARASITES FROM TREE AND FLYING SQUIRREL HOSTS BASED ON PLASTID ORF470 DNA SEQUENCES

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R.S. Seville, Department of Zoology and Physiology, University of Wyoming

The plastid Open Reading Frame (ORF) 470 DNA sequence has been proposed as a suitable phylogenetic marker allowing inference of evolutionary relationships among a variety of apicomplexan parasites from a variety of hosts. DNA from species of *Eimeria* recovered from tree (*Sciurus niger*) and flying squirrels ((*Glaucomys sabrinus*) was isolated and the ORF 470 sequence PCR-amplified, sequenced, and analyzed. Maximum parsimony and neighbor joining analyses were conducted using the new sequences and published and unpublished eimerian ORF 470 sequences from other murid and sciurid rodent hosts and using *Toxoplasma gondii* as an outgroup. Preliminary analyses consistently divide the eimerian species from different rodent hosts into clades reflecting features of the oocyst morphology rather than host relationships (i.e. coevolution). Species with oocysts lacking an oocyst residuum comprised one clade and those with an oocyst residuum formed a second clade. These results are consistent with published results using other sequences (18s rDNA, ITS1) for species of *Eimeria* infecting wild rodent hosts.

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NEW DIPHYLLIDEANS FROM THE SPOTTED SKATE (*RAJA STRAELENI*) FROM SOUTH AFRICA

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The cestodes of the spotted skate, *Raja straeleni,* a host species endemic to Africa, were examined for the first time. Among the cestodes found were multiple specimens of diphyllideans. Specimens of these cestodes were prepared as whole mounts, histological sections, and for scanning electron microscopy (SEM). The results of examination with these methods suggest that 2 forms of *Echinobothrium* are present among these specimens. Although both possess a hook formula of {3–5 6/5 3–5} and 17–20 cephalic peduncle spines per row, they differ conspicuously in bothrial morphology. While one form exhibits small, round bothria, the other exhibits large, elongate bothria. These differences appear to be supported by SEM, which revealed the proximal surfaces of the round form to bear palmate spinitriches with 5 digits, whereas those of at least one specimen of the elongate form exhibited 7 digits. Based on the fact that light and scanning electron microscopy have been used extensively in the past as reliable criteria for the recognition of cestode species, we suspect that these forms represent 2 distinct taxa. The existence of 2 distinct species was tested using sequence data generated for the D1–D3 region of the nuclear gene 28S rDNA, a marker that has been found to show interspecific variation in other cestode taxa. These are the first records of diphyllideans from continental Africa outside of the Mediterranean Sea.

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MORPHOMETRIC ANALYSIS OF *PHOLETER GASTROPHILUS* (DIGENEA: HETEROPHYIDAE): AN EXAMPLE OF CRYPTIC SPECIATION?

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Currently, there is increasing evidence of several helminth parasites representing a complex of cryptic species. *Pholeter gastrophilus* is a digenean found in the stomach of 17 different cetacean species, having a wide geographic range. This raises the question of whether *P. gastrophilus* could be a complex of species. In this study, we used morphometric variation to examine the possible differences among individuals of *P. gastrophilus* from 6 cetacean host species from different localities. Eleven morphometric variables, referred to body length and width, dimensions of suckers, pharynx and testes, and egg size, were made on 127 specimens of *P. gastrophilus* from harbor porpoises (*Phocoena phocoena*), Commerson's dolphins (*Cephalorhynchus commersonii*) and common dolphins (*Delphinus delphis*) from the Atlantic, striped dolphins (*Stenella coerueoalba*) from the Mediterranean sea, and bottlenosed dolphins (*Tursiops truncatus*) and long-finned pilot whales (*Globicephala melas)* from both Atlantic and Mediterranean waters. A Principal Component Analysis was applied since variation in size is usually associated with changes in shape, and it is strongly correlated with others features. The results showed a segregation of *P. gastrophilus* from Mediterranean *T. truncatus* from the rest of samples when the first and the third component was used. When comparing each group of digeneans from different host species and localities with those from Mediterranean *T. truncatus*, a significant difference was detected, the latter having a smaller size. This smaller size for *P. gastrophilus* from Mediterranean bottlenosed dolphins could be due to a crowding effect. Parasites inhabiting an organ within a host are sharing the available resources, and the growth of the worms could be reduced if these are in excess. On the other hand, we cannot rule out the hypothesis of the existence of a complex of cryptic species within *P. gastrophilus*, showing only slight morphometric differences. For this hypothesis to be tested, a molecular study with specific molecular markers is needed. Supported by grant CGL 2009-07465 (MICINN)

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DIAGNOSIS OF *BAYLISASCARIS* HYBRID INDIVIDUALS

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Baylisascaris procyonis and *B. columnaris* are closely related nematodes that infect raccoons and skunks, respectively. Both nematode species are capable of causing visceral larval migrans when they infect non-natural hosts, including humans and domesticated animals. Distributions of raccoons and skunks often overlap in North America, and presumptive hybrid *procyonis-columnaris* individuals have been identified from raccoon hosts based on RFLP-typing of ITS ribosomal DNA. All hybrid individuals are of *B. procyonis* female parentage based on mtDNA lineage. Analysis of ribosomal DNA cannot distinguish between F1 hybrids and individuals resulting from backcrosses to parental individuals. Therefore, nuclear microsatellite markers developed for *B. procyonis* were used to characterize the genetic status of hybrid individuals. The potential for gene flow between different *Baylisascaris* species has implications for pathogenicity of larval migrans in humans and other animals.

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LECANICEPHALIDEAN GENERIC DIVERSITY AND HOST ASSOCIATIONS

K.R. Koch, University of Connecticut
J.J. Cielocha and **K. Jensen,** University of Kansas

Lecanicephalidea is one of seven orders of cestodes that exclusively parasitize elasmobranchs as definitive hosts. Members of the order primarily parasitize batoids, although few records from sharks exist. Currently, the Lecanicephalidea includes 14 valid genera and 87 valid species, with an additional eight genera and 53 species considered to be *genera inquirenda* and *species inquirendae*, respectively. Taxonomic revisions for subsets of taxa are underway. In addition, the order has been the focus of recent survey efforts globally. As a result of the revisionary work, five of the eight *genera inquirenda* should be considered to be valid. These are *Adelobothrium*, *Anthemobothrium*, *Cephalobothrium*, *Flapocephalus*, and *Thysanobothrium*. Moreover, new collections, particularly from Southeast Asia, Australia, and Africa, have revealed hitherto undocumented generic diversity. Specimens representing 13 additional genera have been identified. The new morphological forms exhibited by these new genera, especially with respect to scolex morphology, significantly expand our concept of the order. For example, we document the first lecanicephalidean genus with biloculated bothridia, as well as several new genera possessing multi-tiered, highly complex apical organs. We now consider the Lecanicephalidea to be comprised of at least 32 genera, 30 of which exclusively parasitize batoids. In addition to the generic diversity, the host association of lecanicephalideans is coming into focus. To date, lecanicephalideans have been reported to parasitize 12 of the 23 batoid families. While 26 of the 30 lecanicephalidean genera from batoids appear to be restricted to a single host family, four lecanicephalidean genera parasitize members of greater than two batoid families. For examples, members of *Polypocephalus* and *Tylocephalum* both parasitize members of five different batoid families. The highest lecanicephalidean diversity in terms of genera as well as morphological forms occurs in the ray families Dasyatidae and Myliobatidae. A comprehensive phylogenetic analysis of the Lecanicephalidea, including the new genera, is needed to clarify the interrelationships and with that the familial boundaries in the order.

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MENTORING THE MENTOR

CLARK P. READ MENTOR AWARD LECTURE

B. Christensen, Univiversity of Wisconsin, Madison

Biographical Statement:

Bruce M. Christensen is a faculty member of the Department of Pathobiological Sciences at The University of Wisconsin School of Veterinary Medicine.

Dr. Christensen is an investigator in medical entomology, mosquito-parasite interactions and pathogenesis, mosquito innate immunity, and epidimeiology of mosquito-borne diseases. His lab maintains active collaborations with many research groups in the United States and well as Egypt, Papau New Guinea, and Taiwan.

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ASP Meeting History

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1934 Pittsburgh PA
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1936 Atlantic City NJ
1937 Indianapolis IN
1938 Richmond VA
1939 Columbus OH
1940 Philadelphia PA
1941 Dallas TX
1942 No meeting
1943 No meeting
1944 Cleveland OH
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1954 Memphis TN *
1955 Atlanta GA
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1958 Bloomington IN †
1959 University Park PA †
1960 Los Angeles CA *
1961 Lafayette IN †
1962 Washington DC ‡
1963 Chicago IL *
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1967 Tucson AZ §
1968 Madison WI †
1969 Washington DC *
1970 Washington DC ¶
1971 Los Angeles CA
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1993 Atlanta GA *
1994 Ft. Collins CO
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1996 Tucson AZ ††
1997 Nashville TN
1998 Kona HI
1999 Monterey CA ‡‡
2000 San Juan PR ††
2001 Albuquerque NM
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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
2012 Richmond, VA

* 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