The 90th Annual Meeting of the American Society of Parasitologists

Hilton Omaha
Omaha, Nebraska, June 25-28, 2015

The Old Market

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

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- Sierra Upton (sponsor of the Steve Upton Party for ASP Students; Sierra is the daughter of the late Dr. Steve J. Upton)
- University of Nebraska-Omaha Office of Research and Creative Activity
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The American Society of Parasitologists
ESTABLISHED 1924

Welcome

We would like to welcome you to the 90th 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, Hilton Omaha

Day/Times	Activity/Function	Room/Space
June 25 (Thursday)		
8:00 a.m.-Noon	ASP Council	Hill
2:00-5:00 p.m.	Host-Parasite Interactions I	Grand Ballroom B
2:00-5:15 p.m.	Life Cycles and Epidemiology	Grand Ballroom D
3:15-3:45 p.m.	Coffee Break	Grand Central Foyer
7:00-10:00 p.m.	Welcome Reception	Grand Central Ballroom
June 26 (Friday)		
8:30-10:30 a.m.	ASP President's Symposium	Grand Ballroom C
10:30-11:00 a.m.	Coffee Break	Grand Central Foyer
11:00-Noon	ASP Student Business Meeting	Grand Ballroom B
11:00-Noon	Publishing and Public Access Ideas	Grand Ballroom D
Noon-1:00 p.m.	Editorial Board Luncheon	Hill
1:00-3:00 p.m.	Teaching Parasitology Symposium	Grand Ballroom A
1:00-3:00 p.m.	Taxonomy, Systematics, Phylogeny I	Grand Ballroom D
1:00-3:00 p.m.	Host-Parasite Interactions II	Grand Ballroom B
3:00-3:30 p.m.	Coffee Break	Grand Central Foyer
3:30-5:30 p.m.	ASP Students' Symposium	Grand Ballroom D
5:30-6:30 p.m.	ASP Student Social	Foyer outside of D
3:00-6:00 p.m.	Auction Set Up	Grand Ballroom C
6:00-7:00 p.m.	Auction Preview	Grand Ballroom C
7:00-9:00 p.m.	25th Annual ASP Student Auction	Grand Ballroom C
June 27 (Saturday)		
8:30-10:30 a.m.	Disease Ecology Symposium	Grand Ballroom B
10:30-11:00 a.m.	Coffee Break	Grand Central Foyer
11:00-Noon	US National Parasite Collection	Grand Ballroom B
1:00-2:00 p.m.	ASP President's Address	Blackstone Ballroom B
2:15-6:00 p.m.	Evolutionary Ecology I	Grand Ballroom D
2:15-4:00 p.m.	Taxonomy, Systematics, Phylogeny II	Grand Ballroom B
2:15-4:00 p.m.	Biochemistry/Physiology/ Chemotherapeutic & Drug/Vector	Grand Ballroom A
4:00-4:15 p.m.	Coffee Break	Grand Central Foyer
4:15-5:45 p.m.	Genomics/Molecular/Immunology	Grand Ballroom A
4:00-5:30 p.m.	Authors may set up posters	Blackstone Ballroom A
7:00-10:00 p.m.	Evening at Hot Shops Art Center	
June 28 (Sunday)		
8:00-12:00 p.m.	Evolutionary Ecology II	Grand Ballroom B
8:30-11:30 a.m.	Host-Parasite Interactions III	Grand Ballroom D
9:45-10:15 a.m.	Coffee Break	Grand Central Foyer
8:30-10:30 a.m.	Authors complete poster set up	Blackstone Ballroom A
12:00-1:30 p.m.	Poster Session, coffee, snacks	Blackstone Ballroom A
1:45-2:45 p.m.	H.B. Ward Lecture	Blackstone Ballroom B
3:00-4:30 p.m.	ASP Awards and Business Meeting	Blackstone Ballroom B

Thursday Morning, 2015-06-25

8:00 am – Noon ASP Council Meeting, Hill Room

Presiding: **D. S. Lindsay**, Virginia Tech, Virginia-Maryland College of Veterinary Medicine

Thursday Afternoon, 2015-06-25

2:00-5:00 pm Host-Parasite Interactions I

Location: Grand Ballroom B

Presiding: **A. Shostak**, University of Alberta

Time (Abstract No.)

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

2:00 (1) † **S. Weinstein**. HOW DOES AN INVASIVE SPECIES ALTER NATIVE PARASITE TRANSMISSION?

2:15 (2) † **F.J. Broughton**, M.K. Fentress, S.B. Weinstein, A.M. Kuris. PARASITE BURDEN, HOST SIZE, AND IMMUNE RESPONSE OF *OCTOPUS BIMACULOIDES*.

2:30 (3) † **N.J. Traub**, A.J. Smith-Herron, C.L. Amundson, P.L. Flint. COMPARATIVE HELMINTH COMMUNITY STRUCTURE IN TWO SPECIES OF ARCTIC-NESTING WATERFOWL: BLACK BRANT (*BRANTA BERNICLA NIGRICANS*) AND GREATER WHITE-FRONTED GEESE (*ANSER ALBIFRONS*).

2:45 (4) † **K. Gustafson**, M. Bolek. REMODELING A STOLEN HOME: EFFECTS OF TREMATODE PARASITISM ON THE FUNCTIONAL SHELL MORPHOLOGY OF SNAIL SHELLS IN FLOW AND NONFLOW ENVIRONMENTS.

3:00 (5) † **J.M. Carrillo**, R.M. Overstreet. THE SYMBIOTIC CILIATE *KYAROIKEUS CETARIUS* IN CAPTIVE BOTTLENOSE DOLPHINS.

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

3:45 (6) † **R.P. Shannon**, M.G. Bolek. AMPHIBIAN TRYPANOSOMES FROM NORTH CENTRAL OKLAHOMA: MORPHOLOGY, MOTILITY, AND HOST SPECIFICITY.

4:00 (7) † **V.M. Frankel**. BUILDING COMMUNITIES: THE ROLES OF BIOTIC AND ABIOTIC FACTORS.

4:15 (8) † **A.D. Stumbo**. HOST MANIPULATION VIA TEMPORAL ADJUSTMENT OF OCULAR OBSTRUCTION BY TREMATODE METACERCARIAE IN EYES OF FISH.

4:30 (9) † **C. Williams**, L. Vredevoe, G. Kolluru, B. Hanelt. EFFECTS OF *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA) ON THE CRICKET HOST, *ACHETA DOMESTICUS.*

4:45 (10) † **A.W. Bartlow**. ARE ECOTONES HOTSPOTS FOR PARASITE DIVERSITY?

2:00-5:15 pm Life Cycles and Epidemiology

Location: Grand Ballroom D

Presiding: **U.C. Ngenegbo**, Nnamdi Azikiwe University

Time (Abstract No.)

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

2:00 (11) **O.O. Ikpeze**, U.C. Ngenegbo, I.S. Okwelogu. ABUNDANCE OF FILTH FLIES AT BUTCHERS STALLS, SOUTHERN NIGERIA.

2:15 (12) **F.O. Akinbo**, C.D. Ugboaja. ASYMPTOMATIC *PLASMODIUM FALCIPARUM* INFECTION IN SICKLE CELL DISEASE PATIENTS.

2:30 (13) **U.C. Ngenegbo**, O.O. Ikpeze, D.O. Esu. EFFECTS OF MATERNAL AND NEONATAL MALARIA ON AGE AND BIRTH WEIGHT OF NEONATES IN UYO NIGERIA.

2:45 (14) **U.C. Ngenegbo**, C.M. Egbuche, I. Chukwu, C.K. Ezihe. INTESTINAL PARASITE INFECTIONS AMONG PRIMARY SCHOOL CHILDREN IN IGBARIAM, ANAMBRA-EAST LOCAL GOVERNMENT AREA OF ANAMBRA STATE, SOUTH-EASTERN NIGERIA.

3:00 (15) † **R. Bhattarai**, H. Carabin, J.V. Proaño, J. Flores-Rivera, T. Corona, A. Flisser, C.M. Budke. DIRECT COST OF NEUROCYSTICERCOSIS IN PATIENTS TREATED AT THE INSTITUTO NACIONAL DE NEUROLOGIA Y NEUROCIRUGIA (INNN) IN MEXICO CITY, MEXICO.

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

3:45 (16) † **K. Skinner**, A. Barquin, M.R. Wise de Valdez. INTESTINAL HELMINTH SURVEY OF FERAL HOGS FROM TEXAS.

4:00 (17) **D.J. Larson**. REVIEW OF THE PHYSIOLOGICAL ECOLOGY OF PARASITE OVERWINTERING.

4:15 (18) **I. de Buron**, K.M. Hill-Spanik, L. Haselden, S.D. Atkinson. *KUDOA INORNATA*: A SEASONAL PARASITE?

4:30 (19) † **E.A. Zieman**, M. Schwarzinger, F.A. Jimenez, C.K. Nielsen. *CYTAUXZOON FELIS* (APICOMPLEXA: THEILERIIDAE) IN BOBCATS, DOMESTIC CATS, AND TICK VECTORS IN THE SOUTHERN REGION OF ILLINOIS.

4:45 (20) **C. Stromlund**, J. Vaughan. HEMOPARASITES AND WEST NILE SEROPOSITIVITY OF SONGBIRDS IN A WOODLAND HABITAT WITHIN NORTHWESTERN MINNESOTA.

5:00 (21) **M. Hu**. MICROSATELLITE ANALYSIS OF GENETIC DIVERSITY OF *HAEMONCHUS CONTORTUS* IN CHINA.

Thursday Evening, 2015-06-25

7:00 - 10:00 pm WELCOME RECEPTION

Location: Grand Central Ballroom

Friday Morning, 2015-06-26

8:30-10:30 am ASP President's Symposium

Location: Grand Ballroom C

Presiding: **G.W. Esch**, Wake Forest University

Theme: What genomics is teaching us about Apicomplexan development.

8:30 Introduction.

8:40 (22) **G. Zhu**. *CRYPTOSPORIDIUM* GENOMES AND DRUG TARGETS.

9:10 (23) **D.K. Howe**. "OMICS" INVESTIGATION OF *SARCOCYSTIS NEURONA*.

9:40 (24) **L.D. Sibley**. WHAT GENOMICS IS TEACHING US ABOUT APICOMPLEXANS.

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

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

11:00 am-Noon ASP Student Business Meeting

Location: Grand Ballroom B

Presiding: **E. Kasl**, Texas A&M University

11:00 am-Noon Publishing and Public Access Ideas

Location: Grand Ballroom D

Presiding: **S.L. Gardner**, University of Nebraska-Lincoln

Friday Afternoon, 2015-06-26

Noon – 1:00 pm Editorial Board Luncheon, Hill Room

1:00-3:00 pm Teaching Parasitology Symposium

Location: Grand Ballroom A

Presiding: **S.A. Orlofske**, Northeastern Illinois University

Theme: Enhancing Undergraduate Education: Adding Parasitology to the General Biology Curriculum.

1:00 Introduction.

1:10 (25) **J. Wojdak**. USING GROSS PARASITES TO SNEAK EVEN GROSSER EQUATIONS INTO THE INTRODUCTORY BIOLOGY CLASSROOM.

1:30 (26) **J. Koprivnikar**. PARASITOLOGY AND DISEASE ECOLOGY: A POTENTIAL MUTUALISM FOR UNDERGRADUATE EDUCATION?

1:50 (27) **K. Herrmann**. USING TREMATODES TO TEACH LIFE CYCLES, ECOLOGICAL INTERACTIONS, AND BEHAVIOR.

2:10 (28) **G. Sandland**. AN INTRODUCTION TO THE COLLABORATION ON RIVERINE ECOLOGY (CORE) PROGRAM AND ITS UTILITY AS A MODEL FOR UNDERGRADUATE RESEARCH IN MATHEMATICAL PARASITOLOGY.

2:30-3:00 Questions, Closing Remarks.

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

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

Location: Grand Ballroom D

Presiding: **F.A. Jimenez-Ruiz**, Southern Illinois University

Time (Abstract No.)

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

1:00 (29) † **R. Guyer**, K. Jensen. LECANICEPHALIDEAN TAPEWORMS (CESTODA) OF THE FRESHWATER WHIPRAY, *HIMANTURA POLYLEPIS*, FROM MALAYSIAN AND INDONESIAN BORNEO.

1:15 (30) † **K. Patitucci**, J. Bates, V. Tkach. UNCOVERING HELMINTH DIVERSITY IN SOUTHERN AMAZONIAN BIRDS.

1:30 (31) † **V. Mantovani Bueno**, J. Caira. HOW TO RECOGNIZE A SUCKER WHEN YOU SEE ONE.

1:45 (32) † **M. Tessler**, A. Barrio, E. Borda, R. Rood-Goldman, M. Hill, M. Siddall. DESCRIPTION OF AN EXTANT SPECIES WITH MICRO-COMPUTED TOMOGRAPHY AND PHYLOGENETIC REVISION OF *DUOGNATHOUS* TERRESTRIAL LEECHES (HIRUDINIDA: ARHYNCHOBDELLIDA: HAEMADIPSIDAE).

2:00 (33) † **E.L. Kasl**, W.F. Font, C.D. Criscione. REVISITING THE GENUS A*LLOGLOSSIDIUM* (DIGENEA: MACRODEROIDIDAE): USING MOLECULAR PHYLOGENETIC DATA TO DISENTANGLE EVOLUTIONARY PATTERNS OF LIFE CYCLE COMPLEXITY AND TAXONOMY.

2:15 (34) † **A. Koontz**, J. Caira. AN ENIGMA RESOLVED: THE TRUTH ABOUT THE HOST ASSOCIATIONS AND IDENTITY OF THE ELASMOBRANCH PARASITIZING CESTODE GENUS *CARPOBOTHRIUM*.

2:30 (35) † **S. Galen**, J. Borner, T. Burmester, S. Perkins. PHYLOGENOMIC INSIGHTS INTO THE EVOLUTIONARY HISTORY OF MALARIA PARASITES.

2:45 (36) **A. Tsogtsaikhan**. ENDOPARASITES OF DIPODIDAE (RODENTIA) FROM MONGOLIA.

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

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

Location: Grand Ballroom B

Presiding: **K. Weinersmith**, Rice University

Time (Abstract No.)

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

1:00 (37) † **J. Bell**, A. Fecchio, V. Tkach, J. Weckstein. HAEMOSPORIDIAN PARASITES OF AMAZONIAN BIRDS.

1:15 (38) † **W. Redman**, J.J. Cielocha. ATTACHMENT OF *TYLOCEPHALUM* SP. IN THE COWNOSE RAY, *RHINOPTERA BONASUS*.

1:30 (39) † **J.E. Igetei**, M. Elfaham, S. Liddell, J. Bradley, M.J. Doenhoff. *SCHISTOSOMA MANSONI* TEGUMENT ANTIGENS EXPOSED BY PRAZIQUANTEL TO HOST ANTIBODY REACTIVITY.

1:45 (40) **D. Calhoun**, P. Schaffer, J. Gregory, K. Hardy, P. Johnson. EARLY IMMUNOLOGY AND HISTOPATHOLOGY OF *RIBEIROIA ONDATRAE* (DIGENEA: CATHAEMASIIDAE) IN THE LATERAL LINE OF BLUEGILL, *LEPOMIS MACROCHIRUS*.

2:00 (41) **K. Weinersmith**, V.C. Renick, T. King, E. Payne, A. Sih, R.L. Earley. DOES A BRAIN-INFECTING PARASITE INFLUENCE HOST BEHAVIORAL TYPE AND BEHAVIORAL CORRELATIONS?

2:15 (42) **X. Chen**. NON-CODING RNAS IN *CRYPTOSPORIDIUM*-EPITHELIAL CELL INTERACTIONS.

2:30 (43) **J.J. Morrow**. CHIRIBAYA ENDOHELMINTH INFECTIONS OF THE OSMORE RIVER BASIN.

2:45 (44) **O.M. Amin**. COMMON HUMAN PARASITES AND PATHOGENS AND THEIR NATURAL REMEDIES IN THE USA.

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

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

Location: Grand Ballroom D

Presiding: **E. Kasl**, Texas A&M University

Theme: Science Outreach in the Classroom and Beyond.

Time (Abstract No.)

3:30 Introduction.

3:40 (45) **J.T. Detwiler**. TEACHING PARASITOLOGY WHILE AVOIDING TRANSMISSION AND INFECTING THE NEXT GENERATION.

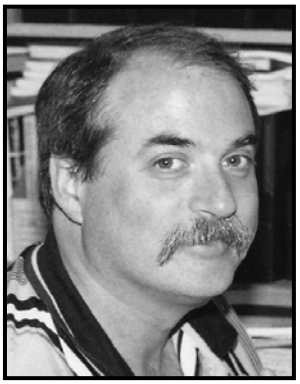
4:10 (46) **K. Weinersmith**. SCIENCE OUTREACH THROUGH BLOGGING AND PODCASTING.

4:40 (47) **M. Siddall**. PRESENCE AND PREPARATION.

5:10-5:30 Questions and Closing Remarks.

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

Location: Foyer outside of grand Ballroom D



Steve J. Upton

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

Friday Evening, 2015-06-26

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

7:00-9:00 pm **25th ANNUAL ASP STUDENT AUCTION**

Location: Grand Ballroom C

Saturday Morning, 2015-06-27

8:30-10:30 am Disease Ecology Symposium

Location: Grand Ballroom B

Presiding: **J. Koprivnikar**, Ryerson University

Time (Abstract No.)

8:30 Introduction.

8:40 (48) **P. Johnson**, C. Wood. LINKING HOST DIVERSITY AND PARASITE INFECTION: A COMMUNITY ECOLOGY APPROACH.

9:00 (49) **C. Wood**. IMPACTS OF HUMAN DISTURBANCE ON PARASITE ASSEMBLAGES: TELESCOPING ACROSS SPATIAL SCALES.

9:20 (50) **T.R. Raffel**, J.P. Sckrabulis, K.A. Altman, E.L. Scott, J.R. Rohr, P.T. Johnson. THERMAL BIOLOGY OF PARASITISM: A METABOLIC APPROACH.

9:40 (51) **P.K. Molnar**. PREDICTING CLIMATE CHANGE IMPACTS ON HOST-PARASITE SYSTEMS: NO LONGER JUST A VISION?

10:00-10:30 Questions, Closing Remarks.

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

11:00-Noon *US National Parasite Collection*

Location: Grand Ballroom B

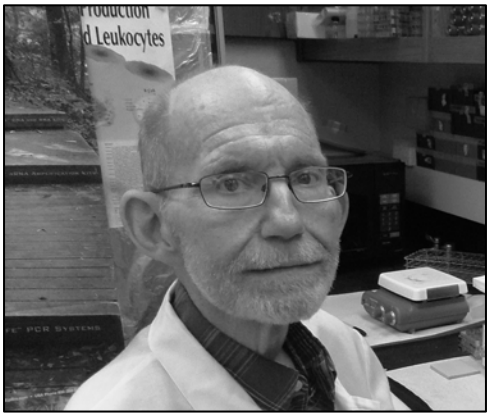
Presiding: **A.J. Phillips**, Smithsonian Institution, National Museum of Natural History
M.E. Moser, Smithsonian Institution, National Museum of Natural History

11:00-12:00 Collections Management Policies and Procedures of the USNPC.

Saturday Afternoon, 2015-06-27

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

Location: Blackstone Ballroom B



David S. Lindsay, President ASP

Presiding: **D.D. Bowman**, Cornell University

1:00 Introduction of **Dr. David S. Lindsay**.

1:10 **D.S. Lindsay**, "My time with parasites."

2:15-6:00 pm Evolutionary Ecology I

Location: Grand Ballroom D

Presiding: **R. Blaylock**, University of Southern Mississippi
S. Seville, University of Wyoming-Casper

Time (Abstract No.)

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

2:15 (52) † **R.L. Grunberg**, M.V. Sukhdeo. TEMPORAL RESOURCE PARTITIONING IN TWO SPECIES OF GREGARINES (*ROTUNDULA* SP. AND *HELIOSPORA* SP.) INFECTING AMPHIPODS (*GAMMARUS FASCIATUS*).

2:30 (53) † **W. Preisser**, N. Dronen, J. Light. PATTERNS OF PARASITISM: THE LATITUDINAL DIVERSITY GRADIENT OF PARASITIC HELMINTHS.

2:45 (54) † **J.A. Harvey**, G. Voelker. AVIAN MALARIA DIVERSIFICATION ACROSS CONTRASTING REGIONS OF AFRICA.

3:00 (55) † **A.M. Gleichsner**. DOES THE PARASITE COMPOSITION ALTER THE OUTCOME OF COMPETITION?: LIFE HISTORY AND VIRULENCE CONSEQUENCES OF INTRASPECIFIC PARASITE CO-INFECTION.

3:15 (56) † **K. Luth**. HELMINTH COMMUNITIES OF SUNFISH (CENTRARCHIDAE) FROM ACROSS THE UNITED STATES.

3:30 (57) † **J.M. Alfieri**, T.K. Anderson. PARASITE LIFE-HISTORY DETERMINES THE RELATIONSHIP BETWEEN ANTHROPOGENIC CHANGE AND PARASITE COMMUNITY STRUCTURE.

3:45 (58) † **H.A. Stigge**, M.G. Bolek. EVALUATING THE BIOLOGICAL AND ECOLOGICAL FACTORS INFLUENCING TRANSMISSION OF LARVAL DIGENETIC TREMATODES: A TEST OF SECOND INTERMEDIATE HOST SPECIFICITY OF TWO *HALIPEGUS* SPECIES IN NORTH AMERICA.

4:00 – 4:15 pm **COFFEE BREAK**

4:15 (59) † **S.A. Zemmer**, L.K. Belden. THE EFFECTS OF STREAM NETWORK CONNECTIVITY AND HOST MOBILITY ON TREMATODE COMMUNITIES.

4:30 (60) † **D. Aguirre-Ayala**, M. Aguirre-Macedo, D. Marcogliese, S. Daoust, V. Vidal-Martínez. POTENTIAL INCREASE OF THE GEOGRAPHICAL DISTRIBUTION OF THE ASIAN TAPEWORM (*BOTHRIOCEPHALUS ACHEILOGNATHI*) DUE TO CLIMATE CHANGE.

4:45 (61) † **J.N. Childress**, S. Rogers, G.J. Langford. REPRODUCTIVE PLASTICITY IN THE NEMATODE *GYRINICOLA BATRACHIENSIS*: IS REPRODUCTIVE STRATEGY DEPENDENT UPON TADPOLE DEVELOPMENTAL TIME?

5:00 (62) † **B. Solorzano**, G. Pérez-Ponce de León. EFFECTS OF HABITAT FRAGMENTATION ON THE GENETIC STRUCTURE OF *TRYPANOXYURIS MINUTUS*, A HOWLER MONKEY PARASITE.

5:15 (63) † **N. Chodkowski**, R.J. Bernot. DIFFERENT ELEMENTAL CONTENT BETWEEN TISSUES OF TREMATODES AND THE FRESHWATER SNAIL, *ELIMIA LIVESCENS*.

5:30 (64) † **B.P. Ruehle**, C. Higgins, K. Herrmann. RELATIONSHIP BETWEEN PARASITIC INFECTION AND REPRODUCTIVE POTENTIAL OF TWO CYPRINIDS WITH DIFFERENT REPRODUCTIVE STRATEGIES.

5:45 (65) † **O.N. Choi**, J.E. Kawaguchi, R.C. Jadin, S.A. Orlofske. SURVEY OF CESTODE BIODIVERSITY IN AVIAN HOSTS.

2:15-4:00 pm Taxonomy, Systematics & Phylogeny II

Location: Grand Ballroom B

Presiding: **V. Tkach**, University of North Dakota

Time (Abstract No.)

2:15 (66) **K. Herzog**, K. Jensen. A NEW GENUS OF LECANICEPHALIDEAN TAPEWORM WITH COMMENTS ON ITS DISTRIBUTION WITHIN A HOST SPECIES.

2:30 (67) **M. Bolek**, C. Szmygiel, R. Shannon, C. Williams, A. Schmidt-Rhaesa, B. Hanelt. THE DIVERSITY AND SURPRISING COMPLEXITY OF LARVAL AND CYST STAGES OF GORDIIDS (NEMATOMORPHA): HOW MANY TYPES ARE THERE?

2:45 (68) **S. Racz**, S. Gardner. PHYLOGENY OF NEW WORLD *HYMENOLEPIS* WEINLAND, 1858 - MORPHOLOGY AND MOLECULES.

3:00 (69) **J.N. Caira**, K. Jensen. GET THE TAXONOMY RIGHT FIRST!

3:15 (70) **T. Ruhnke**. HISTORY AND PROGRESS IN THE SYSTEMATICS OF NON-HOOKED TETRAPHYLLIDEANS: THE ORDER PHYLLOBOTHRIIDEA.

3:30 (71) **S. Monks**, C.E. Bautista-Hernández, G. Pulido-Flores, E.A. Martínez-Salazar. TWO NEW SPECIES OF *PHYLLODISTOMUM* THAT WERENT NEW AFTER ALL: WHEN YOU CANT TRUST MORPHOLOGY!

3:45 (72) **F. Reyda**. MORE TAXONOMY NEEDED: A SURVEY OF NEW YORK LAKE FISH PARASITES.

4:00 – 4:15 pm **COFFEE BREAK**

2:15-4:00 pm Biochemistry, Physiology, Chemotherapy & Drug Resistance, Vector Biology

Location: Grand Ballroom A

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

Time (Abstract No.)

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

2:15 (73) † **S. Ahmad**, M.K. Saifullah, S.A. Abidi. ASSESSMENT OF SOME ANTIOXIDANT ENZYMES IN AMPHISTOME PARASITES, *GASTROTHYLAX CRUMENIFER* AND *GIGANTOCOTYLE EXPLANATUM* INFECTING INDIAN WATER BUFFALO, *BUBALUS BUBALIS*.

2:30 (74) † **G.P. League**, J.F. Hillyer. COMPARATIVE ANALYSIS OF THE LARVAL AND ADULT CIRCULATORY SYSTEM AND ITS ROLE IN PATHOGEN AGGREGATION IN THE MOSQUITO *ANOPHELES GAMBIAE*.

2:45 (75) **Q. Han**. A NOVEL IN VITRO ASSAY OF ANTHELMINTIC ACTIVITY AGAINST LARVAE OF *ASCARIS SUUM*.

3:00 (76) **P.T. LoVerde**, S.R. Stahl, A.B. Taylor, X. Cao, P.J. Hart, S.F. McHardy, A. Lopez, T.J. Anderson. SCHISTOSOMICIDAL OXAMNIQUINE DERIVATIVE DRUG ACTIVITY AGAINST HUMAN SCHISTOSOMIASIS.

3:15 (77) **J.T. Sullivan**, M.K. Nelson, K.L. Buena, B.C. Cru. EFFECT OF ABNORMAL TEMPERATURE AND STARVATION ON THE INTERNAL DEFENSE SYSTEM OF THE SCHISTOSOME-TRANSMITTING SNAIL *BIOMPHALARIA GLABRATA*.

3:30 (78) **J.F. Hillyer**, T.Y. Estevez-Lao. EFFECT OF BLOOD FEEDING ON MOSQUITO HEART PHYSIOLOGY.

3:45 (79) **S.E. Greiman**, V.V. Tkach. QUANTIFICATION OF THE BACTERIAL ENDOSYMBIONT, *NEORICKETTSIA* SP., WITHIN ALL LIFE CYCLE STAGES OF A DIGENEAN HOST BY USE OF REAL-TIME QPCR ANALYSIS.

4:00 – 4:15 pm **COFFEE BREAK**

4:15-5:45 pm Genomics, Molecular Biology & Immunology

Location: Grand Ballroom A

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

Time (Abstract No.)

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

4:15 (80) **N. Lodh**, K. Mikita, C.J. Shiff. LAMP: POINT OF CARE DIAGNOSIS FOR MULTIPLE SCHISTOSOME PARASITES.

4:30 (81) † **C.D. Keroack**, C.G. Decker, J.I. Wurster, S.A. Williams. ABSENCE OF *WOLBACHIA* IN SEAL HEART WORM (ACANTHOCHEILONEMA SPIROCAUDA) WITH EVIDENCE OF LATERAL GENE TRANSFER.

4:45 (82) **K. Tang**, Y. Guo, N. Li, D.M. Roellig, Y. Feng, L. Xiao. CHARACTERIZATION OF APICOPLAST AND MITOCHONDRIAL GENOMES OF *CYCLOSPORA CAYETANENSIS*.

5:00 (83) † **B. Wijyawardena**, D.J. Minchella, J.A. DeWood. TRANSCRIPTOME CHARACTERIZATION OF *S. MANSONI* INFECTED MICE: NOVEL INSIGHTS TO PARASITE INDUCED HOST IMMUNE RESPONSE.

5:15 (84) † **J. Foox**. TRANSCRIPTOMES ILLUMINATE MYXOZOAN EVOLUTION.

5:30 (85) **G. Ahmad**. IMMUNOBIOLOGY OF *ECHINOCOCCUS GRANULOSUS* IN THE DEFINITIVE HOST.

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

Location: Blackstone Ballroom A

Authors may set up posters during this time.

Saturday Evening, 2015-06-27

7:00 – 10:00 pm Hot Shops Art Center

Sunday Morning, 2015-06-28

8:00-NOON Evolutionary Ecology II

Location: Grand Ballroom B

Presiding: **J. Camp**, Purdue University
K. Luth, Wake Forest University

Time (Abstract No.)

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

8:00 (86) † **R. Donnelly**, J. Detwiler. USING INTEGRATIVE TAXONOMY TO INVESTIGATE CRYPSIS WITHIN THE ECHINOSTOME TREMATODES.

8:15 (87) † **E.T. Ebbs**, E.S. Loker, S.V. Brant. INVASION GENETICS OF THE GLOBALLY INVASIVE SNAIL, *PHYSELLA ACUTA* (DRAPARNAUD 1805) AND ITS POTENTIAL AS AN INTERMEDIATE HOST TO LARVAL TREMATODES.

8:30 (88) **S. Brant**, E. Ebbs, E.S. Loker, G. Viozzi, V. Flores. *TRICHOBILHARZIA* IN THE NEW WORLD: ARGENTINIAN SPECIES OFFER A FIRST GLIMPSE OF SPECIES DIVERSITY ACROSS HOSTS AND THE AMERICAN CONTINENTS.

8:45 (89) **M.L. Aguirre-Macedo**. PRELIMINARY STUDY ON THE ROLE OF FISH METAZOAN PARASITES ON THE FOOD WEB OF CELESTUN COASTAL LAGOON, YUCATAN, MEXICO.

9:00 (90) **J. Koprivnikar**, T.M. Urichuk. REMEMBERING PAST THREATS: EFFECTS OF PREDATOR EXPOSURE ON HOST ANTI-PARASITE BEHAVIOR.

9:15 (91) **U.C. Ngenegbo**, O.O. Ikpeze, M.O. Obikwelu. POPULATION DYNAMICS AND ECOLOGY OF FRESHWATER GASTROPODS OF PUBLIC HEALTH IMPORTANCE IN AGULU LAKE NIGERIA.

9:30 (92) **K. Fast**. MALARIA PARASITEMIA AND PREVALENCE IN THE TUFTED TITMOUSE (*BAEOLOPHUS BICOLOR*).

9:45 – 10:15 am COFFEE BREAK

10:15 (93) **J.C. Buck**, W.I. Lutterschmidt. PARASITE ABUNDANCE ACROSS AN URBAN GRADIENT: ADDRESSING PLAUSIBLE MECHANISMS.

10:30 (94) **D. Benesh**, M. Kalbe. THE EFFECT OF A VIRULENT TAPEWORM ON PARASITE COMMUNITY ASSEMBLY IS GENOTYPE DEPENDENT.

10:45 (95) **D. Benesh**, J.C. Chubb, G.A. Parker. THE TROPHIC VACUUM AND THE EVOLUTION OF COMPLEX LIFE CYCLES IN TROPHICALLY TRANSMITTED HELMINTHS.

11:00 (96) **H.F. Tavalire**, M.S. Blouin, M.L. Steinauer. GENOTYPIC VARIATION IN LIFE HISTORY RESPONSE TO INFECTION AND ITS EFFECTS ON PARASITE FITNESS.

11:15 (97) **V.M. Vidal-Martínez**, E. Torres-Irineo, G. Gold-Bouchot, M.L. Aguirre-Macedo. ENVIRONMENTAL AND ANTHROPOGENIC DRIVERS AFFECTING THE GEOGRAPHICAL DISTRIBUTION OF THE HELMINTH PARASITES OF FLATFISHES IN THE SOUTHERN GULF OF MEXICO.

11:30 (98) **V.W. Walstrom**. DIVERSITY AND DISTRIBUTION OF HAEMOSPORIDIAN PARASITES IN THE NORTHERN CARDINAL (*CARDINALIS CARDINALIS*).

11:45 (99) **N. Rubtsova**. PARASITOLOGICAL SURVEY OF PUMPKINSEED (*LEPOMIS GIBBOSUS* (LINNAEUS, 1758)) IN ZAPORIZHZHYA REGION (UKRAINE).

8:30-11:30 am Host-Parasite Interactions III

Location: Grand Ballroom D

Presiding: **K. Jacobson**, NOAA Fisheries
E. Kasl, Texas A&M University

Time (Abstract No.)

8:30 (100) **C. Leaphart**, D. Zelmer. WRECKING THE CURVE: THE INFLUENCE OF TREMATODE INFECTION ON THE FUNCTIONAL RESPONSE OF 2 PREDATORS.

8:45 (101) **K. Bedford**, A. Fedynich, D. Rollins. PARASITOLOGICAL SURVEY OF SCALED QUAIL FROM WEST TEXAS.

9:00 (102) **M.P. Firkins**. PREVALENCE AND DISTRIBUTION OF AMPHIBIAN PARASITES IN NORTH DAKOTA.

9:15 (103) **N. Zymonas**, M. Kent, M. Scheu, M. Hogansen. PATHOGEN RISK TO BULL TROUT POPULATIONS AND REINTRODUCTION EFFORTS IN THE UPPER WILLAMETTE BASIN.

9:30 (104) **J.C. Parrott**. SURVEY OF ENDOPARASITES INFECTING 6 *PRISTIMANTIS* SPECIES OF PERUVIAN FROG.

9:45 – 10:15 am COFFEE BREAK

10:15 (105) **K.M. Wielgus**, B.J. Wielgus, C. Dick, C. Davis. COMPARED PREVALENCE OF *BAYLISASCARIS PROCYONIS* IN RACCOONS (*PROCYON LOTOR*) IN KENTUCKY.

10:30 (106) **A. McElwain**, R. Fleming, M. Lajoie, C. Maney, B. Springall, S.A Bullard. GROSS AND HISTOPATHOLOGICAL CHANGES ASSOCIATED WITH THE EGGS, LARVAE, AND CUTICULAR REMNANTS OF *UNIONICOLA* SP. (ACARI, UNIONICOLIDAE) INFECTING *STROPHITUS CONNASAUGAENSIS* (BIVALVIA, UNIONIDAE).

10:45 (107) **J.G. Bucci**, M.L. Harless. LOCAL SURVEY OF LARVAL DIGENETIC TREMATODES INFECTING PHYSID AND PLANORBID SNAILS WITH IMPLICATIONS FOR NATIVE AMPHIBIAN POPULATIONS IN NORTHWEST NEW JERSEY.

11:00 (108) **I.C. Mgbemena**. REPELLENT ACTIVITIES OF THE METHANOLIC LEAF EXTRACTS OF *MORINGA OLEIFERA* AND *STARCHYTARPHETA INDICA* AGAINST *AEDES AEGYPTI* MOSQUITO.

11:15 (109) **I.C. Mgbemena**, R.I. Okechukwu. THE SYNERGISTIC LARVICIDAL ACTIVITIES OF THREE LOCAL PLANTS ON *AEDES AEGYPTI*.

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

Sunday Afternoon, 2015-06-28

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

Location: Blackstone Ballroom A

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

BIOCHEMISTRY/PHYSIOLOGY

(110) **B.S. Chapman**, P. Pradhan, W.A. Wilson, A. Brittingham. VARIATION IN CARBOHYDRATE UTILIZATION BY TRICHOMONADS OF MAN INHABITING DISTINCT ANATOMICAL NICHES.

CHEMOTHERAPY AND DRUG RESISTANCE

(111) **S. Saeed**. INTERACTIONS BETWEEN ANTIMALARIAL AND ANTIRETROVIRAL DRUGS.

(112) **C.R. Bader**, J.R. Jesudoss Chelladurai, K. Poel, B. Miatke, C. Hall, M. Brewer. PERFORMANCE OF ANTI-BACTERIAL AND ANTI-PROTOZOAL COMPOUNDS AGAINST *TRITRICHOMONAS FOETUS* IN AN IN VITRO DRUG SUSCEPTIBILITY ASSAY.

EVOLUTIONARY ECOLOGY

(113) **E. Barnes**, K.K. Herrmann, N. Carpenter. IS DIVERSITY OF THE PARASITIC HELMINTH COMMUNITY IN *CYPRINELLA VENUSTA* AFFECTED BY ANTHROPOGENIC DISTURBANCE IN EPHEMERAL RIVERS?

(114) **R.W. Koch**, M.V. Sukhdeo. PARASITE COMMUNITIES ALONG A RIVER CONTINUUM IN THE NEW JERSEY PINELANDS.

(115) **J.D. López**, R. Mata-López, M. García-Varela, G. Pérez-Ponce de León. GENETIC VARIATION OF *OLIGACANTHORHYNCHUS MICROCEPHALUS*, PARASITE OF THREE SPECIES OF OPOSSUMS ACROSS CENTRAL AND SOUTHEASTERN MEXICO.

(116) **T. Iakovidis**, G.J. Langford. SURVEY OF HELMINTHS FROM THE INTRODUCED CANE TOAD AND NATIVE TOADS IN CENTRAL FLORIDA.

(117) **N. Svitlica**, Y. Hu, J. Detwiler. DENSITY DEPENDENT IMMUNE RESPONSE OF FRESHWATER SNAILS.

GENOMICS AND MOLECULAR BIOLOGY

(118) **A. Rosser**, A. Emery, F. Allan, D. Rollinson, B. Webster. DEVELOPMENT OF A POINT OF CARE NUCLEIC ACID AMPLIFICATION TEST TO DIAGNOSE *SCHISTOSOMA HAEMATOBIUM* INFECTION.

HOST-PARASITE INTERACTIONS

(119) **N.R. Dunham**, S.T. Peper, R.J. Kendall. THE RESURGENCE OF EYEWORM (*OXYSPIRURA PETROWI*) INFECTION IN NORTHERN BOBWHITE (*COLINUS VIRGINIANUS*) AND SCALED QUAIL (*CALLIPEPLA SQUAMATA*) FOUND IN THE ROLLING PLAINS OF TEXAS.

(120) **S.T. Peper**, N.R. Dunham, R.J. Kendall. PREVALENCE OF CECAL WORMS IN NORTHERN BOBWHITE AND SCALED QUAIL IN THE ROLLING PLAINS OF WEST TEXAS.

(121) **N.M. Dinguirard**, M. Mezera, K.K. Geyer, K.F. Hoffmann, T.P. Yoshino. EPIGENETIC REGULATION OF SCHISTOSOME-ASSOCIATED PARASITIC CASTRATION IN SNAILS: A PRELIMINARY STUDY.

(122) **A. Gong**, Y. Wang, S. Ma, X. Chen, X. Chen. DELIVERY OF PARASITE NON-CODING RNAS TO HOST INTESTINAL EPITHELIUM CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION.

(123) **Y. Wang**, A. Gong, X. Chen, C. Lin, X. Chen. HSP70-DEPENDENT NUCLEAR IMPORT OF PARASITE NON-CODING RNAS IN INTESTINAL EPITHELIAL CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION.

(124) **H. Liu**, Y. Shen, A. Gong, X. Chen, S. Ma, J. Cao, X. Chen. LINCRNAS IN INTESTINAL EPITHELIAL DEFENSE AGAINST *CRYPTOSPORIDIUM* INFECTION.

(125) **X. Chen**, Y. Shen, A. Gong, J. Cao, X. Chen. SHUTTLING OF PARASITE NON-CODING RNAS IN EXOSOMES RELEASED FROM GASTROINTESTINAL EPITHELIAL CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION.

(126) **X. Zhang**, A. Gong, Y. Wang, X. Chen. DEVELOPMENT OF AN EX-VIVO MODEL WITH MURINE ENTEROIDS FOR *CRYPTOSPORIDIUM* INFECTION.

(127) **S. Griffin**, N. Carpenter, K. Herrmann, A. Smith-Herron. MICROHABITAT SELECTION AND EYEFLUKE INFECTION LEVELS WITHIN WESTERN MOSQUITOFISH (*GAMBUSIA AFFINIS*).

(128) **S.A. Shea**, K.A. Bedford, A.C. Olsen, A.M. Fedynich, D. Rollins. *OXYSPIRURA PETROWI* AND *AULONOCEPHALUS PENNULA* IN SCALED QUAIL FROM WEST TEXAS AND SOUTH TEXAS.

(129) **K. Lasater**, W. Preisser. A SURVEY OF THE BLOOD-BORNE AND INTESTINAL PARASITES OF RODENTS FROM TEXAS AND COSTA RICA.

(130) **A. Fedynich**, A. Bruno, A. Olsen, K. Bedford, S. Villarreal, D. Rollins. OCCURRENCE OF *TETRAMERES PATTERSONI* IN QUAIL FROM TEXAS.

(131) **N. Heller**, F. Reyda. THE HISTOPATHOLOGY OF *CATOSTOMUS COMMERSONI* (WHITE SUCKER) INFECTED WITH *POMPHORHYNCHUS BULBOCOLLI* (ACANTHOCEPHALA).

(132) **J.E. Kawaguchi**, O.N. Choi, R.C. Jadin, S.A. Orlofske. TRANSMISSION OF STRIGEIDAE (PLATYHELMINTHES: TREMATODA) IN WISCONSIN AND ILLINOIS FRESHWATER WETLANDS.

(133) **J. Ermer**. SURVEY OF BOBCAT INTESTINAL HELMINTHS ON THE PINE RIDGE INDIAN RESERVATION.

(134) **M. Hanten**. MANIPULATION OF CRICKET (*ACHETA DOMESTICUS*) GEOTAXIS TENDENCIES BY HORSEHAIR WORMS (NEMATOMORPHA) TO INDUCE WATER-SEEKING BEHAVIOR

(135) **J. Eells**, A. Varela-Stokes, S. Guo-Ross, E. Kummari, H. Smith, E. Cox, D. Lindsay. CHRONIC *TOXOPLASMA GONDII* IN NURR1-NULL HETEROZYGOUS MICE EXACERBATES ELEVATED OPEN FIELD ACTIVITY.

IMMUNOLOGY

(136) **A. Kimball**. IMMUNE MECHANISMS IN TREMATODE-*HELISOMA TRIVOLVIS* INTERACTIONS.

LIFE CYCLES AND EPIDEMIOLOGY

(137) **A.D. Acholonu**. PRELIMINARY STUDIES ON HELMINTH PARASITES OF GASTROINTESTINAL TRACT OF CATFISH (*ICTALURUS PUNCTATUS*) AND BUFFALO FISH (*ICTIOBUS CYPRINELLUS*) FROM LOWER MISSISSIPPI RIVER.

(138) **K. McAndrews**, G. Orcutt, T. Herzog, M. Barger. IS PARASITE BIODIVERSITY IN FRESHWATER FISH HIGHER IN PROTECTED AREAS? A CASE STUDY IN THE BIG THICKET NATIONAL PRESERVE.

(139) **K. Jacobson**, A. Aceves, L. Weitkamp. MARINE-ESTUARINE TROPHICALLY TRANSMITTED PARASITES INDICATE ESTUARINE FORAGING AND SUGGEST DIFFERENCES BETWEEN NATURAL-ORIGIN AND HATCHERY-PRODUCED MID/UPPER COLUMBIA RIVER SPRING CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*).

(140) **D.H. Graham**, C. Sarkissian. MICROGEOGRAPHIC POPULATION GENETIC STRUCTURE OF *BAYLISASCARIS PROCYONIS* (NEMATODA: ASCAROIDAE) IN WESTERN MICHIGAN INDICATES THE GRAND RIVER IS A BARRIER TO GENE FLOW.

(141) **S. Rogers**, R. Countess, M. Francois, G.J. Langford. COMPARATIVE ANALYSIS OF HEMOGREGARINES COLLECTED FROM SNAKES (*NERODIA* SPP.) IN FLORIDA.

(142) **M. Jamison**, A.M. Watson, I. de Buron, P.R. Kingsley-Smith, T. Darden, J. Robinson, S.A. Arnott. DETECTION OF AN INVASIVE PARASITE, *ANGUILLICOLOIDES CRASSUS*, OF AMERICAN EELS USING QPCR.

(143) **K.M. Hill-Spanik**, V.A. Connors, M. Babrowicz, W.A. Roumillat, I. de Buron. *DONAX VARIABILIS*: A VECTOR FOR A DIGENEAN OF THE FLORIDA POMPANO *TRACHINUS CAROLINUS*.

(144) **S.D. Atkinson**, I. de Buron, S.L. Hallett, D. Diaz Morales, J.L. Bartholomew. HUNTING FOR THE ALTERNATE HOST OF *KUDOA INORNATA*, A MYXOZOAN PARASITE OF SPOTTED SEATROUT.

(145) **R.O. Sawyer**. DEMONSTRATION OF *SARCOCYSTIS FALCATULA* AND S. *FALCATULA* ARG-LIKE PARASITES IN HEART AND BREAST MUSCLES FROM RAPTORS.

TAXONOMY, SYSTEMATICS AND PHYLOGENY

(146) **I. Delgado**, E. Dedrick, F.B. Reyda. EXAMINATION OF A NEW SPECIES OF RHINEBOTHRIIDEAN CESTODE FROM *HIMANTURA PASTINACOIDES* (ROUND WHIPRAY).

(147) **P. Lado**, D. Hibbs, S. Nava, L. Beati. IS *AMBLYOMMA PARVUM* A COMPLEX OF CRYPTIC SPECIES?

(148) **K. Forti**, T. Aprill, F. Reyda. EXAMINATION OF A NEW SPECIES OF RHINEBOTHRIIDEAN CESTODE FROM A NEW SPECIES OF STINGRAY (*HIMANTURA UARNAK* 2) FROM COASTAL AUSTRALIA.

(149) **B. Solorzano**, S.A. Nadler, G. Pérez-Ponce de León. PINWORM DIVERSITY IN PRIMATES INHABITING RAINFOREST IN MEXICO.

(150) **D.I. Hernández-Mena**, B. Mendoza-Garfias, P. Ornelas-García, G. Pérez-Ponce de León. TESTING THE SYSTEMATIC POSITION OF *MAGNIVITELLINUM SIMPLEX* KLOSS, 1966 WITHIN THE FAMILY MACRODEROIDIDAE (DIGENEA) BY USING SEQUENCES OF THE 28S RRNA.

(151) **J.R. Jesudoss Chelladurai**, C. Bader, T. Snobl, C.A. West, S. Verma, R.J. Martin, M.T. Brewer. CHARACTERIZATION OF A*SCARIS* FROM PIGS USING MITOCHONDRIAL AND NUCLEAR MARKER GENES.

(152) **B. Kozinski**, K. Huberty, R. Colling, A. Choudhury. UNCOVERING THE HIDDEN DIVERSITY OF *BOTHRIOCEPHALUS* SPP. IN NORTH AMERICAN FRESHWATER FISHES.

(153) **D. Yanda**, E. Manlick, A. Grahn, P. Nelson, A. Choudhury. DIVERSITY OF *LISSORCHIS* SPP. (TREMATODA: LISSORCHIIDAE) EXPLORED THROUGH MORPHOLOGY AND MOLECULES.

(154) **C. Wert**, F. Reyda. CRYPTOGONIMID TREMATODES OF THE FISHES OF OTSEGO LAKE, NEW YORK.

(155) **R. Salas-Montiel**, A. Oceguera-Figueroa. PHYLOGEOGRAPHIC ANALYSIS OF THE NORTH AMERICAN MEDICINAL LEECH *MACROBDELLA DECORA* (ANNELIDA: HIRUDINEA).

(156) **N.G. Ruiz Torres**, A. Oceguera-Figueroa. PHYLOGENETIC POSITION OF *SYNDESMIS FRANCISCANA* (RHABDOCELA: UMAGILLIDAE), SYMBIONT OF ECHINOIDS BASED ON MOLECULAR MARKERS.

(157) **A.J. Phillips**, W.E. Moser. COLLECTIONS MANAGEMENT POLICIES AND PROCEDURES OF THE USNPC.

VECTOR BIOLOGY

(158) **J.T. Sullivan**, R.A. Manuel, J.K. White, R.V. Beltran. HEMOPOIETIC TISSUE VOLUME IS A HERITABLE TRAIT IN THE SCHISTOSOME-TRANSMITTING SNAIL *BIOMPHALARIA GLABRATA*.

(159) **C. Chevalier**. PREVALENCE OF RACCOON ROUNDWORM (*BAYLISASCARIS PROCYONIS*) IN A SEMI-URBAN ENVIRONMENT IN NORTHWEST MISSOURI: PRELIMINARY FINDINGS.

(160) **A. Barquin**, A. Vasquez, M. Mendoza, M. Wise de Valdez. MOSQUITO SPECIES DISTRIBUTION IN RESIDENTIAL AREAS ACROSS SAN ANTONIO, TEXAS.

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

Location: Blackstone Ballroom B

Presiding: **B. Christensen,** University of Wisconsin-Madison

1:45 Introduction of 2015 H. B. Ward Medal Recipient.

1:55 **J.F. Hillyer**, Acceptance of the 2015 Henry Baldwin Ward Medal.

Julián F. Hillyer
Henry Baldwin Ward Medal

3:00 PM - 4:30 pm ASP Awards and Business Meeting

Location: Blackstone Ballroom B

Eric S. Loker
Clark P. Read Mentor Award

ASP AWARDS

CLARK P. READ MENTOR AWARD LECTURE

Presiding: **P. Hanington**, University of Alberta

3:00 Introduction of 2015 C.P. Read Mentor Award Recipient

3:10 **E.S. Loker**, "Mentoring… some perspectives from both sides of the desk."

DISTINGUISHED SERVICE AWARD

John Janovy Jr.
Distinguished Service Award

Presiding: **J. Detwiler**, University of Manitoba
M.G. Bolek, Oklahoma State University

WILLIS A. REID JR. STUDENT RESEARCH GRANTS

Presiding: **G. Mayer**, Mahattan College

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: **G. Langford**, Florida Southern College

ASP BUSINESS MEETING

Presiding: **D. S. Lindsay**, Virginia Tech, Virginia-Maryland College of Veterinary Medicine

Thank you for attending this year's ASP meeting and have a safe trip home.
*See you **July 11-14, 2016** at our next meeting in **EDMONTON, ALBERTA***

Abstract Listings

(1)

HOW DOES AN INVASIVE SPECIES ALTER NATIVE PARASITE TRANSMISSION?

S. Weinstein, Ecology, Evolution, and Marine Biology University of California, Santa Barbara

Invasive rats transmit human disease, destroy crops and decimate native fauna. The introduced black rat, *Rattus rattus*, occurs throughout the native range of the raccoon roundworm, *Baylisascaris procyonis*, and those rats may be incorporated into the parasite life cycle if they consume parasite eggs, acquire viable infections, and are subsequently eaten by raccoons. I tested the potential for rats to amplify transmission of this zoonotic parasite by monitoring animal behavior at raccoon latrines, surveying wild rodent populations for *B. procyonis* infection, and conducting scavenger trials using motion activated cameras. Compared to native mice, *Peromyscus maniculatus* and *Reithrodontomys megalotis*, rats occupy more contaminated habitat and have greater contact with latrines. This exposure leads to viable infections with rats harboring mean parasite intensities 100 times greater than that of co-occurring native rodents. Raccoons compete with opossums and skunks for rodent carcasses, but even if raccoon predation is relatively infrequent, the high worm burdens in these invasive rodents likely increase the total parasite population.

(2)

PARASITE BURDEN, HOST SIZE, AND IMMUNE RESPONSE OF *OCTOPUS BIMACULOIDES*

F.J. Broughton
Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara
M.K. Fentress
Department of Molecular, Cellular and Developmental Biology, University of California, Santa Barbara
S.B. Weinstein and **A.M. Kuris**
Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara

We examined the California two-spot octopus, *Octopus bimaculoides*, for prevalence and intensity of pathogens, macroparasites, and trophically transmitted parasites across host size and age classes. The coccidian *Aggregata millerorum* is ubiquitous in *O. bimaculoides* and may be its most important pathogen. Sporozoites of *A. millerorum* invade the digestive tract of *O. bimaculoides*; schizogony ensues, producing presumably host-limited cysts. These are hypothesized to accumulate, enlarge, and spread to other organs as the host ages. At high intensities, organ architecture can become severely compromised. However, in our samples, neither infection intensity nor individual lesion size of *A. millerorum* appear to be associated with an increase in body mass, which we used as a proxy for host age. This result is interpreted with respect to the life cycle of *O. bimaculoides*. These octopuses also frequently harbor several other parasites, including juvenile nematodes, larval trypanorhynch and tetraphyllid tapeworms, dicyemids, and an undescribed species of tisbeid copepod. Other than the dicyemids, these neither multiply within the host nor do their intensities significantly increase in relation to increasing host size.

(3)

COMPARATIVE HELMINTH COMMUNITY STRUCTURE IN TWO SPECIES OF ARCTIC-NESTING WATERFOWL: BLACK BRANT (*BRANTA BERNICLA NIGRICANS*) AND GREATER WHITE-FRONTED GEESE (*ANSER ALBIFRONS*)

N.J. Traub and **A.J. Smith-Herron**, Texas Invasive Species Institute, Sam Houston State University
C.L. Amundson and **P.L. Flint**, U.S. Geological Survey, Alaska Science Center

Waterfowl can have relatively high parasite burdens in some cases resulting in demographic consequences for the hosts; however, little is known about the timing and pathways of infection and if there is inter- and intra-specific transfer on the breeding grounds. This study investigates the helminth communities of two waterfowl species, greater white-fronted geese (*Anser albifrons*) and Pacific black brant (*Branta bernicla nigricans*), breeding in Sub-Arctic (Yukon Delta National Wildlife Refuge in Western Alaska (YK)) and Arctic Alaska (Beaufort Sea coast in Northern Alaska (N)) collected during July–August 2014. Black brant and greater white-fronted geese breed sympatrically, but differ in both migration route and wintering areas. Thus, similarities in helminth communities between species suggest inter-specific transmission of helminthes on the breeding grounds. We sampled brant from both N and YK to evaluate the relative contribution of site (Arctic and sub-arctic) on helminth community structure. We collected both species from N to assess evidence of interspecific transmission. To date, 100% of necropsied hosts are infected. Fourteen species of helminths have been identified from 5 microhabitats (gizzard, proventriculus, duodenal loop, gastric ceca, and small intestine). *Trichostrongylus tenuis*, the dominant nematode, occurred in 77.59% of hosts examined. *Tschertkovilepis setigera*, the dominant cestode, occurred in 70.69% of hosts examined. Preliminary findings suggest that parasite communities are somewhat similar between host species at a site, but community differences exist between sites. Thus, helminth community structure in this area may be driven by host habitat or climate. With the exception of direct lifecycle nematodes, component communities differ between host wintering and breeding grounds. Our results provide baseline information with which to better investigate infra- and component community dynamics of helminths transmitted at high latitudes, and understand helminth infection of migratory waterfowl hosts throughout the annual cycle.

(4)

REMODELING A STOLEN HOME: EFFECTS OF TREMATODE PARASITISM ON THE FUNCTIONAL SHELL MORPHOLOGY OF SNAIL SHELLS IN FLOW AND NONFLOW ENVIRONMENTS

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

It is well understood that the primary function of the gastropod shell is protection. However, shells that function well in one environment may be maladaptive in another. For example, a large, crush-resistant shell may be well-suited for resisting predation but would be a burden in a stream environment where a smaller, light shell can better resist wave action, which is a major source of mortality for stream snails. Upon infection, the shell of a snail becomes the home for a trematode and it is to the parasite's advantage optimize, or not interfere with, the function of the shell to increase its chances of survival and life cycle completion. However, trematodes are also known to be pathogenic to their hosts and it is not clear if parasitism will cause gastropods to express specific morphological changes dependent on their environment or as a result of pathology. To address these hypotheses, we conducted a field study and complimentary laboratory experiment to examine the effects of trematode parasitism on the functional shell morphology (shape, size, and crush resistance) of *Physa acuta* snails in flow and non-flow environments. For the field study, we used naturally infected and non-infected *P. acuta* snails collected from ponds (i.e., nonflow) and streams (i.e., flow). In addition, we conducted a complimentary laboratory experiment to better isolate the effects of parasitism on shell plasticity using experimentally-infected

snails and flow/nonflow tanks. We used geometric morphometrics to measure snail size and shape and used crush assays to calculate the force required to crush snail shells. Our field results indicate that pond snails had larger, more crush resistant shells with narrow apertures and tall spires. In contrast, stream snails had smaller, weaker shells with wide apertures and short spires. Trematode parasitism had no apparent effect on the crush resistance of pond snails but significantly reduced the crush resistance of stream snails. However, parasitism had no significant effect on overall shell shape in stream or pond snails. Laboratory *P. acuta* snails from nonflow tanks were also generally, but not significantly, larger than flow tank snails. Similar to our field study results, nonflow snails had significantly more crush resistant shells than flow snails. Additionally, the shapes of flow and nonflow snails significantly differed where nonflow snails exhibited shapes consistent with pond snails and flow snails exhibited shapes similar to stream snails. For laboratory snails, trematode parasitism reduced crush resistance regardless of their flow/nonflow environment. Our results demonstrate that habitat and/or flow environment was the primary factor affecting *P. acuta* shell size, shape, and crush resistance. Interestingly, laboratory snails from flow and nonflow tanks showed functional morphologies consistent with wild stream and pond snails, respectively. Trematode parasitism played a secondary role and reduced the crush resistance of wild stream snails and laboratory raised snails which is likely a result of parasite-induced pathology. However, it is unclear why this was not observed in ponds as well. Differences in trematode species, nutrition, or other factors between ponds and streams need to be explored further.

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(5)

THE SYMBIOTIC CILIATE *KYAROIKEUS CETARIUS* IN CAPTIVE BOTTLENOSE DOLPHINS

J.M. Carrillo and **R.M. Overstreet**, University of Southern Mississippi

Some symbiotic ciliates live restricted within the blow-hole of several cetacean species where they probably feed on bacteria and mucus. Perhaps the most common and abundant ciliate in this particular habitat is *Kiaroikeus cetarius*. A preliminary study was conducted on captive bottlenose dolphin (*Tursiops truncatus*) to examine the mean intensity and prevalence infection relative to geographic captive location, sex and age of host. We examined 30 bottlenose dolphins in four dolphinaria located in Florida and Mississippi along the Gulf of Mexico. Expectorated products from a consistent number of blows were collected from each dolphin previously trained to blow on demand. The expectorations were fixed immediately on site after collection and then stained and studied in our laboratory. Examination showed no statistically significant difference in prevalence of infection with regard sex, age, or geographic location. However, adults had a statistically significant higher mean intensity of *K. cetarius* than calves ($p<0.05$). The lower mean intensity in calves might be an indication that the intensity of the infection increases as the dolphin ages or, as shown by Overstreet, there is a positive association between the mean intensity of *K. cetarius* and the health of the dolphin.

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(6)

AMPHIBIAN TRYPANOSOMES FROM NORTH CENTRAL OKLAHOMA: MORPHOLOGY, MOTILITY, AND HOST SPECIFICITY

R.P. Shannon and **M.G. Bolek**, Oklahoma State University

During May-August of 2014, a total of 140 amphibians from 5 families and 9 species were collected from 5 locations in Oklahoma and examined for blood parasites, leeches and leech hematomas. Of those, only aquatic bullfrogs (*Rana catesbeaiana*) and semi-terrestrial southern leopard frogs (*Rana sphenocephala*) were infected with blood parasites, but no leeches or leech hematomas were observed on any of the amphibians examined. Five species/morphotypes of blood protozoa infected adult southern leopard frogs from 2 locations and 1 species of blood protozoan infected adult bullfrogs (*R. catesbeiana*) from 1 location. Bullfrogs and southern leopard frogs were both infected with *Hepatozoon catesbianae*; whereas 4 trypanosome morphotypes were present in southern leopard frogs and conform to previous descriptions of (1) *Trypanosoma ranarum*, (2) *Trypanosoma rotatorium*, and (3) *Trypanosoma chattoni*. Among

trypanosome morphotypes, video-microscopy revealed distinct differences in trypanosome motility in frog blood plasma. The larger morphotype of *T. rotatorium* moved laterally in relation to its anterior-posterior axis; whereas the smaller morphotype of *T. rotatorium* moved anteriorly with its curved anterior end. In contrast, *T. chattoni* did not exhibit any motility. Both leeches and hematophageous dipterans have been reported as vectors for amphibian trypanosomes. However, little information is available on the specific vectors for species of *Trypanosoma* infecting southern leopard frogs in our study area. To address this issue, a preliminary host specificity study was performed. Amphibian leeches *Placobdella picta* collected on salamanders infected with *Trypanosoma ambystomae* from Nebraska were fed on frogs infected with Oklahoma trypanosomes. Frogs acquired additional infections of *T. ambystomae*, however subsequent leech feedings on uninfected southern leopard frogs only transmitted the salamander trypanosome, suggesting Oklahoma trypanosomes might not use leeches as vectors. Although differences were found in morphology and swimming behavior, it remains unclear if these morphotypes represent distinct species. We are in the process of sequencing these morphotypes to elucidate additional characters for species identifications.

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(7)

BUILDING COMMUNITIES: THE ROLES OF BIOTIC AND ABIOTIC FACTORS

V.M. Frankel, Smithsonian Tropical Research Institute and McGill University

Parasitism is the most common life-history strategy on Earth but surprisingly little is known about the drivers of parasite species assemblages and community dynamics. Host population stability has long been recognized as an important factor governing parasite population dynamics yet recent research suggests that biotic factors such as host diversity and abundance are strong predictors of parasite community dynamics. While biotic and abiotic factors are logical factors affecting species assemblages, they are rarely factored together to understand changes in parasite communities across spatial and temporal scales. Here, we integrate both biotic and abiotic factors to evaluate the extent to which both biotic factors and abiotic habitat variables better predict the abundance and diversity of parasites. To do this, we quantified the abundance and diversity of specialist trematode parasites infecting an invasive host snail across 26 lake and stream sites in the Isthmus of Panama. We find that the predictive power of our models is significantly improved by integrating both biotic and abiotic factors and discuss both theoretical and practical applications for our understanding not only of parasite assemblages, but of other ecological communities.

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(8)

HOST MANIPULATION VIA TEMPORAL ADJUSTMENT OF OCULAR OBSTRUCTION BY TREMATODE METACERCARIAE IN EYES OF FISH

A.D. Stumbo, University of Otago

Parasitic infection often results in alterations to the host's phenotype, and may modify selection pressures for host populations. It is important to understand the mechanisms of these changes to further understand how parasites shape the evolution of their hosts. A variety of mechanisms may result in changes in the host's behavioural phenotype, ranging from a simple by-product of infection to chemicals directly released by the parasite to alter behaviour. Another possibility may involve parasites freely moving into certain tissues, or sites within tissue, at specific times of the day to induce behavioural changes in the host. We observed the metacercarial activity of a *Tylodelphys* sp. trematode that remains unencysted in the eye of their second intermediate fish host, the New Zealand common bully (*Gobiomorphus cotidianus*). Ocular obstruction and metacercarial activity were assessed within the sedated host's eye at three time points per 24 hour period, using video captured via an ophthalmoscope. Ocular obstruction was significantly reduced at night and metacercarial activity did not change between time periods. A parallel study showed that greater levels of infection correlate with reduced host response to a light stimulus and increased response to tactile stimuli during the day, though no correlation is seen

for behavioural measurements taken during the evening hours. Together, these studies show increased visual obstruction during the foraging time of the most likely definitive host, the crested grebe (*Podiceps cristatus*). This *Tylodelphys* sp. has only been documented in Central Otago, New Zealand, and achieves high local prevalence in fish populations. The rapidly growing grebe population may soon spread *Tylodelphys* sp. across the country. Further studies will explore the extent of behavioural alterations in infected fish populations, and comparisons between infected and uninfected populations may reveal evolutionary differences resulting from contrasting selective pressure from parasites.

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(9)

EFFECTS OF *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA) ON THE CRICKET HOST, *ACHETA DOMESTICUS*

Williams, **L. Vredevoe** and **G. Kolluru,** California Polytechnic State University
B. Hanelt, University of New Mexico

Freshwater gordiids have complex life cycles which include multiple hosts and a free-living aquatic phase. At the end of their parasitic phase, gordiids manipulate the behavior of their terrestrial arthropod hosts, causing them to enter aquatic environements where adult worms emerge often at the expense of host mortality. All gordiids develop in the hemocoel of their terrestrial arthropod host. Incredibly, within the host, gordiids grow from a small length of 60-100 um to a length of over 2 m for some species. Anecdotal field observations indicate that arthropod hosts appear to show a high degree of hairworm induced pathology. Some reports indicate that after worms emerge from their hosts, only the gut remains within the arthropod's body cavity, whereas other studies indicate that the production of eggs by female arhtorpod hosts is inhibited or absent altogehter. The focus of this investigation was to evaluate if infection by hairworms alters growth rate, depletes fat body, and reduces fecundity in their arthropod host. To test the effect of hairworm parasitism on the arthropod host, 4 week old female house crickets (*Acheta domesticus*) were infected with the hairworm *Paragorius varius.* once worms emerged from their cricket hosts, cricket body length, femur length, and ovipositor length as well as fat body content and egg production were measured and compared with sham-infected crickets. Our results indicate that cricket body length and ovipositor length, as well as fat body content and egg production were significantly reduced in infected crickets compared to sham-infected control crickets. This work is the first to experimentally document the negative effects of hairworm parasitism on their arthropod hosts and will be discussed and compared to field observations on arthropod hairworm infections.

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(10)

ARE ECOTONES HOTSPOTS FOR PARASITE DIVERSITY?

A.W. Bartlow, University of Utah

Ecotones are transition zones between two different habitats. Ecotones frequently have a higher number of free-living species than the primary habitats on either side. Ecotones have relatively high species richness because the ranges of free-living species from the different primary habitats overlap in the ecotone, and some species may specialize on the ecotone itself. The effect of ecotones on parasite diversity, however, remains largely unknown. As in free-living systems, parasites may have higher species richness in ecotones because they are places where parasite species from hosts in different habitats overlap, and because there may parasites that are endemic to the ecotone itself. To test the hypothesis that ecotones have higher parasite species richness, we compared the helminth communities of deer mice (*Peromyscus maniculatus*) across a sagebrush–ecotone–pinyon/juniper habitat gradient in the Great Basin. Initial surveys indicate differences in helminth community composition among the three habitats; however, the ecotone does not differ significantly from either sagebrush or pinyon/juniper in helminth species richness. The prevalence and intensity of helminths differed significantly among habitats. Helminth prevalence was similarly high in both ecotone and pinyon/juniper habitats. Helminth intensity did not differ significantly

between ecotone and pinyon/juniper habitats, but were both significantly higher than in sagebrush. Sagebrush may support a smaller helminth community compared to pinyon/juniper and ecotone habitats.

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(11)

ABUNDANCE OF FILTH FLIES AT BUTCHERS STALLS, SOUTHERN NIGERIA

O.O. Ikpeze, **U.C. Ngenegbo** and **I.S. Okwelogu,** Nnamdi Azikiwe University, Awka, Nigeria.

Lack of government-owned abattoirs in Anambra State, Nigeria has led to proliferation of private, illegal and unhygienic slaughtered slabs resulting in absence or inadequate inspection of more than 75% of cattle slaughtered in the State. Carcasses were mostly brought in blood-smeared and stinking push-trucks to butchers stalls and displayed openly on wooden tables for sale or hawked nearby with disregard to proper sanitation, thereby attracting filth flies. This situation would be compounded by prevailing absence of Vet inspection services in rural areas of the State. Abundance of filth flies in Butchers Stalls at 3 major Ethnic Foods Markets in Anambra State namely, Afo-Igwe Umudioka, Oye-Olisa Ogbunike, and Nkwo Ogidi were recorded monthly in 2014. Collections using sweep-nets were made on first Saturdays (8.00a.m-11a.m), second Saturdays (12noon-3.00p.m) and third Saturdays (4.00p.m-7.00p.m) of each month simultaneously in all butchers' stalls by three respective teams, each led by an Entomologist supported by Entomology Technicians. Filth flies caught were identified by morphological features using identity Keys of Armed Forces Pest Management Board Technical Guide No. 30. Altogether 123130 filth flies were caught by making 3600 sweep nets, giving an average of 34.2 flies per sweep net. However, average filth fly per sweep net thrown in Afo-Igwe was 47.01, Oye-Olisa (40.94) and Nkwo-Ogidi (14.61) while total number and relative percentages of identified species were *Musca domestica* (116540;94.6%), *Chrysomyia putoria* (5353;4.3%), *Calliphora* species (103; 0.1%) which were significantly different (P<.05). Interestingly, average flies per sweep net and relative percentages of total collections were in evenings (49.03; 47.8%), mornings (33.34;32.5%) and afternoons (20.24; 19.7%) but their numerical values increased gradually during November-March dry season (63299;51.4%) and fluctuated during April-October rainy season (59831;48.6%).

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(12)

ASYMPTOMATIC *PLASMODIUM FALCIPARUM* INFECTION IN SICKLE CELL DISEASE PATIENTS

F.O. Akinbo and **C.D. Ugboaja**, University of Benin

Plasmodium falciparum infection is widely considered a major cause of death in children and adolescent born with sickle cell anaemia (SCA) in sub-Saharan Africa. This study was conducted to determine asymptomatic *P. falciparum* infection in sickle cell patients in Edo State, Nigeria. A total of 302 participants consisting of 202 sickle cell disease patients (101 males and 101 females) and 100 apparently healthy non-sickle cell subjects that served as control were enrolled in this study. Blood specimen was obtained from each participant for haemoglobin concentration, complete blood count and the detection of malaria parasite using standard procedures. A prevalence of 48% of asymptomatic *P. falciparum* infection was observed among sickle cell disease patients. Total white blood count, lymphocyte and monocyte counts were significantly higher among sickle cell patients. Measures to reduce asymptomatic malaria and its associated sequelae in sickle cell disease patients are advocated.

(13)

EFFECTS OF MATERNAL AND NEONATAL MALARIA ON AGE AND BIRTH WEIGHT OF NEONATES IN UYO NIGERIA

U.C. Ngenegbo, **O.O. Ikpeze** and **D.O. Esu**, Nnamdi Azikiwe University, Awka, Nigeria.

Plasmodium falciparum (*Pf*) malaria in pregnancy results in pre-term, underweight and malaria infected neonates in Nigeria. Prevalence of maternal and cord-blood malaria, gestation period and birth weight of resultant neonates were determined at a hospital in southern Nigeria between September and October 2013. One hundred and six (106) pregnant women and associated cord blood were examined for malaria parasitaemia soon after delivery at St Luke's Hospital Uyo, Southern Nigeria. Neonatal status (pre-term, full term and birth weights) and mothers' compliance with long lasting insecticidal nets (LLIN) and intermittent preventive treatment (IPT) of malaria in pregnancy were recorded. Peripheral blood of mothers and venous cord blood of neonates were examined for malaria parasites with Giemsa staining technique employing conventional thin and thick blood films to establish presence and identity of *Plasmodium* species. Only *P. falciparum* was identified. Prevalence of maternal and neonatal malaria was 54.7% and 45.3% respectively. Among infected mothers, 48(45.3%) had *Pf* positive neonates while 10(9.4%) had *Pf* negative babies. All *Pf* negative mothers delivered full term *Pf* negative neonates but 27(25.5%) *Pf* positive mothers had full-term neonates, and 31(29.2%) had pre-term neonates. Also, 6(5.7%) *Pf* positive neonates had normal birth weight of ≥2.5kg while 42(39.6%) had under birth weight of ≤2.5kg. However, mean birth weight (MBW) of neonates 75(70.8%) delivered full term at ≥ 37 weeks was 2.92±0.1519 kg while 31(29.2%) delivered pre-term at <37 weeks was 2.18±0.1661kg. Difference between MBW of under birth weight neonates with *Pf* positive cord blood (2.24±0.1814kg) and normal birth weight neonates with *Pf* positive cord blood (3.08±0.4689kg) was statistically different ($P<.05$). Observed low compliance with LLIN (46.2%) and IPT (48.1%) in pregnancy may be responsible for high prevalence and consequences of maternal and neonatal malaria in Uyo, southern Nigeria.

(14)

INTESTINAL PARASITE INFECTIONS AMONG PRIMARY SCHOOL CHILDREN IN IGBARIAM, ANAMBRA-EAST LOCAL GOVERNMENT AREA OF ANAMBRA STATE, SOUTH-EASTERN NIGERIA

U.C. Ngenegbo, **C.M. Egbuche** and **I. Chukwu**, Nnamdi Azikiwe University, Awka, Nigeria.
C.K. Ezihe, National Arbovirus and Vector Research Enugu

A study of intestinal parasites that infect primary school children in Igbariam was conducted between April to September, 2014. A total of 130 stool samples were collected from the pupils randomly selected for the study. Microscopic examination of the specimens was done using both saline mount and floatation techniques. The number of infected people was 36 (27.7%) with no case of mixed infection. Among the parasites encountered, *Entamoeba histolytica* was the most occurring parasite, infecting 26 (20.0%) subjects. The prevalence of other intestinal parasites encountered were 3.8%, 2.3% and 1.5% for *Ascaris lumbricoides*, *Strongyloides stercoralis* and hookworm respectively. Prevalence by gender showed no significance difference ($P > 0.05$) even though more males were infected than females. The study shows that intestinal parasites still thrive and persists in some areas in Nigeria even in the face of some control measures that have been put in place.

(15)

DIRECT COST OF NEUROCYSTICERCOSIS IN PATIENTS TREATED AT THE INSTITUTO NACIONAL DE NEUROLOGIA Y NEUROCIRUGIA (INNN) IN MEXICO CITY, MEXICO

R. Bhattarai, Texas A&M University
H. Carabin, University of Oklahoma Health Sciences Center
J.V. Proaño, Instituto Mexicano del Seguro Social
J. Flores-Rivera and **T. Corona**, National Institute of Neurology and Neurosurgery
T. Corona, National Institute of Neurology and Neurosurgery
A. Flisser, Universidad Nacional Autónoma de México
C.M. Budke, Texas A&M University

The objective of this study was to estimate the annual direct costs related to the diagnosis and treatment of 54 patients that were hospitalized for neurocysticercosis (NCC) at the Instituto Nacional de Neurologia y Neurocirugia (INNN) in Mexico City, Mexico from July 2007 to August 2008. Information on presenting clinical manifestations, diagnostic tests, hospitalizations, surgical procedures and other treatments received by patients was collected via medical chart reviews. Uncertain values for costs and frequency of treatments were imputed using bootstrap techniques, with results presented as average costs and 95% Confidence Intervals (95% CIs). Total annual direct cost for the 54 inpatients was US$ 310,314, with an annual average direct cost of US$ 2,972 (95% CI: 2,264 – 3,681) per patient. Individuals who were suffering from a combination of seizures, severe chronic headaches, and hydrocephalus had the greatest direct costs compared to NCC patients presenting with other clinical manifestations or combinations thereof. The annual average direct cost per patient corresponded to 260% of an annual minimum wage salary. This study suggests that significant economic losses occur, in Mexico, due to clinical manifestations associated with NCC.

(16)

INTESTINAL HELMINTH SURVEY OF FERAL HOGS FROM TEXAS

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Program of Biology, Texas A&M University-San Antonio

Feral hogs, or *Sus scrofa*, are known widely throughout Texas as an overall pest to land management and livestock enterprises in general. Close to half of the nation's feral hog population resides in Texas potentially creating a health risk for domesticated livestock; for this reason knowing more about the intestinal helminthes of feral hogs is important. We collected a total of 43 feral hog large and small intestines on day of slaughter from a USDA processing facility in south Texas from September of 2014 to February of 2015. We will continue to collect at least 10 hogs weekly throughout the remainder of the year. The facility accepts hogs from holding facilities located throughout the state; each serves a specific region which was noted on day of intestine collection. Our findings thus far have shown that 14 of the 43 hogs were infected. Parasites collected included six *Ascaris spp*., 31 *Macracanthorhynchus hirudinaceus*, five smaller, yet to be identified, Acanthocephalans, and 375 yet to be identified hookworms. With a potentially unlimited supply of feral hogs, we will be able to continue these studies indefinitely which will give us multiple opportunities to investigate any trends in this host-parasite system.

(17)

REVIEW OF THE PHYSIOLOGICAL ECOLOGY OF PARASITE OVERWINTERING

D.J. Larson, University of Alaska Fairbanks, Biology and Wildlife Department, Institute of Arctic Biology

Subarctic and arctic winters exhibit extreme conditions with temperatures remaining below 0°C for 6 months or longerand-40°C or lower for extended periods. The impact of these conditions on parasite transmission and host-parasite interactions is poorly understood; however, parasites may cope with winter using similar strategies as their hosts or even usurp host responses for protection from winter. This review will examine the strategies parasitic helminths and arthropods use to survive winter. When confronted with winter, animals cope with one of four strategies: migration, seek thermal refugia, hibernate, or acclimatize and stay active. Animals that hibernate depress metabolism and keep body temperatures above freezing or overwinter with body temperatures below freezing. Organisms that overwinter body temperature below freezing tolerateextracellularice formation, inhibit ice growth, or avoid ice formation. Ice formation is inhibited by producingcolligative solutes and supercoolingbodywater by removing ice nucleators; for freeze avoidant species internal ice formation is lethal. Ice inhibiting organisms produce antifreeze proteins and glycolipids that attach to ice crystals and prevent ice propagation. Freeze-tolerant animals survive extracellular freezing by controlling ice formation, reducingfreezing induced desiccation, and preventing intracellular ice formation. Climate change is altering parasite life histories by shifts in phenology, altering geographical ranges, shortening life cycles, and crashing host populations. Despite the large changes in winter climate, the impact of climate change on parasite overwintering strategies, especially at high latitudes is difficult to determine since little information exists on parasite adaptations to winter. Most studies on parasite winter adaptations have focused freeze-tolerance with regards to food safety or zoonotic diseases. How parasite life histories are affected by the overwintering strategies of their hosts is important to understanding how climate change in the Arctic and Subarctic will impact disease transmission, parasite-host interactions, and host populations.

(18)

KUDOA INORNATA: A SEASONAL PARASITE?

I. de Buron, College of Charleston
K.M. Hill-Spanik, **L. Haselden** and **S.D. Atkinson**

Kudoa inornata is a muscle-dwelling myxozoan that infects the spotted seatrout, *Cynoscion nebulosus*. Over 80% of adult spotted seatrout in South Carolina wild populations are infected. The purpose of this study was to determine if infection of spotted seatrout by *K. inornata* follows a seasonal pattern. During a two year experiment (2013-2014), two replicates of 10 naïve sentinel seatrout were exposed monthly to raw water from Charleston Harbor. At the end of each four week exposure, the presence of myxospores was determined via microscopic observation of squashed muscle biopsies. When no myxospores were visualized, samples were screened for *K. inornata* rDNA using PCR. In both years, peak infection by myxospores was observed during the summer with no infection November through April. However, PCR results indicate the presence of *K. inornata* in fish muscle over a longer period of time (April through January). Because only naïve fish were used, these results indicate that actinospores of *K. inornata* are likely to be released by the annelid vector (yet to be identified) throughout the year except for the two coldest months. The results show that the seasonal presence of myxospores in seatrout muscle is a reflection of the different development rates of myxospores at different times of the year, most likely associated with water temperature. Future studies should focus on temporal quantification of waterborne actinospores and identification of the annelid vector.

(19)

CYTAUXZOON FELIS (APICOMPLEXA: HEILERIIDAE) IN BOBCATS, DOMESTIC CATS, AND TICK VECTORS IN THE SOUTHERN REGION OF ILLINOIS

E.A. Zieman and **M. Schwarzinger**, Southern Illinois University Carbondale
F.A. Jimenez and **C.K. Nielsen**, Southern Illinois University

Cytauxzoon felis is an intraerythrocytic Apicomplexan parasite of felines in the southeastern US. Infection in domestic cats (*Felis catus*) can result in the highly fatal cytauxzoonosis. Bobcats (*Lynx rufus*) are the natural host and often show no apparent pathology associated with infection by *C. felis*. The lone star tick (*Amblyomma americanum*) and the American dog tick (*Dermacentor variabilis*) are competent vectors of *C. felis*. Previous work on *C. felis* has addressed the infection in one host species in a specific geographic region. In particular, distribution of the parasite in tick vectors was based on ticks removed from domestic animals and humans. A comprehensive study of the distribution of the parasite in both questing ticks and felines is necessary. Our study had two general objectives: i) to determine the prevalence and parasitemia of *C. felis* in bobcats and prevalence in questing tick vectors, and ii) to compare the genetic diversity of *C. felis* among different hosts. We screened tissues of 122 bobcats, and 218 ticks (117 *A.* americanum, 101 *D.* variabilis) and 8 domestic cats suspected to suffer cytauxzoonosis for the presence of *C. felis* using polymerase chain reaction (PCR) with specific primers. Bobcats from Illinois showed a prevalence of 66%., whereas ticks had a prevalence of 15.6% with no difference between species. Eight cases of cytauxzoonosis were confirmed in domestic cats. This is the first study to examine a local population of ticks, domestic cats and bobcats. Our data indicate a very high prevalence in ticks and bobcats. More research is necessary to evaluate the causes of these high prevalences, specifically exploring the possibility that domestic cats may be acting as reservoirs and that localized foci of infections may have elevated the prevalence in ticks.

(20)

HEMOPARASITES AND WEST NILE SEROPOSITIVITY OF SONGBIRDS IN A WOODLAND HABITAT WITHIN NORTHWESTERN MINNESOTA

C. Stromlund and **J. Vaughan**, University of North Dakota

One hundred and ten songbirds (29 species) were captured by mist-net in a woodland habitat within Roseau County, Minnesota from April until July 2014. Birds were held in captivity until midnight and then bled from the wing vein. Blood was collected in capillary tubes, centrifuged and the buffy coats were examined for microfilariae and trypanosomes. Hematocrits were also recorded. Each tube was cut and the cellular portion was extracted for DNA and subsequent PCR for detection of hemosporidians. The serum fraction was analyzed by ELISA for antibodies to West Nile virus (WNV). Overall, prevalence for microfilariae, trypanosomes, *Plasmodium*, *Hemoproteus*, *Leucocytozoon* and anti-WNV antibodies were 9%, 40%, 25%, 17%, 18% and 29%, respectively. The most commonly captured species, American Robin, had prevalence for microfilariae, trypanosomes, *Plasmodium*, *Hemoproteus*, *Leucocytozoon* and anti-WNV antibodies of18%, 32%, 57%, 0%, 4%, and 43%, respectively. Only a quarter of the birds captured had no evidence of blood infection and indeed 44% of all birds had evidence of having more than one concurrent infection. Even so, most hemacrit values were within the normal range of ca. 50%.

(21)

MICROSATELLITE ANALYSIS OF GENETIC DIVERSITY OF *HAEMONCHUS CONTORTUS* IN CHINA

M. Hu, Huazhong Agricultural University

Haemonchus contortus is a trichostrongyloid nematode infecting small ruminants. The blood-feeding activity of adult worms causes anaemia, oedema, diarrhoea and even death, consequently resulting serious production and economic losses. As there is no commercial vaccine available against haemonchosis, the control of *H. contortus* relies largely on anthelmintics. However, extensive and uncontrolled use of anthelmintics caused serious drug resistance problem worldwide. Knowledge of genetic variation of *H. contortus* can provide a foundation for understanding the spread of drug resistance alleles and assisting in the control of haemonchosis. However, little is known about the genetic diversity of *H. contortus* in China. In the present study, we explored genetic variation within and among populations of *H. contortus* from seven different geographical regions of China, employing microsatellites as markers. *Haemonchus contortus* adult worms from seven populations in China were collected and applied to microsatellite analysis. Parameters of genetics such as allele number, heterozygosity and PIC implied the selected eight microsatellite markers which could accurately reflect the information of population genetics were polymorphism locus. Genetic analyses based on AMOVA analysis, Fst analysis, phylogenetic analysis, structure analysis, mantel test and population dynamics test revealed high within-population variation, low population genetic differentiation and high gene flow of *H. contortus* in China. The findings provide valuable information for predicting the spread of anthelmintic resistance and further studying the molecular epidemiology.

(22)

CRYPTOSPORIDIUM GENOMES AND DRUG TARGETS

G. Zhu, Texas A&M University

Cryptosporidium is a genus of apicomplexan parasites that infect humans and/or animals with varied host specificities. In humans, cryptosporidia frequently cause water-borne outbreaks and deadly opportunistic infection in AIDS patients (AIDS-OI). However, no drugs are currently approved by FDA to treat cryptosporidiosis in immunocompromised patients, although a single drug (nitazoxanide) is FDA-approved for use in immunocompetent individuals. Therefore, there is an urgent need to identify drug targets and develop new anti-cryptosporidial drugs, particularly those that are effective in AIDS patients. Because of the lack of genetic tools and difficulties in manipulating the parasite, we mainly rely on the genomics and biochemical analysis to learn the *Cryptosporidium* biology. Since *C. parvum* and *C. hominis* genomes were first sequenced and reported in 2004, a number of genomes from other *Cryptosporidium* species and related apicomplexans have been sequenced or being sequenced. By data-mining their genomes, we have learned that cryptosporidia are metabolically divergent not only from the hosts, but also from other apicomplexans. A number of potential new drug targets are also identified and being pursued by a number of laboratories for target-based drug discovery. In this presentation, we will discuss the genomic and metabolic features and current progress in our laboratory on the drug discovery by targeting essential enzymes in the parasite, including those involved in the energy metabolism and fatty acid biosynthesis.

(23)

"OMICS" INVESTIGATION OF *SARCOCYSTIS NEURONA*

D.K. Howe, Department of Veterinary Science, University of Kentucky

Sarcocystis neurona is the leading cause of neurologic disease in horses and an emerging pathogen of marine mammals. *Sarcocystis neurona* cycles between multiple small-mammal intermediate hosts and the opossum definitive host, which restricts this parasite species to the Western Hemisphere. However, the genus *Sarcocystis* is cosmopolitan and encompasses well over 100 species that collectively infect a very broad host range including mammals, birds, reptiles, and fish. To accelerate gene discovery and enable current investigative technologies (e.g., transcriptomics, proteomics, etc.), the genome from two different strains of *S. neurona* has been sequenced and annotated. The assembled genome sequences for both strains indicated an approximate genome size of 125 Mb, which is ~2X the *Toxoplasma gondii* genome. Despite the doubled genome size, the predicted gene content for *S. neurona* was approximately 7000, or about 1500 genes fewer than *T. gondii.* Nearly 20% of the predicted *S. neurona* genes had no identifiable homologue, so some of these genes may be unique to this species. Importantly, the *S. neurona* sequences and annotations have been submitted to EuPathDB so that the information can be accessed by the research community. As part of our efforts to capitalize on the new *S. neurona* genome information, we are examining transcriptional changes that occur during *S. neurona* asexual development. Extracellular merozoites and intracellular schizonts of *S. neurona* each have discrete functions that must be accomplished for the parasite to survive and disseminate. To identify changes in the parasite transcriptome during asexual development, RNA-Seq data were generated from extracellular merozoites and 5 different time-points during intracellular schizont development. Not surprisingly, the schizont transcriptome was enriched for genes involved in nucleotide and protein synthesis, consistent with cell growth and budding of new merozoites. Information from the annotated *S. neurona* genome is being incorporated to better document differential gene expression during intracellular development. The resulting catalogue of novel and differentially-expressed transcripts will be a useful resource for identifying *S. neurona* genes involved in intracellular survival and propagation by this and other apicomplexan parasites.

(24)

WHAT GENOMICS IS TEACHING US ABOUT APICOMPLEXANS

L.D. Sibley, Washington University School of Medicine

The development of affordable and efficient methods for NextGen sequencing of RNA and DNA samples has lead to an expansion of genomic studies and fostered a range of comparative analyses. For example, recent transcriptomics studies have given us a window into the sexual cycle that occurs when *Toxoplasma gondii* infects enterocytes of the cat. Dramatic changes in the expression of metabolic enzymes, surface antigens, and secretory effectors accompany the development of merozoites. NextGen sequencing has also provided new insight into the genetic diversity of *T. gondii* populations from around the world. Sequencing of more than 60 strains of *T. gondii* identified many gene families that encode surface and secretory proteins have been amplified in tandem blocks within the genome. These secretory determinants control key aspects of pathogenesis, and also show strong signatures of selective pressure. Comparative genome sequencing of *T. gondii* and close relatives such as *Hammondia hammondi* and *Neospora caninum* indicate that these same pathogenic secretory determinants are responsible for the key differences between these taxa. The evolution of apicomplexan parasites is reflected in their genomes, and our ability to efficiently decode these signatures provides insight into adaptations that lead to successful parasitism, transmission, and host range.

(25)

USING GROSS PARASITES TO SNEAK EVEN GROSSER EQUATIONS INTO THE INTRODUCTORY BIOLOGY CLASSROOM

J. Wojdak, Department of Biology, Radford University

College faculty that teach introductory courses often struggle to strike a successful balance between covering the requisite content, introducing students to the array of scientific skills they will need, and maintaining the student's interest. Mathematics, modeling, simulation, and statistics are all more important for a successful career in science than ever, yet in most schools the curriculum hasn't kept pace with the changing demands. Parasitologists might be in a particularly good position to contribute to needed reforms. Many parasitologists use reasonably sophisticated mathematical models or statistical analyses in their own research, and many teach these methods in their upper-level parasitology courses. The incorporation of more quantitative approaches, which sometimes students are not excited about, could be made more palatable by the genuinely fascinating stories in which we can embed the need for quantitative tools. For this approach to be impactful, though, we will need to produce and share materials for use by non-parasitologists. As a by-product, more of the students at our institutions might gain exposure to basic parasite biology, which is often given short shrift in introductory courses.

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PARASITOLOGY AND DISEASE ECOLOGY: A POTENTIAL MUTUALISM FOR UNDERGRADUATE EDUCATION?

J. Koprivnikar, Ryerson University

Organismal-level courses at the undergraduate level, including those related to parasitology, have become increasing rare at many institutions. The wide diversity of parasites, their important roles, and complexity of host-parasite interactions make it possible to incorporate the teaching of parasitology into various courses; however, the emerging field of disease ecology also presents an opportunity for directed study of parasites. This rapidly growing area of research spans multiple disciplines, representing a broadly thematic field that is now favored by many institutions with respect to undergraduate programs. Here, common elements of disease ecology and parasitology courses will be explored, as well as challenges to teaching basic parasitology in the context of a course in disease ecology. By adapting to changes in the educational landscape, parasitology and disease ecology represent a potential mutualism that can benefit both fields.

(27)

USING TREMATODES TO TEACH LIFE CYCLES, ECOLOGICAL INTERACTIONS, AND BEHAVIOR

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With complex life cycles that include multiple life stages in multiple hosts, trematodes are ideal organisms to teach ecological relationships and life cycles of animals. Trematodes are common in aquatic systems, both freshwater and marine. Snails typically serve as the first intermediate host, making trematodes easy to bring into the lab to observe and use for teaching exercises. Besides being convenient for teaching about life cycles and the multitude of strategies utilized for transmission and infection, trematodes are useful in illustrating direct and indirect ecological interactions. Trematodes can have direct detrimental effects on their hosts and can cause changes in population dynamics and competitive interactions. Parasite transmission is an invisible but important part of the natural food web, and for trematodes, exploitation of predator-prey relationships for transmission to the definitive host is common. Host

responses also provide opportunities to teach about immunity and behavior. Students are often surprised by anti-parasite behavior and amazed by the ways parasites manipulate host behavior (and morphology) to increase transmission. Additionally, dissections of hosts allow students to learn about anatomy of those organisms. Clearly, the abundance and widespread nature of trematodes in aquatic systems make them excellent teaching models to demonstrate a variety of ecological phenomena.

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(28)

AN INTRODUCTION TO THE COLLABORATION ON RIVERINE ECOLOGY (CORE) PROGRAM AND ITS UTILITY AS A MODEL FOR UNDERGRADUATE RESEARCH IN MATHEMATICAL PARASITOLOGY

G. Sandland, University of Wisconsin-La Crosse

Methodologies employed by mathematicians have emerged as critical tools for modeling complex biological systems. Yet interactions rarely occur among researchers from math and the life sciences. In 2011, members from the Mathematics and Biology Departments at the University of Wisconsin–La Crosse were awarded a collaborative grant from the National Science Foundation (NSF) to establish an undergraduate program in Mathematical Biology. The UBM-Collaboration on Riverine Ecology (UBM-CORE) program was a year-long research, learning, and peer-mentoring experience designed to facilitate the development of biologists and mathematicians with broad, interdisciplinary training. Research investigations centered on species invasions and waterfowl disease in the upper Mississippi River. This talk will provide an overview of the CORE program, its recent outcomes, and its potential use as a template for future teaching collaborations between parasitologists and mathematicians.

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(29)

LECANICEPHALIDEAN TAPEWORMS (CESTODA) OF THE FRESHWATER WHIPRAY, *HIMANTURA POLYLEPIS*, FROM MALAYSIAN AND INDONESIAN BORNEO

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The lecanicephalidean cestodes parasitizing the spiral intestine of the endangered (IUCN, 2013) freshwater whipray, *Himantura polylepis* (Bleeker, 1852), are investigated for the first time. A total of seven hosts were collected between 2003 and 2008 at two collection sites off the east coast of Borneo: five from freshwater about 16 km up the Kinabatangan River (Malaysia) and two in the estuarine/marine waters off Tarakan (Indonesia). Collectively, these hosts were parasitized by seven new species representing four genera of lecanicephalideans: three new species of *Tetragonocephalum* Shipley and Hornell, 1905; two new species of *Polypocephalus* Braun, 1878; and one species each of two as of yet undescribed genera. Specimens of each of the new taxa were prepared for light and scanning microscopy to examine morphological features. Molecular sequence data using the D1-D3 28S rDNA region confirmed morphological assessment of species boundaries exhibiting genetic differences between two of the new species of *Tetragonocephalum* (19 base pairs) and the two new species of *Polypocephalus* (59-61 base pairs). Five of the seven species were only present at either the Kinabatangan River (freshwater) or Tarakan (estuarine/marine) localities; two were present at both collection sites. These seven new species bring the total number of known cestodes from *H. polylepis* to seventeen species across nine genera of four orders (i.e. Lecanicephalidea, Onchoproteocephalidea, Rhinebothriidea, and Trypanorhyncha). Despite the characterization of the freshwater whipray as an obligate freshwater species, overall the composition of tapeworms that parasitize this species is consistent with those of other dasyatid stingrays from euryhaline environments (e.g. *H. dalyensis*) and marine environments in the Indo-Pacific and elsewhere.

(30)

UNCOVERING HELMINTH DIVERSITY IN SOUTHERN AMAZONIAN BIRDS

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J. Bates, Museum of Natural History in Chicago, Illinois
V. Tkach, University of North Dakota

Very little is known about the diversity, distribution, and host associations of avian helminths in southern Amazonia. The majority of avian species, families and even orders in the region have not been examined for parasitic worms so far. At the same time, the expected helminth diversity is high, given that Amazonian birds are extremely diverse and their fauna is characterized by a high level of endemism. In this work, we studied helminth fauna of birds from the westernmost region of endemism, Inambari and from the easternmost region, Bélem. Two hundred and thirty-four birds belonging to 9 orders were examined for endoparasites in Inambari in November, 2013 and 199 birds belonging to 15 orders were examined in Bélem in July, 2013. Birds were examined and parasites were fixed following standard endoparasite collecting protocols. Specimens were processed in the laboratory for morphological and molecular analyses. Morphology was studied on total permanent (cestodes, digeneans) or temporary (nematodes, acanthocephalans) mounts. When necessary, DNA sequences of nuclear ribosomal and mitochondrial genes were obtained to aid in species differentiation and/or phylogenetic analysis. In Inambari, 71 birds (30%) were infected with helminths. Cestodes were the most prevalent group of parasites. They were found in 45 birds (19.2%), followed by digeneans (21; 9%), nematodes (13; 5.6%) and acanthocephalans (2; 0.9%). In Bélem, 54 birds (27%) were infected with helminths. Prevalence of infection with nematodes (28 birds; 14.1%) was nearly equal to that of cestodes (26; 13.1%), followed by digeneans (12; 6%) and acanthocephalans (6; 3%). The prevalence of infection with digeneans in Inambari was almost twice higher than in Bélem which can be explained by the close proximity of Inambari collecting sites to water. Taxonomic diversity and distribution of helminths among systematic and ecological groups of birds is discussed with an emphasis on digeneans. Our study revealed several new species belonging to the families Brachylaimidae, Diplostomidae, Renschtrematidae and a likely new genus of the Schistosomatidae. Among other notable discoveries, *Mesocestoides* tethrathiridia have been found for the first time in South American birds. DNA sequences obtained in our study have been incorporated into phylogenetic analyses of corresponding groups. The resulting phylogenies will be presented and discussed.

(31)

HOW TO RECOGNIZE A SUCKER WHEN YOU SEE ONE

V. Mantovani Bueno and **J. Caira**, University of Connecticut

The recent re-structuring of the order Rhinebothriidea into four families has greatly contributed to our understanding of these taxa. The phylogenetic relationships among rhinebothriidean families resulting from molecular analyses proposed in that study suggest the existence of two subclades of families, each defined by the presence or absence of diagnostic morphological features. One clade, composed of the families Escherbothriidae and Anthocephaliidae is comprised of species bearing apical suckers on their scoleces and therefore having a clear anterior/posterior orientation to their bothridia. The other clade, comprised of the families Echeneibothriidae and Rhinebothriidae, are very unusual in their apparent lack of such features. As noted by Ruhnke and collaborators, detecting the apical sucker in species that exhibit large numbers of marginal loculi can be difficult and may be have misled past interpretations of bothridial morphology. For instance, the purported absence of apical suckers in members of the Echeneibothriidae dates back to the description of the genus *Echeneibothrium* in 1850 and has not been questioned until now. Detailed morphological studies of newly collected specimens of multiple species of *Echeneibothrium* was undertaken to confirm the absence of suckers in this genus. Indeed, observations under light microscopy failed to definitively resolve this issue. However, scanning electron microscopy revealed a very different picture. In fact, all species examined were found to bear apical suckers and thus, the

anterior/posterior orientation of their bothridia became clear. These new findings have prompted the emendation of the descriptions of these species and the genus in general. Future studies should focus on careful morphological examination of additional species belonging to Echeneibothriidae. Furthermore, these findings question the reported absence of apical suckers in members of the Rhinebothriidae.

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(32)

DESCRIPTION OF AN EXTANT SPECIES WITH MICRO-COMPUTED TOMOGRAPHY AND PHYLOGENETIC REVISION OF DUOGNATHOUS TERRESTRIAL LEECHES (HIRUDINIDA: ARHYNCHOBDELLIDA: HAEMADIPSIDAE)

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Two-jawed (duognathous) terrestrial leeches in the Haemadipsidae are major pests across their wide geographic range, represented by numerous endemic species spread across many islands in the Indian and Pacific Oceans. However, haemadipsid taxonomy largely remains in conflict with apparent phylogeny, including genetically distinct undescribed diminutive species. We capitalize on the power of micro-computed tomography (μCT), allowing for the first description of an extant species with this technology. Higher taxonomy of duognathous haemadipsids is valuated with phylogenetic reconstruction of DNA sequence data, expanding on prior studies. Whereas monophyly of duognathous leeches was supported, substantial conflict remained with respect to named genera. Consequently, the genus *Chtonobdella* is revised to include all duognathous leech species previously distributed in over 30, mostly monotypic genera in the subfamily Domanibdellinae. Several fixation strategies for soft-bodied invertebrates in μCT scanning applications are also evaluated.

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(33)

REVISITING THE GENUS *ALLOGLOSSIDIUM* (DIGENEA: MACRODEROIDIDAE): USING MOLECULAR PHYLOGENETIC DATA TO DISENTANGLE EVOLUTIONARY PATTERNS OF LIFE CYCLE COMPLEXITY AND TAXONOMY

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The digenean genus *Alloglossidium* is notable for a high amount of intraspecific variation in life cycle complexity (host number and species needed to complete development). Some species exhibit a 3-host life cycle, sexually reproducing in a vertebrate final host (e.g. catfish) and other species exhibit a 2-host pattern wherein precocious development leads to sexual maturation in what is typically considered the second intermediate host (e.g. crustacean, leech). The genus *Alloglossidium* has long been used as a system with which to study the origin of changes in lice cycle pattern. Nonetheless, with the exception of two recent studies, prior inferences on taxonomy and life cycle evolution have relied exclusively on morphological data. Here we present a molecular phylogenetic reassessment of the genus *Alloglossidium* by incorporating updated taxonomic and life history findings from ongoing survey efforts. Our data set includes 17 of the 18 nominal species (excluding only the most recently described species from a leech) plus a number of additional specimens collected from our surveys. Mitochondrial (ND1) and ribosomal (partial 18S, ITS1-5.8S-ITS2, partial 28S) DNA sequence data were used to confirm species identifications from type localities and revisit phylogenetic relationships. Although morphologically similar, genetic differences supported delineation of 2, and possibly up to 5, new species, further expanding the genus. In addition, collections from the type locality of *A. kenti* indicate that specimens currently identified in the literature as *A. kenti* require taxonomic revision. Overall, our molecular-based phylogeny found a well-supported early divergence between those species utilizing leech final hosts and the remaining *Alloglossidium* species. Thus, the 2-host life cycle pattern was shown to have derived independently in leeches and crustaceans. Moreover, the species utilizing crustacean hosts show 2 and possibly 3

independent losses of the vertebrate host. Future work will attempt to assess if there are reliable morphological traits that reflect the molecular phylogeny.

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(34)

AN ENIGMA RESOLVED: THE TRUTH ABOUT THE HOST ASSOCIATIONS AND IDENTITY OF THE ELASMOBRANCH PARASITIZING CESTODE GENUS *CARPOBOTHRIUM*

A. Koontz and **J. Caira**, University of Connecticut

The tapeworm genus *Carpobothrium* Shipley and Hornell, 1906, was erected in 1906 with the species *Carpobothrium chiloscylli* Shipley and Hornell, 1906, collected from the Slender bambooshark (*Chiloscyllium indicum* [Gmelin, 1789]) in Sri Lanka, as its type species. However, subsequent emendation of the generic diagnosis based on specimens collected from batoid hosts, rather than the type shark host, has lead to substantial confusion with respect to the morphology and thus also identity of this genus. Collection of new material from a third species of bambooshark, *Chiloscyllium hasselti* Bleeker, 1852, as well as additional material of *C. chiloscylli* from *C. indicum*, in Borneo provided an opportunity for the host associations and morphology of *Carpobothrium* to be re-evaluated. Light microscopy, histological sections, and scanning electron microscopy were used to investigate the morphology of the material from both host species. This work suggests that *C. hasselti* hosts a novel species of *Carpobothrium* and also provides insights regarding the enigmatic nature of the bothridial morphology of this genus as it is currently interpreted. Most intriguing was the discovery of a sucker on the anterior bothridial flap of both species, thereby eliminating the feature that had originally been used to set *Carpobothrium* well apart from other "tetraphyllidean" genera. Discovery of some of Southwell's specimens identified as belonging to this genus, but collected from batoid hosts, allowed the duplicitous nature of *Carpobothrium* to be formally examined. That material makes it clear that the specimens from batoids that were originally identified as belonging to *Carpobothrium* in fact belong to an undescribed genus, which although superficially resembling *Carpobothrium*, in scolex structure, represents a distinct lineage, a fact that is supported by recent comprehensive molecular analyses. This work sets the stage for the future establishment of a new genus to house the species parasitizing batoids.

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(35)

PHYLOGENOMIC INSIGHTS INTO THE EVOLUTIONARY HISTORY OF MALARIA PARASITES

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Resolving the evolutionary relationships among the protozoan blood parasites of the order Haemosporida (the "malaria parasites") has remained a vexing problem despite a broad application of modern molecular systematic approaches to this system. Previous studies have recovered conflicting phylogenetic hypotheses based on different character sets and methods of inference, with the basal taxon of this clade proving particularly unstable. In addition, several enigmatic Haemosporidian genera (e.g. *Polychromophilus*, *Nycteria*, *Haemocystidium*) have been poorly represented in previous phylogenetic treatments, making it difficult to confidently reconstruct the evolution of host switches and life-history characters within the order. To address these issues, we generated sequence data for 21 nuclear protein-coding genes (over 20,000 bp) for 43 Haemosporidian taxa representing 8 genera, making this the most comprehensive estimate of malaria phylogeny to date. We explored this dataset using multiple methods of phylogenetic inference, character subsets, and partitioning strategies to evaluate topological concordance across analyses. We observed instability among analyses associated with our treatment of third codon positions, particularly at the base of the tree. However, several previously controversial relationships among major clades were robust to analytical approach, including a sister relationship between *Leucocytozoon* and *Parahaemoproteus* as well as a close relationship between the bat parasite *Polychromophilus* and malaria parasites of saurian hosts. This study provides novel insights into the

evolution of malaria parasites, and supports previous findings that host switching and life-history characters have followed a dynamic evolutionary history within this group.

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ENDOPARASITES OF DIPODIDAE (RODENTIA) FROM MONGOLIA

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This paper is a partial report of results from the NSF funded Mongolian Vertebrate Parasite Project (1999-2012). The project goal was to discover and describe the parasites of vertebrates of the Gobi desert and grassland steppe regions of south central and south western Mongolia. Our team collected approximately 4000 mammals, 2000 birds, and 1000 reptiles and amphibians. The present analysis focuses on insectivorous rodents including more than 500 individuals of the family Dipodidae representing at least 11 species. From the jerboas (Rodentia: Dipodidae) and relatives alone, 120 individuals were infected with endoparasites, representing 7 species including: *Allactaga balikunica*, *A. bullata*, *A. sibirica*, *Dipus sagitta*, *Pygeretmus pumilio*, *Stylodipus andrewsi* and *S. sungorus*. Up to the current time, we identified *Mastophorus muris*, *Protospirura sp.*, *Subulura citelli*, and *Skrjabinocerina sp.* (Nemata). Also, a species of *Mathevotaenia* (Cestoda: Anoplocephalidae) and three species of *Catenotaenia* (Cestoda: Catenotaeniidae) were found including an undescribed species *C. dendritica,* and *Catenotaenia sp.* Cestodes of the family Catenotaeniidae were some of the most commonly recorded parasites from these rodents. A molecular phylogeny confirms morphological placement of these Cestodes in the Catenotaeniidae and provides some insight into the biogeography of these host-parasite communities.

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HAEMOSPORIDIAN PARASITES OF AMAZONIAN BIRDS

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Birds possess the most diverse assemblage of haemosporidian parasites, represented by three genera, *Plasmodium*, *Haemoproteus* and *Leucocytozoon*. Currently there are over 200 morphologically identified avian haemosporidian species, although the true diversity is unknown, due to high genetic diversity and vastly insufficient in highly diverse habitats and regions, such as the BrazilianAmazon. Amazonia supports the world's highest avian diversity and therefore should also support highly diverse haemosporidian diversity which remains mostly undescribed. This study represents the largest sampling effort of avian haemosporidian parasites from Amazonia, with 2664 avian blood samples collected from 323 host species. Blood samples were collected from six distinct areas of avian endemism; Belem (327 samples), Guiana (353 samples), Imeri (164 samples), Inambari (717 samples), Rondonia (1003 samples), and Tapajos (100 samples). DNA extracted from blood samples was initially screened using a newly developed real-timePCR to identify samples positive for at least one genus. A portion of the cytochrome b gene was amplified from positive samples using nested PCR. Two different primer sets were used; one for *Plasmodium/Haemoproteus* and one for *Leucocytozoon*. Due to expected low prevalence, only 1000 samples were tested for *Leucoctyozoon*, none of which turned out positive. Positive sample samplified for *Plasmodium/Haemoproteus* were split into respective genera by DNA sequencing, also allowing for identification of genetic lineages. A total of 465 samples were positive (17.5% prevalence), with *Plasmodium* accounting for 80.8%of infected hosts. A total of 265 genetic lineages of *Plasmodium* (214) and *Haemoproteus* (51) were identified, with 247 (93%) representing new lineages. Lineages were confined by host distribution with 231 lineages (87%) being found within only one area of endemism. Distribution of haemosporidians among systematic and ecological groups of birds is discussed. This study was supported by NSF grants DEB1050525, DEB1120054, DEB1120734.

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ATTACHMENT OF *TYLOCEPHALUM* SP. IN THE COWNOSE RAY, *RHINOPTERA BONASUS*

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The cestode genus *Tylocephalum* Linton, 1890 has been described from an array of elasmobranch hosts families, including cownose rays (Family Rhinopteridae), eagle rays (Myliobatidae), guitarfishes (Families Rhynchobatidae and Rhinobatidae), and the monotypic shark ray (Family Rhinidae). The type species of the genus, *Tylocephalum pingue* Linton, 1890, was originally reported from the cownose ray, *Rhinoptera bonasus* and collected from the Atlantic Ocean off Woods Hole, Massachussettes, U.S.A. Superficial morphological similarities can be seen between *Tylocephalum* and members of the family Lecanicephalidae which includes the genera *Lecanicephalum, Hexacanalis, Floriparicapitus,* and *Stoibocephalum*. Members of three of these genera have been subjects of recent studies on host-attachment. Recent molecular data suggests *Tylocephalum* is more closely related to the Cephalobothriidae, which includes the genera *Cephalobothrium* and *Adelobothrium*. These genera have not yet been the subject of targeted attachment studies. Specimens of *Tylocephalum* sp. were collected from *Rhinoptera bonasus*, off the coast of South Carolina, U.S.A. Specimens were removed from the spiral valve of their host by a piece of host tissue being excised from the spiral valve and scoleces left embedded in or freed of the surrounding host tissue. These specimens were then prepared for histological sectioning by standard methods and stained with Hematoxylin and Eosin. Gross morphology suggests that *Tylocephalum* sp. secretes a substance to aid in attachment, evidenced by a dark ring on the host tissue upon removal of the embedded scolex. Histological sections revealed that the apical organ and apical modification of the scolex proper are crucial in attachment to the host tissue, while the acetabula and scolex proper play little to no role in attachment. Periodic Acid Schiff's reagent will be used to further investigate the secretions and identify whether or not these secretions are released from the apical organ or the apical modification of the scolex proper. Additional studies are needed to confirm if microthrix patterns consistent with attachment strategies observed in members of the Lecanicephalidae are also observed in *Tylocephalum,* or if members of the Cephalobothriidae display different microthrix patterns.

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SCHISTOSOMA MANSONI TEGUMENT ANTIGENS EXPOSED BY PRAZIQUANTEL TO HOST ANTIBODY REACTIVITY

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The tegumental antigens of *Schistosoma mansoni* worms play an important role in the survival of the parasite in its definitive hosts. Here, the tegumental antigens that are exposed by sub-curative doses of praziquantel were investigated using serum from a rabbit that had been infected percutaneously with *S. mansoni* cercariae. The antiserum had previously shown synergistic action with praziquantel in killing adult worms. IgG antibodies in this antiserum reacted with two antigens of, respectively, ~30 kDa and ~40 kDa in Western immunoblots of a detergent extract of *S. mansoni* adult worms. Both antigens were purified by repeated immunoelectrophoresis in, and elution from, one dimensional sodium dodecyl sulphate polyacrylamide gel electrophoreses (SDS-PAGE). After each electrophoresis the part of the gel containing the respective antigen was excised, eluted and re-electrophoresed. The purified ~30 kDa and ~40 kDa antigens were analysed by tandem mass spectrometry (TMS). Data from the purified ~30 kDa antigen was significant for two entries in the NCBInr database, corresponding to two *S. mansoni* tegument antigens: Sm29 and fructose 1, 6-bisphosphate aldolase. TMS analysis of the 40 kDa antigen revealed the presence of *S. mansoni* malate dehydrogenase. In indirect immunofluorescence both the unfractionated rabbit antiserum and anti-30 kDa antigen antibodies purified from the same antiserum reacted on the surface of adult worms treated with a sub-lethal dose of praziquantel, but such reactivity

was not observed on the surface of control untreated worms. These results provide tentative identification of the *S. mansoni* tegument antigens which induce production of host antibodies that act synergistically with praziquantel in killing adult worms.

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(40)

EARLY IMMUNOLOGY AND HISTOPATHOLOGY OF *RIBEIROIA ONDATRAE* (DIGENEA: CATHAEMASIIDAE) IN THE LATERAL LINE OF BLUEGILL, *LEPOMIS MACROCHIRUS*

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Ribeiroia ondatrae is an infamous multi-host trematode known to cause limb malformations in North American amphibian species. Although *R. ondatrae* also infects fishes as second intermediate hosts, less is known about the pathology and immune responses initiated in infected fishes, even though reports of infected fish date back to 1900s. Here we used an experimental approach to examine the consequences of *R. ondatrae* infection over time in bluegill *Lepomis macrochirus*, hosts with varing exposure levels. All exposed fishes became infected with metacercariae, and average infection load increased monotonically with exposure dose. Histologically, infection was associated with acute hemorrhages within the lateral line and local dermis at 36 hours followed by progressive granulomatous inflammation that led to destruction of encysted metacercariae. Correspondingly, over the course of 648 hours we observed an 85% decline in average infection load among hosts, likely reflecting host clearance of the parasite. Infection was not associated with changes in fish growth or survival, but did correlate with leukocytosis (increase in total white blood cells) and neutrophilia (increased neutrophils) in circulating host blood. The pathology caused by *R. ondatrae* metercariae in the lateral line system has the potential to cause alterations of bluegill behavior by interfering with the sensory input. In natural settings, this pathology may lead to increased predation.

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DOES A BRAIN-INFECTING PARASITE INFLUENCE HOST BEHAVIORAL TYPE AND BEHAVIORAL CORRELATIONS?

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T. King, University of Alabama
E. Payne and **A. Sih**, University of California Davis
R.L. Earley, University of Alabama

Parasites that manipulate host phenotype may influence host behavioral type, population-level behavioral correlations (i.e., behavioral syndromes), and induce feedbacks between infection and behavior. While the field of behavioral ecology has become increasingly interested in interactions between parasites and behavior, few studies have explored the role of parasites in inducing or breaking apart behavioral syndromes and even fewer have explored the potential for feedbacks between infection and behavior. Here, we employ controlled infections of a phenotype-manipulating trematode parasite (*Euhaplorchis californiensis*) in a numerically abundant host (California killifish, *Fundulus parvipinnis*) to explore interactions between infection and behavior. We ask the following questions: 1) Does host activity, social behavior, or boldness influence its risk of infection? 2) Does infection then change killifish activity, sociability, and boldness behavior? 3) Does infection modify correlations between these behavioral traits? 4) Are there feedbacks between infection risk and host behavior? We find that *E. californiensis* influences host behavior, and discuss the potential implications of behavioral changes for both host and parasite population dynamics.

(42)

NON-CODING RNAS IN *CRYPTOSPORIDIUM*-EPITHELIAL CELL INTERACTIONS

X. Chen, Creighton University

A large portion of the eukaryotic genome is transcribed as non-protein-coding RNAs (ncRNAs). While once thought of primarily as "junk," recent studies indicate that many of these ncRNAs are functional. At least two classes of ncRNAs, microRNAs (miRNAs) and the long intergenic ncRNAs (lincRNAs), have been shown to play key regulatory roles in diverse biological functions in mammalian cells. While the existence of miRNAs in protozoan parasites is still in doubt, genomic research has revealed the expression of novel long ncRNA genes in the protozoan group of parasites. A detailed analysis of a full length cDNA library constructed from *C. parvum* identified 118 long ncRNAs. We speculate that ncRNAs from either the host or the parasites may be important elements for the host-parasite interactions. Using both *in vitro* and *in vivo* models of gastrointestinal cryptosporidiosis, we have demonstrated that ncRNAs of the host epithelial cell origin modulate mucosal immune responses at every step of the immune network following *Cryptosporidium* infection, including production of antimicrobial molecules, expression of cytokines/chemokines, release of epithelial cell-derived exosomes, and feedback regulation of immune homeostasis. We also identified the shuttling of *C. parvum* ncRNAs in exosomes released from host epithelial cells following infection, suggesting a potential role of exosomal shuttling of parasite ncRNAs in the activation of host systemic immune responses. Moreover, we detected highly selective and specific delivery of parasite ncRNAs into the host epithelial cells following *C. parvum* infection. Such horizontal transfer of parasite ncRNAs to host cells during *C. parvum*-epithelial cell interactions appears to be involved in the modulation of gene transcription in host cells. In summary, we have accumulated data supporting an important regulatory role for ncRNAs in *C. parvum*-epithelial cell interactions, relevant to the development of potential novel therapeutic strategies.

(43)

CHIRIBAYA ENDOHELMINTH INFECTIONS OF THE OSMORE RIVER BASIN

J.J. Morrow, University of Nebraska-Lincoln, School of Natural Resources

The pre-Inca Chiribaya of the Osmore River Basin were hosts to endohelminths that provide proxy information regarding the societal structure and cultural behaviors of these populations. Endohelminth eggs have been recovered from coprolites in mummies excavated from three sites: Chiribaya Alta, Chiribaya Baja, and San Gerónimo. Chiribaya Alta was an administrative center for the ruling elite of this culture while the other two sites were occupied by farmers and fishermen who provided foods for both themselves and for other Chiribaya communities. Endohelminth eggs recovered from these sites include *Diphyllobothrium* sp. and *Trichuris trichiura*. Combining data from multiple archaeoparasitological studies of these sites, Chiribaya Alta had 2/53 (3.7%) coprolites from mummies that tested positive for *Diphyllobothrium* sp. Chiribaya Baja had a total of 13/37 (35%) positive coprolites in addition to 20/29 (69%) other samples that also tested positive for *Diphyllobothrium* sp. San Gerónimo analyses revealed 3/11 (27%) *Diphyllobothrium* sp.-positive coprolites as well as 2/8 (25%) of coprolites containing the eggs of *T. trichiura*. The parasitological disparity between endohelminth prevalence in material analyzed at Chiribaya Alta, which had little endohelminth evidence, and the other two sites, which demonstrated parasites in 25-69% of samples analyzed, may be explained by putting the parasitological data into a cultural framework. Herein, we incorporate the published data with new data obtained using standard archaeoparasitological techniques for endohelminth egg recovery and discuss the cultural behaviors that affected endohelminth parasitism among the Chiribaya living at these sites between 1000-1350AD. This study highlights the importance of combining parasitological principles with archaeological reconstructions leading to the conclusion that archaeoparasitological data should always be founded on the reconstructions of ancient cultures.

(44)

COMMON HUMAN PARASITES AND PATHOGENS AND THEIR NATURAL REMEDIES IN THE USA

O.M. Amin, Institute of Parasitic Diseases

This presentation is based on our diagnostic work and research at the Parasitology Center, Inc. (PCI), in Scottsdale, Arizona, USA. A brief introduction addresses exposure to parasitic infections, testing, impact on public health, and the diagnosis of common parasitic infections. The most common protozoan and helminth (worm) parasites as well as pathogenic bacteria in the USA are cosmopolitan. Our work and products are, thus, applicable world-wide where they are also distributed. The primary focus here is to introduce our natural herbal anti-parasitic remedy comprising three formulas, FREEDOM/CLEANSE/RESTORE (F/C/R). F/C/R is the most popular and effective anti-parasitic remedy in the USA today. FREEDOM frees and protects the body from parasitic infections. CLEANSE cleanses the intestine from parasite toxins, promotes regularity, and integrates organ system functions. RESTORE supports the integrity and regeneration of tissues damaged by parasite feeding, migration, and toxic byproducts. F/C/R also has a wider application for use in infected pets. At PCI, we also diagnose pet parasites. Published sources used to formulate F/C/R as well as reports from clients who have used the product are included. All topics are presented with illustrated labeled pictures of the various kinds of parasites and bacterial pathogens tested for in our facility and their gross pathology in human tissues, when applicable. GI symptoms caused by pathogenic bacteria are similar to those caused by intestinal parasites.

(45)

TEACHING PARASITOLOGY WHILE AVOIDING TRANSMISSION AND INFECTING THE NEXT GENERATION

J.T. Detwiler, University of Manitoba

Undergraduate and graduate students often fantasize about what it would be like to teach their own course. Some of us get a taste of that experience through teaching assistantships or fellowships, but in those cases you are often working in collaboration with at least one person who gives you feedback on ideas, takes care of the animal care forms, and handles serious issues when they arise. Once your name appears in a course catalog, and you have a few weeks or months before you step into the classroom/lab, the reality hits that YOU are now primarily responsible for everything including training and directing a teaching assistant (TA) that may not know much about the material in your course and have much teaching experience. What is the focus of your course going to be? What is your lecture/lab going to look like? What kind of teaching style will you employ? Are you going to develop everything from scratch, or can you build upon existing materials? What are your expectations for the students, the TA, and yourself? For this talk, I will draw on my own experiences with re-developing and teaching Introductory Parasitology at University of Manitoba for upper-level undergraduates. My goals are to give you some ideas to reflect upon, open the door to thinking about how social media and education outreach can be incorporated into your teaching, and spark conversations about teaching that will continue after this symposium.

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SCIENCE OUTREACH THROUGH BLOGGING AND PODCASTING

K. Weinersmith, Rice University

Blogs and podcasts are two popular ways of engaging in science outreach. Both of these outreach mediums require particular technical know-how, which can present a barrier to entry for those interested in using these mediums. I co-host two science podcasts (www.Sciencesortof.com and www.WeeklyWeinersmith.com) and run a science blog (www.Weinersmith.com). I will share my experience using these mediums for science outreach, and will discuss how to get started with blogging and podcasting, including a discussion of 1) programs for blogging and podcasting, 2) hardware for podcasting, 3) strategies for generating blog and podcast content, and 4) how to disseminate blogs and podcasts. In my personal experience, science outreach using these mediums is not only fun and satisfying, but has also been a fantastic tool for networking and has resulted in favorable reviews of Broader Impacts statements on National Science Foundation grants.

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PRESENCE AND PREPARATION

M. Siddall, American Museum of Natural History

Over the course of the nearly three decades of my parasitological career, I have increasingly been called upon to represent science in the public sphere. Those opportunities (and burdens) have ranged from a now near constant attention from print, internet and broadcast media, to television specials on major networks like Discovery and NatGeo, and on-stage public speaking engagements like TED, the EG conference, and the World Science Festival. Everything, all of it, I trace back to my first student paper presentation at the ASP meeting in East Lansing Michigan 25 years ago, and the encouragement I received on that day. The public is hungry for your science and your insight. Whether you accept the challenge, or have it thrust upon you, it will probably now almost inevitably happen. I will discuss a variety of issues that intersect with putting a public face on science including how to prepare, what to expect, presentation stylistics, and above all the responsibility that we each have to our science to be ready and willing to be the go-to personalities, without which we risk losing influence in an increasingly attention-deficient world.

(48)

LINKING HOST DIVERSITY AND PARASITE INFECTION: A COMMUNITY ECOLOGY APPROACH

P. Johnson, University of Colorado
C. Wood, University of Michigan

Community ecology seeks to understand the factors structuring complex communities and how they vary with scale. With respect to parasites, host diversity has consistently been identified as a positive correlate of parasite richness, which is often interpreted as a reflection of habitat availability for infectious organisms. A key yet unresolved question, however, is how this relationship varies with spatial scale and the level of biological organization. Addressing this question has become especially important in light of increasing interest and ongoing debate about the diversity-disease relationship (e.g., the dilution effect). Here we use a large-scale data set on parasite assemblages (20 taxa of helminths, viruses, fungi and protists) from 1671 amphibian hosts representing seven species to address the following questions: (1) How do shifts in host composition and diversity affect parasite richness? (2) How do these relationships vary with spatial grain (from within-pond to among-metacommunities) and by host type (e.g., upstream and downstream)? And (3) are similar relationships observed for alternative response metrics such as

parasite abundance and transmission, particularly for pathogenic species? Using analytical approaches from community ecology, we find that parasite richness and community composition exhibit non-random structuring in which host community functions as a primary driver. Host richness is a consistent, positive predictor of parasite richness; however, this relationship varies with spatial grain (becoming stronger at coarser grains) and with the host community considered. The effects of host community on parasite abundance and transmission success are more complex, such that diversity tends to reduce transmission but can nonetheless exhibit neutral or positive relationships with infection abundance owing to associations between host richness and parasite colonization. We highlight the need for more hierarchical tools to allow cross-scale analyses to parasite metacommunities, which may provide ideal systems in which to further develop and test such techniques.

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IMPACTS OF HUMAN DISTURBANCE ON PARASITE ASSEMBLAGES: TELESCOPING ACROSS SPATIAL SCALES

C. Wood, University of Michigan

A primary goal of ecology is to understand how anthropogenic environmental change affects populations, communities, and ecosystems. But despite the overwhelming ubiquity of parasites, relatively few studies have comprehensively assessed the response of parasitic species to human impacts like biodiversity loss. Substantial disagreement exists as to whether parasite diversity and abundance will increase or decrease in response to disturbance, whether these relationships will hold across spatial scales, and even whether such generalizations are possible. To address this knowledge gap, I present summary results from several systems, indicating that relationships between disturbance and parasite assemblage composition are complex but predictable, and that spatial scale is a key element in explaining this variability. First, I present results at two divergent spatial scales from a study in which my collaborators and I assessed the abundance of fish parasites of seven coral reef fishes collected from three fished and three unfished islands of the Northern Line Islands archipelago in the central equatorial Pacific. We found that fishing depressed parasite taxon richness and that the response of parasite abundance (# of parasites per host) varied substantially among parasite taxa. However, predictable patterns emerged at higher levels of taxonomic organization, with meta-analysis demonstrating that directly transmitted parasites were significantly more abundant on fished than on unfished islands, while trophically transmitted parasites were significantly more abundant on unfished than fished islands. This might arise because increasing life cycle complexity increases the probability that some obligately required host will be negatively affected by fishing, and because parasites with a single parasitic life stage can take advantage of fishing-driven, compensatory increases in abundance of some hosts within the host range. The overall pattern of directly transmitted parasites thriving and trophically transmitted parasites declining in the presence of fishing also held at a smaller spatial scale – across a gradient of fishing pressure within one of the fished islands. However, there was no relationship between parasite diversity and fishing at this smaller spatial scale, perhaps because – at small spatial scales – locally extirpated parasite species experience a “rescue effect” from nearby source populations of parasites. Together, these results suggest that, in this system, fishing disturbance erodes parasite species richness only at a coarse spatial resolution, but has consistent impacts on parasite abundance across orders-of-magnitude differences in spatial resolution. How general are these patterns across ecosystems? In the second part of my talk, I will link my earlier findings from marine ecosystems with preliminary results from a meta-analysis of the relationship between host diversity and parasite diversity across a variety of studies. I will highlight the key values (e.g., definitions of “host”, spatial grain, spatial extent, spatial autocorrelation) that govern the strength of this relationship. My work shows that, by uniting epidemiological and biodiversity theory and using novel empirical approaches, it is possible to uncover some general rules governing how human impacts shape transmission of parasites. The next step is for the explicit inclusion of variability in spatial scale for empirical studies addressing the host diversity– parasite diversity relationship.

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THERMAL BIOLOGY OF PARASITISM: A METABOLIC APPROACH

T.R. Raffel, **J.P. Sckrabulis**, **K.A. Altman** and **E.L. Scott**, Oakland University
J.R. Rohr, University of South Florida
P.T. Johnson, University of Colorado at Boulder

As climate change alters patterns of environmental temperature variability, understanding the thermal biology of disease and parasitism takes on new importance. In species interactions like parasitism, both interacting organisms have potentially temperature-dependent physiological processes (e.g., parasite infectivity & host resistance) that could be described using separate physiological performance curves. However, this approach is complicated by the fact that both parasite infectivity and host resistance influence measureable outcomes of infection (e.g., parasite growth/survival in hosts), making it notoriously challenging to tease apart the separate effects of temperature on these processes. One potential solution is suggested by recent work on the metabolic theory of ecology, which has revealed generalizable patterns among taxa and physiological processes in key parameters such as the activation energy for metabolism E_A. Based on these patterns, we postulated that key parameters of the thermal performance curves for parasite infectivity and host resistance might be derived from measurements of other physiological processes (e.g., host respiration or parasite swimming speed). We tested the utility of this approach by applying it to experimental infection data from two parasite-host systems, chytridiomycosis (*Batrachochytrium dendrobatidis*) in Cuban treefrogs (*Osteopilus septentrionalis*) and trematode infection (*Ribeiroia ondatrae*) in green frog tadpoles (*Lithobates clamitans*). We found that this approach successfully described multiple aspects of temperature-dependence for parasite-host interactions and allowed estimation of remaining model parameters via non-linear model fitting. Furthermore, this approach accurately predicted an unexpected non-linearity in the effect of thermal acclimation on tadpole clearance of encysted trematodes. Based on these results, we conclude that metabolic theory provides a reasonable and highly useful framework for developing predictive models of parasite thermal biology.

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PREDICTING CLIMATE CHANGE IMPACTS ON HOST-PARASITE SYSTEMS: NO LONGER JUST A VISION?

P.K. Molnar, University of Toronto Scarborough

Ongoing climate change is affecting host-parasite systems globally, and further dramatic changes are expected in the future. Predicting these changes is necessary to facilitate proactive control strategies in wildlife conservation, livestock management, and human health, but this remains difficult due to the complexity of biological systems. Recent work has suggested that physiological host-parasite models based on the Metabolic Theory of Ecology may allow predicting climate change impacts on host-parasite interactions even in data-scarce systems, primarily because these models can capture the temperature-dependencies of host and parasite life history (e.g. development, mortality, reproduction), adaptability (e.g. acclimatization to new temperatures) and interactions (e.g. parasite uptake). First, I will review these approaches, showing how metabolic models can predict changes in parasite fitness, range and phenology. I will then extend existing approaches to show how metabolic models can predict climate change impacts on essential dynamic properties of host-parasite systems, such as the threshold host density allowing parasite persistence, the stability of stationary states, and the parasite burden and prevalence in hosts. Through select examples, I will in particular illustrate how certain characteristics of host-parasite interactions, such as transmission mode or the strength of parasite-dependent host mortality, may dramatically alter the qualitative response of host-parasite systems to climate change. These results emphasize the urgent need to quantify the temperature-dependence of host and parasite characteristics in a variety of systems, and I will finish by presenting novel analytical tools for extracting such metrics from experimental and field data. A predictive framework for the impacts of climate change on host-parasite

systems is possible through considering the physiological bases of population-level dynamics, but developing this framework requires concerted efforts from experimental parasitologists, field biologists, and theoretical epidemiologists.

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TEMPORAL RESOURCE PARTITIONING IN TWO SPECIES OF GREGARINES (*ROTUNDULA* SP. AND *HELIOSPORA* SP.) INFECTING AMPHIPODS (*GAMMARUS FASCIATUS*)

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

Predation and competition exert strong selective pressures on free-living communities, but these forces are generally not expected to determine parasite infection patterns. However, in co-infections of a single host, infra-community dynamics may be shaped by antagonistic interactions between competing parasite species. In this study, we surveyed two parasites that infect the same host to investigate potential competitive interactions. We sampled a population of amphipods, *Gammarus fasciatus*, bimonthly for two years in the North Branch of the Raritan River. These amphipods were infected with *Rotundula* sp. and *Heliospora* sp., both direct lifecycle gregarine parasites. Infections were seasonal with prevalence of *Rotundula* sp. peaking in the fall (79 ± 6.8% in 2012 and 98 ± 0.9% in 2013) and *Heliospora* sp. in early spring (42 ± 10.6 % and 46 ± 7.7%). Although mixed species infections were infrequent (overall prevalence of 4.6%), when these gregarines infected the same host there was a significant negative relationship between the two species (Spearman's rho = -0.4378), indicating active interspecific interactions within the host. Mean intensity in single infections was 36.2 ± 1.2 and 10.8 ± 0.7 for *Rotundula* sp. and *Heliospora* sp. respectively. In concurrent infections interactions were asymmetric; the mean intensity of *Rotundula* sp. significantly decreased ($p<0.001$), while *Heliospora* sp. mean intensity did not change ($p=0.902$). There was no significant relationship between gregarine infections and host density for either species of gregarine. However, *Heliospora* sp. infection intensity and prevalence was positively correlated with amphipod size ($R^2 = 0.207$, $p= 0.002$; $R^2 = 0.242$, $p < 0.001$), and there was no significant relationship found with *Rotundula* sp. The mean wet weight value of amphipods infected with *Heliospora* sp. was 20.7 ± 1. 2 mg and with *Rotundula* sp., 8.1 ± 0.2 mg, which suggests that there may be host partitioning in these species based on age or size. Temporal partitioning of this host may be a mechanism to reduce interspecific interactions between these gregarine species. We conclude that competition may influence the seasonal patterns of infection in these gregarine populations, and could be a key factor in regulating host infection patterns.

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(53)

PATTERNS OF PARASITISM: THE LATITUDINAL DIVERSITY GRADIENT OF PARASITIC HELMINTHS

W. Preisser, **N. Dronen** and **J. Light**, Texas A&M University

The tropics are host to the greatest diversity of animal fauna, with species diversity generally decreasing as latitude increases. Less attention, however, has been given to parasite latitudinal diversity gradients (LDG). Given their physiological and biological requirements, parasites might be expected to follow a similar LDG pattern as their hosts. However, there is not a clear consensus on a general latitudinal pattern of parasite diversity, and more studies investigating this topic are needed. It is important to note that latitude itself cannot explain parasite species distributions; rather, multiple abiotic and biotic factors vary with latitude, and the amount of pressure they exert on parasite species may vary across geography. Therefore, this research assessed the parasite LDG by field sampling rodents and their helminth parasites across a latitudinal gradient. Additionally, abiotic and biotic factors were correlated with helminth diversity at various latitudes to reveal the underlying mechanisms shaping the LDG of parasites. Notably, this research will have important implications in determining the latitudinal patterns of helminth diversity, as this pattern in rodents has never been closely examined. Rodents were trapped and collected from specific sites along a latitudinal gradient across North and Central America. Captured rodents were

humanely euthanized and dissected for internal parasite collection. Collected helminths were identified to the species level using morphological and molecular methods and preserved using standard techniques. At each trapping locality, abiotic and biotic factors were measured, including average rainfall, temperature, host sex, and host geographic range. These factors were combined with helminth diversity in a generalized linear mixed model to find significant correlates with parasite diversity, with analyses performed both across localities and within host species. Results of the helminthic diversity of collected rodents will be discussed, as will preliminary results of correlations between various abiotic and biotic factors and diversity.

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AVIAN MALARIA DIVERSIFICATION ACROSS CONTRASTING REGIONS OF AFRICA

J.A. Harvey and **G. Voelker**, Texas A&M University

Avian haemosporidians, the broad suite of malaria and related parasites (*Plasmodium*, *Leucocytozoon* and *Haemoproteus*), demonstrate a high degree of diversification, with 1,873 currently known unique molecular haplotypes (Malavi database; Bensch 2009). Despite this diversity little is known about their distributions and host associations, particularly in underexplored regions like Africa. Our research examines malaria parasites sampled from avian hosts collected in Benin and the Democratic Republic of the Congo (DRC) (n=211 and n=427 hosts respectively), two countries where no avian malaria parasite sampling has been done. These countries contrast sharply in habitat types and environmental variables. The DRC has tropical to subtropical forests while Benin has some subtropical forest along with savanna and savanna forest mosaics, leading us to the hypothesize that DRC will have a higher infection rate as this habitat type would indicate a year-round host-vector contact. We collected mitochondrial DNA sequence data from the *Cytb* gene of infected hosts. We use maximum likelihood and Bayesian analyses to reconstruct a phylogenetic hypothesis and provide estimates of support for haemosporid diversification and relationships. Further, we assess the diversity across contrasting sampling regions, habitats and in the context of the already known haemosporid diversity to inform the broader avian haemosporid phylogeny.

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DOES THE PARASITE COMPOSITION ALTER THE OUTCOME OF COMPETITION?: LIFE HISTORY AND VIRULENCE CONSEQUENCES OF INTRASPECIFIC PARASITE CO-INFECTION

A.M. Gleichsner, Purdue University

Parasites do damage to their hosts (virulence) and cause disease which impacts human, wildlife, and livestock populations. Competition between parasites within a host has been shown to influence the amount of damage they do, but few studies have tried to tease apart what factors alter the direction of virulence and whether they do so in a predictable way. Additionally, studies that have looked at intraspecific competition are limited in their conclusions because of their short-term duration and failure to validate co-infection status. The goal of this study was to expand upon our previous work to investigate whether competitive effects on virulence vary depending on the strain of the interacting parasites. Using *Schistosoma mansoni* parasites and *Biomphalaria glabrata* snails we conducted a long-term study investigating the impact of different strain combinations on virulence. We used molecular tools (SYBR Green qPCR) to validate and track co-infections over time and gain novel insight into competition dynamics throughout an infection. To monitor the impacts of competition on host and parasite life history strategies we recorded host mortality, growth, and host and parasite reproductive output. Preliminary data indicated that co-infections between two Puerto Rican strains of *S. mansoni*, NMRI and PR, resulted in lower host *and* parasite reproductive output, suggesting that infections between non-relatives were more virulent to their host, but that virulence was not correlated with higher transmission. We added a Brazilian strain, LE, to our design to determine whether these trends are retained when these strains are with a different competitor. Our findings suggest that 1) strains differ in their virulence. LE is similar to NMRI in its infection patterns, having lower cercariae output and higher host reproduction than PR. PR is

hyper virulent but becomes less virulent when in a competitive interaction. 2) Strain identity can influence host life history and parasite virulence. For example, exposure to LE and PR resulted in higher longevity of infected snails than exposure to only LE or PR parasites, but exposure to NMRI and LE or PR did not alter the length and number of surviving snails. 3) Competition between strains changes over the course of the infection, with dominance switching occurring frequently throughout the infection, and often delayed emergence of one of the strains until later in the infection. Together, these findings indicate that intraspecific competition is a dynamic process where the genetic composition of parasites within a host could alter disease outcomes.

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(56)

HELMINTH COMMUNITIES OF SUNFISH (CENTRARCHIDAE) FROM ACROSS THE UNITED STATES

K. Luth, Wake Forest University

The current study sought to understand the factors influencing the structure of helminth communities in sunfish (Centrarchidae). When possible, 10 fish were collected via angling from 230 lakes in 30 states across the United States during the summer months of 2011-2013. The most commonly collected centrarchid hosts were bluegill (*Lepomis macrochirus*), green sunfish (*L. cyanellus*), and largemouth bass (*Micropterus salmoides*). Prevalence, intensity, and parasite richness were considered as response variables to factors including host age, host gender, host size, host species, host community richness, host trophic level, parasite life history (e.g., allogenic/autogenic, transmission route), water body surface area, water depth, year of sampling, geographic location, mean annual precipitation, mean annual temperature, and Omernick/Bailaeys/freshwater ecoregion. Several analysis procedures were used for analysis of this geographically-expansive and sampling-intensive data set, including generalized linear mixed modelling (GLMM) and ordination. Although analysis is still underway, it appears that important factors in structuring these freshwater fish helminth communities include host species, host trophic level, and whether parasites display autogenic or allogenic life history strategies.

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PARASITE LIFE-HISTORY DETERMINES THE RELATIONSHIP BETWEEN ANTHROPOGENIC CHANGE AND PARASITE COMMUNITY STRUCTURE

J.M. Alfieri and **T.K. Anderson**, Department of Biology, Georgia Southern University

Parasites may be indicators of salt marsh functioning because of their dependence on multiple host organisms to complete their life cycle and potential sensitivity to environmental contaminants. To determine whether complex life cycle parasites are indicators of salt marsh functioning, we surveyed the parasite community of *Fundulus heteroclitus*, a common inhabitant of salt marshes in Georgia. Five salt marsh sites along coastal Georgia (St. Mary's, Shellman Bluff, Skidaway Island, and Tybee Island) were selected using a proxy for anthropogenic disturbance (impervious surface) and which also fell along a latitudinal gradient. Percent impervious surface within a 100 m buffer from the collection site ranged from 5% (Skidaway Island) to 60% (St. Mary's). 30 fish were necropsied from each site: 78% of fish were infected with parasites, and included 10 parasite taxa and 1,532 individual parasites. The most abundant parasite was a larval tapeworm, *Glossocercus caribaensis*, that uses fish-eating birds (Family Ardeidae) as a definitive host. Prevalence of complex life cycle parasites was dependent on site ($G=66.5$, $df=4$, $p<0.0001$), while prevalence of directly transmitted parasites was independent of site ($G=8.02$, $df=4$, $P=0.09$). Parasite intensity was associated with fish length ($\rho=0.3299$, $P<0.0001$) and mass ($\rho=0.2481$, $P=0.0036$) but did not differ among sexes ($t=37$, $df=128$, $p=0.7153$). Further, parasite species richness, intensity, and prevalence depended on an urbanization threshold ($\lambda=0.01$, $F=3120.7$, $df=4,137$, $p<0.0001$). This study suggests that complex life cycle parasites can act as proxies for human disturbance and ecosystem functioning. Further, these data reveal how landscape patterns can affect fine-scale parasite transmission dynamics.

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EVALUATING THE BIOLOGICAL AND ECOLOGICAL FACTORS INFLUENCING TRANSMISSION OF LARVAL DIGENETIC TREMATODES: A TEST OF SECOND INTERMEDIATE HOST SPECIFICITY OF TWO *HALIPEGUS* SPECIES IN NORTH AMERICA

H.A. Stigge and **M.G. Bolek**, Oklahoma State Univeristy

Host specificity or the extent to which a parasite can infect different host species is a fundamental concept of parasitology. Traditionally, most helminths are thought to be highly host specific and most have been reported from only a single or few host species. However, recent studies suggest that host ranges of many parasites are grossly underestimated based on field surveys alone, and few studies have experimentally examined host specificity. This study evaluated the specificity of 2 trematode species for their 2nd intermediate hosts. First, 3 species of microcrustaceans (*Cypridopsis* sp., *Phyllognathus* sp., and *Thermocyclops* sp.) were used to assess the extent to which the growth and development of metacercariae of 2 *Halipegus* species differed within phylogenetically distinct host groups. Each species of microcrustacean was exposed to a single metacercaria of 1 of the 2 *Halipegus* species. Then, worms were examined on wet mounts for body length, sucker size, and the loss of the excretory bladder every 3 days. After examining the development of worms within each host, the extent that each of the 3 microcrustacean species contributed to transmission of the 2 *Halipegus* species was evaluated by documenting the rate that microcrustacean species were consumed by the next odonate paratenic host. Damselflies were placed in a cup with 20 infected individuals of the assigned microcrustacean species, and after 24 hours, the number of microcrustaceans eaten was determined. After an additional 24 hours, odonates were dissected, and the number of worms that established from each species of microcrustacean was determined. *Halipegus* species were capable of infecting all 3 species of microcrustaceans, although not all exposed individuals became infected. There were significant differences in the abundance of worms in the 3 microcrustaceans with *Cypridopsis* sp. having the highest prevalence and abundance of both *Halipegus* species. Metacercariae of both *Halipegus* species did not grow at the same rate in the 3 microcrustacean species. For both *Halipegus* species, metacercariae grew fastest and had the largest suckers within the ostracods than within either of the copepods. Additionally, there was a significant difference in the rate that each of the microcrustaceans were consumed by an odonate and in the number of worms that established within them. A copepod, *Thermocyclops* sp., was always consumed less frequently than the other 2 hosts. Lastly, worms from *Cypridopsis* sp. establish significantly more often than the other 2 species. Collectively, these results suggest that although these 3 intermediate hosts are all capable of becoming infected, they are not all equally good hosts. The ostracod, *Cypridopsis* sp., is the best option of these 3 hosts. Worms infected *Cypridopsis* sp. most frequently, developed fastest, and then had the highest rates of transmission to subsequent hosts. These results are important because understanding how different hosts contribute to the development and transmission of parasites is critical to fully understand host specificity of helminths and evaluate transmission dynamics within natural systems.

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THE EFFECTS OF STREAM NETWORK CONNECTIVITY AND HOST MOBILITY ON TREMATODE COMMUNITIES

S.A. Zemmer and **L.K. Belden**, Virginia Tech

Dispersal is one of the major processes that structures ecological communities. Dispersal patterns are determined by the particular dispersal abilities of individual species, as well as by physical factors such as landscape features and habitat connectivity. For many parasitic organisms, hosts play a key role in parasite dispersal. Trematodes are multi-host parasites with complex life cycles that may be entirely aquatic or include terrestrial hosts. The primary goal of this study was to explore the role of dispersal in structuring trematode component communities in stream networks, dendritic systems with continuous, unidirectional water flow that results in downstream drift. Trematodes that use fish as definitive hosts are

limited to within stream dispersal, whereas species with avian or mammalian definitive hosts are likely able to disperse across landscapes more easily. We examined first-intermediate host infection (in stream snails *Elimia proxima*) at eight locations within a headwater stream network in southwestern Virginia, including sites within multiple headwaters and the mainstem. The prevalence of infection (proportion of infected snails) progressively decreased from upstream to downstream (headwaters to mainstem), and community composition changed from predominately parasites of birds and mammals to parasites of fish. Molecular identification of these parasites is now underway and will provide a higher level of resolution for examining patterns in community structure to assess the relative importance of host dispersal versus downstream drift in this system.

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POTENTIAL INCREASE OF THE GEOGRAPHICAL DISTRIBUTION OF THE ASIAN TAPEWORM (*BOTHRIOCEPHALUS ACHEILOGNATHI*) DUE TO CLIMATE CHANGE

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The introduction of alien host species and their parasites is a serious problem worldwide because it has direct implications on the biota of the invaded habitat. Theory on climate change suggests a potential increase in the geographical distribution of alien species and their parasites due to global warming with increasing risk of epizootiological outbreak. To test this hypothesis, we have chosen the Asian fish tapeworm (Bothriocephalus acheilognathi) introduced globally in fresh waters together with the grass carp. We aim to estimate the potential distribution of B. acheilognathi under four scenarios of climate change (RCP 2.6, RCP 4.5, RCP 6.0 and RCP 8.5) proposed by the Intergovernmental Panel on Climate Change (IPCC). We used the Maximum Entropy Model (Maxent), which is based on the idea of a realized distribution constrained by the values of the environmental variables at the spatial scale under study. We built a global data set based on the published records of presence of the Asian fish tapeworm. For background data, we used the record distribution of fish species that could be parasitized by B. acheilognathi from Fishbase. The climatic data were obtained from the Bioclim dataset from the NASA GISS-E2 satellite. The results showed that the distribution probability increased in every one of the four scenarios by over 50%, especially in temperate latitudes. These results suggest that B. acheilognathi will increase its geographical distribution under any climate change scenario, with the concomitant increase in the risk of infection of potentially susceptible freshwater species in temperate latitudes. The current distribution of B. acheilognathi is the result of the introduction of alien species under current climate conditions but this likely would be expanded under climate change increasing also the potential of infection in native and threatened species, with special emphasis in fishes of temperate latitude.

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REPRODUCTIVE PLASTICITY IN THE NEMATODE *GYRINICOLA BATRACHIENSIS*: IS REPRODUCTIVE STRATEGY DEPENDENT UPON TADPOLE DEVELOPMENTAL TIME?

J.N. Childress, **S. Rogers** and **G.J. Langford**, Florida Southern College

The nematode *Gyrinicola batrachiensis* (Oxyuroidea: Pharyngodonidae) infects the gastrointestinal tract of tadpoles, and female worms are known to have a complex reproductive strategy. Specifically, females use either (1) didelphic haplodiploidy with thick-shelled eggs that are resistant to desiccation and thin-shelled eggs that are autoinfective, or (2) monodelphic parthenogenesis with only thick-shelled, resistant eggs, although it is unclear whether this system is genetically determined or phenotypically plastic. Previous studies suggest that a haplodiploidy strategy is used only in long-developing tadpoles, such as ranids (true frogs), whereas a parthenogenetic strategy is only found in short-developing tadpoles, such as hylids and bufonids (treefrogs and toads); however, a recent study found an intermediate strategy with didelphic worms (but not haplodiploidy) in short-developing toad tadpoles collected in sympatry with

long-developing tadpoles in nature. Taken together, these data suggest that *G. batrachiensis* are developmentally plastic dependent on the host species infected and possibly the tadpole community in a pond. To elucidate this complex reproductive system, this project used an outdoor mesocosm system to conduct a multiple species cross-infection and development study. In brief, hylid egg masses (two species) were exposed to infected ranid tadpoles, ranid egg masses to infected hylid tadpoles, and egg masses of all species, as a group, to infected tadpoles of both anuran families (controls were used in all experimental groups). A total of 525 experimental tadpoles were analyzed for this study, which produced thousands of worms for developmental and morphological analysis. Preliminary results suggest that the nematodes are reproductively plastic – dependent on the species of tadpole infected, although some exceptions were found and will be discussed.

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EFFECTS OF HABITAT FRAGMENTATION ON THE GENETIC STRUCTURE OF *TRYPANOXYURIS MINUTUS*, A HOWLER MONKEY PARASITE

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Habitat fragmentation and the consequent isolation of host's populations could be a key factor determining parasite genetic variation and population structure, and hence the processes of evolution. The howler monkey *A. palliata* is one of the three primates inhabiting tropical rainforests in Mexico, and it is considered as a threatened species. The habitat loss and transformation has left its populations isolated throughout its distribution range. In this study we conducted an analysis at different spatial scales (regional, sub-regional and local) in order to determine the effects of habitat fragmentation in the genetic structure of the howler monkey oxyurid, *Trypanoxyuris minutus,* using non-invasive sampling techniques and sequences of the COI gene. Feces were collected from 14 fragments in 4 regions across southeastern Mexico in the states of Veracruz, Tabasco and Chiapas. Genetic diversity was high in the different populations of this nematode, and the analysis of genetic differentiation showed significant variation among regions within the distribution range, and among sub-regions within a region, suggesting limited gene flow. No genetic differentiation was found among fragments within a locality, indicating that habitat fragmentation and host isolation may be occurring too recently to have caused genetic differentiation among pinworm populations at this scale. Studies such like this one will help to understand the effects of environmental change on parasite microevolution which is essential for developing landscape management plans and wildlife conservation strategies

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DIFFERENT ELEMENTAL CONTENT BETWEEN TISSUES OF TREMATODES AND THE FRESHWATER SNAIL, *ELIMIA LIVESCENS*

N. Chodkowski and **R.J. Bernot**, Ball State University

Parasites are infectious agents present in every ecosystem, but their effects on ecosystem functioning are largely unexplored. Ecological stoichiometry uses the mass balance of multiple elements to predict and understand energy and elemental fluxes across different levels of ecological organization and provides a framework for understanding the role of parasites in ecosystems. A specific prediction of ecological stoichiometry is that organisms with faster growth or reproductive rates will require higher phosphorus content for nucleic acid and protein synthesis. We examined the carbon (C), nitrogen (N), and phosphorus (P) content and biomass of parasitic trematodes and their intermediate host, the freshwater snail *Elimia livescens*, from the White River in east-central Indiana. Snails ranged in size from 10.0 to 16.5 mm and were dissected to separate snail tissue from trematode sporocyst, rediae, and cercariae. We hypothesized that the N:P ratio of trematodes will be lower (more P per unit N) than snails due to rapid asexual reproduction of the trematodes. Trematode tissues contained lower N:P than the snail tissues, which was driven by greater P in trematodes. The N:P of trematode tissues was similar to the N:P of the snail gonadal tissues. Trematodes tissue also had greater C:N than snail foot tissues, but not snail gonadal tissues. The gonadal tissues of parasitized snails had lower N:P (more P per unit N) than the gonadal

tissues of non-parasitized snails. The foot tissues of parasitized snails had 2x lower N:P (more N per unit P) than the foot tissues of non-parasitized snails. N:P was 20x greater in snail foot tissue and 12x greater in snail gonadal tissues than the trematode tissues. Foot and gonadal snail tissues N:P was higher in non-parasitized individuals. Overall, the elemental content of snails and trematodes differed substantially, potentially leading to differences in snail nutrient recycling. Ongoing studies are relating trematode infection to host nutrient recycling dynamics and metabolism to elucidate the functional role of parasites and their effects on nutrient dynamics in ecosystems.

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RELATIONSHIP BETWEEN PARASITIC INFECTION AND REPRODUCTIVE POTENTIAL OF TWO CYPRINIDS WITH DIFFERENT REPRODUCTIVE STRATEGIES

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Parasites can inflict a number of effects on their hosts; of interest to this study are the effects on the reproductive potential of the host. It has been hypothesized that during the breeding season energy is reallocated from the immune system to reproduction. As a result the individuals with the most pronounced sexual characteristics (e.g. gonad size and mating coloration) will also harbor to the highest parasite load. Alternatively, it has been hypothesized that parasitic infection utilizes the host's energy, resulting in less energy being available for reproduction. In the case of fishes few studies have compared this relationship between males and females and between species with different reproductive strategies. So, the first objective of this study is to determine if there is a relationship between parasite load and reproductive potential in fish and whether this relationship differs between males and females. The second objective is to examine two cyprinids, *Cyprinella venusta*, a crevice-spawner and *Notropis volucellus*, a broadcast-spawner, to determine if this relationship varies between the two species. Fish were collected from a single site on the Paluxy River, TX and returned to the lab to measure parasite load, distinguished as either endo- or ectoparasites, and reproductive potential using the gonadosomatic index (GSI). Prevalence was calculated for the four major groups of parasites for *C. venusta*: trematodes (86.4%), cestodes (8.4%), nematodes (43.5%), and protozoans (39.0%); for *N. volucellus*: trematodes (24.0%), cestodes (0.60%), nematodes (33.3%), and protozoans (62.3%). Preliminary results show a significant, positive correlation between number of endoparasites and ectoparasites and GSI in male *C. venusta*, and between number of endoparasites and GSI in female *C. venusta*. These correlations indicate that the individuals with the highest GSI also harbor the most parasites, suggesting a relationship between reproductive potential and infection.

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SURVEY OF CESTODE BIODIVERSITY IN AVIAN HOSTS

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Biodiversity loss is an undeniable fact of modern society. However, less understood is how the loss of biodiversity inevitably alters communities including those of parasites. As parasites make up a large portion of the worldwide biodiversity, it is important to conduct surveys to address this knowledge gap. Birds are a useful system for wildlife parasite surveys due to their role as the definitive host for many helminth parasites. While there are a considerable number of studies conducted on helminth parasites of birds throughout the United States, studies in northeastern Illinois are limited and those surveys that exist need to be updated particularly in urban areas. Therefore, our research objective was to describe the parasite communities of a variety of avian hosts collected from urban areas in northeastern Illinois. We necropsied 53 birds: 5 American robins, 36 European starlings, 4 Mallard ducks, 5 Mourning doves, 2 Pigeons, and 1 Wood thrush. Birds were donated by regional airports, the Field Museum Chicago, IL and collected from the Northeastern Illinois University campus as part of a bird window collision study. We used standard parasitological methods for parasite isolation and collection. We obtained morphological information from permanent, whole mounts of specimens. We extracted DNA from select specimens for sequencing using 28S, NAD1, 16S, and COX1 gene fragments to aid in cryptic species identification. Of the

four helminth groups, cestodes showed the highest prevalence at 55% followed by nematodes (45%), acanthocephalans (36%), and trematodes (13%). Within the cestodes, 100% of all ducks were infected (4 birds, mean intensity 5.5 individuals), 80% of robins (4, mean intensity 6.25), 58% of starlings (21, mean intensity 2.8), and none in doves, pigeons, and thrushes. We identified five different species of cestodes from the families Dilepididae and Hymenolepididae including *Fimbriaria* and *Cloacotaenia*. Based on the diet of these birds, it is unsurprising that doves and pigeons showed no cestode infections. The lone thrush was not infected with cestodes, however this is likely due to the single individual sampled. Both the robins and ducks exhibited higher than expected prevalence of cestodes, but additional specimens are needed. The host specificity of these cestode species can be determined as well as the role of diet by determining transmission. Similarities between host species may indicate the specific host resource(s) used by the parasites. This can lead to better predictions of infection dynamics and parasite communities within changing host communities through species introduction and urbanization. While many recent advances have been made in the roles of wildlife parasites in ecosystems, more precise information is needed on their diversity and life cycles to increase our understanding of these processes.

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A NEW GENUS OF LECANICEPHALIDEAN TAPEWORM WITH COMMENTS ON ITS DISTRIBUTION WITHIN A HOST SPECIES

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Generic diversity within the Lecanicephalidea has nearly doubled within the last two decades; to date, 24 genera are recognized, parasitizing primarily batoid hosts. Examination of eight specimens of the dasyatid stingray *Himantura granulata* collected in 2012 from the Solomon Islands revealed the presence of two species of lecanicephalideans—a large and a small-bodied species—representing a new genus. Individual specimens representing this new genus have also been found parasitizing several other dasyatid hosts from elsewhere in the Indo-Pacific region (i.e., at least six other species of *Himantura* and one species of *Neotrygon*). This new genus most closely resembles *Seussapex* in its possession of a scolex proper with four acetabula in the form of suckers, a large, complex, retractable apical structure, and a single column of testes. However, it can be distinguished from *Seussapex* and the remaining valid lecanicephalidean genera most readily by the unique morphology of its apical organ, which is in the form of a large, scalloped, muscular disk with eight marginal sucker-like depressions. The two new species exhibiting this unusual apical organ morphology are readily distinguishable from one another in that the larger species is at least two orders of magnitude larger than the smaller species and possess two to three times the number of immature proglottids. Moreover, the two species exhibit an intriguing distribution among the eight stingray specimens examined: the larger species was found only in smaller, immature stingray specimens (disk width <35cm) while the smaller species was found mostly in larger, mature stingray specimens (disk width >100cm) and, on rare occasion, in some immature specimens as well. Despite the morphological differences noted between the two species, their sequence data for the D1-D3 28s rDNA gene region is essentially identical. Ultimately, differences in the complete cestode fauna between immature and mature host specimens may be attributable to a host diet shift, or an age-diversity relationship.

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THE DIVERSITY AND SURPRISING COMPLEXITY OF LARVAL AND CYST STAGES OF GORDIIDS (NEMATOMORPHA): HOW MANY TYPES ARE THERE?

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Freshwater hairworms or gordiids infect terrestrial arthropods as juveniles but are free-living in aquatic habitats as adults. Estimates suggest that only 18% of hairworm species have been described globally and biodiversity studies on this group have been hindered by unreliable ways of collecting adult free living worms over large geographical areas. However, recent work indicates that non-adult cyst stages of hairworms may be the most commonly encountered stages of gordiids in the environment, and can be used for discovering the hidden diversity of this group. Unfortunately, little information is available on the morphological characteristics of non-adult stages of hairworms. To address this problem, we describe and compare morphological characteristics for larval and cyst stages for 10 species of African and North American gordiids from 4 genera (*Chordodes*, *Gordius*, *Neochordodes* and *Paragordius*) using differential interference contrast microscopy and/or scanning electron microscopy. Additionally, we substantiate our observations by evaluating larval and cyst morphology from field collections of gordiid larvae and/or cysts from various locations in Africa, Asia and North, Central, and South America. Our study indicates that three distinct morphological larval and cyst types are present among the gordiids. Although species identification based on larval and/or cyst characteristics is not always possible among different species of gordiids, larval and cyst morphology appears to be conserved among some genera and/or related genera of gordiids and may represent useful synapomorphic characters for hairworm systematics. Additionally, our work indicates that gordiid larval morphology can be used for predicting cyst morphology in gordiid genera for which cyst stages are unknown. The capability to identify and predict gordiid genera and/or clades based on cyst morphology will be useful for culturing gordiids in the laboratory from field collected cysts and these new techniques will undoubtedly allow others to discover new species of gordiids from around the world.

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PHYLOGENY OF NEW WORLD *HYMENOLEPIS* WEINLAND, 1858 - MORPHOLOGY AND MOLECULES

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The phylogenetic relationships of several species of *Hymenolepis* from the new world were estimated using both morphology and molecules. Several species of *Hymenolepis* were studied, including: *H. citelli* McLeod, 1933, *H. diminuta* Rudolphi, 1819, *H. geomydis* Gardner and Schmidt, 1988, *H. neurotrichi* Rausch, 1962, *H. pitymi* Yarinsky, 1952, *H. robertrauschi* Gardner, 2014, *H. scalopi* Schultz, 1939, *H. tualatinensis* Gardner, 1985, and *H. weldensis* Gardner and Schmidt, 1988. Character matrices used in the phylogenetic analyses included mensural, morphological, and molecular data analyzed both separately and in combination. Several phylogenetic methods were used to analyze the data-set and results showed a general convergence in topologies.

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GET THE TAXONOMY RIGHT FIRST!

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In the context of the present—almost frenzied—focus on the synthesis of biological data it is easy to loose sight of the importance of ensuring the accuracy of the basic facts on which such "big data" contributions are based. Ironically, because the generation of primary data is tedious, time consuming, and when conducted in a global context requiring fieldwork is also particularly formidable, this type of work has begun to loose its appeal. However, perhaps the most daunting of these endeavors is the taxonomic work required to ensure the accurate identification of the taxa that represent the foundation of synthetic contributions. The results of our multiyear NSF-funded Planetary Biodiversity Inventory project aimed at "surveying the tapeworms of the vertebrate bowels of the earth" attest to the remarkable value of careful taxonomic studies of *both* host and parasite species. It is now clear that, as a group, elasmobranchs (sharks and rays) are *much* more speciose than originally thought. Furthermore, their cestode faunas are both substantially more diverse *and* more host specific than historical records would suggest. In fact, this parasite system now appears to rank among the most host-specific of any of those formally characterized to date. But what is also now painfully clear is that, despite its very high degree of host-specificity, this system shows little evidence of cophylogeny, let alone cospeciation. Instead, a substantial geographic signal underlying the observed host associations appears to exist. A way to move forward to disentangle the various factors potentially contributing to the observed host associations is presented.

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HISTORY AND PROGRESS IN THE SYSTEMATICS OF NON-HOOKED "TETRAPHYLLIDEANS": THE ORDER PHYLLOBOTHRIIDEA

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The Phyllobothriidae of 20-25 years ago (e.g., Schmidt, 1986; Euzet, 1994) was an unwieldy beast, a classic "not-A" group *sensu* Eldredge and Cracraft (1980). The past quarter century has been an exercise of "peeling back the onion" to get at the actual phylogenetic nature of the taxa once allocated to this family. Early molecular systematic surveys (Olsen et al., 1999, 2001) revealed two clades of phyllobothriids, one hosted by sharks and the other batoids. The batoid hosted clade was formalized as the Rhineobothriidea by Healy et al. (2009), with familial categories added by Ruhnke et al. (2015). Ruhnke (2011) critically analyzed all taxa historically allocated to the Phyllobothriidae and made recommendations on what might constitute it members. In "Orders out of Chaos", Caira et al. (2014) erected the order Phyllobothriidea and tapped the genera *Calyptrobothrium, Chimaerocestos, Marsupiobothrium, Nandocestus, Orectolobicestus, Orygmatobothrium, Paraorygmatobothrium, Phyllobothrium, Ruhnkecestus, Scyphophyllidium* and *Thysanocephalum* as members. They listed *Alexandercestus Bibursibothrium, Cardiobothrium, Clistobothrium, Crossobothrium, Flexibothrium* and *Pelichnibothrium* as likely members. Evidence exists to suggest the inclusion of *Doliobothrium Hemipristicola* and *Monorygma* in the order. Phyllobothriid systematics exemplifies the value of reciprocal illumination in combining critical historical research, careful morphological work and modern phylogenetic analyses to improve biological classifications.

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TWO NEW SPECIES OF *PHYLLODISTOMUM* THAT WEREN'T NEW AFTER ALL: WHEN YOU CAN'T TRUST MORPHOLOGY!

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Two geographically separated populations of *Phyllodistomum* were discovered in fish from Hidalgo, México; one was from the headwaters of a branch leading to Río Pánuco (northeastern Hidalgo) and the other from a small artisian spring in the Reserve of the Biosphere Barranca de Metztitlán (central Hidalgo). Waters from both localities eventually drain in the same river, connected to the Gulf of Mexico (east of Hidalgo), but, because of the altitude of each locality, water cannot flow from one to the other. Individuals from each population were distinct from each other morphologically and were different from any other species reported in North America. Because there is a robust phylogenetic hypothesis that included North American species, it was decided to confirm the unique identity of each putative taxon using the same sequences used in that study. Specimens for molecular analyses were collected from fish from the two localities and genomic DNA was extracted and sequenced according to the methodology used in that study. Comparison of the sequences of 28s DNA from individuals from each locality indicated that both of the two populations were members of *P. inecoli*, described previously from *Heterandria bimaculata* (Teleostei: Poeciliidae). That species was collected in the Río La Antigua basin, Veracruz, Mexico, which drains into the southern Gulf of Mexico. The Hidalgo localities are about 400 km northeast of the locality in Veracruz, and the two are separated mountains and several unconnected river drainages. The presence of the population in Barranca de Metztitlán can be explained by supposed translocation of fish (*Xiphophorus hellerii*; Teleostei: Poeciliidae) from Veracruz or the more eastern states, although the presence of the other, in a more pristine part of Hidalgo, cannot be explained. Morphological details of each population are compared and discussed, including problems with the use of morphological characters for the identification of species of *Phyllodistomum*.

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MORE TAXONOMY NEEDED: A SURVEY OF NEW YORK LAKE FISH PARASITES

F. Reyda, State University of New York College at Oneonta

This presentation discusses the need for more taxonomic work in the context of a longterm survey of fish parasites in a lake in New York State. A survey of the intestinal parasites of fishes of Otsego Lake and its tributaries (Cooperstown, New York) took place from 2008 to 2014. Over 500 individual fish were collected by hook and line, seine, gill net, or ElectroFisher, and subsequently examined for intestinal parasites, and in many cases, for parasites in other fish organs. Helminths encountered in the alimentary canal were prepared as whole mounts using conventional methods and subsequently examined with light microscopy, and often scanning electron microscopy. In addition, DNA sequence data (mitochondrial cytochrome oxidase I) was obtained for a subset of the helminth species, and those data were compared with other published sequence data. The survey included a total of 27 fish species, consisting of six centrarchid species, one ictalurid species, eleven cyprinid species, three percid species, three salmonid species, one catostomid species, one clupeid species, and one esocid species. Thirteen of the 27 fish species examined were infected with parasitic worms in the alimentary canal, including four species of acanthocephalans, seven species of cestodes, seven species of digenetic trematodes, and at least six species of nematodes. Additional species of helminths were encountered as larvae in the body cavity, or the viscera, in at least 18 of the 27 fish species examined. Among the intestinal parasitic worms in fish in Otsego Lake, the most prevalent and least host specific is the cryptic acanthocephalan, known as *Leptorhynchoides thecatus* 'Large form' (see Steinauer 2004). Our survey work included the discovery of at least one species new to science, of the nematode genus *Spinitectus.* In many cases, generic identifications of helminths were possible based on the published literature, but unequivocal species identifications were not tenable owing to a deficiency of reference information. This was the case for species of *Neoechinorhynchus*, *Proteocephalus, Crepidostomum* and *Spinitectus,* signifying the need for revisionary work on these taxa.

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ASSESSMENT OF SOME ANTIOXIDANT ENZYMES IN AMPHISTOME PARASITES, *GASTROTHYLAX CRUMENIFER* AND *GIGANTOCOTYLE EXPLANATUM* INFECTING INDIAN WATER BUFFALO, *BUBALUS BUBALIS*

S. Ahmad, **M.K. Saifullah** and **S.A. Abidi**, Aligarh Muslim University

Amphistomosis is a neglected ruminant disease causing high morbidity and mortality, resulting in substantial economic losses in tropical and subtropical countries across the world. Livestock form an indispensible part of Indian agronomy and the flourishing dairy industry. The two most common amphistomes which parasitize the Indian water Buffalo, *Bubalus Bubalis* are recognized as *Gastrothylax crumenifer,* infecting rumen and *Gigantocotyle explanatum* infecting bile ducts of hepatic tissues. Generally, the migrating immature forms of *G. crumenifer* cause hemorrhagic inflammation of the alimentary tract, edema and anemia whereas *G. explanatum* infection causes thickening of bile duct wall with parietal chronic inflammation involving mucosa and submucosa. Poor animal health affects various animal based industries and ultimately, the Indian economy. This needs a reliable control measure to tackle amphistomosis in our livestock. Many explanations exist describing how these parasites survive in known hostile conditions of their host. Immune evasion strategies, efficient detoxification of xenobiotic load coupled with organized tools to tackle host generated reactive oxygen species (ROS) are seen as effective technique for the successful establishment in a host. In the present study we assessed the activities of some antioxidant enzymes like Glutathione-S-transferase (GST), Superoxide Dismutase (SOD), Catalase and the levels of Lipid Peroxidation. We observed that the specific activity of GST, SOD, Catalase and lipid peroxidation level were comparatively higher in *G. crumenifer* than *G. explanatum*. Native polyacrylamide gel elecectrophoresis revealed a total of three isozyme of SOD in both *G. crumenifer* and *G. explanatum*. Higher level of activity of antioxidant enzymes in *G. crumenifer* suggests a higher level of host generated ROS in rumen of definitive host than their biliary counterparts. A more efficient phase-II detoxification process mediated by GST was observed in *G. crumenifer* than *G. explanatum*. Modulation of antioxidant enzymes in response to host generated oxidative stress indicates a dynamic state of host-parasite interactions including immune evasion mechanism and their possible role in anthelmintic drug resistance.

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COMPARATIVE ANALYSIS OF THE LARVAL AND ADULT CIRCULATORY SYSTEM AND ITS ROLE IN PATHOGEN AGGREGATION IN THE MOSQUITO *ANOPHELES GAMBIAE*

G.P. League and **J.F. Hillyer**, Vanderbilt University

Insects transport hemolymph (blood) throughout their hemocoel (body cavity) via a muscular dorsal vessel, which is comprised of a thoracic aorta and an abdominal heart. In adult mosquitoes, the heart contracts both toward the head (anterograde) and toward the posterior of the abdomen (retrograde), and contains ostia (valves), which serve as both the major inlets for hemolymph into the lumen of the vessel and the primary sites of pathogen aggregation following infection. Because mosquitoes undergo drastic morphological changes during metamorphosis, we investigated how hemolymph flow dynamics, dorsal vessel structure, and pathogen aggregation differ between the larval and adult stages. Intravital imaging of the larval abdomen showed that, unlike adults, the larval heart contracts solely in the anterograde direction, and does so at a rate that is significantly slower than that of adults. Similarly, tracking of fluorescent microspheres showed that hemolymph velocity inside the larval heart is 68% slower than hemolymph velocity inside the adult heart. Fluorescence imaging of the larval dorsal abdomen following treatment with AlexaFluor-conjugated phalloidin (which binds F-actin) revealed a heart that is structurally similar to that of adults, including the presence of intersegmental ostia. However, unlike adults, hemolymph enters the larval heart primarily through incurrent openings located in the 8th abdominal segment. This difference in hemolymph flow results in a different pattern of heart-associated

pathogen aggregation, as quantification of fluorescence emitted from injected GFP-*E. coli* revealed that bacteria aggregate primarily in the 8th abdominal segment tracheal tufts rather than the periostial regions.

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A NOVEL IN VITRO ASSAY OF ANTHELMINTIC ACTIVITY AGAINST LARVAE OF *ASCARIS SUUM*

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Q. Liu and **Q. Wang**, National Laboratory of Veterinary Protozoology, College of Veterinary Medicine, China Agricultural University

In this study we tested effects of bile concentrations, pH values, and CO_2 on *Ascaris suum* egg hatching. New hatched larvae were separated from unhatched eggs and debris by the agar gel method and washed with sterile PBS and culture medium. The larvae were pre-incubated in Dulbecco's modified Eagle's medium in presence of anthelmintics in 48 well plates for 3 days at 38°C in 5% CO_2. Drugs tested were thiabendazole, mebendazole, fenbendazole, pyrantel, and levamisole. The percentages of larvae that migrated to the surface of each treated and control well were used to calculate the drug concentration which inhibits 50% of the larvae migration (EC_{50}). The reasonable values of EC_{50} of fenbendazole, mebendazole, levamisole, pyrantel and thiabendazole against *A. suum* isolates were obtained successfully. Seemingly, this combined multiwell culture and agar gel larval migration assay was a sensitive bioassay for anthelmintic activity and could serve as an *in vitro* method to detect anthelmintic resistance against *A. suum* and possibly to detect *Ascaris lumbricoides* as well.

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SCHISTOSOMICIDAL OXAMNIQUINE DERIVATIVE DRUG ACTIVITY AGAINST HUMAN SCHISTOSOMIASIS

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Human schistosomiasis is a disease caused by species of the genus *Schistosoma*, which globally affects over 200 million people. The major species effecting humans are *S. mansoni*, *S. haematobium*, and *S. japonicum*. There is currently only one method of treatment (monotherapy), the drug Praziquantel. Constant selection pressure through mass chemotherapy - this year alone will see the administration of over 250 million doses - has yielded evidence of resistance to PZQ. This has been observed in both the laboratory and field. The purpose of this research is to develop a second drug for use in conjunction with PZQ. Previous treatment of *S. mansoni* included, among others, the use of oxamniquine (OXA), a prodrug that is enzymatically activated in *S. mansoni* but is ineffective against *S. haematobium* and *S. japonicum*. The OXA activating enzyme was identified, described, and crystallized by our laboratories as being a sulfotransferase (SmSULT). The focus of this research is to reengineer OXA to be effective against *S. haematobium* and *S. japonicum*. Twelve OXA derivatives were synthesized, of which three showed schistosomicidal activity as good as or better than OXA. A further 5 drugs were designed based on the most schistosomicidal derivative and yielded 2 more drugs with even higher schistosomicidal activity in vitro. Further structure-activity relationship studies to improve activity produced an additional 9 analogs. Of these derivatives, 3 lead analogs showed schistosomicidal effects, making a total of 8 derivatives discovered that may potentially be used to treat schistosomiasis. Further in vitro tests of these 8 derivatives against *S. haematobium* and *S. japonicum* are ongoing. This iterative process of using structural data to inform chemical synthesis of derivatives, which are then tested in vitro, continues to provide us with novel compounds with improved anti-schistosomal activity. The information gleaned from these early studies will be used to optimize OXA derivative design. The most active derivatives will

be used in an in vivo model of schistosomiasis to evaluate efficacy before moving to safety and toxicity studies.

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EFFECT OF ABNORMAL TEMPERATURE AND STARVATION ON THE INTERNAL DEFENSE SYSTEM OF THE SCHISTOSOME-TRANSMITTING SNAIL *BIOMPHALARIA GLABRATA*

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The internal defense system (IDS) of freshwater gastropods is comprised of phagocytic hemocytes as well as soluble plasma factors. Physiological stress caused by non-optimal environmental conditions potentially could interfere with the IDS and as a result the ability to resist infection with larval trematodes. To explore this hypothesis, we examined the effect of supra- and sub-optimal temperatures as well as starvation on 3 parameters of the IDS of the schistosome-resistant Salvador strain of *Biomphalaria glabrata*: circulating hemocyte concentrations, mitotic activity in the amebocyte-producing organ (APO), which is located in the anterior wall of the pericardial sac, and resistance to infection with *Schistosoma mansoni*. Salvador *B. glabrata* (10.5-13 mm, shell diameter) in individual 500-ml jars were subjected to abnormally low (20 C) or high (33 C) temperatures, or to starvation at 27 C for 7 or 14 days. Control snails were maintained at 27 C with food, conditions deemed as optimal. A total of 30 snails was used for each treatment category. Hemocyte concentrations were obtained by counting all hemocytes in a 2-µl sample of hemolymph. Mitotic activity was estimated by counting total numbers of mitotic figures in the 5 largest 7-µm histological sections of the APO in serially sectioned pericardial sacs. Additionally, snails subjected to these 4 treatments in groups of 11-15 were individually challenged with 25 miracidia each of *S. mansoni* (total of 32-37 snails/treatment category). Infection controls consisted of susceptible M-line *B. glabrata* that had been reared in aquaria at 23-25 C prior to miracidial challenge. Following exposure to miracidia, snails were maintained at 27 C, with food, and were monitored for development of daughter sporocysts. Compared to the controls, starved snails had significantly higher hemocyte counts at both 7 and 14 days. Conversely, mitotic activity in the APO of starved snails was significantly lower than that of controls at both time periods. These results suggest that leukocytosis in starved snails did not result from increased hemopoiesis in the APO, but from other mechanisms, e.g., hemocyte proliferation in other locations, recruitment of hemocytes from tissues and/or prolonged hemocyte residence time in the hemolymph. Exposure to 20 C or 33 C for 7 or 14 days did not have a statistically significant effect on hemocyte counts compared to controls. However, APO mitotic activity in snails exposed to 20 C was higher at both time periods, and this difference was statistically significant at 14 days, whereas mitotic activity in snails exposed to 33 C was lower at both times, and this difference was statistically significant at 7 days. Moreover, none of the treatments altered the resistance phenotype of Salvador snails, with only 1 of 277 developing an infection, versus 36 of 44 M-line controls. In summary, starvation for 7 or 14 days strongly affects hemocyte concentrations and APO mitotic activity in Salvador *B. glabrata*, albeit in opposite directions, whereas abnormally high and low temperatures affect APO mitotic activity but not hemocyte concentrations, and none of these treatments eliminate resistance to infection with *S. mansoni*.

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EFFECT OF BLOOD FEEDING ON MOSQUITO HEART PHYSIOLOGY

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As anautogenous insects, the females of many mosquito species are required to take a blood meal in order to obtain the necessary nutrients to produce eggs. This act of blood feeding causes skin irritation in vertebrate animals, and can lead to the transmission of diseases such as malaria, lymphatic filariasis, and dengue fever. Blood feeding also imposes significant physiological challenges. For example, it often results in the doubling or tripling of the weight of a mosquito, which can affect normal processes such as flight. In the present study we tested the effect of blood feeding on the physiology of the dorsal vessel of the malaria mosquito, *Anopheles gambiae*. The dorsal vessel is the mosquito's primary circulatory organ. It is a

muscular tube that extends the length of the body and is divided into an abdominal heart and a thoracic aorta. As a first experiment, we blood fed five-day-old mosquitoes and measured their heart physiology. We found that blood feeding increases the heart rate, and that the heart rate remains elevated for at least the first six days following feeding. The mosquito heart periodically reverses contraction direction, and the elevated heart rate was observed regardless of the direction in which heart contractions propagated. We then repeated the experiment using ten-day-old mosquitoes and obtained similar results. For both age groups, blood feeding increased the abdominal width, and this increase remained for at least six days following feeding. However, it remains unclear whether this increase correlates with the cardiac phenotype observed. Currently, we are undertaking additional experiments in efforts to uncover the mechanism that leads to the cardiac phenotype observed. For example, we are measuring the effect of blood feeding on the protein, carbohydrate and lipid content of the mosquito, and we are testing the effect of oviposition on cardiac physiology.

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QUANTIFICATION OF THE BACTERIAL ENDOSYMBIONT, *NEORICKETTSIA* SP., WITHIN ALL LIFE CYCLE STAGES OF A DIGENEAN HOST BY USE OF REAL-TIME QPCR ANALYSIS

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Neorickettsia (Rickettsiales, Anaplasmataceae) is a genus of obligate intracellular bacteria transmitted by digenean (fluke) hosts. These endosymbionts pass through all stages of digenean life cycles via vertical transmission. Importantly, they may also be passed to the vertebrate hosts of digeneans including humans, domestic animals, and wildlife, via horizontal transmission. Despite the increasing interest in this group of bacteria and their role as pathogens in domestic animals, wildlife and humans, the fundamental biology of these bacteria remains poorly known. The present study quantified the abundance of *Neorickettsia* within all stages of the life cycle of a digenean, *Plagiorchis elegans*. *Lymnaea stagnalis* snails were collected from a single pond in Towner County, North Dakota and screened for the presence of digenean cercariae. Cercariae were identified to species by sequencing of the 28S rRNA gene. *Neorickettsia* infections were initially detected using real-time PCR targeting a 152-bp portion of the 3' end of the heat shock protein coding gene, GroEL. A total of 3 *L. stagnalis* were found to shed *P. elegans* cercariae infected with *Neorickettsia*. The three snails were used to initiate three separate laboratory life cycles to obtain all digenean life cycle stages for bacterial quantification. A quantitative real time PCR assay targeting the GroEL gene was developed to enumerate *Neorickettsia* sp. within individuals at all stages of the digenean life cycle. The number of bacteria significantly increased throughout all stages of the digenean life cycle, from eggs to adults. The two largest increases in number of bacteriae occurred from eggs to cercariae and from 6 day metacercariae to 48 hour juvenile worms. This is the first study to quantify *Neorickettsia* within life cycle stages of a digenean. This study was supported by an NIH grant R15AI092622.

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LAMP: POINT OF CARE DIAGNOSIS FOR MULTIPLE SCHISTOSOME PARASITES

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Schistosomes are easily transmitted and multiply considerably so if control strategies based on targeted mass drug administration (MDA) are to succeed it is essential to have a simple to operate sensitive and accurate test. As the control programs operating become more and more effective in reducing the parasite burden in the individual, the issue of diagnostic sensitivity will become more critical in the assessment of program effectiveness. We have demonstrated that species-specific DNA can be detected in human urine by PCR when some specimens are apparently egg negative. This method is effective in detecting and amplifying DNA from urine residue on Whatman No. 3 filter paper that is dried after filtration and can be stored for several months without freezing and easy to transport. In the current study done in a low to moderate transmission area in Ghana, we assessed the efficacy of detection of either or both *Schistosoma mansoni* and *S. haematobium* specific DNA from 86 urine residues both by PCR and loop mediated

isothermal amplification (LAMP). We also compared the DNA extraction techniques by standard extraction kit and field usable LAMP PURE kit and have evaluated these procedures on species-specific DNA detection. With *S. haematobium* all three methods showed similar sensitivity and specificity when compared with PCR amplification (100%). For *S. mansoni* sensitivity was highest for LAMP amplification (100%) than PCR and LAMP PURE (99% and 94%). The LAMP PURE extraction produced false negatives, which require further investigation for this field usable extraction kit. Overall high positive and negative predictive values (90% - 100%) for both species were indicative of a highly robust approach. The same pattern was observed when stratified for sex specific analysis. LAMP approach is close to point of care use and more sensitive than detection of parasite eggs in urine or stool. Our approach with LAMP can be an effective means to detect low intensity infection and would enhance the effectiveness of surveillance and MDA control programs of schistosomiasis.

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ABSENCE OF *WOLBACHIA* IN SEAL HEART WORM (*ACANTHOCHEILONEMA SPIROCAUDA*) WITH EVIDENCE OF LATERAL GENE TRANSFER

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The symbiotic relationship of *Wolbachia* was first observed in insects, and has since been established in helminthes. Specifically, *Wolbachia* is known to be a bacterial endosymbiont of many parasitic filarial nematodes. This bacterium is believed to provide metabolic or possibly developmental assistance to the parasite, although the details of the relationship have yet to be fully elucidated. Furthermore, the presence of Wolbachia is inconsistent over the phylogeny of filarial nematodes, with notable species lacking the endosymbiont such as *Loa loa*. Additionally, all tested members of filarial worms of the genus *Acanthocheilonema,* such as *Acanthocheilonema viteae,* have been shown to lack *Wolbachia*. In this study we present molecular evidence against the presence of *Wolbachia* in seal heartworm (*Acanthocheilonema spirocauda*) a filarial parasite primarily infecting phocid seals. We also present sequence data that supports lateral gene transfer between *Wolbachia* and *A. spirocauda* and *A. viteae,* suggesting the presence of a symbiotic relationship between *Acanthocheilonema* and *Wolbachia* in the past.

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CHARACTERIZATION OF APICOPLAST AND MITOCHONDRIAL GENOMES OF *CYCLOSPORA CAYETANENSIS*

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To improve understanding of the basic biology of *Cyclospora* spp. and development of molecular diagnostic tools and therapeutics, the complete apicoplast and mitochondrial genomes of *C. cayetanensis* were sequenced using 454 and Illumina technologies. They were 34,155 and 6,229 bp in size and coded for 65 and 5 genes, respectively. Comparative genomic analysis showed high similarities between *C. cayetanensis* and *Eimeria tenella* in apicoplast and mitochondrial genomes; they had 85.6% and 90.4% nucleotide sequence similarities, respectively, and complete synteny in gene organization. Like in other coccidia, both genomes of *C. cayetanensis* were transcribed bi-directionally, and the apicoplast genome had the complete machinery for protein biosynthesis and contained two inverted repeats that differed slightly in lsurRNA gene sequences. In-frame TGA codon was presented in both the apicoplast (20) mitochondrial (1) genomes. Phylogenetic analysis of the genomic sequences confirmed the genetic

similarities between cecum-infecting avian *Eimeria* spp. and *C. cayetanensis*. The availability of sequence data of the complete apicoplast and mitochondrial genomes could facilitate studies of *C. cayetanensis* biology and development of advanced molecular tools for investigations of cyclosporiasis outbreaks.

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TRANSCRIPTOME CHARACTERIZATION OF *S. MANSONI* INFECTED MICE: NOVEL INSIGHTS TO PARASITE INDUCED HOST IMMUNE RESPONSE

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Schistosomiasis is a chronic and debilitating disease of substantial medical importance, contributing to 200 million cases in the tropics. The causative agents of schistosomiasis are trematode parasites of the genus *Schistosoma,* the species *S. mansoni* being the most widespread. Adult *S. mansoni* parasites reside in mesenteric veins, where they lay hundreds of eggs per day. These eggs become lodged in host liver, provoking granulomatous reactions and portal hypertension. In fact, much of the pathology of schistosomiasis is accredited to the host granulomatous response induced by eggs of the parasite, which ultimately leads to obstruction of blood flow, increases portal blood pressure, and development of portal-systemic venous shunts. Identification of such host immune responses provides insights to host-parasite interplay, at the cellular level. Microarray based techniques have been used to identify differential gene expression in *S. mansoni* infected hosts. Next Generation Sequencing technologies now provide in-depth characterization of transcriptomes. We employed Next Generation RNAseq (Illumina HiSeq) to deep sequence the liver transcriptome of infected Balb/cj mice (2 control; 2 mildly infected; 2 highly infected) to identify novel transcripts, corresponding to *S. mansoni* infection. Our sequencing effort produced ~200 million reads which we de novo assembled producing 198859 putative genes. Thereafter, we analyzed differential expression, comparing the liver transcriptomes of infected and uninfected mice and mice infected at different intensities. Genes associated with metabolism, immunity and inflammatory responses were differentially expressed in infected mice. In addition, we observed significant differences in gene expression based on infection level. Our findings provide a better understanding of the pathology and host immune repertoire involved in response to *S. mansoni* infections.

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TRANSCRIPTOMES ILLUMINATE MYXOZOAN EVOLUTION

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Owing to extreme morphological degeneracy and resistance to culturing, the Myxozoa, a group of oligocellular, obligate endoparasites of poikilothermic vertebrates such as fish and frogs and vermiform invertebrates such as oligochaetes, has long been poorly understood in an evolutionary context. Recent genomic studies have confirmed their cnidarian affinity, sister to the Medusozoa, a clade that includes true jellyfish, box jellies, hydras, and other medusa-formers. Transcriptomic sequencing (known also as RNA-Seq) enables unprecedented insight into the expressed genetic underpinnings of the Myxozoa, including intercellular development, extracellular matrix construction, and defense against host-derived immunoresponse. This increasingly popular sequencing tool was implemented on *Myxobolus pendula*, a cyst-forming parasite of the gill arch of the common creek chub *Semotilus atromaculatus*. Several transcriptomic libraries were prepared from distinct stages of cyst formation, including early stage and fully mature cysts. Polyadenylated sequencing captured hundreds of thousands of mature transcripts, a proportion of which was identified as host-derived and decoupled from parasite-derived sequences through an *in silico* hybridization pipeline. The final myxozoan data set allowed us to explore aforementioned host-parasite interaction, sporogenesis, and other elements comprising myxozoan biology. We also characterized structural and venomic proteins that are canonical nematocyst elements, thereby further contextualizing the evolution of the Myxozoa within the phylum Cnidaria. The workflow constructed for *M. pendula* of transcriptomic sequencing, *in silico* identification, and phylogenetic comparison acts as a foundation for future study of the genetic evolution of this bizarre group of parasites.

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IMMUNOBIOLOGY OF *ECHINOCOCCUS GRANULOSUS* IN THE DEFINITIVE HOST

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Echinococcus granulosus is the causative agent of hydatidosis, which is a major economic and public health importance worldwide. The adult parasites infect dogs and other canines, whereas herbivorous and omnivorous animals serve as an intermediate host. Human beings may also accidently harbor the infection due to close contact with infected dogs. In man and other intermediate hosts the larvae form hydatid cyst and the conditions is referred to as hydatidosis. Most of the available literatures are in respect to the larval stages of the parasites in the intermediate host but the adult parasite and the responses of the definitive host remained somewhat neglected. The present investigation concerns the immunobiology of the adult parasite in the intestine of the definitive host dogs. After isolations of the protoscolices from the infected organs of Indian water buffaloes, the soluble protein antigens were isolated and purified in order to investigate the cellular and humoral immune response of dog. A number of biochemical and immunological techniques including affinity chromatography, SDS-PAGE, western blotting, ELISA and immunohistochemistry have been used to dissect the immunological responses of dogs once the parasite lodge in the intestine of canines. The immunogenicity of the identified antigens of the protoscolices has been investigated using various immunoenhancers to determine the role of adjuvants in the immunoprotective strategies of the definitive hosts. Details of the results of the investigation will be presented and discussed during the presentation.

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USING INTEGRATIVE TAXONOMY TO INVESTIGATE CRYPSIS WITHIN THE ECHINOSTOME TREMATODES

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As more cryptic helminths are being recognized, stronger efforts are needed to understand their biology especially to elucidate the evolutionary processes underlying their speciation. Some primarily genetic studies have suggested that the echinostome trematode group includes several complexes of cryptic species that can co-occur within the same definitive host. This in itself is intriguing given that one primary way parasites may speciate is via isolation and specialization for a particular host species. In these prior studies, the degree of crypsis was not well established as detailed morphological analysis of the adult and larval stages was not completed. We used integrative taxonomy (morphology, genetics, and intermediate and definitive host specificity) to examine the diversity of echinostomes present in the Lake Winnipeg watershed. Larval echinostomes were collected from freshwater snails at four different sites, while adults were obtained from mammals (muskrats, otters, and minks) via local fur trappers. Clustering analysis was performed on 29 adult characters to determine if there were any morphological differences within and amongst definitive host species, and to identify the most informative characters for morphological species discrimination. From the same set of specimens, the 28S ribosomal RNA was sequenced to obtain a molecular identification. We will discuss the concordance between these three pieces of evidence to estimate echinostome species diversity in both intermediate and definitive hosts. This study helps illuminate how much crypsis occurs within the echinostome group, informs speciation hypotheses, and aids in accurate identification of a ubiquitous wildlife parasite.

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INVASION GENETICS OF THE GLOBALLY INVASIVE SNAIL, *PHYSELLA ACUTA* (DRAPARNAUD 1805) AND ITS POTENTIAL AS AN INTERMEDIATE HOST TO LARVAL TREMATODES

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Invasive snails can dramatically affect ecosystems due in part to the trematodes comminutes they harbor. *Physella acuta* is a globally invasive snail, native to North America where it is a common host to a variety of trematodes. Prior to this study global genetic diversity and host-parasite relationships were unknown. In the old world *P. acuta* is common but its role as an intermediate host is unclear; trematode survey data suggests the maintenance of life cycles within Europe but possibly not Africa or Asia. Does time since invasion and genetic diversity of invasive populations explain the heterogeneity of trematode infections across geography? We investigated the invasion genetics of *P. acuta* across multiple temporal and spatial scales. We used a molecular population genetic approach to 1) characterize global population genetic structure, 2) identify potential founding populations, 3) estimate between population migration rates and 4) reconstruct demographic histories of global populations over a 10-year period. Genetic structure and diversity are dissimilar between native and invasive snail populations. Within the invasive range we find highly structured and genetically homogenized subpopulations, with low between population migration suggesting that founding events were independent and relatively recent. Further, historical demographic analyses support that founding populations invaded Europe over 150 years prior to Africa. These results may explain the discrepancies in trematode survey data between the two regions, and provide insight into the amount of genetic diversity and time invasive snail populations require to establish trematode assemblages. Suggesting that with time parasite spillback may become more common and *P. acuta* may become an important intermediate host across its invasive range; potentially impacting the epidemiology of snail transmitted disease around the globe. These findings are discussed within the context of the dermatitis producing avian schistosome, *Trichobilharzia querquedulae* (*Physella* transmitted), which was recently reported as globally distributed. Results from this study, in conjunction with trematode surveys of *P. acuta* and other invasive snails (*Potamopyrgus, Bithynia*), allows us to make predictions about the future distribution of *Physella* mediated cercarial dermatitis and the frequency of outbreaks.

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TRICHOBILHARZIA IN THE NEW WORLD: ARGENTINIAN SPECIES OFFER A FIRST GLIMPSE OF SPECIES DIVERSITY ACROSS HOSTS AND THE AMERICAN CONTINENTS

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The genus *Trichobilharzia*, commonly responsible for cercarial dermatitis, is globally distributed. But until recently, little was known about their species diversity in South America. This poses an interesting question, since some species of North American ducks are known to migrate to South America (and vice versa), and it is not known if South America duck species host distinct species of *Trichobilharzia*, or if they harbor the same species as found in North America, or both. Eleven species of indigenous South American ducks from northern Argentina were examined for schistosomes over the last two years. Two lineages of *Trichobilharzia* were found, one from one species of diving ducks and the other from three species of dabbling ducks, both endemic to South America. The species from diving ducks is distinct from dabbling ducks, but similar to the physid-transmitted North American species *T. physellae,* also from diving ducks. Similarly, the schistosome from South American dabbling ducks is distinct from, yet most similar to, the physid-transmitted species *T. querquedulae* from North American dabblers. This pattern reinforces the finding that at least within Clade Q of *Trichobilharzia*, one species group appears to prefer diving ducks (*Netta, Aythya, Bucephala*) and another prefers dabbling ducks (*Anas*), a trend also seen in

flyways along the Eastern Hemisphere. This suggests that Clade Q has diversified into two host groups that are separated both by their descent and by their habitat use preferences. The global distribution of both groups of schistosomes has been favored by their use of now widely distributed snail host families, Lymnaeidae (*Radix, Stagnicola*) and in Physidae (*Physa*). Diving duck- or dabbler-specific schistosomes have been spread across two continents by virtue of their use of definitive hosts that are inherently migratory, and because their required snail host species are also widely distributed, yet we find that these lineages have undergone diversification between the two continents. This is explained in part by the particular host ecologies (and distributions) most frequently encountered by the schistosome, as well as the fact that the duck host that travels the farthest may mix with more local populations infrequently.

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PRELIMINARY STUDY ON THE ROLE OF FISH METAZOAN PARASITES ON THE FOOD WEB OF CELESTúN COASTAL LAGOON, YUCATáN, MEXICO

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We investigated the metazoan parasites of 22 fish species, 4 crabs, 3 snails and 4 bird species collected between 1996 and 2014 from Celestún coastal lagoon to determine the role of metazoan parasites linking host species of different thropic levels and the similarity of the parasite community of sympatric fish. A checklist was prepared including all available records (1996-2014) of parasites of marine, brackish water and freshwater fishes using Celestún coastal lagoon as permanent habitat or as shelter, feeding or reproduction area. All of these data were included in a presence/absence database and used to determine similarity via Jaccard's index. The results indicate the presence of 62 metazoan parasites. The number of metazoan parasite species found in the fishes from the Celestún lagoon is apparently the highest reported worldwide for a tropical coastal lagoon. The parasites included 12 species of adult digeneans, 27 in the metacercarial stage, 6 monogeneans, 3 metacestodes, 2 acanthocephalans, 9 nematodes, 2 crustaceans and 1 annelid. Thirty-nine species were autogenic and 23 allogenic. The overall similarity among all of the fish species with respect to the metazoan parasites they share was low (0.08 ± 0.12), with few similarity values above 0.4 being obtained. This low similarity was due primarily to the presence of suites of parasites exclusive to specific species of fish. The autogenic component of the parasite fauna (39 species) dominated the allogenic component (23 species). Thirteen of the parasite species identified from fishes were found infecting either, the snails, crabs or birds examined. The most likely explanation for the large number of fish parasites found at Celestún is the good environmental condition of the lagoon, which allows the completion of parasite life cycles and free circulation of euryhaline fishes from the marine environment, thus bringing marine parasites into the lagoon.

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REMEMBERING PAST THREATS: EFFECTS OF PREDATOR EXPOSURE ON HOST ANTI-PARASITE BEHAVIOR

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Anti-parasite behaviors are an important first line of defense for hosts. These include avoidance, evasion, and removal of infectious stages, such as those of trematodes. Previous studies have shown that larval amphibians exhibit highly effective anti-parasite behaviors, including increased activity and twisting movements that reduce the prevalence and intensity of trematode infection. Because these defensive behaviors are also likely to attract the attention of various predators, hosts may not display them if they perceive a threat of predation. Many animals, including tadpoles, reduce their activity in the presence of predators. In the simultaneous presence of both natural enemies, hosts often choose to engage in anti-predator versus anti-parasite behaviors if these present a conflict. However, it is not clear whether there is a temporal component to such choices, i.e. if hosts favor responses to the immediate threat at hand and disregard previous ones. We examined the behavior of larval toads in the absence and presence of

echinostomatid cercariae, comparing tadpoles that had been previously exposed to chemical cues signifying the presence of a predator to those which had not. Previous predator exposure had a significant negative effect on overall tadpole activity level, with a marginally insignificant activity increase in the presence of cercariae. However, there was a significant interaction of these two factors as larval toads not previously exposed to predator cues reacted strongly to cercariae whereas those subjected to predation threat displayed relatively little activity in the absence or presence of parasites. Our results indicate that hosts may exhibit stronger responses to predators than parasites in certain circumstances, even if the threat of predation is not immediate.

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POPULATION DYNAMICS AND ECOLOGY OF FRESHWATER GASTROPODS OF PUBLIC HEALTH IMPORTANCE IN AGULU LAKE NIGERIA

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Agulu Lake is among 366 geo-referenced endemic foci for schistosomiasis in Nigeria. Freshwater gastropods serve as intermediate hosts for *Schistosoma haematobium* responsible for urinary schistosomiasis but there is a dearth of published information on gastropods of Agulu Lake. Gastropod abundance was determined by sampling eight-20m^2 quadrats on Agulu Lake shorelines from November 2012 to October 2013 using scoop net sampling and hand picking techniques, supplemented by a 20-minute manual search on each quadrat and over aquatic plants and suspended materials. Monthly collections of water samples from each quadrat were analyzed for dissolved oxygen and calcium ion concentrations while water temperature, transparency, depth, and pH were measured in-situ with standard procedures. Samples of aquatic plant that served as gastropod habitats were identified in our Herbarium. Annual abundance of gastropods was 6866, comprising five species identified with malacological keys as *Bulinus globosus* 1957(28.5%), *Bulinus truncatus* 1832(26.7%), *Bulinus forskalii* 964(14%), *Lymnaea natalensis* 2089(30.4%) and *Melanoides tuberculata* 24(0.4%). Mean annual density of gastropod/m^2 was 4.29±2.44 with significant difference (P<.05) between dry season mean (5.4±13.28) and rainy season mean density (3.77±2.63). *Bulinus* species are known worldwide as intermediate hosts for *S. haematobium*. Mean monthly water parameters temperature (27.84±0.16^{o}C), transparency (22.48±4.32cm), depth (27.03±3.57cm), dissolved oxygen (6.2±0.2mg/l), Ca^{++} (5.705±0.805mg/l) and pH (7.785±0.685). There was strong and positive relationship between gastropod density and Ca^{++} (R^2=0.7861); also strong and negative with water transparency (R^2=0.9036). Other parameters showed unremarkable influence on gastropod abundance. Eight identified aquatic plant species were associated with gastropod habitats while unabated human-water-contact activities in Agulu Lake could positively influence gastropod infectivity and epidemiology of urinary schistosomiasis in the area.

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MALARIA PARASITEMIA AND PREVALENCE IN THE TUFTED TITMOUSE (*BAEOLOPHUS BICOLOR*)

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Haemosporidians, including the avian malaria parasites, are an incredibly diverse group of blood parasites that infect terrestrial vertebrates on every continent except for Antarctica. One remarkable characteristic of avian malaria parasites is their complicated life cycle which requires very specific dipteran insects to transmit different parasite genera. This intricacy generates numerous host-parasite interactions that produce variability in parasite prevalence (parasite presence) and parasitemia (infection intensity). These host-parasite interactions include parasite lineage virulence, host health, and other characteristics of the bird host. The extent of the parasite's detriment to the avian host is also irregular and can range from virtually inconsequential to lethal. Among the suitable hosts for this parasite is the Tufted Titmouse (*Baeolophus bicolor*) which belongs to the order of birds with the greatest assortment and prevalence of malaria parasites. Parasites from the genera *Plasmodium* and *Parahaemoproteus* are

detected and quantified from bird blood using microscopy and amplification of the cytochrome *b* (cyt *b*) gene. Several different lineages of malaria parasites have been found in Tufted Titmice, which may include both specialists and generalists. Prevalence in this host species is relatively high based on polymerase chain reaction (PCR) amplification of the cyt *b* gene. Data collected by microscopy indicate that circulating parasite levels are low. Avian malaria prevalence is independent of host sex, age, and body condition. Infection in this bird as observed in a natural population provides details on host susceptibility that is applicable to the understanding of malaria parasites in other avian hosts collectively.

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PARASITE ABUNDANCE ACROSS AN URBAN GRADIENT: ADDRESSING PLAUSIBLE MECHANISMS

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Anthropogenic stressors such as pollution, climate change, and habitat alteration represent a substantial and increasing threat to organisms. However, it is not always clear how anthropogenic stressors might interact with natural stressors such as parasites. Theoretical predictions and empirical evidence suggest that environmental stress may exacerbate or moderate parasitic disease through direct or indirect mechanisms. A stressor might be associated with greater parasite abundance if it (1) increases the susceptibility of hosts to parasites, (2) decreases host density leading to greater parasite load per host, or (3) positively influences density of other hosts in the parasite lifecycle. A stressor might be associated with lower parasite abundance if (1) parasites are more susceptible to the stressor than hosts, (2) infected hosts suffer differentially high mortality, or if the stressor (3) increases host density leading to reduced parasite load per host, or (4) negatively influences density of other hosts in the parasite lifecycle. Two species of Lepomid fishes (*Lepomis macrochirus* and *L. auritus*) were collected in the Bull and Upatoi Creeks watershed of Muskogee County, Georgia across two seasons in eight creeks spanning an urban gradient. Fish (n=428) were measured for standard length, dissected, and their trematodes and cestodes identified to species. We found higher abundance of metacercariae of the dominant trematode, *Posthodiplostomum minimum*, in host fishes near the urban center. The observed pattern may be driven by any of the three hypotheses outlined above. Chronic stress associated with urbanization may lower immune response and increase susceptibility to disease. Alternatively, positive influences of urbanization on first intermediate or final hosts of *P. minimum* may be driving the observed pattern. While we cannot rule out these two hypotheses, we present evidence that the observed pattern is driven, at least in part, by changes in density of host fishes. If host density is reduced by environmental stressors, then the same number of infective stages of parasites would be divided among fewer host fish, leading to greater parasite load per host. Using generalized linear mixed models with creek as a random effect, we found host density to be a significant predictor of parasite abundance. We conclude that changes in density of host fishes are one mechanism behind the positive association between urbanization and the abundance of *P. minimum* in Lepomid fishes.

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THE EFFECT OF A VIRULENT TAPEWORM ON PARASITE COMMUNITY ASSEMBLY IS GENOTYPE DEPENDENT

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Many experiments indicate that parasite species can interact, positively or negatively, within their hosts. However, it remains unclear whether interactions between parasite species strongly shape the assembly of parasite communities. We experimentally infected three-spined sticklebacks with a virulent tapeworm (*Schistocephalus solidus*), before placing them into cages in a lake to expose them to the natural parasite community. The tapeworms came from two populations and were characterized by either high or low growth in sticklebacks. After approximately three months in the cages, sticklebacks were dissected and their parasites recorded. Changes in the abundance of parasite species, relative to that in control fish (no *S.*

solidus), occurred mainly in fish infected with the high-growth *S. solidus*. The abundance of one eye fluke species increased significantly, whereas that of a second decreased, suggesting that elevated *S. solidus* growth, and the presumed immune manipulation necessary to achieve it, does not result in a generally higher parasite burden. Additional experimental infections confirmed that the increased susceptibility to a diplostomatid eye fluke has a physiological basis. Fish kept in cages separated by a few meters had significantly different parasite communities, suggesting fine-scale heterogeneity in parasite exposure. While interspecific interactions clearly occur, their apparent genotype-dependence and their small magnitude relative to the effect of spatial heterogeneity, suggests that they may often be of secondary importance in structuring parasite communities.

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THE TROPHIC VACUUM AND THE EVOLUTION OF COMPLEX LIFE CYCLES IN TROPHICALLY TRANSMITTED HELMINTHS

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Parasitic worms frequently have complex life cycles in which they are transmitted trophically between two or more successive hosts. Reproduction often takes place in high trophic-level (TL) vertebrates, where parasites can grow to large sizes with high fecundity. Direct infection of high TL hosts, while advantageous, may be unachievable for parasites constrained to be transmitted trophically, simply because helminth propagules are unlikely to be ingested by large predators. We refer to the lack of niche overlap between propagule and definitive host as a 'trophic vacuum', and suggest that it may explain the evolutionary origin and/or maintenance of intermediate hosts, which overcome this transmission barrier. We find that nematodes infecting high TL definitive hosts tend to have more successive hosts in their life cycles. This relationship was modest, though, driven mainly by the minimum TL of hosts, suggesting that the shortest trophic chains leading to a host define the boundaries of the transmission vacuum. We suggest that widespread omnivory as well as parasite adaptations to increase transmission probably reduce, but do not eliminate, the barriers to the transmission of helminths through the food web.

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GENOTYPIC VARIATION IN LIFE HISTORY RESPONSE TO INFECTION AND ITS EFFECTS ON PARASITE FITNESS

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Disease outcome is determined by an interaction among pathogen genotype, host genotype, and the environment. Together, these variables drive host-parasite co-evolution and disease risk. We investigated how unique host genotypes influence parasite reproduction, and presumably fitness, in the vector host of an important pathogen of humans, *Schistosoma mansoni*. We infected 5 inbred lines of *Biomphalaria glabrata* with 2 doses of parasites and followed their growth, reproductive output and mortality throughout the course of infection. We also monitored parasite fitness by measuring weekly cercarial output of individual snails, and length of the pre-patent and patent periods. Although we found no difference in the ability of the genotypes to become infected, we found that the 5 genotypes of snails varied in their response to infection. They differed in their defense against parasite induced castration (reproductive death), namely the ability to extend the pre-patent period and thus increase egg output before complete castration. The success of this strategy was influenced by parasite dose. None of the genotypes showed fecundity compensation in which infected individuals reproduce more than unexposed controls. Parasite reproduction within snails differed among lines. Some lines showed enhanced early growth after infection (gigantism) that led to an increase in parasite production, but this effect was not consistent among all genotypes and decreased with increasing parasite dose. Upon infection, the lines differed in their relative allocation of energy to reproduction or growth indicating that some genotypes

were better able to defend against castration and divert resources into energy while others were directed toward growth. The former showed increased host fitness and decreased parasite reproductive rate, and the latter showed decreased host fitness and an increase in parasite reproductive rate. The patent period was strongly influenced by snail survival which was dose and genotype dependent. The genotype with the lowest cercarial production rate also displayed highest survivorship especially at high doses; however, there was no overall correlation among production rate and snail survivorship. Together, these results further define the intricacies of snail schistosome compatibility. Host genotype played a strong role in determining parasite reproductive rate, which is a critical parameter in determining infection risk to humans and is a driving force for parasite evolution.

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ENVIRONMENTAL AND ANTHROPOGENIC DRIVERS AFFECTING THE GEOGRAPHICAL DISTRIBUTION OF THE HELMINTH PARASITES OF FLATFISHES IN THE SOUTHERN GULF OF MEXICO

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Understanding the environmental factors influencing the geographical distribution of marine parasitic species is fundamental to determining the circumstances under which they can produce disease. The aim of this study was to determine whether physicochemical variables, polycyclic aromatic hydrocarbons (PAHs) or sewage discharge affect the probability of occurrence of the larval cestode *Oncomegas wageneri*, and the adult acanthocephalan *Acanthocephaloides plagiusae* infecting the flatfishes *Syacium gunteri* (n = 165), *Cyclopsetta chittendeni* (n = 240), *C. spilopterus* (n =80), *Syacium papillosum* (n = 16), *Bhotus robinsi* (n = 37) and *Symphurus plagiusa* (n = 158)) from 162 sampling sites in the southern Gulf of Mexico. We used boosted generalised additive models (boosted GAM) and MaxEnt to examine potential statistical relationships between the environmental variables and the probability of occurrence of these parasites. In all, 3283 individual helminths (3162 *O. wageneri* and 121 *A. plagiusae*) were collected. *Oncomegas wageneri* occurred in 34 out of the 162 (21%) sampling sites and infected 104 out of 563 flatfishes of the species *S. gunteri*, *C. chittendeni* and *S. plagiusa*. *Acanthocephaloides plagiusae* was present in 14 out of the 162 (9%) sampling sites, infecting 35 out of 563 of the same three flatfish species mentioned above. The boosted GAM accurately predicted the probability of occurrence of *O. wageneri* and *A. plagiusae* in the study area. By contrast, poor probabilities of occurrence were obtained with the MaxEnt models. For both parasite species, the variables with the highest percentage of appearance in the models (a proxy for the explained variability) were the high molecular weight PAHs (PAHH, 95%), followed by a combination of nutrients, spatial variables and low molecular weight PAHs (PAHL) (5%). The PAHH contribution to variability was explained by the fact that that these compounds, together with N and P, are carried by rivers discharging into the ocean enhancing growth of hydrocarbonoclastic bacteria, productivity and the number of intermediate hosts. Overall, the results indicated that PAHH apparently affect the probability of occurrence of these helminth parasites.

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DIVERSITY AND DISTRIBUTION OF HAEMOSPORIDIAN PARASITES IN THE NORTHERN CARDINAL (*CARDINALIS CARDINALIS*)

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Avian malaria parasites provide a model system for understanding ecological and evolutionary host-parasite interactions. The diversity and distribution of these parasites is largely unknown, and we provide the first range-wide assessment of avian malaria in a continentally distributed host, the Northern Cardinal (Cardinalis cardinalis). We specifically address the following three questions: 1) what is the prevalence of avian malaria parasites in the Northern Cardinal and does it vary between host subspecies populations? 2) What is the lineage diversity and biogeographic distribution of these parasites? 3) Is there evidence of

parasite lineage structuring with respect to host subspecies? Based on molecular techniques, we show geographical differences in prevalence and lineage diversity between host subspecies and identify several novel lineages. We use phylogenetic reconstruction to show where these lineages fit into the expanding evolutionary tree of known avian malaria lineages. All except one subspecies of Northern Cardinal are highly parasitized by a wide diversity of Plasmodium and Parahaemoproteus. Compared to published studies that used microscopy to determine prevalence in this host, we find a much higher number of infected individuals (66.3% versus 45% or less). Consistent with previous studies, Parahaemoproteus from the Northern Cardinal was found to be highly host specific and geographically structured, whereas Plasmodium was less host specific and spread across a large geographic range.

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PARASITOLOGICAL SURVEY OF PUMPKINSEED (*LEPOMIS GIBBOSUS* (LINNAEUS, 1758)) IN ZAPORIZHZHYA REGION (UKRAINE)

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Pumpkinseed, *Lepomis gibbosus* (Centrarchidae, Perciformes) was brought from North America to Western Europe at the end of 19th century as an ornamental fish and probably accidentally invaded small and later larger water bodies of Europe and Asia. There is an assumption, that *L. gibbosus* was a favored competitor to native fish species and can cause damage to fisheries by eating away eggs, larvae and fry of economically important aboriginal species. *Lepomis gibbosus* reached Ukrainian waters through a cascade of the Dnieper reservoirs and has become a common fish in lower parts of rivers of the Black Sea basin. In Kakhovske reservoir *L.gibbosus* was registered in 2000. While the parasitic fauna of *L. gibbosus* has been studied in many European locations, there are no published reports on any parasitological research on parasites of this alien species in Ukrainian waters. Two species of monogeneans were found in the Romanian part of Danube. Fourteen parasite species were reported in Polish waters in 1994. Four species of monogeneans were reported from Italy in 2003. Four other species of monogeneans were also reported In 2011 in Czech Republic's in Danube waters in 2011. In the same year, 2011, all specimens of *L. gibbosus* were infected with monogenean species in southern England. Present parasitological survey of *L. gibbosus* was carried out using the methods developed by Bykhovskaya-Pavlovskaya, and included studying of all organs of fresh-caught or refrigerated fish under stereomicroscope. Since spring 2013 to spring 2015 we studied 42 mature specimens of *L. gibbosus*. Only two specimens were infected with nematode larvae, found in mesentery. These results show still poor infection of *L. gibbosus* by parasites compared to geographically close locations (Romanian and Czech Republic waters). These results can be explained by the "parasite release hypothesis" of Zhang.

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WRECKING THE CURVE: THE INFLUENCE OF TREMATODE INFECTION ON THE FUNCTIONAL RESPONSE OF 2 PREDATORS

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The representation of parasites in food webs, in terms of both trophic linkages and biomass, suggests that they have a tremendous potential for influencing ecosystem dynamics. Although the influence of parasitism on prey behavior has been examined extensively, the consequences of parasitism are less well-known for predators. In the present investigation, the influence of trematode infection on the functional response of predators was examined in 2 model systems: odonate naiads feeding on *Daphnia magna* and bluegill sunfish (*Lepomis macrochirus*) feeding on oligochaetes (*Eisenia fetida*). Ten predators were fed a range of prey abundances to determine their functional response, after which 5 randomly selected predators were exposed to trematode cercariae. Odonates were exposed to cercariae of *Haematoloechus floedae*, and bluegills were exposed to cercariae of *Posthodiplostomum minimum*. The feeding trials were repeated for the same range of prey abundances. Both experiments were repeated with a second set of predators. Nonlinear least-squares regression was utilized to fit a type II functional response model to the

data, and an indicator variable approach was used to estimate between-trial differences in model parameters. Handling time was significantly reduced for odonates exposed to *H. floedae*, indicating more time spent feeding, while there was no significant difference in the functional response of exposed und unexposed bluegill. The increased feeding time of the exposed odonates reflects a metabolic cost that likely is a result of the encapsulation response produced by the odonates.

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PARASITOLOGICAL SURVEY OF SCALED QUAIL FROM WEST TEXAS

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With the decline of quail in Texas, there is an interest in quail helminths and their impacts on quail populations. Little research has been conducted in the last few decades on the helminth communities of the scaled quail (*Callipepla squamata*). Our objectives are to (1) document the helminth species infecting scaled quail in west Texas, (2) determine helminth prevalence, intensity, and abundance, and (3) assess whether infections are influenced by host age, host sex, host weight, precipitation, and season of collection. Twenty-eight and 95 scaled quail were donated during the 2012–2013 and 2013–2014 hunting seasons, respectively. Fourteen quail were also trapped in August and October 2012 and 20 in August and October 2013. Seven helminth species were found; of these, three species (all nematodes) occurred in ≥ 25% prevalence: the cecal worm *Aulonocephalus pennula* (98%), the eye worm *Oxyspirura petrowi* (52%), and the gizzard worm *Procyrnea pileata* (25%). In addition, *A. pennula* numerically dominated, accounting for 94% of the total worms found (9,245). Prevalence of *O. petrowi* was influenced by host age and season, whereas host sex was not a factor influencing prevalence for each of the three species. *Oxyspirura petrowi* abundance varied in relation to host age between seasons, whereas no differences were observed in abundance of the other species for host age, sex, or season. Additional samples will be collected during the 2014–2015 Texas quail-hunting season and additional analysis of precipitation and body weight will be conducted. Our research provides insight about helminth community structure and pattern in scaled quail and is the first survey to compare helminth infections over multiple years in west Texas.

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PREVALENCE AND DISTRIBUTION OF AMPHIBIAN PARASITES IN NORTH DAKOTA

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The diversity and ecology of parasites is an integral aspect of all biotic communities. Knowledge of the diversity, distribution, and host associations of parasites in North Dakota amphibians is very limited. In this project, we report on the first statewide survey for amphibian parasites in North Dakota. Our objective are to estimate geographic distribution and prevalence of helminth parasites infecting amphibians across North Dakota, and to test for patterns related to general ecological context. We sampled broadly across the state, including all major ecoregions and land use categories. Specimens were processed in the laboratory for morphological and molecular analyses. For mature helminths, morphology was studied on permanent (cestodes, digeneans) or temporary (nematodes) mounts. For immature helminths, DNA sequences of nuclear ribosomal genes were obtained to aid in species differentiation. In 2013 and 2014, 707 amphibians were collected from 171 sample locations. Six species of amphibians were represented in the total sample, with northern leopard frogs (*Lithobates pipiens*) outnumbering, as expected, in terms of sample locations and sample size (N=402). Other amphibians included wood frogs (*Lithobates sylvaticus*) (N=109), chorus frogs (*Pseudacris maculata*) (N=106), Canadian toads (*Anaxyrus hemiophrys*) (N= 45), Great Plains toads (*Anaxyrus cognatus*) (N=29), and tiger salamanders (*Ambystoma mavortium*) (N=14). We found at least 18 species of helminths across all amphibians. The total prevalence across all amphibian species for common genera found was 20.1% for *Alaria*, 16.8% for *Echinostoma*, 13.0% for *Heamatoloechus*, and 8.2% for *Rhabdias*. Prevalence of unidentified nematodes was 8.6% and prevalence of unidentified digeneans (mostly larval stages) was 26.6% across all amphibian

species. We are continuing to identify parasites so prevalence will likely change. Upon identification of all helminths, we will test for associations between helminth occurrence and geographic range, amphibian species, and predominant land use. Results of concurrent screening of amphibians for chytrid fungus *Batrachocytrium dendrobatidis* and Ranavirus will be presented.

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PATHOGEN RISK TO BULL TROUT POPULATIONS AND REINTRODUCTION EFFORTS IN THE UPPER WILLAMETTE BASIN

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Populations of bull trout (*Salvelinus confluentus*) drastically declined in the Willamette River basin in the past century, and a coordinated recovery effort has been underway since the 1990s. One component of this effort has been a reintroduction program beginning in 1993 that included head-start rearing of early juveniles at Leaburg Hatchery in 2007–2013. High mortality (82%) occurred among the cohort collected in 2013, and the surviving fish showed a high incidence of physical deformities. Furthermore, monitoring data has indicated unexplained declines and continued low spawning abundance in the donor population. To assess factors adversely affecting early survival of bull trout in the hatchery and in the donor population, we conducted a study involving radiography, necropsy, and histology on the remaining fish from 2013, preserved mortalities from 2012 and 2013, specimens brought in directly from the donor population in 2014, and specimens reared at Leaburg Hatchery in 2014. Bull trout reared in the hatchery in 2013 and 2014 exhibited skeletal deformities such as severe kyphosis and fusion of vertebrae. Histology revealed heavy infections by metacercariae of the trematode parasite *Nanophyetus salmincola* directly associated with the lesions. In contrast, we found no infections or deformities in specimens brought directly from the spawning tributary, suggesting that deformities may have stemmed from *N. salmincola* surviving passage through the UV disinfection system in the hatchery. We are conducting an experimental infection study in 2015 to assess *N. salmincola* as the cause of elevated rates of mortality and deformity. To further assess pathogen risk to wild populations of bull trout, we conducted distribution surveys for *Juga* snails (the obligate first intermediate host of *N. salmincola*) and associated parasites and began an ongoing effort to provide surrogate fishes and bull trout incidental mortalities to the ODFW Fish Health Laboratory for examination. Our survey thus far indicates that bull trout spawning and early rearing tributaries in the basin are located in colder reaches upstream of where *Juga* snails occur, but larger bull trout and other fishes in downstream reaches may acquire relatively heavy loads of metacercariae. Infections of *N. salminicola* commonly occur without associated obvious skeletal deformities in other salmonid species in watersheds that are warmer and endemic for the infection in Oregon. It is plausible that the infection is more pathogenic to early juvenile bull trout, which have not co-evolved with the parasite. Moreover, parasites such as *N. salmincola* may contribute to higher mortality among juvenile bull trout that move downstream too early. These results hold implications for bull trout reintroduction efforts.

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SURVEY OF ENDOPARASITES INFECTING 6 *PRISTIMANTIS* SPECIES OF PERUVIAN FROG

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The helminthological record of South American anurans is summarized in surveys completed in the lowlands. These surveys account for the diversity and distribution of parasites across a wide range of anuran hosts throughout many habitats. However, to our knowledge, there is no test that accounts for the role of phylogeny and lifestyle in the distribution of parasites infecting direct developing terrestrial breeding frogs. We investigated these effects in a specialized group of frog, the direct developing and terrestrial breeding members of the Pristimantis genus. We were able to compare the effect of phylogeny and habitat to test the distribution of parasites in six species of Pristimantis and some other aquatic-

breeding species. We screened 73 individuals of six species of Pristimantis from Manu National Park, Peru. Five of these species have never before been screened for parasites and four are inhabitants of specific altitudinal ranges within the highlands of the Peruvian Andes. This is part of an ongoing mission to understand anuran host-parasite dynamics and the helminth diversity of Peru.

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COMPARED PREVALENCE OF *BAYLISASCARIS PROCYONIS* IN RACCOONS (*PROCYON LOTOR*) IN KENTUCKY

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Baylisascaris procyonis is a nematode that lives in the small intestine of its definitive host, the raccoon. Female worms produce between 115,000 and 179,000 eggs/worm/day, and many raccoons harbor multiple worms. Eggs are released in feces, and become infective in the soil in 2-4 weeks. Human infection and resulting disease has been facilitated by the expansion of raccoons into peridomestic habitats in the U.S.A. There have been approximately 20 confirmed cases of baylisascariasis, with the majority of these cases involving children. The associated mortality rate is high, and only one surviving patient has recovered without residual neurological damage. Despite the obvious relevance to public health, the prevalence of *B. procyonis* in raccoons has not been determined in Kentucky. Results of a pilot study in 2007 showed a prevalence of 28% in raccoons trapped in Warren County, Kentucky. The purpose of the present study is to determine the current prevalence of *B. procyonis* infection in raccoons in Warren County, and to determine if prevalence of raccoon roundworm infection varies between rural, suburban, and urban localities. Preliminary results, with 52 raccoons examined to date, show 14/52 raccoons (29%) positive for *B. procyonis*. Between the three localities tested, 4/10 raccoons (40%) were positive in urban locations, 4/14 raccoons (29%) were positive in suburban locations, and 6/28 raccoons (21%) were positive in rural locations. There was no significant difference found between the three localities ($p = 0.51$).

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GROSS AND HISTOPATHOLOGICAL CHANGES ASSOCIATED WITH THE EGGS, LARVAE, AND CUTICULAR REMNANTS OF *UNIONICOLA* SP. (ACARI, UNIONICOLIDAE) INFECTING *STROPHITUS CONNASAUGAENSIS* (BIVALVIA, UNIONIDAE)

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Symbiotic water mites that associate with, or infect, freshwater invertebrates comprise at least 247 nominal species assigned to 35 subgenera, 3 genera, 3 subfamilies, and 3 families (Hygrobatidae, Hygrobatinae, *Dockovida* = 2 spp.; Pionidae, Najadicolinae, *Najadicola* =1 sp.; Unionicolidae, Unionicolinae, *Unionicola* = 244 spp.). Species of *Najadicola* and *Unionicola* commonly occur in freshwater mussels (Bivalvia, Unionoida). *Najadicola ingens* has been reported from at least 30 species representing Unionidae, while only 137 species of *Unionicola* are known to occur in mussels representing Iridinidae, Hyriidae, Mycetopodidae, and Unionidae. While describing tissues of *Strophitus connasaugaensis* for a histological atlas for Unionidae, we observed larvae, nymphs, and adults crawling in the mantle cavity. Additionally, we observed eggs, larvae, nymphs, and cuticular remnants in histological sections of various tissues. Herein, we characterize the gross and histopathological changes associated with *Unionicola* sp. in the mantle, gill, and visceral mass of 25 Alabama creek mussels, *S. connasaugaensis*, collected during May 2010 through July 2012 from South Fork of Terrapin Creek, and Shoal Creek, Alabama. A preponderance (estimated mean intensity >100) of mite eggs and larvae typically infected mantle, gill, and visceral mass integument of mussels. Pathology associated with eggs (prevalence = 0.57) and larvae (prevalence = 0.39) typically consisted of localized distension of the infection site.

While a host response to these infections was indeterminate, larval mites embedded in the suprabranchial cavity were typically encapsulated by hemocytes and connective tissue fibers (prevalence = 0.89). Mite remnants (prevalence = 0.5) were observed in the mantle, gill, visceral mass integument, foot, heart, pericardial gland, intestinal lamina propria, and were typically encapsulated. We speculate that *S. connasaugaensis* clears some infections but is re-colonized by autoinfection or horizontal dispersal of mites in the stream. Noteworthy is that high-intensity infections seemingly do not markedly impact the structure of mussel tissues, suggesting that mites are relatively benign symbionts that are of little concern to mussels under normal environmental conditions.

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LOCAL SURVEY OF LARVAL DIGENETIC TREMATODES INFECTING PHYSID AND PLANORBID SNAILS WITH IMPLICATIONS FOR NATIVE AMPHIBIAN POPULATIONS IN NORTHWEST NEW JERSEY

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Digenetic trematode diversity in snail populations was assessed in Northwestern New Jersey. These parasites are characterized by complex life cycles, requiring snails for development. Consequences of trematode infection have dramatic effects upon hosts including decreased reproduction in snails, visceral pathologies, and limb deformities in larval anurans. Molluscan dependence for life cycle completion makes snails a convenient source for trematode diversity surveys. *Physid* and *Planorbid* snails were collected from five sites and examined for cercariae production. Snails collected at all sites produced cercariae, based upon morphology, representing eight digenetic trematodes families *Plagiorchidae, Echinostomatidae, Diplostomatidae, Psilostomatidae, Strigeidae, Paramphistomatidae, Schistosomatidae,* and *Spirochidae*. No significant difference in trematode diversity was observed over survey duration. One site demonstrated lower snail infection rates than the other four sites ($p<0.02$) although no infection rates varied over time. Genera associated with amphibian pathology including *Plagiorchis, Echinostoma, Echinoparyphium,* and *Ribeiroia* were observed at all sites sampled. Infection experiments with native amphibian larvae and three trematode families suggest these parasites vary in their ability to infect a host when in direct competition. Metacercariae of each species demonstrated a preference for host tissue encysting in the dermis, nephric system, or liver of infected tadpoles. *Ribeiroia* and *Echinostoma* cercariae successfully encysted in a lower amount of larval *Anaxryus americanus* than *Lithobates clamitans* suggesting tolerance to trematodes varies by amphibian species. This could impact the fitness and demography of local amphibian species using infected water bodies as a nursery. This work expands the knowledge by identifies diverse parasite/host relationships in Northwestern New Jersey and how these impact local anuran communities.

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REPELLENT ACTIVITIES OF THE METHANOLIC LEAF EXTRACTS OF *MORINGA OLEIFERA* AND *STARCHYTARPHETA INDICA* AGAINST *AEDES AEGYPTI* MOSQUITO

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Methanolic extract of *Moringa oleifera* and *Stachytarpheta indica* leaves was evaluated for repellent effect against *Aedes aegypti* mosquito. Repellent effect of the treatment was assessed at different concentrations (20, 25, 30, 35 and 40mg/ml) after 5mins, 10mins and 15mins of exposure against 45 *Aedes aegypti* adult mosquitoes in a cage. All extracts were evaluated in different cages. Percentage Repellency (PR) was determined for each extract following the procedure of WHO. All the tested extracts showed moderate to good repellent activities; however the maximum repellency potential was detected in the 40mg/ml concentration of *S. indica* while the minimum percentage repellency was detected in the 20mg/ml concentration of *M. oleifera*. The repellent activity of the extracts was performed with human volunteers and dose-response method was used to estimate the percentage protection. The results indicated that the significant effect of the treatments and the effectiveness increased with extended

exposure interval and enhanced dose rate. There was a statically significant difference between the 3 test groups (Control, *M. oleifera* and *S. indica*) as determined by a one way Analysis of Variance (ANOVA) ($F(22, 1) = 20921.216$, $P = 0.000$. Since the p-value $0.000 < 0.05$, a Turkey Post-hoc test revealed that at 95% confidence level, *S. indica* yielded a different (highest) mean value of percentage repellency from those of *M. oleifera* and the control (which also yielded different mean values). The LC_{50} value recorded for *M. oleifera* and *S. indica* are 66.0mg/ml and 18.2mg/ml respectively. The test plant extracts were screened for phytochemicals such as alkaloids, flavonoids, saponins, tannins, steroids, anthraquinones and terpenes. The findings of the present study clearly revealed that methanol extracts of *M. oleifera* and *S. indica* leaves are good repellent agents for the control of *A. aegypti*, however the efficacy depends on dose rates and the exposure interval.

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THE SYNERGISTIC LARVICIDAL ACTIVITIES OF THREE LOCAL PLANTS ON *AEDES AEGYPTI*

I.C. Mgbemena and **R.I. Okechukwu**, Public Health and Parasitology Society of Nigeria

The synergistic activity of extracts of *Lantana camara*, *Stachytarpheta indica* and *Allamanda blanchetii* against *Aedes aegypti* mosquito larvae were investigated. Ethanolic leaf extracts of these plants were tested separately and combined on *Ae. aegypti* larvae with concentration ranging from 5, 10, 20, 30 and 40mg/ml. In 72 hours bioassay experiment, mortalities were observed at the different time intervals but were highest at 40mg/ml concentration for the three plants independently, with the *L. camara* extract showing better larvicidal activity over the other plant extracts at 48 hours and 72 hours exposure. The LC_{50} of *L. camara* (6.08mg/ml), *S. indica* (8.15mg/ml) and *A. blanchetii* (6.44g/ml) indicates their ability to cause 50% larval mortality at such low concentrations. For the synergistic effects all the concentrations exhibited high mortality at 48 hours and 72 hours exposure. The 40mg/ml showed the highest larvicidal activity (100% mortality) after 48 hours exposure with the L2:A1:S1 combination. Synergistic factor (S.F.) of 1.00, 1.27 and 0.94 were obtained for *L. camara*, *S. indica* and *A. blanchetii*. Synergism was recorded for *L. camara* and *S. indica*, while antagonism was recorded for *A. blanchetii*. Phytochemical analyses showed the presence of some active compounds including flavonoids, tannins, saponins, alkaloids and cardiac glycosides which may account for their mosquitocidal effects and at same time present them as an effective replacement to chemical insecticides. Combination of plant extracts is therefore strongly recommended to serve as a better mosquitocidal agent over the use of individual plants in mosquito control programs.

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VARIATION IN CARBOHYDRATE UTILIZATION BY TRICHOMONADS OF MAN INHABITING DISTINCT ANATOMICAL NICHES

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There are three Trichomonads that infect humans; *Trichomonas vaginalis* in the urogenital tract, *Trichomonas tenax* in the oral cavity, and *Pentatrichomonas hominis* in the large intestine. *T. vaginalis* is the causative agent of trichomoniasis, the most common non-viral sexually transmitted infection world-wide, with an estimated 160 million new infections occurring annually. *P. hominis* and *T. tenax* are generally regarded as non-pathogenic commensal flora. During in vitro cultivation, all 3 species can metabolize and grow in media supplemented with either glucose or maltose as a carbon source. *T. tenax* and *T. vaginalis* have also been reported to metabolize exogenous glycogen. The carbohydrate metabolism of *P. hominis* is less well defined. We hypothesize that the different ecological / anatomical niche inhabited by each trichomonad species is reflected in the diversity of carbohydrates that can support their in vitro growth. To test this, we compared the growth of all 3 species of trichomonads in media supplemented with 9 different carbohydrates. All 3 species grow on glucose, glycogen, and galactose; however, *T. vaginalis* required 24-40 hrs of adaptation before growing in galactose. Only *P. hominis* grew in media supplemented with melibiose, sucrose or raffinose, but required a 40 hour period of adaptation to grow on the latter two sugars. None of the organisms grew on lactose or trehalose, and only *P. hominis*

showed modest growth on cellobiose. Our studies show that the species of trichomonads infecting man demonstrate differing patterns of carbohydrate utilization which may be related to the ecologic niche in which they are found. For example *T. vaginalis*, which encounters mainly glucose and glucose polymers, has rather limited carbohydrate degrading capacity. In contrast *P. hominis*, which is exposed to a wide variety of sugars in the gut, has a much broader capacity. Future studies will characterize the delayed / adaptive growth of *P. hominis* in sucrose and *T. vaginalis* in galactose, as well as the expression of the enzymes involved in carbohydrate metabolism.

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INTERACTIONS BETWEEN ANTIMALARIAL AND ANTIRETROVIRAL DRUGS

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Malaria and AIDS are two infectious diseases that are prevalent in sub-Saharan Africa due to geographic overlap. Malaria, caused by the protozoan parasite *Plasmodium*, is transmitted to humans by the female *Anopheles* mosquito. The Human Immunodeficiency Virus (HIV), which can lead to AIDS, is a retrovirus that damages the immune system by destroying CD4 T-cells. It is transmitted both parentally and sexually. Previous research in our laboratory has shown that co-infected patients in Benin City, Nigeria, taking both antiretroviral and antimalarial drugs, still had *Plasmodium* present in their bloodstream. We have demonstrated that *P. falciparum* was the only species present in these patients at a 28.7% prevalence. We have also shown a lack of correlation between the levels of CD4 T-cells and *Plasmodium* in these patients suggesting no interaction between HIV and *Plasmodium*. Therefore, we hypothesized that antiretroviral drugs are inhibiting the antimalarial drugs. This was tested by performing a 3H-hypoxanthine incorporation assay in the presence of antimalarial and antiretroviral drugs, used individually and in combination. We found that the antimalarial drugs, sulfadoxine and lumefantrine, were inhibited by the antiretroviral drugs, zidovudine, lamivudine, and stavudine, respectively. We also found that stavudine had the most inhibitory effects on all of the antimalarial drugs, except for artemisinin.

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PERFORMANCE OF ANTI-BACTERIAL AND ANTI-PROTOZOAL COMPOUNDS AGAINST *TRITRICHOMONAS FOETUS* IN AN IN VITRO DRUG SUSCEPTIBILITY ASSAY

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Tritrichomonas foetus is a sexually-transmitted parasite infecting cattle in the United States. In cows, *T. foetus* causes early embryonic death and abortion which has led to millions of dollars in lost revenue. Current control measures focus on testing and slaughter of infected animals; no vaccines or treatments are available. In addition, metronidazole is not approved for use in food animals in the United States. In the present study, we evaluate fluorometric assays for high-throughput screening of putative anti-*T. foetus* compounds. We discuss the assessment of a panel of antibacterial and antiprotozoal drug compounds which provides a roadmap for future studies in bovine models of disease.

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IS DIVERSITY OF THE PARASITIC HELMINTH COMMUNITY IN *CYPRINELLA VENUSTA* AFFECTED BY ANTHROPOGENIC DISTURBANCE IN EPHEMERAL RIVERS?

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Parasites in aquatic environments can serve as indicators of ecosystem health. Ecosystems in good health tend to support a higher diversity of species, both free living and parasitic, than those in poor condition. For parasites with complex life cycles, multiple host species must be present in order for a parasite species to exist in that system. Further, many parasites have transmission stages that are highly sensitive to changes in water quality. Therefore endoparasitic helminthes make excellent bioindicators. In order to understand the effect of anthropogenic disturbance on parasite abundance and diversity in ephemeral aquatic ecosystems of north central Texas, we examined the endohelminth communities of blacktail shiners (*Cyprinella venusta*) in the Paluxy River, historically undisturbed, and the Bosque River, historically disturbed. Twenty fish were collected from three sites on each river and dissected in the laboratory. Overall prevalence and abundance of trematodes and nematodes was greater in the undisturbed river, as well as cestodes which were not found at any site on the disturbed river. Five species of trematode were recovered from these fish, one adult and four metacercaria. For the two most common trematode species, *Posthodiplostomum* sp. 4 had a greater prevalence and abundance in the undisturbed river (81.7% and 4.37, respectively) than in the disturbed river (58.3% and 1.63, respectively). *Clinostomum marginatum* also had a greater prevalence in the undisturbed river (18.3%) than disturbed one (5.0%). While abundance of *C. marginatum* was higher on the disturbed river than the undisturbed (0.367 and 0.183, respectively), a single fish accounts for this discrepancy. Nematodes followed a similar pattern with prevalence and abundance greater in the undisturbed (45.0% and 1.417, respectively) than on the disturbed river (28.3% and 0.533, respectively). Preliminarily, diversity and abundance of endohelminths in *C. venusta* seem to be greater in the less disturbed river system.

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PARASITE COMMUNITIES ALONG A RIVER CONTINUUM IN THE NEW JERSEY PINELANDS

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Free-living community composition changes along a river gradient from upstream to downstream, and the River Continuum Concept (RCC) predicts shifts in macroinvertebrate communities that are linked to the physical characteristics of the river. While this idea has been developed for free-living communities, it is largely unknown how parasite community composition also changes along the river continuum. This study will test the hypothesis that parasite diversity correlates with host communities along the continuum. We sampled two rivers, the Mullica and the Batsto, located in Wharton State Forest in the New Jersey Pinelands, in August and September of 2014. Three sites were selected from each river based on variation in stream depth, width, and canopy cover. Sunfish (family Centrarchidae) were collected (n=20) from each site and necropsied for macroparasites. Macroinvertebrate samples were collected from each site using a dip net (n=3), sorted into functional feeding groups (FFG), and examined for parasites. A total of 8 parasite species were recovered from these sampling locations, and most sites were dominated by parasitic nematodes. Shannon's diversity index was used to evaluate parasite diversity among sites. In the Mullica River, parasite diversity declined as we sampled downstream (upstream = 1.36, midstream = 1.06, downstream = 0.6). The invertebrate community of the Mullica River followed the RCC and consisted of 35% shredders and 20% collectors upstream and 3% shredders and 92% collectors downstream. However, in the Batsto River, parasite diversity increased as we sampled downstream (upstream = 0.88, midstream = 1.12, downstream = 1.5), and the invertebrate community did not follow the RCC. Shredder abundance was positively and strongly correlated with acanthocephalan abundance ($R^2 = 0.8352$, and $p \leq 0.05$). These results suggest that macroinvertebrate functional feeding groups may be important in structuring parasite communities along these two rivers. This study measured both biotic

and abiotic factors along rivers, and the data suggests that the biotic component is the dominant force controlling parasite communities in these rivers.

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GENETIC VARIATION OF *OLIGACANTHORHYNCHUS MICROCEPHALUS*, PARASITE OF THREE SPECIES OF OPOSSUMS ACROSS CENTRAL AND SOUTHEASTERN MEXICO

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Universidad Nacional Autónoma de México

Oligacanthorhynchus microcephalus is a typical parasite of opossums (Didelphidae). This species exhibits a wide distributional range (from Brazil to as far north as the US) but no data on the genetic variation of this species has been provided thus far along its entire geographic range. The fact that *O. microcephalus* shows a relatively wide geographic range in Mexico, and it has been recorded in three species of opossums, allows us to conduct a molecular prospecting study to assess the genetic variation among individuals and populations, and to detect potentially exclusive lineages indicating the presence of a species complex. In total, 81 specimens identified as *O. microcephalus* were collected from the intestines of three species of opossums in eight localities across central and southeastern Mexico. DNA sequences of two genes, cytochrome *c* oxidase subunit 1 (cox 1) of the mitochondrial DNA and the domains D2 and D3 from Large Subunit of the nuclear ribosomal RNA (LSU) were generated. Maximum parsimony, maximum likelihood and Bayesian inference analyses were performed for each data set alone and for the combined data sets (LSU + cox 1). All the phylogenetic analyses yielded three major clades, with high support values and with relatively high genetic divergence levels for both markers. However, the morphological study of specimens through light and scanning electron microscopy, as well as morphometric data show that specimens allocated into Clade I are smaller than those contained in Clades II and III. Lower genetic divergence values, as well as no clear-cut morphometric differences indicate that probably Clades II and III are not independent lineages. Our results show at least two genetic lineages that may represent independent species, but we refrain at the moment on describing a new species in the lack of evidence gathered from a wider geographic range.

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SURVEY OF HELMINTHS FROM THE INTRODUCED CANE TOAD AND NATIVE TOADS IN CENTRAL FLORIDA

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While the helminths of cane toads are known from their native lands and some invasive locations, few data are available from the toad's invasive range in Florida. Specimens of *Rhinella marina* (cane toad) were surveyed from an established population in Tampa, Florida and an invasion front population in Lakeland, Florida from summer 2014 to spring 2015. In addition, two native toads, *Anaxyrus terrestris* (southern toad) and *Scaphiopus holbrooki* (eastern spadefoot toad), were surveyed from Lakeland, Florida in sympatry with cane toads, and from Winter Haven, Florida where cane toads are not present. To date, we have collected the following helminths from over 70 Florida toads: *Rhabdias* spp., *Cosmocercoides variablis*, *Mesoceolium* sp., *Distoichometra bufonis*, and an unidentified nematode (encysted). The southern toad has the most diverse helminth assemblage, whereas the cane toad is only infected by nematodes; thus, few differences have been noted in parasite assemblages between invasion front and established cane toad populations.

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DENSITY DEPENDENT IMMUNE RESPONSE OF FRESHWATER SNAILS

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While animal aggregation benefits individuals such as by reducing predation, grouping can also induce costs including creating an increased risk of parasite infection. This is especially true for freshwater snails, which often aggregate in large numbers in nature, and are commonly infected with trematode parasite stages (redia, sporocysts) that produce another stage (cercariae) that can infect conspecific and heterospecific snails. To counteract this increased risk of infection, snails may utilize their immune systems, and in particular produce hemocytes that will encapsulate and kill larval trematodes. Thus, we investigated whether snails living in high densities invested more in their immune systems than snails raised at lower densities, and whether this resulted in a life history trade-off with growth. Three species of freshwater snails were lab-raised at low, medium, and high densities (*Lymnaea elodes*, *Helisoma trivolvis*, *Stagnicola reflexa*). From unexposed and exposed snails, hemocytes and growth were counted and measured once per week. At the end of three weeks, metacercarial parasite intensity was counted in the exposed snails. Results from generalized linear models showed that low-density group snails (unexposed and exposed) exhibited significantly lower hemocyte counts, growth, and greater intensities of infection, compared to medium or high-density snails. Immune response in infected snails was affected by density, in particular, low density snails had more parasites than medium density snails. This study demonstrates the significant effect of host population density on immune investment in three freshwater snail species and the potential ecological and life history trade-offs involved in animal aggregation.

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DEVELOPMENT OF A POINT OF CARE NUCLEIC ACID AMPLIFICATION TEST TO DIAGNOSE *SCHISTOSOMA HAEMATOBIUM* INFECTION

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Schistosoma haematobium infection causes significant morbidity and mortality, mostly in sub Saharan Africa. Control programs require sensitive and specific tests for accurate diagnosis and surveillance, particularly important when shifting emphasis from control to elimination. Rapid diagnostic tests are gaining importance as control programs scale up but currently are insufficiently sensitive and specific. Recombinase polymerase amplification (RPA) is a new isothermal nucleic acid amplification technology suitable for point of care use in low resource settings. We developed an RPA test for *S. haematobium* with lateral flow strip detection. Candidate primers for the *S. haematobium* Dra1 repeat sequence were empirically evaluated and the best performing primer pair combined with a specifically designed TwistAmp® nfo probe enabling amplicon detection on oligochromatographic lateral flow strips. The lateral flow RPA (LF-RPA) assay analytical specificity and sensitivity were tested against a panel of prokaryotic, schistosomal and human DNA samples and a serial dilution of *S. haematobium* DNA. The diagnostic performance of the assay was compared to a Dra1 polymerase chain reaction (PCR) and urine microscopy using urine collected from children resident in Zanzibar that had been stored on Whatman FTA cards. The LF-RPA limit of detection for *S. haematobium* was 100fg with an analytical specificity of 100% against human and prokaryotic DNA. Cross amplification with *S. mansoni* genomic DNA was noted to a limit of 100pg. Amplification was possible across a broad range of temperatures from 30-45^{o}C. Time taken from incubation to result availability was 25 minutes. When compared to Dra1 PCR the LF-RPA assay showed a sensitivity and specificity of 60%.The LF-RPA a promising isothermal nucleic acid amplification test with potential applicability to the point-of-care setting. Further assay optimization is required before field testing is undertaken.

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THE RESURGENCE OF EYEWORM (*OXYSPIRURA PETROWI*) INFECTION IN NORTHERN BOBWHITE (*COLINUS VIRGINIANUS*) AND SCALED QUAIL (*CALLIPEPLA SQUAMATA*) FOUND IN THE ROLLING PLAINS OF TEXAS

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There is unequivocal evidence that quail, Northern Bobwhites (*Colinus virginianus*) and Scaled quail (*Callipepla squamata*), are steadily declining throughout their native range. While the causes are unclear, many have pointed to extremes in weather, declining quality of habitat, and habitat fragmentation; however, often overlooked is the potential impact that parasites can have on their host. The eyeworm *Oxyspirura petrowi* has received recent interest in the role it may play in negatively impacting gamebirds. Anecdotal reports have occurred of eyeworm-infected bobwhites found dead after flying into buildings and other anthropogenic structures, while others have reported infected bobwhites behaving erratically. These reports have led to speculation that eyeworms may be causing visual obstruction. Recently, high numbers of *O. petrowi* were observed connected to orbital tissue and ingesting blood which caused inflammation and localized petechiae/spot hemorrhaging to the lacrimal duct. During the summer and fall of 2013 in Mitchell County, Texas, eyeworm infections were witnessed in over 90% of Northern Bobwhite sampled (n=51) with an average abundance of 10.4±11.5 (range:0-69) and over 84% in Scaled quail (n=31) with an average of 5.1±7.5 (range:0-41). A follow-up study was conducted in the summer and fall of 2014 in the same location in Mitchell, County, Texas. Both Northern Bobwhite (n=51) and Scaled quail (n=38) were sampled for eyeworm prevalence and mean abundance. A total of 1,218 eyeworms were recovered from 49 of 51 Northern Bobwhite (96% prevalence). Eyeworm infections ranged from 1-92 with a mean abundance of 23.8±17.9. Adult bobwhite (n=39) exhibited a mean abundance of 29±16.9, while juveniles (n=12) averaged 7.9±8.5. Approximately 283 eyeworms were collected from 33 of 38 Scaled quail (87%). Eyeworm infections ranged from 0-52 with a mean abundance of 7.4±10.8. Adult Scaled quail (n=35) had a mean abundance of 8.1±11, while juveniles (n=3) were uninfected with eyeworms. More quail were documented to have a heavier infection in 2014 than in 2013. With mean abundance doubling in 2014 compared to 2013, the data suggests that eyeworm infection is a cumulative process, meaning that a host can continuously build up the amount of eyeworms it is infected with. Additionally, given the rise in both eyeworm mean abundance and prevalence in just over a year, parasites could be a contributing factor in regulating quail populations throughout the Rolling Plains of Texas.

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PREVALENCE OF CECAL WORMS IN NORTHERN BOBWHITE AND SCALED QUAIL IN THE ROLLING PLAINS OF WEST TEXAS

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Northern Bobwhite (*Colinus virginianus*) and Scaled Quail (*Callipepla squamata*) have experienced dramatic population declines over the past decade in the Rolling Plains of West Texas, the cause of which is still heavily debated. Several theories exist as possible explanations for this decline including semiarid environments linked to survival and reproduction success, lack of suitable habitat, habitat fragmentation, and toxicity from neonicotinoid pesticides, to name a few. More recently, the impact of parasitic eyeworms have been thought to be a leading cause in this population decline. This study investigated the prevalence of a similar parasite nematode (Cecal worms; *Aulonocephalus pennula*) in Northern Bobwhite and Scaled Quail. A similar cecal worm, found in the Red Grouse (*Lagopus lagopus scoticus*), was shown to be the leading cause for the drastic population decline in Scotland. From April to October of 2014, 107 quail (69 Northern Bobwhite and 38 Scaled Quail) were trapped in Mitchell County, Texas for necropsy using standard walk-in funnel traps. Upon necropsy, the cecum from each quail was removed and teased apart. The total number of worms found within each cecum was counted. The prevalence of cecal worm

infection in the 107 quail was 100%. Northern Bobwhites averaged 145.83 ±94.73 (Range = 12-504) worms per bird and Scaled Quail averaged 62.24±67.37 (Range = 3-255) worms per bird. Adult Northern Bobwhites (n = 58) averaged 160.32±91.5 (Range = 30-504) while juveniles (n = 11) averaged 56.09±81.23 (Range = 12-141). Adult Scaled Quail (n = 35) averaged 66.43±68.62 (Range = 3-255) while juveniles (n = 3) averaged 13.33±6.03 (Range = 7-19). Work is currently underway to look at the prevalence of infection during the winter months (November through March) for comparison. Current work is also focused on the impact this parasite may have on the Northern Bobwhite and Scaled Quail. Nesting and reproductive success, survivability, hunter bias are several areas of concern where the cecal worm may have an influence on these quail.

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EPIGENETIC REGULATION OF SCHISTOSOME-ASSOCIATED PARASITIC CASTRATION IN SNAILS: A PRELIMINARY STUDY

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Parasitic castration, a parasite-induced cessation of host egg production, is well documented in snails infected with larval trematodes. It has been hypothesized that chemicals secreted by larvae may be involved in the early disruption of host reproduction by targeting the neuroendocrine system of the cerebral ganglia (CG) or by direct action on the ovotestis (OT). However, the mechanism(s) by which larval secretions may be mediating interference with reproductive function is currently unknown. The present study explores the hypothesis that parasitic castration associated with prepatent *Schistosoma mansoni* infection of adult *Biomphalaria glabrata* may be mediated, at least in part, through larval influence on the epigenetic regulation of reproduction-associated gene expression in the CG or OT. To begin addressing this hypothesis, groups of adult susceptible *B. glabrata* snails (NMRI strain) were exposed to 15-20 *S. mansoni* miracidia/snail or left unexposed, and then monitored for egg production at 1, 2, 3 and 4-weeks (wk) post-exposure (PE). Significant decreases in egg #/snail were noted in exposed snails at 3 and 4 wk PE (N=3). Concurrently, the OT and CG were dissected from subsets of exposed and unexposed snails on days 4, 15 and 21 and subjected to quantitative PCR to determine the steady-state transcript levels of DNA (cytosine-5-)-methyltransferase 1 (Dnmt1) and Methyl-CpG-binding domain protein 2/3 (MBD2/3). Dnmt1 expression in the OT of exposed snails exhibited a transient spike at day 15 before returning to control levels, whereas there was a significant increase in CG Dnmt1 transcript levels at day 21 in exposed snails relative to controls. Similarly, compared to control levels, MBD2/3 gene expression was elevated at days 15 and 21 in the CG, but not the OT. As Dnmt1 and MBD2/3 are core DNA methylation machinery components involved in developmental biology, the observed changes in their transcript expression in the CG and OT temporally-associated with the onset of castration suggests that epigenetic mechanisms may be involved in this phenomenon.

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DELIVERY OF PARASITE NON-CODING RNAS TO HOST INTESTINAL EPITHELIUM CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION

A. Gong, **Y. Wang**, **S. Ma**, **X. Chen** and **X. Chen**, Creighton University

Horizontal gene transfer, the process of swapping genetic materials between neighboring “contemporary” organisms in a manner other than traditional reproduction, has been shown to be an important factor in the evolution of many organisms. Horizontal transfer between bacteria is well studied, representing the primary reason for bacterial antibiotic resistance. Emerging evidence indicates that horizontal transfer may be especially important in the evolution of a parasitic lifestyle, as infection-related factors could be transmitted, and many of these factors would presumably confer an immediate selective advantage. In this study, we addressed the question of whether *C. parvum* non-coding RNAs (ncRNAs) can be delivered

into infected host cells. Using *in vitro* infection models employing several murine and human intestinal epithelial cell lines, we tested the delivery of parasite ncRNAs into the nuclei of infected host cells following *Cryptosporidium* infection. We used the nuclear extracts from infected host cells because it is not technically feasible to separate the internalized intracellular parasites from the cytoplasmic components of infected cells. Using primers for the 118 *C. parvum* ncRNAs identified in *C. parvum* sporozoites, we reliably detected the presence of a panel of *C. parvum* ncRNAs in the nuclear extracts from infected cells by PCR, which was further confirmed by *in situ* hybridization. The host nuclear presence of a *C. parvum* ncRNA is not correlated to its expression level in the parasite. This selective nuclear delivery of *C. parvum* ncRNAs is not due to the nonspecific endocytosis (phagocytosis or macropinocytosis) of the parasite molecules by epithelial cells. Our data demonstrate the highly selective and specific delivery of parasite ncRNAs into the host epithelial cells following *C. parvum* infection, suggesting the horizontal transfer of parasite ncRNAs to host cells during *C. parvum*-epithelial cell interactions.

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HSP70-DEPENDENT NUCLEAR IMPORT OF PARASITE NON-CODING RNAS IN INTESTINAL EPITHELIAL CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION

Y. Wang, **A. Gong**, **X. Chen**, **C. Lin** and **X. Chen**, Creighton University

Cryptosporidium spp. infects the gastrointestinal epithelium of vertebrate hosts and is an important protozoan parasite for human, in particular, in HIV/AIDS patients and young children. Genomic analysis of a full length cDNA library constructed from *C. parvum* identified 118 non-coding RNA (ncRNA) transcripts. We recently made a novel observation on the nuclear delivery of *C. parvum* ncRNAs into infected intestinal epithelial cells. In this study, we investigated the underlying molecular mechanisms of their nuclear import. Several *in vitro* infection models employing murine and human intestinal epithelial cell lines were used. We identified that the main partner protein binding for nuclear transfer of *C. parvum* ncRNAs is the heat-shock protein 70 (HSP70), a chaperone protein that has been implicated to be hijacked by some RNA viruses for their replication or nuclear import. By RNA immunoprecipitation analysis, we detected the physiological interactions between HSP70 and four nuclear imported *C. parvum* ncRNAs, including *Cdg7_0990 and Cdg2_0220*. Our *in vitro* binding assay using recombinant human HSP70-His protein and isolated whole parasite RNA further confirmed the direct binding of HSP70 to associated *C. parvum* ncRNAs, but not the non-related control ncRNAs. By Western blot, we detected a cytoplasmic – to – nuclear translocation of HSP70 in infected cells, but not in cells exposed to the whole parasite lysate or stimulated with bacterial lipopolysaccharides. Moreover, transfection of host epithelial cells with a siRNA designed for human HSP70 significantly decreased the nuclear delivery of *Cdg7_0990* and *Cdg2_ 0220* in infected epithelial cells. Our findings indicate that host HSP70-mediated nuclear import of RNA cargos is involved in the highly selective and specific delivery of parasite ncRNAs into the host epithelial cells following *C. parvum* infection.

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LINCRNAS IN INTESTINAL EPITHELIAL DEFENSE AGAINST *CRYPTOSPORIDIUM* INFECTION

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Members of the genus *Cryptosporidium* infect intestinal epithelium of a wide range of vertebrates, including humans. Because of the "minimally invasive" nature of *Cryptosporidium* infection, epithelial cells are critical to the host's anti-*Cryptosporidium* immunity. LincRNAs are long non-coding transcripts (> 200 nt) from the intergenic regions of annotated protein-coding genes. Emerging evidence supports a key regulatory role for lincRNAs across diverse biological functions, including gene transcription. Here, we measured alterations in lincRNA expression profile in intestinal epithelial cells following *C. parvum* infection and explored the role of lincRNA-mediated gene transcription in the regulation of epithelial

anti-*C. parvum* defense. Several *in vitro* infection models employing murine and human intestinal epithelial cell lines were used. We found that intestinal epithelial cells displayed significant alterations in lincRNA expression profile following infection. Two of these upregulated lincRNAs, lincRNA-Chr1a and LincRNA-Chr10a, are early-responsive lincRNAs induced in infected cells through the activation of the NF-κB signaling pathway. Knockdown of lincRNA-Chr1a or LincRNA-Chr10a in intestinal epithelial cells resulted in a significant increase in the *C. parvum* infection burden, reflecting a deficiency in epithelial anti-*C. parvum* defense. Knockdown of both lincRNAs caused reprogram of the gene expression profile in intestinal epithelial cells in response to infection, including several anti-microbial defense genes. Our findings suggest that host epithelial cells activate NF-κB signaling to regulate lincRNA expression in response to *C. parvum* infection. Moreover, lincRNA-mediated gene transcription may be critical to the regulation of intestinal epithelial anti-*C. parvum* defense.

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SHUTTLING OF PARASITE NON-CODING RNAS IN EXOSOMES RELEASED FROM GASTROINTESTINAL EPITHELIAL CELLS FOLLOWING *CRYPTOSPORIDIUM* INFECTION

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J. Cao, Institute of Parasite Disease
X. Chen, Creighton University

Cryptosporidium spp. is a ubiquitous pathogen that infects the gastrointestinal (GI) epithelium and other mucosal surfaces in vertebrate hosts, including humans. This parasite is of great medical importance as infections in immunocompromised humans often lead to life-threatening illness. After rotavirus, *Cryptosporidium* is the most common pathogen responsible for moderate-to-severe diarrhea in children in the developing countries. Because of the "minimally invasive" nature of infection, epithelial immune responses are critical to the host's mucosal defense. Exosomes are extracellular vesicles derived from cells that function as "bioactive vesicles" to promote cell-cell communication and immunoregulation. Exosomes derived from GI epithelial cells have been demonstrated to modulate lymphocyte immune responses during mucosal infection. Here, we reported a novel observation on the presence of *C. parvum* non-coding RNAs (ncRNAs) in the released exosomes. Using both *in vitro* and *in vivo* models of GI (either intestinal or biliary) cryptosporidiosis, we first demonstrated the release of exosomes from the biliary and intestinal epithelium following infection by *C. parvum*. We found that release of exosomes involves activation of TLR4 signaling through SNAP23-associated vesicular exocytotic process. Intriguingly, released exosomes carry a panel of non-coding RNAs (ncRNAs) of parasite origin, including *Cdg2_0220*, *Cdg2_0170*, and *Cdg7_0990*. Exposure of macrophages to released exosomes displayed significant alterations in cytokine/chemokine expression profiles in treated macrophages. Our data demonstrate the shuttling of parasite non-coding RNAs in exosomes released from gastrointestinal epithelial cells following *Cryptosporidium* infection, suggesting a potential role of exosomal shuttling of parasite ncRNAs in the activation of host systemic immune responses.

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DEVELOPMENT OF AN EX-VIVO MODEL WITH MURINE ENTEROIDS FOR *CRYPTOSPORIDIUM* INFECTION

X. Zhang, **A. Gong**, **Y. Wang** and **X. Chen**, Creighton University

The human intestinal epithelium is the largest of the body's mucosal surfaces with a single layer of cells organized into crypts and villi. Although the majority of cells bordering the intestinal lumen are absorptive enterocytes, additional specialized epithelial cell lineages are also important to intestinal homeostasis, including intestinal stem cells, goblet cells and Paneth cells. Enteroids are cultured functional intestinal epithelial units, which are comprised of all four types of normal epithelial cells and develop a crypt–villus differentiation axis. *Cryptosporidium spp.* is a ubiquitous pathogen that infects the intestinal epithelium in humans. Although this parasite primarily only infects the absorptive enterocytes

of the villus region, significant pathological changes have been identified along the entire epithelium and underlying mechanisms are unclear. Here, we report the development of murine enteroids for an *ex-vivo* model of intestinal cryptosporidiosis. Adult intestinal crypt-derived enteroids from mouse tissues were collected and cultured according to a previous report by Sato *et al* (Nature 2009;459:262-265). The integrity of isolated enteroids in culture showed characteristics of intestinal crypts and villi by morphological analysis. The +4 cell population is identified based on the expression of several markers including Lgr5. Exposure of the enteroids to *C. parvum* sporozoites caused an increase of epithelial cell apoptotic death and a decrease of the stem cell markers from the infected enteroids. Our initial findings suggest that adult intestinal crypt-derived enteroids support *C. parvum* infection and could be an important model for studying intestinal cryptosporidial pathogenesis.

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MICROHABITAT SELECTION AND EYEFLUKE INFECTION LEVELS WITHIN WESTERN MOSQUITOFISH (*GAMBUSIA AFFINIS*)

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Eyefluke studies commonly document microhabitat locations within the eyes of many fish species. Some eyefluke species have a preference for the vitreous humour, some for the retina, and others the lens. Preliminary data indicated high infection levels of flukes in the pigment layer of eyes in mosquitofish (*Gambusia affinis*) in local study sites. Interestingly, although these species of eyeflukes have been well studied, *G. affinis* have not been documented as a host. The objective of this study was to examine eyefluke infections in *G. affinis* and document the microhabitat selection of the various species. Twenty *G. affinis* were collected from the Paluxy River near Glen Rose, Texas, and processed resulting in 40 eye dissections. Individual weight, length, and sex were recorded prior to dissection. Left and right eyes were differentiated to reveal potential eye preference. Eye layers were separated, and specific location and quantity of metacercariae were recorded. Tissues from an additional 7 *G. affinis* eyes were histologically analyzed to confirm microhabitat location. Four of these were from the original collection site, while 3 were collected from the Bosque River in Hico, Texas, which demonstrated minimal to no infection rates as controls. Histology confirmed that infections in the pigment layer were specifically in the vitreous layer of the choroid. A total of 465 metacercariae were collected with 444 metacercariae being in the vitreous layer of the choroid, 9 metacercariae found in the lens, and 12 metacercariae in the eye orbit. Results show an average of 11.1 metacercariae per eye in the vitreous layer of the choroid with a 100% prevalence and abundance of 22.2 flukes per fish. Lens metacercariae averaged 0.23 individuals per eye with 40% prevalence and abundance of 0.45 flukes per fish. Eye orbit metacercariae averaged 0.3 individuals per eye with 40% prevalence and abundance of 0.6 flukes per fish. This data represents the first documentation of eyefluke microhabitat within the vitreous layer of the choroid in *G. affinis*.

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OXYSPIRURA PETROWI AND *AULONOCEPHALUS PENNULA* IN SCALED QUAIL FROM WEST TEXAS AND SOUTH TEXAS

S.A. Shea, **K.A. Bedford**, **A.C. Olsen** and **A.M. Fedynich**
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Scaled quail (*Callipepla squamata*) have been declining since the 1980s and the possible correlation between parasitic infections and this decline is of interest to quail biologists and parasitologists. *Oxyspirura petrowi* and *Aulonocephalus pennula* are two common nematodes found in scaled quail. *Oxyspirura petrowi* has an indirect lifecycle and is found under the nictitating membrane and within the conjunvtival sacs, lacrimal canals, and the Hardarian glands of the eye. Thus, *Oxyspirura petrowi* may impair the quail's vision, reducing their survivability. *Aulonocephalus pennula* also uses an intermediate

host. In the definitive host, this species occurs in the ceca and intestines and may cause intestinal blockage. We assessed *O. petrowi* and *A. pennula* prevalence, intensity, and abundance in scaled quail collected in west Texas and south Texas during the 2012-2013 and 2013-2014 hunting seasons. Findings from this study provide insight on helminth communitites in scaled quail from these two distinct ecoregions in Texas.

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A SURVEY OF THE BLOOD-BORNE AND INTESTINAL PARASITES OF RODENTS FROM TEXAS AND COSTA RICA

K. Lasater and **W. Preisser**, Texas A&M University

Rodents are known to host multiple species of blood-borne parasites throughout the world, including the causative agents of Chagas disease and babesiosis. However, little is known about the blood-borne parasites infecting rodents in Texas, where it is likely that rodents harbor multiple blood-borne parasites, serving as intermediate, definitive, and/or sylvatic hosts for multiple species of protozoa and filarial nematodes. Furthermore, very few studies have examined blood-borne parasites of rodents in Costa Rica, where Chagas disease is endemic. In addition to the lack of information on rodent blood-borne parasites, recent surveys on the intestinal helminths of rodents in these localities are scarce. While often overlooked, parasitic species of nematodes, trematodes, cestodes, and protozoa may have large effects on the ecology of a region. To survey blood-borne and intestinal parasites in Texas and Costa Rica, rodents were live-captured at multiple localities throughout east and south Texas and from one locality in north central Costa Rica. Using a tail snip technique, where the distal tip of the tail was removed with a sharp blade, blood was collected from captured rodents and thin smears were prepared in the field. Dried smears were fixed in methanol and brought back to the lab for analysis. Fecal samples were opportunistically collected and returned to the lab for screening. In the lab, blood smears were stained with Giemsa stain and scanned under the 100x objective to search for blood-borne parasites, particularly filarial nematodes and parasitic protozoa such as *Trypanosoma cruzi*, *Babesia microti*, *Plasmodium* spp., and *Hepatozoon* spp. Fecal samples were prepared using standard floatation and sedimentation techniques and screened under a microscope for the detection of the eggs of intestinal helminths. Multiple species of rodents were sampled, and the blood-borne and intestinal parasite species of each host species will be presented.

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OCCURRENCE OF *TETRAMERES PATTERSONI* IN QUAIL FROM TEXAS

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Two species of *Tetrameres* (*T. pattersoni* and *T. americana*) have been described from the proventriculus of Galliformes in North America of which *T. pattersoni* is considered more pathogenic to its definitive host. Previous to this study, it was unclear which species was found in wild quail occurring in Texas. We have identified *T. pattersoni* in wild bobwhites (*Colinus virginianus*) and scaled quail (*Callipepla squamata*) occurring in Texas and report its prevalence and intensity of infection in distinct geographic regions of Texas spanning a 5-year period. Prevalence of *T. pattersoni* in bobwhites from the Rolling Plains of Texas collected during 2010–2011 (n = 142), August and October 2011–2013 (n = 161), and South Texas during the 2012–2013 and 2013–2014 hunting seasons (n = 209) was 26%, 14%, and 10%, respectively, whereas mean intensity was 2.9 ± 0.3 (range 1–8), 3.0 ± 0.5 (range 1–10) and 2.8 ± 0.7 (range 1–9), respectively. Prevalence of *T. pattersoni* in 23 scaled quail collected during the 2012–2013 and 2013–2014 hunting seasons in South Texas and in 126 collected in west Texas was 9% and 2%, respectively, and averaged 4.3 ± 3.0 (range 1–7) and 1.0 (range 1), respectively. Based on our findings, *T. pattersoni* represents a species that occurs with sufficient frequency in bobwhites (10–26%) to have a

negative effect at the host-population level. Additional study is needed to determine specific pathology associated with infection and assess potential negative effects at the host-population level.

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THE HISTOPATHOLOGY OF *CATOSTOMUS COMMERSONI* (WHITE SUCKER) INFECTED WITH *POMPHORHYNCHUS BULBOCOLLI* (ACANTHOCEPHALA)

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This study was undertaken in order to assess the damage caused by *Pomphorhynchus bulbocolli* to *Catostomus commersoni* (white sucker). Three specimens of *C. commersoni* were collected during early September 2014 via gill net from Canadarago Lake (Otsego County, New York) and dissected for intestinal parasites. Upon dissection, damage to the fish intestine was macroscopically visible, with the intestine perforated when infected with *P. bulbocolli*. Intestines observed to be infected with *P. bulbocolli* were opened with a longitudinal incision and fixed in neutral buffered formalin with the acanthocephalans remaining attached. Histological sections of intestinal tissue infected with *P. bulbocolli* were generated according to conventional methods. Histological sections of intestine with *P. bulbocolli* attached were compared with histological sections of intestine in which no worms were present. Examination of sections revealed extensive damage in the form of profound tissue destruction, as well as proliferation of cells at the sites of wounds. These changes were observed at the mucosa, submucosa, and muscularis layers of the fish intestine, eventually penetrating the connective tissue.

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TRANSMISSION OF STRIGEIDAE (PLATYHELMINTHES: TREMATODA) IN WISCONSIN AND ILLINOIS FRESHWATER WETLANDS

J.E. Kawaguchi, **O.N. Choi**, **R.C. Jadin** and **S.A. Orlofske**, Northeastern Illinois University

Freshwater communities consist of many species interactions, including predator-prey and parasite-host relationships. For trematodes, the life cycle is dependent on trophic interactions, leading to the proposal of parasites as bio-indicators of predator-prey interactions, host diet range, and of species occurrence at the landscape level. During field surveys of wetlands (N=4) in Southeastern Wisconsin and Northeastern Illinois, we observed cercariae and tetracotyle (metacercariae) of the family Strigeidae in *Lymnaea* sp. (snails). We identified these strigeid larval stages from three total sites and during each visit to those sites. Only two of the four sites presented both the cercariae and tetracotyle ($p = 0.277$, Chi-square). The snails were less likely to be infected by both life stages of the parasite simultaneously ($p = 0.002$, Chi-square). Based on field observations, we hypothesized that these life stages were the same species; we conducted transmission experiments where we exposed uninfected *Lymnaea* snails to the free-living infective stage. Between 16 and 31 days, with temperatures at 18°C and 22°C, tetracotyle formed from underdeveloped stages to fully formed tetracotyle. The mean percent of tetracotyle per exposed *Lymnaea* was 41%. Our future research includes using DNA sequence analysis to compare our samples to other members of Strigeidae, confirming species identity. We can then determine the distribution of the trematode species across wetland sites. Once positively identified, we propose that this species can potentially serve as an indicator of the presence of migratory waterfowl that may have applications to investigating food web functions in wetland restoration. These parasites are not major factors to morbidity but would serve as good indicators of waterfowl because they can indicate long-term bird activity rather than single point observations.

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SURVEY OF BOBCAT INTESTINAL HELMINTHS ON THE PINE RIDGE INDIAN RESERVATION

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Because state and federal agencies do not survey Native American Reservations, they have been referred to as "black holes" of biological knowledge. One gap in our knowledge of reservation species is in bobcat (*Lynx rufus*) intestinal helminths. A survey of bobcat intestinal helminths was conducted in early January 2015 on the Pine Ridge Indian Reservation in South Dakota. In addition to surveying the reservation for the first time, a significant snowstorm impacted the area in the previous winter killing much of the wildlife, including thousands of cattle. We wanted to see if this had an effect on the parasites diversity in bobcats. Specimens were obtained from the Oglala Sioux Parks and Recreation for dissection and examination. Identification of parasite species was done by microscopy of distinguishing structures. Although analysis is still being conducted, results will be compared to intestinal parasite diversity of bobcats in previous studies from the Upper Midwest.

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MANIPULATION OF CRICKET (*ACHETA DOMESTICUS*) GEOTAXIS TENDENCIES BY HORSEHAIR WORMS (NEMATOMORPHA) TO INDUCE WATER-SEEKING BEHAVIOR

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Parasite-induced behavior alterations have been observed in infected hosts in numerous parasite-host relationships. The abnormal and erratic behavioral changes in terrestrial crickets infected by horsehair worms (Nematomorpha) results in a water-seeking behavior. The cause of this behavior is generally unknown despite many possible reasons suggested in the literature, such as an attraction to light reflected off water surfaces or a manipulation of the cricket's central nervous system. I intend to discover whether this behavior is a result of the parasite modifying the cricket's geotaxis response to gravity. Uninfected crickets show a statistically significant negative geotaxis, tending to seek higher points of elevation. I expect crickets infected with *Paragordius varius* to show the reverse trend in an attempt to make their way down a gravitational gradient, towards potential water sources to release the mature, aquatic parasite. This was tested with a slope gradient of a flat board elevated at a 45-degree angle on which the crickets were released and direction of movement recorded. Crickets (*Acheta domesticus*) were placed in the center of a circle in order to utilize directional statistics for analysis of the geotaxis tendencies of the uninfected versus infected crickets over the course of infection.

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CHRONIC *TOXOPLASMA GONDII* IN NURR1-NULL HETEROZYGOUS MICE EXACERBATES ELEVATED OPEN FIELD ACTIVITY

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Latent infection with *Toxoplasma gondii* is common in humans (approximately 30% of the global population) and is a significant risk factor for schizophrenia. Since prevalence of *T. gondii* infection is far greater than prevalence of schizophrenia (0.5-1%), genetic risk factors are likely also necessary to contribute to schizophrenia. To test this concept in an animal model, Nurr1-null heterozygous (+/-) mice and wild-type (+/+) mice were evaluate using an emergence test, activity in an open field and with a novel object, response to bobcat urine and prepulse inhibition of the acoustic startle response (PPI) prior to and

6 weeks after infection with *T. gondii*. In the emergence test, *T. gondii* infection significantly decreased the amount of time spent in the cylinder. *Toxoplasma gondii* infection significantly elevated open field activity in both +/+ and +/- mice but this increase was significantly exacerbated in +/- mice. *T. gondii* infection reduced PPI in male +/- mice but this was not statistically significant. Aversion to bobcat urine was abolished by *T. gondii* infection in +/+ mice. In female +/- mice, aversion to bobcat urine remained after *T. gondii* infection while the male +/- mice showed no aversion to bobcat urine. Antibody titers of infected mice were a critical variable associated with changes in open field activity, such that an inverted U shaped relationship existed between antibody titers and the percent change in open field activity with a significant increase in activity at low and medium antibody titers but no effect at high antibody titers. These data demonstrate that the Nurr1 +/- genotype predisposes mice to *T. gondii*-induced alterations in behaviors that involve dopamine neurotransmission and are associated with symptoms of schizophrenia. We propose that these alterations in murine behavior were due to further exacerbation of the altered dopamine neurotransmission in Nurr1 +/- mice.

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IMMUNE MECHANISMS IN TREMATODE-*HELISOMA TRIVOLVIS* INTERACTIONS

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We often think of host specificity evolving from ecological and physiological factors, however, the immunological elements of phenomenon are poorly understood. A field which is studied even less is the immunological interactions between parasites and their primary hosts. Questions like: 'why are some gastropods resistant to some trematodes, but susceptible others?', 'what immunological trends are found in infected communities?', and 'how does the parasite successfully hide from the host immune system?' we lack answers to, and are essential to our understanding of curing or preventing human parasitic infections as well. In this study, I aimed to establish methods for analyzing gastropod immunity, map out the immune systems of *Helisoma trivolvis* and get a basic understanding of how infection changes this network of cells, so that I could further research this topic and provide procedures for other researchers interested in this subject. I began by doing a mass literature review which contained papers whose publication date ranged from 1976-2014 and discussed a wide variety of species of freshwater invertebrates to establish what type of immune systems I could expect to see in *H. trivolvis* and to get acquainted with the vocabulary and previous research in this field of study. I then developed methods for obtaining hemolymph samples from the primary hosts, staining and fixing the immune cells, measuring, categorizing, and identifying various types of hemocytes in this species. I also established effective ways of counting these cells, as well as calculating basal levels of hemocytes in uninfected snails in order to compare to snails infected with different parasites. In conclusion, my study has provided me with valuable background research, establishment of methods, and the beginnings of understanding these trematode-*H. trivolvis* immune interactions for future study.

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PRELIMINARY STUDIES ON HELMINTH PARASITES OF GASTROINTESTINAL TRACT OF CATFISH (*ICTALURUS PUNCTATUS*) AND BUFFALO FISH (*ICTIOBUS CYPRINELLUS*) FROM LOWER MISSISSIPPI RIVER

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Catfish (*Ictalurus punctatus*) are named for their whisker-like structures called barbells on their face which they use to detect food in the water. It is one of the most consumed fish of Mississippians. They are known as bottom dwellers. Buffalo fish (*Ictiobus cyprinellus*) has large oblique and lakes and considered to be omnivores. The purpose of this study is to know the helminth parasites prevalent in this fish that is the favorite of people from Mississippi and buffalo fish also consumed a lot by the Mississippi people. The next purpose is to find out which of the two species of fish that harbors more helminth parasites than the other. From July 2012 to November 2014, the two species were obtained from a fish market located in

Port Gibson, Mississippi as they become available. They were taken to the laboratory and autopsied. The parasites they harbored were removed, put in petri dishes, killed, fixed and preserved in 10% formalin pending staining and identification to species. They were next grossly identified with a dissecting microscope. The results were recorded and the parasites preserved in 10% formalin pending staining and identification to species. Ninety percent of the catfish so far autopsied were infected with helminths. The kinds of helminths found were cestosdes, trematodes, nematodes and acanthocephalans. With respect to the buffalo fish, 50% were infected with acanthocephalans and trematodes. This is a preliminary report. Work on this study is continuing.

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IS PARASITE BIODIVERSITY IN FRESHWATER FISH HIGHER IN PROTECTED AREAS? A CASE STUDY IN THE BIG THICKET NATIONAL PRESERVE

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T. Herzog
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A long-term effort is ongoing to determine if the Big Thicket National Preserve (BTNP) in Texas effectively protects its aquatic habitats. Previous work demonstrated that parasite diversity and abundance in select catfishes (*Ictalurus punctatus* and *Ameiurus natalis*) is higher inside the BTNP than outside, largely because of higher diversity of adult endohelminths, particularly trematodes and nematodes. The present investigation expands this study to include results on parasite diversity in 4 species of ictalurid catfishes (*A. natalis*, *Ameiurus melas*, *I. punctatus*, and *Ictalurus furcatus*) and 6 species of suckers (Catastomidae) in 5 genera. Since 2006, 137 ictalurids (73 inside BTNP) from 20 sites (10 inside BTNP) and 133 catostomids (64 inside BTNP) from 15 sites (10 inside BTNP) were collected and examined for parasites. Observed parasite diversity was higher inside the BTNP than outside for ictalurids (34 vs. 20 species), primarily due to more adult nematodes, acanthocephalans, and adult trematodes. In addition, measures of abundance for catfish specialists and adult endohelminths, in general, were higher inside the Preserve than outside. These results suggest that the BTNP has some positive effects on the aquatic communities it was intended to protect via maintaining larger and more interactive fish and invertebrate communities. However, parasite diversity was similar for catostomids inside and outside the BTNP (26 vs. 24 species). The different feeding habits of catfishes and suckers might be responsible for the observed differences in patterns of parasite diversity. In addition, most catostomid species have been collected from only 1 or a few locales, statistically confounding host species and locale to some extent. Additional sampling is underway to fill in gaps in coverage and to include additional host groups, e.g., topminnows (*Fundulus*) and sunfishes (centrarchids).

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MARINE-ESTUARINE TROPHICALLY TRANSMITTED PARASITES INDICATE ESTUARINE FORAGING AND SUGGEST DIFFERENCES BETWEEN NATURAL-ORIGIN AND HATCHERY-PRODUCED MID/UPPER COLUMBIA RIVER SPRING CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*)

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Recent studies have shown that the Columbia River estuary serves as an important habitat for subyearling Chinook salmon for foraging and refuge from predators. However, it is unclear if salmonids with a life history type that move rapidly through the estuary use estuarine habitats for foraging. To help assess this, we used trophically transmitted parasite assemblages to provide an extended diet history for a rapidly moving Chinook salmon stock group, the Mid/Upper Columbia River Chinook salmon. This stock group is one of the evolutionary significant units listed as endangered under the Endangered Species Act. Seventy-

five yearling Chinook salmon collected in the lower Columbia River estuary during 2007-2011 were examined for trophically transmitted parasites. Results show that these yearling salmon harbor a parasite community that consists of freshwater and marine-estuarine parasite taxa, including trematodes, nematodes and acanthocephalans. A total of 161 parasites were recovered representing 13 taxa. The prevalence of any marine taxa recovered (38.6%) was higher compared to freshwater taxa (24.0%). A relatively high prevalence of the marine-estuarine nematode *Hysterothylacium aduncum* (26.7%), which uses the amphipod *Americorophium* sp. as an intermediate host, demonstrates that the Columbia River estuary is used for foraging by yearling Chinook salmon. Comparison between hatchery and natural origin salmon indicated there was a trend for natural origin fish to harbor more freshwater and marine parasites than the hatchery origin fish (50% vs 14% and 50% vs. 35%, respectively), suggesting that juvenile hatchery origin Chinook salmon may not be consuming at the same rate, or diversity of diet, as natural origin Chinook salmon as they migrate down river and through the estuary.

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MICROGEOGRAPHIC POPULATION GENETIC STRUCTURE OF *BAYLISASCARIS PROCYONIS* (NEMATODA: ASCAROIDAE) IN WESTERN MICHIGAN INDICATES THE GRAND RIVER IS A BARRIER TO GENE FLOW

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Baylisascaris procyonis, the raccoon roundworm, is increasingly being recognized for its zoonotic and public health importance. Fine-scale analyses of the population genetics of this species have been problematic due to a lack of appropriate genetic marker. We developed eight polymorphic microsatellites for *B. procyonis*. Amplification of these loci in a sample of 74 worms collected from 10 raccoons in Western Michigan revealed significant population structure. Bayesian clustering indicates two subpopulations, one on either side of the Grand River, which bisects the region sampled. Estimates of F_{ST}, and results from AMOVA and isolation by distance, further corroborate a scenario whereby the river is acting as a barrier to gene flow, a rather unusual finding given the high vagility of raccoons and microgeographic scale (~500 km^2) of the analysis. We describe one possible mechanism for how this pattern of structure could have become established

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COMPARATIVE ANALYSIS OF HEMOGREGARINES COLLECTED FROM SNAKES (*NERODIA* SPP.) IN FLORIDA

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The host specificity and life history of hemogregarines from snake hosts are poorly known through much of the United States, with a major exception occurring in northern and southern peninsular Florida. Previous studies conducted at the University of Florida (Sam Telford, Jr. and colleagues) characterized the specificity and morphology of several species of *Hepatozoon* from wild snakes collected in Florida, which clearly showed strict specificity for most species of hemogregarines, but found *Hepatozoon sauritus* to be a generalist that infected at least 5 snake species in 4 genera. In this study, we sampled (primarily) watersnakes: *Nerodia fasciata pictiventris, Nerodia floridana,* and *Nerodia taxispilota* from a natural wetland and lake (Circle B Bar Reserve) and an urban lake (Lake Hollingsworth) that are approximately 15 km apart and are connected by a small stream in Polk County, Florida. Previous studies have not sampled snakes from central Florida, nor compared infection parameters between urban and natural areas. Giemsa stained blood smears revealed that only *N. f. pictiventris* (18/25) were infected, whereas *N. floridana* (0/4) and *N. taxispilota* (0/1) were uninfected at Circle B Bar Reserve; interestingly, 3 species of *Hepatozoon* were present in *N. f. pictiventris*: *Hepatozoon fasciate, Hepatozoon pictiventris,* and *Hepatozoon sirtalis*. In total, 60% of the snakes were infected with *Hepatozoon* species at Circle B Bar Reserve. *Nerodia taxispilota* (n = 16) was the only watersnake noted and collected at Lake

Hollingsworth, which were not infected with hemogregarines. Currently, additional efforts are underway to (1) collect more snakes and (2) complete *Hepatozoon* spp. life cycles in the laboratory to determine experimental specificity and confirm parasite identification using oocysts and sporocysts in the mosquito host.

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DETECTION OF AN INVASIVE PARASITE, *ANGUILLICOLOIDES CRASSUS*, OF AMERICAN EELS USING QPCR

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Anguillicoloides crassus is a nematode parasite of Asian origin that infects the swim bladder of its native host, the Japanese eel *Anguilla japonica*. The parasite was unintentionally introduced to the U.S. and Europe, with the earliest detections of the species in U.S. waters occurring during the mid-1990s. In the introduced range, *A. crassus* now infects both the American eel, *Anguilla rostrata,* and the European eel, *Anguilla anguilla*. The parasite may be associated with declining populations of both eel species because it causes more extensive host pathology and mortality compared with infected native Japanese eels. Methods of preventing introductions and/or the spread of such invasive species are a priority in the early detection and rapid response to aquatic invasions. The ultimate goal of this project is to develop a molecular tool that will accurately detect and quantify *A. crassus*. To achieve this, *A. crassus*-specific regions of the *Cox I* gene were identified and used to develop and optimize species-specific primers appropriate for qPCR. The primers were tested against closely related nematode species and *A. rostrata* DNA to verify their specificity. To establish limits of detection, gravid *A. crassus* worms were removed from infected eels to obtain eggs harboring L_2 larvae (the free-living stage that infects crustacean intermediate hosts). L_2 larvae were allowed to hatch from the eggs and triplicate qPCR assays were performed using 1, 5, 20, 50 and 100 L_2 larvae to generate standard curves for quantification. Once developed, the molecular tool should enable *A. crassus* to be detected in water, sediments, potential vectors, and both intermediate and definitive hosts.

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DONAX VARIABILIS: A VECTOR FOR A DIGENEAN OF THE FLORIDA POMPANO *TRACHINUS CAROLINUS*

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The coquina clam, *Donax variabilis* is a known host of multiple digenean larvae. Sporocysts infect the clam's gonads and are thought to induce castration, while metacercariae inhabit various locations within the host, such as foot muscle or siphon. Despite the fact that such parasites have been known for some time, several of these larvae have not been taxonomically identified; further, their life cycles have yet to be resolved. This work focused on the molecular identification of gonadal sporocysts and foot-muscle metacercariae found in *D. variabilis* collected from Folly Beach, South Carolina in the summer of 2013. Prevalence of infection by metacercariae in foot muscle was 100% and mean intensity was 30 ± 1.84 (N = 448). Infection by sporocysts was not tabulated. DNA was isolated from a subsample of metacercariae and sporocysts, and a portion of small subunit ribosomal DNA (SSU rDNA) was PCR-amplified and sequenced. Resulting sequences from sporocysts and metacercariae were identical. In order to identify the definitive host of the metacercariae, we collected digeneans from the digestive tract of Atlantic croaker (*Micropogonias undulatus*) and Florida Pompano (*Trachinus carolinus*), which are known predators of coquina clams. DNA from individual digeneans was isolated and the same portion of SSU rDNA was amplified and sequenced for comparison. Whereas sporocyst and metacercaria SSU rDNA sequences were only 96% similar to the digenean sequence from the Atlantic croaker, they were 100% identical to the

digenean sequence from the Florida Pompano. We conclude that the parasite studied use coquina clams as both first and second intermediate hosts and the Florida Pompano as a definitive host. Morphological identification and additional sequencing of this parasite are currently being carried out in order to establish definitive species identification.

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HUNTING FOR THE ALTERNATE HOST OF *KUDOA INORNATA*, A MYXOZOAN PARASITE OF SPOTTED SEATROUT

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Kudoa spp. are widespread parasites of marine fishes. No *Kudoa* life cycles are known, but they probably require annelid worm alternate hosts. *Kudoa inornata* is a parasite of spotted seatrout, a commercially important species and an indicator of biological integrity of coastal resources. Both wild and captive seatrout become infected with *K. inornata* at high prevalence and intensity in Charleston Harbor, SC. To find the putative alternate host, we sampled annelids in summer 2014, by hand and by grab from the intertidal zone to 5m deep water. We examined 2287 polychaetes and 871 oligochaetes. We found a low diversity of oligochaete species (2 families, 5 species), but the level of overt myxozoan infections was relatively high: 45/871 (5%) with >20 genetically distinct actinospore types. For polychaetes, species diversity was very high (>20 families) but we found myxozoan infections only in 1 species of spionid 6/574 (1%); 0/1713 other polychaetes. We sequenced 18S rDNA from 34 infections. Four myxozoans were found twice each, but the rest were unique sequences, which indicated high local myxozoan diversity. The polychaete infections were genetically identical. BLAST searches showed no similarities >98% with GenBank myxozoan sequences. Phylogenetic analyses showed striking correlation between polychaetes as hosts of "marine" lineage myxozoans and oligochaetes as hosts of "freshwater" lineage myxozoans. This pattern leads us to hypothesize that the invertebrate host of *K. inornata* is a marine polychaete worm, probably a Spionid, Serpulid or Sabellid (which are known to host other myxozoan species). Collectively, these data are the first description of myxozoan infections in marine annelids from North America, and only the fifth species found in a marine polychaete worldwide.

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DEMONSTRATION OF *SARCOCYSTIS FALCATULA* AND *S. FALCATULA* ARG-LIKE PARASITES IN HEART AND BREAST MUSCLES FROM RAPTORS

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The present investigation is part of a long-term study designed to examine the evolutionary biology of *Sarcocystis* species in opossums. *Sarcocystis falcatula* encephalitis has been identified in the brains of great horned owls, golden eagles, and bald eagles in raptor rehabilitation centers. Opossums, *Didelphis virginiana* are the definitive host (DH) for *S. falcatula, S. falcatula* Arg-like, *S. lindsayi*, *S. speeri*, and *S. neurona* (*S. falcatula/S. neurona* complex), the opossums shed the sporocysts in their feces. Sarcocysts of *S. falcatula* have been observed in skeletal muscles from raptors indicating that they can serve as true intermediate hosts (IH). We found that 27 of 114 raptors were positive for *Sarcocystis* spp. using histology, PCR-RFLP, and ITS based PCR sequencing. Of these 27 ITS PCR positive samples 9 were also positive for JNB33/54 PCR and RFLP placing them in the *S. falcatula/S. neurona* complex. This indicates that the18 samples positive by ITS PCR but negative by JNB33/54 PCR are potentially new species of *Sarcocystis*. We will sequence the ITS gene of the 18 DNA samples that were positive only for *Sarcocystis* ITS and compare them to the ITS sequence from the 9 DNA samples that are in the *S. falcatula/S. neurona* complex. This will allow us to create a phylogenetic tree, which will reveal more about the relationships of these *Sarcocysitis* spp. based on ITS gene sequence. With this information, we will be able to run the necessary molecular tests (using different primers and restriction enzymes) to confirm the species of

Sarcocystis that the raptors are serving as IH for. We hypothesize that new species of *Sacrocytsis* using raptors as IH will be discovered. Additionally, using the phylogenetic tree we generate we can determine if *Sarcocystis* spp. using raptors as the IH (*Sarcocystis*-Arg, and *S. falcatula*) are more closely related than *Sarcocystis* spp. using mammals as IH (*S. neurona* and *S. speeri*) even though they all use the same DH (*D. virginiana*).

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EXAMINATION OF A NEW SPECIES OF RHINEBOTHRIIDEAN CESTODE FROM *HIMANTURA PASTINACOIDES* (ROUND WHIPRAY)

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This study of a new species of rhinebothriidean cestode is part of a continuous survey of parasites, including cestodes, from elasmobranchs in Borneo, Australia, and Senegal. In this study, a morphologically unique species of tapeworm from a rhinebothriidean genus referred to by Healy et al., 2009 as new genus 3 was collected from several specimens of *Himantura pastinacoides* in Borneo. Unique characteristics for this species were identified using methods such as light microscopy, histological sectioning, and scanning electron microscopy. Through analysis using these methods it was observed that the arrangement of loculi on the bothridia showed a pattern of anterior, posterior, and marginal loculi, with marginal locui specific to the posterior end. Other unique features found were filitriches and spinitriches in restricted areas along the posterior margin of the proximal bothridial surface. The unique combination of locular arrangements and microtriches enable distinction of this new species from other members of the new genus to which it belongs. This work, among numerous other studies, further emphasizes the diversity of cestodes that still exist and have yet to be defined in elasmobranchs.

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IS *AMBLYOMMA PARVUM* A COMPLEX OF CRYPTIC SPECIES?

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Amblyomma parvum is a hard tick species with a wide distribution, spanning from Mexico to Argentina (Guglielmone et al 2003). In the last years it has also been found in the US imported by parasitized animals entering the country from South and Central America (Corn et al 2012). Some ticks species with wide geographic distribution are indeed a cluster of cryptic species: morphologically identical species, but with different bioecological and pathogen-transmission capacities (Szabo et al 2005; Labruna et al 2009, 2011; Mastropaolo et al 2011, Beati et al., 2013). Recent studies suggest that this may apply to *A. parvum*. The analyses of 16S Nava et al (2008) determined values of genetic divergence between Argentine and Brazilian populations indicating that these could actually be different species. Taking this into account, the main objective of our research was to reassess the taxonomic status of *A. parvum* by using 6 different molecular markers, and extending the analysis to more northern latitudes. *A. parvum* specimens were obtained from different Central and South American countries. The molecular markers employed were the fast evolving 12SrDNA, 16SrDNA, D-loop, COI, COII (mitochondrial) and ITS2 (nuclear) genes. The phylogenetic analyses were consistent in identifying three different genetic clades within *A. parvum*. Two of them, from Brazil and Argentina, are sufficiently closely related to be conspecific, but the Central American specimens differ from other specimens by divergence values compatible with the occurrence of a different species.

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EXAMINATION OF A NEW SPECIES OF RHINEBOTHRIIDEAN CESTODE FROM A NEW SPECIES OF STINGRAY (*HIMANTURA UARNAK* 2) FROM COASTAL AUSTRALIA

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Recent survey work of elasmobranch parasites in northern Australia led to the discovery of several new cestode species. This study utilizes light and scanning electron microscopy to characterize a new species of the cestode order Rhinebothriidea, belonging to an undescribed genus referred to by Healy et al (2009) as "new genus 3." This cestode was found in an undescribed species of stingray referred to by Naylor et al (2012) as *Himantura uarnak* 2. Examination using light microscopy demonstrated that this new cestode possesses bothridia with three horizontally oriented loculi on the anterior region and seven vertically oriented loculi on the posterior region, a feature similar to that seen in another new species of this genus collected from Borneo. The vagina of the species in the present study, however, is distinctive in that it does not recurve anteriorly. This study is part of broad international endeavor to discover and classify parasites, including cestodes, of elasmobranchs around the world.

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PINWORM DIVERSITY IN PRIMATES INHABITING RAINFOREST IN MEXICO

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Three species of primates are found in Mexico, two howler monkeys, *Alouatta palliata* and *A. pigra*, and the spider monkey *Ateles geoffroyi*. All three are considered threated species due to pressures that compromise their conservation. Although numerous studies of primates have been conducted in Mexico, the parasite diversity of these primates has not been investigated in detail. In this study we determined the pinworm diversity in Mexican primates using morphological and molecular data. We employed non-invasive sampling techniques to collect the pinworms from these three primates in several localities throughout their distribution. Four different pinworm species were identified, including *Trypanoxyuris minutus, T. atelis,* and *T. atelophora*. Mixed infections were common, with two pinworm species per host species. Species delimitation was based on morphological and molecular data; a phylogenetic analysis was also completed to understand the evolutionary relationships among these nematodes. Our results show that pinworm diversity in Neotropical primates may be higher than expected. Increased sampling effort to study pinworms from different primate species is needed to better estimate parasite biodiversity and phylogenetic history

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TESTING THE SYSTEMATIC POSITION OF *MAGNIVITELLINUM SIMPLEX* KLOSS, 1966 WITHIN THE FAMILY MACRODEROIDIDAE (DIGENEA) BY USING SEQUENCES OF THE 28S RRNA

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Magnivitellinum simplex is a parasite of characids of the genus *Astyanax* (*A. aeneus, A. bimaculatus, A. eigenmanniorum, A. fasciatus* and *A. mexicanus*) and *Oligosarcus* (*O. jenynsii*) whose distributional range extends across the America (Argentina, Brazil, Nicaragua and Mexico). It was originally recorded by Kloss (1966) as a parasite of *Astyanax bimaculatus* in Mogi-Guassu River, State of Sao Paulo, Brazil. In Mexico, this species has been found as a parasite of *Astyanax aeneus* and *A. mexicanus* in 26 localities (Chiapas, Durango, Guerrero, Hidalgo, Nuevo León, Oaxaca, Quintana Roo, San Luis Potosí, Veracruz and Yucatán). This parasite is characterised by the tegumental spines along the body, oral sucker equal size as the acetabulum, muscular pharynx and short esophagus, with vitellaria extending from intestinal bifucartion to posterior margin of posterior testis. It has been allocated into the family Macroderoididae. However, its phylogenetic relationships with other members of the family have not been established. Recently, we conducted fieldwork in 14 localities across Mexico and we sampled 140 individuals of *Astyanax aeneus* and *A. mexicanus* mainly from north and southeastern of Mexico. Specimens of *M. simplex* were collected and that gave us the opportunity to study their morphology by using light and scanning electron microscopy. DNA sequences were obtained. We sequenced the domains D1-D3 of the rRNA of three individuals from three localities (Chiapas, San Luis Potosí and Tabasco). An alignment was built including all the representative members of the family, and our sequences were included. Our results reveal that *M. simplex* is the sister taxon of the genus *Alloglossiidium* which are a mostly parasites of freshwater fishes in North America.

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CHARACTERIZATION OF *ASCARIS* FROM PIGS USING MITOCHONDRIAL AND NUCLEAR MARKER GENES

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Ascaris is a common soil transmitted helminth with a worldwide distribution and a high zoonotic potential. Ascariasis is caused by both *Ascaris lumbicoides* and *Ascaris suum* in humans and pigs. Up to 6 different genotypes based on the ITS1 gene and greater than 29 haplotypes based on mt-DNA have been described from around the world. However, there is no genetic data available from North America. In the present study *Ascaris* obtained from pigs, originating from different farms in Iowa and other states, were characterized using the mitochondrial genetic marker - cyclooxygenase1 (cox1), and the nuclear marker - internal transcribed sequence 1 (ITS1). The gene sequences of the isolates were compared with sequences on GenBank, and neighbor joining trees were constructed. Past studies in endemic areas have shown that two host-associated transmission cycles with limited cross-transmission are common. Although there is evidence for limited cross-transmission in non-endemic areas like the United States, differences in farming practices may contribute to different population structures in humans and pigs. We will discuss the relevance of the molecular epidemiological data collected, for prospective studies of *Ascaris* transmission dynamics, host association, and dispersal.

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UNCOVERING THE HIDDEN DIVERSITY OF *BOTHRIOCEPHALUS* SPP. IN NORTH AMERICAN FRESHWATER FISHES

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Survey work in Canada and the U.S. in the last decade has shown that what was once considered a single species, *Bothriocephalus cuspidatus*, is an assemblage of several species that can be differentiated using a combination of morphology (DIC light microscopy, SEM) and molecular data. This study continues that exploration and the prospecting for new species from several hosts and localities, including goldeye (*Hiodon alosoides*) from Manitoba, Canada, centrarchids from Wisconsin and Michigan, and darters (Etheostomini) from Wisconsin. *Bothriocephalus* spp. from these hosts show different levels of molecular and morphological differences when compared with *Bothriocephalus cuspidatus* from the type host, walleye (*Sander vitreus*) in Canada and the U.S. So far, our studies have identified at least 3 (possibly 4) different species of *Bothriocephalus*, with their own host specificities in darters, centrarchids, and goldeye. The midwest alone is home to 4 of these 5 species of *Bothriocephalus* in question.

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DIVERSITY OF *LISSORCHIS* SPP. (TREMATODA: LISSORCHIIDAE) EXPLORED THROUGH MORPHOLOGY AND MOLECULES

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The genus *Lissorchis* comprises an assemblage of at least 17 nominal species that typically parasitize hosts of the mainly Nearctic fish family Catostomidae (suckers). This study is based on recent surveys of fishes in Manitoba, Canada, as well as in Wisconsin and Oregon in the U.S. that allow for a more detailed morphological study of unflattened specimens using light (DIC) microscopy and Scanning Electron Microscopy (SEM), as well as sequence data from the rRNA genome. These studies have revealed that closely related hosts such as the ictiobines *Carpiodes cyprinus* and *Ictiobus cyprinellus* In Manitoba, Canada, have morphologically and genetically similar yet distinct species of *Lissorchis* that were conflated in the past as *Lissorchis gullaris*, and that the external features such as spination, tegumental papillae and gross acetabular morphology provide informative characters in describing and differentiating new species of *Lissorchis*.

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CRYPTOGONIMID TREMATODES OF THE FISHES OF OTSEGO LAKE, NEW YORK

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This study is part of a survey of the intestinal parasites of fishes of Otsego Lake and its tributaries (Cooperstown, New York) that began in 2008. To date, over 500 individual fish were collected by hook and line, seine, gill net, or ElectroFisher, and subsequently examined for intestinal parasites, and in many cases, for parasites in other fish organs. The survey included a total of 27 fish species, consisting of six centrarchid species, one ictalurid species, eleven cyprinid species, three percid species, three salmonid species, one catostomid species, one clupeid species, and one esocid species. Intestinal trematodes were studied by light microscope examination of specimens that were whole-mounted using conventional methods. Scanning electron microscopy was also used. The survey work revealed a relatively low diversity of trematodes occurring as adults in the alimentary canal of fishes in Otsego Lake; for the first six years a total of only six species of trematodes were encountered, including one species of cryptogonomid, *Crytogonimus chili*, from *Ambloplites rupestris* and *Micropterus dolomieu*. In winter 2014, however, a

second as yet unidentified species of cryptogonimid was found in the intestine of *Esox niger* that were collected via ice fishing. This specimen, which possesses an elongate body and a terminally oriented oral sucker, is recognized as a member of Cryptogonimidae because of its possession of a ventral sucker that is embedded in a pouch. The discovery of an additional species of trematode after six years of routine survey work is testimony for the importance of the continued acquisition of parasitological data in water bodies.

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PHYLOGEOGRAPHIC ANALYSIS OF THE NORTH AMERICAN MEDICINAL LEECH *MACROBDELLA DECORA* (ANNELIDA: HIRUDINEA)

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The term "medicinal leech" commonly refers to any hirudinean whose feeding habits are hematophagous and has been used to cause phlebotomies in order to treat a variety of human diseases in several cultures around the world. In accordance with such definition, species of *Macrobdella* have been considered as the North American medicinal leech. *Macrobdella decora* is the most widely distributed species of the genus, inhabiting in most of the southeastern states of Canada, the northeastern states of the United States and Northern Mexico. *Macrobdella decora* has three pairs of jaws armed with fine denticles and conspicuous green and orange coloration patterns on the dorsal surface. It can easily be distinguished from other species of the genus by the presence of two pairs of copulatory glands located under the female gonopore. Its geographical distribution has been considered disjunct due to the absence of populations between the USA and Mexican populations. It is generally thought that glaciations during the Pleistocene (11,000 years ago) could have had a great impact on the current geographical distribution of several organisms of the region and *M. decora* might be a good model to study that problem. In order to investigate the potential impact of the last glaciation on the distribution and genetic configuration of the current populations of *M. decora* all across its geographical distribution, we have collected specimens of *M. decora* from Eastern USA and Southern Canada and investigated the variation of two mitochondrial markers: the mitochondrial cytochrome *c* oxidase subunit I (COI) and nicotinamide adenine dinucleotide dehydrogenase subunit I (ND1) and three nuclear microsatellites generated in previous studies. Preliminary analyses indicate higher levels of nucleotide variation than expected under the assumption that *M. decora* represents a single species. For example, ND1 from populations separated by less than 500 km differ in seven positions (fixed nucleotides). Further analysis including specimens from other localities, especially from the East of the Appalachians might provide valuable information in order to better characterize the molecular variation of *M. decora* and detect possible new species as well as to investigate the effects of the last glaciation on the distribution and genetic structure of the current populations.

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PHYLOGENETIC POSITION OF *SYNDESMIS FRANCISCANA* (RHABDOCELA: UMAGILLIDAE), SYMBIONT OF ECHINOIDS BASED ON MOLECULAR MARKERS

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The phylum Platyhelminthes includes more than 20,000 species of organisms with an enormous variation in form, size and ecological requirements. Neodermata is one of the most important groups of platyhelminths and includes many of the most pathogenic animal and human parasites such as *Taenia solium*, *Schistosoma mansoni* and *Fasciola hepatica*. Phylogenetic relationships within Neodermata have been investigated on multiple occasions and are relatively well known. However, investigations in non-parasitic flatworms, historically included in the class Turbellaria, have been neglected; in consequence

many aspects of their basic biology and their evolutionary relationships remain unknown. Establishing the phylogenetic position of species proposed as “intermediate” between free-living and parasitic forms is a key element to better understand the evolution of parasitism and in more modern terms, to identify the sister group of Neodermata. Umaguillidae (Neodalyellida) includes arround 68 species of turbellarians, some of them endosymbiotic of echinoderms inhabiting their coelom and intestine. Species of Umaguillidae are distributed in European seas (Mediterranean Sea including the Barents Sea), Caribbean, Pacific Ocean and the Indian Ocean. General information about umaguillids from the Americas is scarce and little is known about their phylogenetic relationships and position between flatworms. In the present study, the phylogenetic relationships of Umaguillidae were re-investigated in order to allocate the planarian genus *Syndesmis* in a phylogenetic context. The phylogenetic analysis included newly generated DNA sequences of the nuclear 18S rDNA and 28S. Specimens of *Syndesmis franciscana* were collected in sea urchins (*Echinometra viridis*) from several places of the Gulf of Mexico, in the State of Veracruz, Mexico. Newly generated sequences, along with information from other flatworms available in GenBank, were integrated to generate phylogenetic analyses using different approaches (Parsimony and Bayesian inference). Our results confirm the monophyly of Umagillidae including *Whalia*, *Seritia* and *Anoplodium*, all of them symbionts of echinoderms. Mapping the ecological traits (i.e. host associations and habitat) in the phylogenetic trees, suggests that multiple origins of association between planarians and echinoderms have occurred in the course of evolution.

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COLLECTIONS MANAGEMENT POLICIES AND PROCEDURES OF THE USNPC

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Since its founding in 1894, the United States National Parasite Collection (USNPC) has been maintained by scientists and curators of the Agricultural Research Service (ARS) of the United States Department of Agriculture (USDA) initially in Washington, D.C., and then for over 70 years at the Beltsville Area Research Center in Maryland. The USNPC holdings include approximately 210,000 lots (20,000,000 specimens) consisting of 35 phyla of parasitic taxa and including over 14,000 type lots (3,000 holotypes and 7,000 type series). The USNPC is a cornerstone for global and North American parasitology and serves as an irreplaceable resource for research programs emphasizing biodiversity and systematics of parasites and complex host-parasite systems. In 2013 an agreement was articulated between the USDA/ARS and the Smithsonian Institution to transfer the USNPC in its entirety (fluid specimens, slide specimens, frozen tissues, and reprints) to the National Museum of Natural History (NMNH) in Washington, D.C. The relocation of the USNPC to the NMNH is underway. Curatorial control now lies with the NMNH and collections management policy of the NMNH is implemented by the Department of Invertebrate Zoology (NMNH-IZ) and the Department of Entomology (NMNH-Ent). Information about procedures for donation of specimens, policies for loans, including requests for destructive sampling, and arranging scientific visits can be found at the website for the NMNH-IZ (http://invertebrates.si.edu/collections.htm). The entire USNPC Collection Database can be downloaded on the NMNH-IZ website (http://invertebrates.si.edu/parasites.htm). The web interface of the NMNH-IZ specimen catalog can be accessed at: collections.nmnh.si.edu/search/iz/.

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HEMOPOIETIC TISSUE VOLUME IS A HERITABLE TRAIT IN THE SCHISTOSOME-TRANSMITTING SNAIL *BIOMPHALARIA GLABRATA*

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Hemocytes are the main effector cell in the internal defense system (IDS) of the snail *Biomphalaria glabrata*. The amebocyte producing organ (APO) in the anterior wall of the pericardial sac is a site for hemopoiesis in this snail, and undergoes hyperplasia in response to trematode infection and several other types of challenge with non-self. Consequently, the APO may play a role in interactions between the IDS and invading larval trematodes. In this study we developed a method for measuring total APO volume and explored whether APO size was a heritable trait. Juvenile snails (4.5-5 mm, shell diameter) from 3 laboratory strains of *B. glabrata* were initially compared: the schistosome-resistant, wild-type Salvador strain, which has a well-developed APO, and 2 schistosome-susceptible, albino (M-line) strains, one from the Biomedical Research Institute, Rockville, MD (BRI-M), and the second from the University of San Francisco (USF-M), which unlike BRI-M appears to lack an APO as adults. Total APO volumes were measured in serial histological sections of pericardial sacs with the use of a graphics tablet and Image J software. Total numbers of mitotic figures in the largest APO section also were counted, providing a mitotic index (mitotic figures/μm^3). Additionally, hemocyte concentrations were measured in hemolymph samples from 30 adult specimens (10.5-13 mm) of each strain. Among the 3 strains, APO size was highest in Salvador snails and lowest in USF-M snails, with that in BRI-M snails intermediate, and differences between strains were statistically significant. Hemocyte counts in adult Salvador snails also were higher than in the other 2 strains, although counts in USF-M snails (that lack an APO) were slightly higher than those in BRI-M snails (that possess an APO). Next, individual Salvador and USF-M snails were paired, and APO volumes were measured in F_1 hybrid progeny of the albino parent, and in F_2s produced by pooled F_1 hybrids. Finally, juvenile and adult specimens of USF-M and BRI-M snails were exposed to 50 miracidia each of *Schistosoma mansoni* to test whether susceptibility to infection was correlated with APO size. APO volume in F_1 hybrids from Salvador-USF-M crosses was nearly identical to that of Salvador snails, showing that this trait is dominant. Among F_2s, APO volume was approximately 50% of that in the Salvador strain, but still significantly higher than that of the USF-M strain. Despite significant differences in APO volumes between laboratory strains and between F_1s and F_2s from Salvador-USF-M crosses versus USF-M snails, mitotic indices did not differ. Moreover, infection prevalence was similar in USF-M and BRI-M snails. These data suggest that APO volume in juvenile *B. glabrata* is a heritable trait, and does not correlate with APO mitotic activity, hemocyte concentrations, or susceptibility to infection with *S. mansoni*. Finally, absence of an APO in adult USF-M snails suggests that hemocyte formation occurs in a location outside the pericardial sac.

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PREVALENCE OF RACCOON ROUNDWORM (*BAYLISASCARIS PROCYONIS*) IN A SEMI-URBAN ENVIRONMENT IN NORTHWEST MISSOURI: PRELIMINARY FINDINGS

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Raccoons are the only member of the raccoon family to naturally occur in Missouri, and are very adaptable to life around humans. Their proximity to humans can cause some health concerns. They can carry diseases and parasites that could be transmitted to humans. One such parasite is raccoon roundworm (*Baylisascaris procyonis*). Raccoon roundworm larvae can infect the central nervous system of humans, causing disease and in rare cases death. Since raccoons live in urban and suburban environments, there is increasing awareness of the possibility of human infection from raccoon roundworm. Roundworm eggs are shed in raccoon feces, and can remain viable in the environment for long periods of time. We began a survey of raccoon latrines on the Missouri Western State University campus to determine the distribution and prevalence of raccoon roundworm. We established 100 x 100 m

grids on the campus of MWSU and have begun to systematically search each grid. We recorded the location of each fecal sample and latrine using mapping grade global positioning systems (Trimble Navigation, Ltd., Sunnyvale, CA). We then analyzed each sample for raccoon roundworm using standard fecal floatation technique. So far, we have evaluated 53 samples and found raccoon roundworm eggs in 9; an approximately 17% infection rate. The extent, to which our preliminary results accurately reflect infection rate and prevalence, will depend upon analyzing additional samples.

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MOSQUITO SPECIES DISTRIBUTION IN RESIDENTIAL AREAS ACROSS SAN ANTONIO, TEXAS

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The purpose of this study is to provide a preliminary survey of mosquito species of veterinary and medical importance in residential backyards across San Antonio, Texas. The number of stray dogs in San Antonio is approximately 150,000 and they are known reservoirs for heartworm, *Dirofilaria immitis*, posing a risk to companion pets. According to data collected in 2014 by The Companion Animal Parasite Council, 19.75% of all positive heartworm cases in U.S. come from Texas, and 8.19% of all positive cases in Texas are from Bexar County. In addition, because San Antonio is in close proximity to areas where mosquito-vectored diseases such as Dengue Fever and West Nile are endemic, assessing the presence of mosquitoes known to vector these human diseases is important. Seventeen zip codes across San Antonio were sampled for mosquito species during the summer and early fall of 2014. Both CDC light traps baited with dry ice and BG-Sentinel traps (non-baited) were used to collect mosquito species. We identified 28 mosquito species within six genera: *Aedes, Culex, Ochelrotatus, Orthopodomyia, Psorophora, and Anopheles*. *Aedes* was the most prevalent genus, with *Aedes aegypti* found in all zip codes sampled. Five of the mosquito species known to vector *D. immitis* were found, including *Ae. aegypti*. Additionally, eleven of the mosquito species known to carry and transmit West Nile Virus were present. In future studies we aim to improve our collection methods, sample additional locals, correlate data with weather patterns, and include various

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ASP Meeting History

1925 Kansas City MO
1925 Philadelphia PA
1927 Nashville TN
1928 New York NY
1928 Des Moines IA
1930 Cleveland OH *
1931 New Orleans LA
1932 Atlantic City NJ
1933 Boston MA
1934 Pittsburgh PA
1935 St Louis MO
1936 Atlantic City NJ
1937 Indianapolis IN
1938 Richmond VA
1939 Columbus OH
1940 Philadelphia PA
1941 Dallas TX
1942 No meeting
1943 No meeting
1944 Cleveland OH
1945 St. Louis MO
1946 Boston MA
1947 Chicago IL
1948 New Orleans LA *
1949 New York NY
1950 Cleveland OH
1951 Chicago IL *
1952 Ithaca NY †
1953 Madison WI †
1954 Memphis TN *
1955 Atlanta GA
1956 Storrs CT †
1957 Philadelphia PA *
1958 Bloomington IN †
1959 University Park, PA †
1960 Los Angeles CA *
1961 Lafayette IN †
1962 Washington DC ‡
1963 Chicago IL *
1964 Boulder CO †
1965 Atlanta GA
1966 San Juan PR *
1967 Tucson AZ §
1968 Madison WI †
1969 Washington DC *
1970 Washington DC ¶
1971 Los Angeles CA
1972 Miami Beach FL *
1973 Toronto ON, Canada
1974 Kansas City MO
1975 New Orleans LA *
1976 San Antonio TX
1977 Las Vegas NV
1978 Chicago IL *
1979 Minneapolis MN
1980 Berkeley CA
1981 Montreal QB, Canada
1982 Toronto ON, Canada
1983 San Antonio TX *
1984 Snowbird UT
1985 Athens GA
1986 Denver CO *
1987 Lincoln NE #
1988 Winston-Salem NC
1989 Vancouver BC, Canada
1990 East Lansing MI
1991 Madison WI
1992 Philadelphia PA
1993 Atlanta GA *
1994 Ft. Collins CO
1995 Pittsburgh PA **
1996 Tucson AZ ††
1997 Nashville TN
1998 Kona HI
1999 Monterey CA ‡‡
2000 San Juan PR ††
2001 Albuquerque NM
2002 Vancouver BC, Canada ¶§§
2003 Halifax NS, Canada
2004 Philadelphia PA **
2005 Mobile AL
2006 Glasgow, Scotland ¶
2007 Merida Yucatan, Mexico §§¶ ¶
2008 Arlington TX
2009 Knoxville TN
2010 Colorado Springs CO
2011 Anchorage AK
2012 Richmond VA
2013 Quebec City QB, Canada ***
2014 New Orleans LA
2015 Omaha NE
2016 Edmonton, Alberta, Canada

* With American Society of Tropical Medicine; since 1952, American Society of Tropical Medicine and Hygiene
† With American Institute of Biological Sciences
‡ With Helminthological Society of Washington
§ With American Microscopical Society
¶ With the International Congress of Parasitology; 1970 (ICOPA-II), 1982 (ICOPA-V), 2002 (ICOPA-X), 2006 (ICOPA-XI)
# With Wildlife Disease Associaton
** With American Association of Veterinary Parasitologists
†† With Society of Protozoologists
‡‡ With Society of Nematologists
§§ With Sociedád Méxicana de Parasitología
¶¶ With Parasitology Section, Canadian Society of Zoologists
*** With Québec Molecular Parasitology