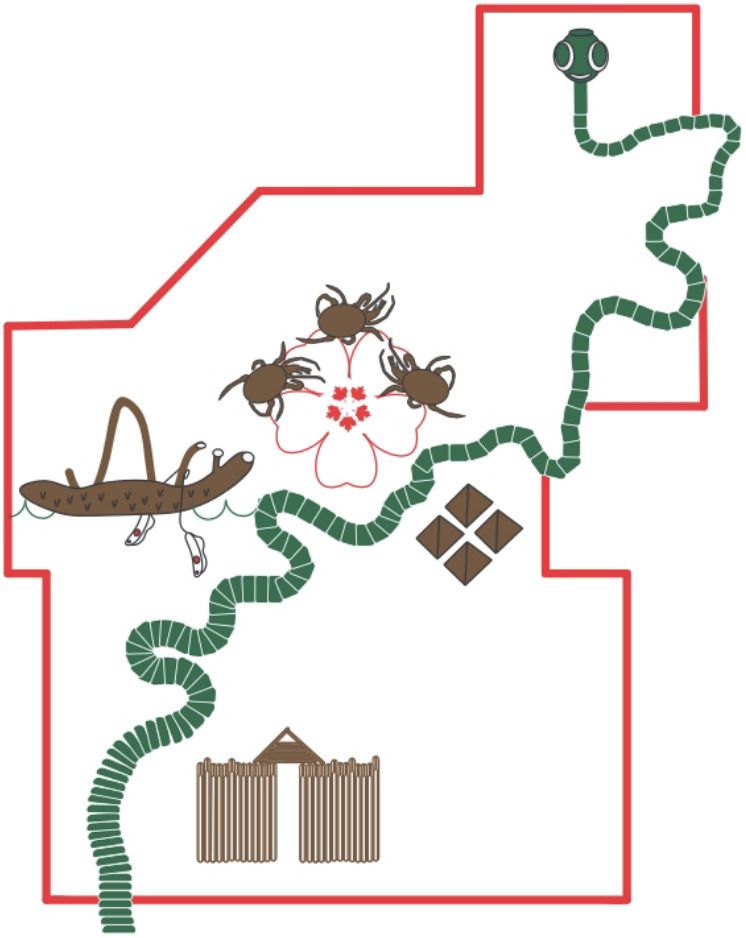
The 91st Annual Meeting of the American Society of Parasitologists

The Westin Edmonton



Edmonton, Alberta, Canada

July 11-14, 2016

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 Organizing Committee

Al Shostak, Chair – University of Alberta

Mike Belosevic - University of Alberta

Patrick Hanington - University of Alberta

Lien Luong - University of Alberta

Dr. John C. Holmes, Honorary Committee Member

Scientific Program Officers

Herman Eure, Wake Forest University

Kelli Sapp, High Point University

Sponsors

- Sierra Upton (sponsor of the Steve Upton Party for ASP Students; Sierra is the daughter of the late Dr. Steve J. Upton)
- Robert Grieve, ASP Past Predsident
- Faculty of Science, University of Alberta

The American Society of Parasitologists
ESTABLISHED 1924

Welcome

We would like to welcome you to the 91st annual meeting of the American Society of Parasitologists (ASP).

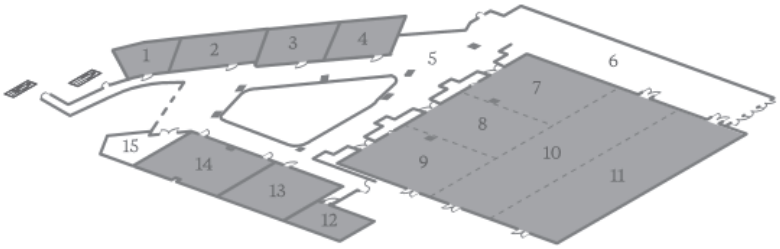
The ASP is a diverse group of over 1500 scientists from industry, government, and academia who are interested in the study and teaching of parasitology. Founded in 1924, ASP members have contributed not only to the development of parasitology as a discipline, but also to primary research in systematics,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

Herman Eure and Kelli Sapp, Scientific Program Officers

Floor Plan, The Westin Edmonton, Lobby Level and Second Floor

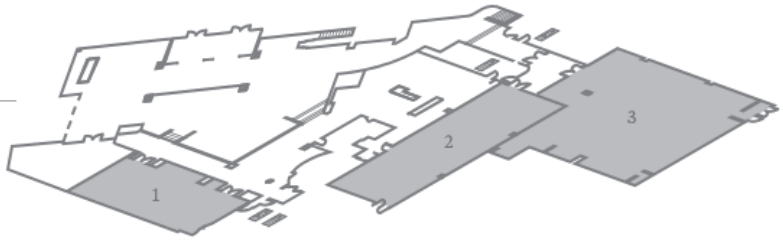
SECOND FLOOR

1. DIRECTOR
2. CONSULATE
3. CHANCELLOR
4. CHAIRMAN
5. WEST FOYER
6. NORTH FOYER
7. BRITISH COLUMBIA
8. ALBERTA
9. YUKON
10. SASKATCHEWAN
11. MANITOBA
12. ATHABASCA
13. LEDUC
14. TURNER VALLEY
15. TANGENT



LOBBY LEVEL

1. STRATHCONA
2. CENTENNIAL
3. DEVONIAN



American Society of Parasitologists Discrimination Policy

Statement of Policy: In accordance with the bylaws of the American Society of Parasitologists (ASP), the Society will afford an environment free from discrimination, harassment, and retaliation. The ASP will not tolerate actions, statements, or contacts that discourage the free expression and exchange of scientific ideas. This includes unequal treatment or harassment of any person based on their age, gender, gender identity or expression, marital status, sexual orientation, race, color, national or ethnic origin, religious identifications, beliefs or practices, disabilities, veteran status, or any other reasons or expressions that are unrelated to their scientific merit. Harassment, sexual or otherwise, shall be considered as a form of misconduct and violators will be subject to disciplinary actions, including expulsion from a society function or from the society itself.

Definition of Sexual Harassment: Sexual harassment refers to unwelcome sexual advances, requests for sexual favors, and other verbal or physical conduct of a sexual nature. Sexual harassment does not refer to occasional compliments of a socially acceptable nature. It refers to behavior that is not welcome, is personally offensive, debilitates morale, and therefore, interferes with a collegial atmosphere. The following are examples of behavior that, when unwelcome, may constitute sexual harassment: sexual flirtations, advances, or propositions; verbal comments or physical actions of a sexual nature; sexually degrading words used to describe an individual; a display of sexually suggestive objects or pictures; sexually explicit jokes; unnecessary touching. What is perceived as acceptable to one person may be unwelcome by another. Those who have positions of authority or higher rank should be aware that others may be reluctant to outwardly express objections or discomfort regarding unwelcome behavior or language.

Other Types of Harassment: Remarks and behaviors based on other protected characteristics are also unacceptable to the Society. These include stereotyping, slurs, derogatory jokes or statements, and any hostile or intimidating acts.

Policy Scope: This policy applies to all attendees and participants at ASP meetings and functions, including social functions, tours, or off-site activities during the course of meetings and functions, and includes all members, guests, staff, contractors, and exhibitors.

Reporting an Incident: If any individual covered by this policy believes that they have experienced or witnessed harassment or bullying they should contact the society's designated individual **[Dr. Sara Brant, sbrant@unm.edu]**. No complainant will be required to discuss any incident with a respondent; no respondent will be required to discuss any incident with a complainant. All individuals (complainant or respondent) may bring an accompanying individual of their choice with them for support at any point when they discuss the matter with the society's designated individual, or during any course of an ensuing investigation.

Because allegations of discrimination, harassment and misconduct are sensitive matters with the potential to negatively impact the reputation of individuals, institutions, and/or our Society, confidentiality and discretion throughout the process is expected from all parties involved and is assured from the ASP's designated individual and all involved in the investigation.

Regardless, a complainant may speak in confidence with the society's designated individual without involving an official report, an investigation or a respondent. All complaints that are received will be treated seriously, and will be addressed promptly if that is the wish of a complainant. Any incidents of sexual assault should be immediately reported to the police. Note that many local and regional governments also consider a variety of behaviors to be reportable crimes regardless of the wishes of the complainant, respondent or of the society.

Investigation: Following the official report of an incident, the Society's designated individual, in consultation with ASP Council, will name an impartial investigator, usually an elected officer or Council member, and the respondent will be promptly notified. No one who has a conflict of interest with respect to the complainant or respondent will serve in this role. A complainant will be asked to

file a formal written complaint; the respondent will be notified immediately and prior to any discovery procedures. A respondent will be invited to respond to the complaint and allowed to bring evidence. The Council of the society reserves the right to interview other individuals as witnesses at its own discretion. The investigator is allowed to seek counsel if they are in doubt as to how to proceed. When the investigation is complete, the findings will be communicated to the elected officers, as well as both to the complainant and respondent. Those officers without a conflict of interest will decide on appropriate disciplinary actions.

Retaliation: The Society will not tolerate any form of retaliation against individuals who report an incident, against those who are subject to a complaint, nor against those who participate in an investigation. Retaliation will be considered a form of discrimination in and of itself and offenders will be subject to disciplinary action, up to and including ejection from the society.

Disciplinary Action: If an individual harasses, retaliates, or knowingly makes a false claim, they will be subject to disciplinary action. These actions might range from a verbal warning to a request to leave the meeting or function without refund of fees and a reporting of the incident to the person's employer. Should repeated complaints, patterns of inappropriate behavior, or other events emerge, the society's by-laws permit its Council to exclude and eject members through a process that has no appeal.

Appeal & Questions: Should any person be dissatisfied with the result of an investigation or disciplinary action, they may appeal to the President of the Society, or to the highest ranking officer without a conflict of interest. Questions concerning the policy can be directed to an ASP officer or the ASP designated individual.

Congratulations to American Society of Parasitologists Member and Nobel Laureate Dr. William “Bill” C. Campbell!

2016 Recipient of the Nobel Prize in Physiology or Medicine

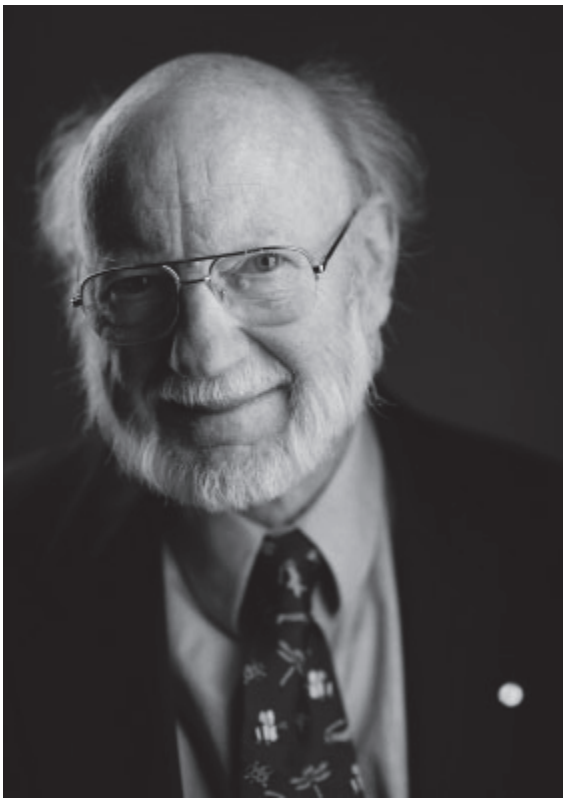


Photo: A. Mahmoud

2016 Recipient of the ASP Eminent Parasitologist Lectureship Award

Day/Times	Activity/Function	Room/Space
July 11 (Monday)		
8:00 a.m.-Noon	ASP Council	Strathcona
2:00-6:00 p.m.	Host-Parasite Interactions I	Yukon
2:00-5:45 p.m.	Life Cycles and Epidemiology	Alberta
3:45-4:15 p.m.	Coffee Break	West Foyer
7:00-10:00 p.m.	Welcome Reception	Manitoba/Saskatchewan
July 12 (Tuesday)		
8:30-10:30 a.m.	ASP President's Symposium*	Saskatchewan
10:30-11:00 a.m.	Coffee Break	North/West Foyer
11:00-Noon	ASP Student Business Meeting	Saskatchewan
Noon-1:00 p.m.	Editorial Board Luncheon	Chairman
1:00-3:00 p.m.	Teacher Education Symposium	British Columbia
1:00-3:00 p.m.	Taxonomy, Systematics, Phylogeny I	Alberta
1:00-3:00 p.m.	Host-Parasite Interactions II	Yukon
3:00-3:30 p.m.	Coffee Break	North/West Foyer
3:30-5:30 p.m.	ASP Students' Symposium	Saskatchewan
5:30-6:30 p.m.	ASP Student Social	North Foyer
3:00-6:00 p.m.	Auction Set Up	Manitoba
6:00-7:00 p.m.	Auction Preview	Manitoba
7:00-9:00 p.m.	26th Annual ASP Student Auction	Manitoba
July 13 (Wednesday)		
8:00-10:30 a.m.	Host Parasite Interactions III	Yukon
8:30-10:30 a.m.	Associate Editor's Symposium	British Columbia
10:30-11:00 a.m.	Coffee Break	North/West Foyer
11:00-Noon	ASP President's Address	Saskatchewan
1:30-5:45 p.m.	Evolutionary Ecology I	British Columbia
2:00-5:15 p.m.	Taxonomy, Systematics, Phylogeny II	Alberta
2:00-4:45 p.m.	Biochemistry/Physiology/Immunology Chemotherapeutic & Drug/Vector	Yukon
3:30-4:00 p.m.	Coffee Break	North/West Foyer
7:00-10:00 p.m.	Evening at Muttart Conservatory**	
July 14 (Thursday)		
8:00-11:45 a.m.	Genomics & Molecular Biology	Alberta
8:00-12:00 p.m.	Evolutionary Ecology II	British Columbia
8:30-11:30 a.m.	Host-Parasite Interactions IV	Yukon
8:30-10:00 a.m.	Authors complete poster set up	Manitoba
9:45-10:15 a.m.	Coffee Break	North/West Foyer
12:00-1:30 p.m.	Poster Session, coffee, snacks	Manitoba
1:45-2:45 p.m.	H.B. Ward Lecture	Saskatchewan
3:00-4:00 p.m.	ASP Awards and Business Meeting	Saskatchewan

* ASP President Symposium will include the Eminent Parasitologist Lecture.

** Buses will leave The Westin between 6:45 - 7:00 p.m., and return to The Westin from 9:00 - 10:00 pm. Food and beverage stations, and conservatory access, will be open throughout the event.

Monday Morning, 2016-07-11

8:00 am – Noon ASP Council Meeting, Strathcona

Presiding: **M.E. Siddall**, American Museum of Natural History

Monday Afternoon, 2016-07-11

2:00-6:00 pm Host-Parasite Interactions I

Location: Yukon

Presiding: **R. Cole**, US Geological Survey

Time (Abstract No.)

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

2:00 (1) † **A.E. Matthews**, J.L. Larkin, D.W. Raybuck, M.C. Slevin, S.H. Stoleson, T.J. Boves. FEATHER MITE ABUNDANCE VARIES BY ECOLOGICAL CONTEXT, BUT SYMBIOTIC NATURE OF MITE-HOST RELATIONSHIP DOES NOT DIFFER IN TWO WARBLER SPECIES.

2:15 (2) † **C.C. Pierce**, M.G. Bolek. DISTRIBUTION AND REPRODUCTIVE STRATEGIES OF *GYRINICOLA BATRACHIENSIS* (OXYUROIDEA: PHARYNGODONIDAE) AND THEIR FUNGAL SYMBIONTS IN TADPOLE STAGES OF FIVE SPECIES OF ANURANS.

2:30 (3) **E. Pila**, M. Tarrabain, A. Kabore, P. Hanington. A NOVEL TOLL-LIKE RECEPTOR INFLUENCES COMPATIBILITY BETWEEN *BIOMPHALARIA GLABRATA* (GASTROPODA) AND THE HUMAN BLOOD FLUKE *SCHISTOSOMA MANSONI* (DIGENEA).

2:45 (4) **R. Krause**. INCREASED INFECTION OF PRESCHOOL CHILDREN WITH SOIL-TRANSMITTED HELMINTHS DURING EXPOSURE TO AGRICULTURE DIMINISHES IMPROVEMENTS OF AN AGRICULTURAL INTERVENTION ON PRESCHOOL CHILD GROWTH IN RURAL PANAMA.

3:00 (5) † **J. Bell**, A. Fecchio, J. Weckstein, V. Tkach. HOST LIFE HISTORY TRAITS PREDICT THE PROBABILITY OF AVIAN MALARIA INFECTION IN THE BRAZILIAN AMAZON.

3:15 (6) † **C. Li**, J. Detwiler. IMPROVING ESTIMATES OF WILDLIFE DIET: INTEGRATING PARASITES AND STABLE ISOTOPE ANALYSIS.

3:30 (7) **L.H. Du Preez**. MORPHOLOGICAL SPECIALIZATION FOR ATTACHMENT BY POLYSTOMES (MONOGENEA: POLYSTOMATIDAE).

3:45-4:15 pm **COFFEE BREAK**

4:15 (8) **D. Colwell**, F. Leggett, C. Goater, B. van Paridon. WHAT'S ON YOUR MIND: INFECTION OF THE SUB-OESOPHAGEAL GLAND OF ANTS INFECTED BY METACERCARIAE OF *DICROCOELIUM DENDRITICUM*.

4:30 (9) † **P. Selseleh**, T. Chakraborty, L. Eliuk, J. Detwiler. DNA SEQUENCING REVEALS UNEXPECTED VARIATION IN FIRST INTERMEDIATE HOST SPECIFICITY IN ECHINOSTOME TREMATODES.

4:45 (10) † **K. Speer**. A FLY ON THE CAVE WALL: USING BAT FLIES (STREBLIDAE) TO UNDERSTAND HOST BAT DISPERSAL.

5:00 (11) † **L. Lu**, S. Zhang, M.W. Mutuku, G.M. Mkoji, E.S. Loker. RELATIVE COMPATIBILITY OF *SCHISTOSOMA MANSONI* WITH *BIOMPHALARIA SUDANICA* AND *B. PFEIFFERI* FROM KENYA AS ASSESSED BY PCR AMPLIFICATION OF THE *S. MANSONI* ND5 GENE IN CONJUNCTION WITH TRADITIONAL METHODS.

5:15 (12) **Z.W. Dempsey**. ECOLOGICAL EPIDEMIOLOGY OF EMERGING LIVER FLUKE, *DICROCOELIUM DENDRITICUM*, IN OREOHELID LANDS SNAILS IN CYPRESS HILLS PARK, ALBERTA.

5:30 (13) † **S.Y. Wang**, G.J. Tattersall, J. Koprivnikar. UNDERSTANDING EFFECTS OF TREMATODE-INFECTION ON TEMPERATURE SELECTION IN TADPOLES.

5:45 (14) **M.M. Nazir**, M. Akhtar, A. Waheed, A.N. Ahmed, M.A. Sajid, M.A. Ali, M.A. Alam and D. S. Lindsay. EFFECT OF CONTRIBUTING RISK FACTORS ON THE PREVALENCE OF *TOXOPLASMA GONDII* INFECTION IN THE SERA OF PREGNANT AND NON-PREGNANT WOMEN AT NISHTAR HOSPITAL, MULTAN, PAKISTAN.

2:00-5:45 pm Life Cycles and Epidemiology

Location: Alberta

Presiding: **N. Lodh**, Marquette University

Time (Abstract No.)

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

2:00 (15) A. Janik, D. Markle, V. Tkach, A. Choudury, **M. Kent**. PARASITE ASSOCIATED MORTALITY IN SHORTNOSED (*CHASIMISTES BREVIROSTRIS*) AND LOST RIVER SUCKERS (*DEKTISTES LUXATUS*).

2:15 (16) **D.S. Lindsay**, S.K. Verma, D. Scott, J.P. Dubey, A.C. Rosypal. DEVELOPMENT OF SARCOCYSTIS ISOLATED FROM A COOPER'S HAWK (*ACCIPITER COOPERI*) AND A RED-SHOULDERED HAWK (*BUTEO LINEATUS*) IN CELL CULTURE.

2:30 (17) † **S. Hopkins**. QUANTIFYING THE BARRIERS AND BRIDGES TO INTERSPECIFIC TRANSMISSION IN A COMMON HOST-SYMBIONT SYSTEM.

2:45 (18) † **E.A. Zieman**, F.A. Jimenez, C. Nielsen. *CYTAUXZOON FELIS* INFECTIONS IN BOBCATS, DOMESTIC CATS, AND TICK VECTORS IN THE SOUTHERN REGION OF ILLINOIS.

3:00 (19) **R. Blaylock**, J. Lotz, M. Muhammad, S. Curran. RESERVOIR COMMUNITIES AND THE MAINTENANCE OF WHITE SPOT SYNDROME VIRUS IN THE NORTHERN GULF OF MEXICO.

3:15 (20) **S. Michalski**, Z. Williams, L. Mann, Z. Heimark, L. Bowen, S. Schaar. ADVANCES TOWARD LARGE SCALE PRODUCTION OF *ACANTHACHEILONEMA VITEAE*.

3:30 (21) **J.M. Porter-Kelley**. BLENDING TEACHING AND RESEARCH IN A DOG TAPEWORMS STUDY.

3:45-4:15 pm **COFFEE BREAK**

4:15 (22) † **S.G. Sapp**, L.N. Rascoe, P.P. Wilkins, S. Handali, E.B. Gray, M. Eberhard, D.M. Woodhall, S.P. Montgomery, E.W. Lankau, K.L. Bailey, M.J. Yabsley. SUBCLINICAL BAYLISASCARIASIS AND ASSOCIATED RISK FACTORS IN WILDLIFE REHABILITATORS FROM THE UNITED STATES AND CANADA.

4:30 (23) **J. Leaphart**, D. Zelmer. THE LIFE CYCLE OF *HAEMATOLOECHUS FLOEDAE* HARWOOD, 1932 (DIGENEA: PLAGIORCHIIDAE).

4:45 (24) **N.M. Orji**. DISTRIBUTION OF LOIASIS INFECTION IN EHIME MBANO AND EZINIHITTE MBAISE LOCAL GOVERNMENT AREAS OF IMO-STATE NIGERIA.

5:00 (25) **T.R. Olariu**, V. Dumitrascu, C. Petrescu. HYMENOLEPIASIS IN INSTITUTIONALIZED ROMANIAN CHILDREN.

5:15 (26) **E.A. Omudu**, C.F. Okafor, A.D. Yaji. DETECTION OF LYMPHATIC FILARIASIS USING CLINICAL EXAMINATION AND IMMUNOCHROMATOGRAPHIC CARD TEST AND FILARIASIS RELATED KNOWLEDGE, ATTITUDES AND PERCEPTION AMONG THREE ETHNIC GROUPS IN BENUE STATE, NIGERIA.

5:30 (27) **M.E. Idu**, E.A. Omudu, A.D. Yaji. EPIDEMIOLOGY OF CO-INFECTION OF INTESTINAL PARASITES AND TUBERCULOSIS IN BENUE STATE, NIGERIA.

Monday Evening, 2016-07-11

7:00 - 10:00 pm WELCOME RECEPTION

Location: Manitoba/Saskatchewan

Tuesday Morning, 2016-07-12

8:30-10:30 am ASP President's Symposium
*Eminent Parasitologist Lecture**

Location: Saskatchewan

Presiding: **S.L. Perkins**, American Museum of Natural History

Theme: Magic Bullets and Windows of Opportunity.

8:30 **S. L. Perkins**. Introduction.

8:40 **T. Ruhnke**. Presentation of the 2016 Eminent Parasitologist Lectureship Award Recipient.

8:50 (28)* **W.C. Campbell**. DOES CHEMOTHERAPY HAVE A FUTURE IN PARASITE CONTROL?

9:20 (29) **J.M. Carlton**. THE E-WORD: IS MALARIA ERADICATION A REALISTIC GLOBAL GOAL?

9:50 (30) **F.O. Richards**. MAYBE THERE IS REASON FOR OPTIMISM FOR LONG TERM MDA EFFECTIVENESS?

10:20-10:30 Questions, Closing Remarks.

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

11:00 am-Noon ASP Student Business Meeting

Location: Saskatchwan

Presiding: **S. Weinstein**, University of California Santa Barbara

Tuesday Afternoon, 2016-07-12

Noon – 1:00 pm Editorial Board Luncheon

Location: Chairman

1:00-3:00 pm ASP Education Committee Symposium

Location: British Columbia

Presiding: **G. Mayer**, Mahattan College
M.A. Gordy, University of Alberta

Theme: Parasitology Careers Outside of Academia.

1:00 Introduction.

1:10 (31) **K. Jacobson**. IF YOU THINK YOU WANT TO SAVE THE SALMON, OR THE WHALES…, OR REALLY JUST GO FLY FISHING?

1:35 (32) **K.D. Lafferty**. I'M FROM THE GOVERNMENT AND I'M HERE TO HELP.

2:00 (33) **T.G. Geary**. PARASITOLOGY IN INDUSTRY.

2:25-3:00 Questions, Closing Remarks.

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

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

Location: Alberta

Presiding: **A.J. Phillips**, Smithsonian's National Museum of Natural History

Time (Abstract No.)

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

1:00 (34) † **L.E. Camp**, S. Nadler. *BAYLISASCARIS* PHYLOGENETICS: ASSESSING SPECIES VALIDITY.

1:15 (35) † **G. Vasquez**, N.J. Negovetich. A REVIEW OF *SALSUGINUS SECULUS* (PLATYHELMINTHES: MONOGENEA) IN THE WESTERN MOSQUITOFISH (*GAMBUSIA AFFINIS*) FROM TEXAS.

1:30 (36) **A. Smythe**, C. Kline. GENETIC DIVERSITY AND CRYPTIC SPECIES OF THE *ECHINOSTOMA TRIVOLVIS* SPECIES COMPLEX FROM CENTRAL NEW YORK MUSKRATS.

1:45 (37) † **K.S. Herzog**, K. Jensen. DOES SIZE MATTER? TAPEWORM FAUNAL DIVERSITY AND HOST SIZE IN THE MANGROVE WHIPRAY FROM THE SOLOMON ISLANDS AND AUSTRALIA.

2:00 (38) † **K.A. Gallagher**, J.N. Caira, M. Cantino. EXAMINING THE NOVEL INTERNAL ANATOMY OF AN ENIGMATIC TAPEWORM USING TRANSMISSION ELECTRON MICROSCOPY.

2:15 (39) **M. Oros**, A. Choudhury, T. Scholz, R. Kuchta. MONOZOIC TAPEWORMS OF FRESHWATER FISHES IN NORTH AMERICA: AN UPDATE AND PERSPECTIVES.

2:30 (40) **R. Guyer**, K. Jensen. CESTODE FAUNA OF THE GIANT FRESHWATER WHIPRAY COMPARABLE TO THAT OF ITS MARINE RELATIVES.

2:45 (41) † **V. Mantovani Bueno**, J. Caira. UNEXPECTED TAPEWORM FORAYS INTO SKATE HOSTS.

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

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

Location: Yukon

Presiding: **M. Scott**, McGill University
T. Yoshino, University of Wisconsin-Madison

Time (Abstract No.)

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

1:00 (42) † **A.L. Edwinson**. CHARACTERIZATION OF CARBOHYDRATE STRUCTURES THAT TRIGGER REPLICATION IN *CRYPTOSPORIDIUM*.

1:15 (43) **L. Leroux**. *TOXOPLASMA GONDII* AFFECTS TRANSLATION INITIATION IN MACROPHAGES BY TARGETING THE MTORC1 AND MNK1/2 PATHWAYS.

1:30 (44) **I.C. Mgbemena**, K.E. Nweke, C.O. Ezea. SCREENING OF ETHANOL EXTRACT OF *COMBRETUM RACEMOSUM* AND *EUPHORBIA HIRTA* LEAVES FOR POSSIBLE ACTIVITY ON *TRYPANOSOMA BRUCEI BRUCEI* INFECTED MICE.

1:45 (45) † **A.D. Stumbo**, R. Poulin. ALTERATIONS TO NEURONAL ACTIVITY AS A FUNCTION OF METACERCARIAE INFECTION INTENSITY.

2:00 (46) **N. Kovacevic**. ACUTE PHASE RESPONSE DURING THE COURSE OF INFECTION IN *TRYPANOSOMA CARASSII* INFECTED GOLDFISH (*CARASSIUS AURATUS* L.).

2:15 (47) J. Marquez, C.E. Montelongo, G. Overcast, **M.G. Castillo**. EXPRESSION OF THIOESTER-CONTAINING PROTEINS IN THE SNAIL *BIOMPHALARIA GLABRATA* IN RESPONSE TO MICROBIAL CHALLENGE.

2:30 (48) † **R.P. Shannon**, M. Bolek. AMPHIBIAN TRYPANOSOMES FROM NORTH CENTRAL OKLAHOMA: MORPHOLOGY, MOTILITY, AND PHYLOGENETIC RELATIONSHIPS.

2:45 (49) **K.L. Sheehan**, P.N. Albers, R.F. Hechinger. DO ECTOPARASITE INFRACOMMUNITIES OF COASTAL BIRDS FOLLOW THE METABOLIC THEORY OF ECOLOGY?

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

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

Location: North Foyer

Presiding: **S. Weinstein**, University of California Santa Barbara

Theme: Methods in Parasitology.

Time (Abstract No.)

3:30 Introduction.

3:40 (50) **V. Tkach**. MAXIMIZING THE OUTPUT: COLLECTING AND FIXATION OF QUALITY HELMINTH SPECIMENS IN THE FIELD.

3:55 (51) **J.N. Caira**. A TOTAL EVIDENCE APPROACH TO THE IDENTIFICATION AND DESCRIPTION OF HELMINTHS.

4:10 (52) **M.L. Kent**. HISTOLOGY AND FISH PARASITE SURVEYS.

4:25 (53) **A.J. Phillips**. ARCHIVING PARASITES IN SCIENTIFIC COLLECTIONS – SPECIMENS, DATA, AND THE BIOREPOSITORY.

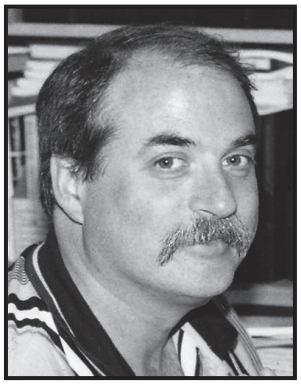
4:40 (54) **S.L. Perkins**, M. Zilversmit, J. Foox. GENOMICS METHODS FOR PARASITOLOGY.

4:55 (55) **K. Lafferty**. ECOLOGICAL METHODS FOR PARASITOLOGY.

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: Saskatchewan



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.

Tuesday Evening, 2016-07-12

Steve J. Upton

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

7:00-9:00 pm ***26th ANNUAL ASP STUDENT AUCTION***

Location: Manitoba

Wednesday Morning, 2016-07-13

8:00-10:30 am *Host Parasite Interactions III*

Location: Yukon

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

Time (Abstract No.)

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

8:00 (56) **S.A. Shea**, A.M. Fedynich, L.A. Brennan, D.B. Wester. ASSESSMENT OF HELMINTH COMMUNITIES IN NORTHERN BOBWHITES FROM SOUTH TEXAS.

8:15 (57) † **S.K. Buddenborg**, S. Zhang, G.M. Mkoji, E.S. Loker. RNA-SEQ RESPONSES OF FIELD-DERIVED SPECIMENS OF THE AFRICAN SNAIL *BIOMPHALARIA PFEIFFERI* TO INFECTION WITH THE HUMAN PARASITE, *SCHISTOSOMA MANSONI*.

8:30 (58) **J. Kvicerova**. SURPRISING EVOLUTIONARY PATTERNS IN COCCIDIA INFECTING *APODEMUS* AND ARVICOLID HOSTS.

8:45 (59) † **R.W. Koch**, R.P. Shannon, K.D. Gustafson, M.G. Bolek. USING MORPHOLOGICAL AND MOLECULAR DATA TO IDENTIFY A *NEOECHINORHYNCHUS* SP. (PHYLUM: ACANTHOCEPHALA) INFECTING A NEW SNAIL HOST (*HELISOMA TRIVOLVIS*).

9:00 (60) **I.C. Mgbemena**, R.C. Asianuba. EVALUATION OF ANTI-MALARIAL AND ANTIOXIDANT ACTIVITIES OF ETHANOLIC LEAF EXTRACT OF *VERNONIA AMYGDALINE* DELILE ON MICE INFECTED WITH *PLASMODIUM BERGHEI*.

9:15 (61) † **T.E. Stewart**, C.E. Cáceres. PLANKTON-PARASITOID INTERACTIONS: A WINDOW INTO WITHIN-HOST DYNAMICS.

9:30 (62) † **B. Shakya**, L. Wang, G.K. Kilili, D.J. LaCount. ANCHORING *PLASMODIUM FALCIPARUM* EXPORTED PROTEINS TO ERYTHROCYTE CYTOSKELETON AND UNDERSTANDING THEIR FUNCTION.

9:45 (63) **S. Shirakashi**, K. Tani, K. Ishimaru, T. Honryo, H. Uchida, K. Ogawa. TEMPORAL AND SPATIAL INFECTION PATTERNS OF TUNA BLOOD FLUKES *CARDICOLA* SPP. IN POLYCHAETE INTERMEDIATE HOSTS AT A TUNA FARM IN JAPAN.

10:00 (64) † **H. Toman**. COMPARATIVE PHYLOGEOGRAPHY OF NORTH AMERICAN PIKA PARASITES: UNRAVELING A HISTORY DRIVEN BY CLIMATE CHANGE.

10:15 (65) † **C. Anaya**, B. Hanelt, MG. Bolek. EFFECTS OF HAIRWORM INFECTION (NEMATOMORPHA: GORDIIDA) ON CRICKET REPRODUCTIVE OUTPUT.

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

8:30-10:30 am Associate Editor's Symposium

Location: British Columbia

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

Theme: Diverse Perspectives in Parasitology – Mechanism of Action of Ivermectin, Species Recognition in Freshwater Tapeworms, and Paleoparasitology.

Time (Abstract No.)

8:30 Introduction.

8:40 (66) **T.G. Geary**. IVERMECTIN AND FILARIAE: THE DAWN OF UNDERSTANDING.

9:10 (67) **A. Choudhury**. EX UNO PLURES: SPECIES RECOGNITION AND DIVERSIFICATION OF FRESHWATER *BOTHRIOCEPHALUS* SPECIES IN NORTH AMERICAN FRESHWATER FISHES.

9:40 (68) **C. Faulkner**. PALEOPARASITOLOGY: A WINDOW TO THE PAST FOR APPRECIATION OF HOST-PARASITE RELATIONS IN SPACE AND TIME.

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

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

11:00-Noon *ASP President's Address*

Location: Saskatchewan

Presiding: S. Desser, President Emeritus, ASP

11:00 Introduction of **Dr. Mark Siddall**.

11:10 **M.E. Siddall**, "Reinvention and Resolve."

Mark Siddall, President

Wednesday Afternoon, 2016-07-13

1:30-5:45 pm Evolutionary Ecology I

Location: British Columbia

Presiding: **A. Choudhury**, St. Norbert College
R. Hechinger, Scripps Institution of Oceanography

Time (Abstract No.)

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

1:30 (69) † **F. Zahlan**, J. Koprivnikar. PARASITISM OF INVASIVE AND NATIVE SPECIES: EVALUATION OF ENDOHELMINTHS IN ROCK BASS AND SMALLMOUTH BASS FROM ALGONQUIN PARK LAKES.

1:45 (70) † **E.S. Durkin**. PARASITE EVOLUTION: HERITABLE VARIATION IN INFECTION STRATEGY IN A FACULTATIVE PARASITE.

2:00 (71) † **N.H. Bird**. SHOULD I STAY OR SHOULD I GO: INFECTION PLASTICITY IN THE FACULTATIVELY PARASITIC MITE *MACROCHELES SUBBADIUS*.

2:15 (72) † **D. Milotic**, J. Koprivnikar. ROAD SALT REDUCES LARVAL AMPHIBIAN PARASITE AVOIDANCE BEHAVIOUR BUT NOT RESISTANCE TO INFECTION.

2:30 (73) † **M. Milotic**, J. Koprivnikar. DENSITY AND COMPLEXITY OF AQUATIC VEGETATION DOES NOT AFFECT LARVAL AMPHIBIAN PARASITISM.

2:45 (74) † **S.R. Gallagher**, K.E. Galbreath. POPULATION DYNAMICS AND PHYLOGEOGRAPHY OF A BERINGIAN CESTODE, *AROSTRILEPIS MACROCIRROSA*.

3:00 (75) † **O.C. Friesen**, C. Lagrue. PARASITE-MEDIATED HABITAT USE BETWEEN CONGENERIC ISOPODS.

3:15 (76) † **A.E. Garcia-Vedrenne**, A. Kuris, R. Hechinger. A PARADIGM SHIFT: SYNTHESIS AND FUTURE DIRECTIONS FOR TREMATODE SOCIALITY.

3:30 – 4:00 pm **COFFEE BREAK**

4:00 (77) † **M.R. Laidemitt**, M.W. Mutuku, G.M. Mkoji, E.S. Loker. BIOTIC DIVERSITY AND HUMAN SCHISTOSOMIASIS TRANSMISSION IN WESTERN KENYA.

4:15 (78) † **S. Weinstein**, A.M. Kuris. INDEPENDENT ORIGINS OF PARASITISM IN ANIMALIA.

4:30 (79) † **N. Chodkowski**, R.J. Bernot. PARASITE EFFECTS ON FRESHWATER SNAIL, *ELIMIA LIVESCENS* ELEMENTAL CONTENT AND METABOLISM.

4:45 (80) † **R.L. Grunberg**, M.V. Sukhdeo. PATTERNS IN PARASITE INFRAPOPULATION ENERGY USAGE.

5:00 (81) † C.L. Amundson, **N.J. Traub**, A.J. Smith-Herron, P.L. Flint. HELMINTH COMMUNITY STRUCTURE IN TWO SPECIES OF ARCTIC BREEDING WATERFOWL.

5:15 (82) † **A.M. DeRogatis**, A.E. Garcia-Vedrenne, A.M. Kuris. LIFE IN A DISH: OPTIMIZATION OF AN IN VITRO SYSTEM FOR TREMATODE PARTHENITAE.

5:30 (83) † **S. Bromagen**, B.C. Reeder, D. Eisenhour. IMPACT OF AGRICULTURAL RUNOFF AND COAL MINE EFFLUENCE ON MINNOW INTESTINAL PARASITES.

2:00-5:15 pm Taxonomy, Systematics & Phylogeny II

Location: Alberta

Presiding: **S. Seville**, University of Wyoming-Casper
V. Tkach, University of North Dakota

Time (Abstract No.)

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

2:00 (84) † **G.M. Haas**, K.E. Galbreath. TRANSBERINGIAN BIOGEOGRAPHY OF A HOLARCTIC TAPEWORM SPECIES COMPLEX.

2:15 (85) † **S. King**, P. Bentzen, D. Marcogliese. A FORAY INTO THE GENETICS OF THE SUPER-DIVERSE GENUS *GYRODACTYLUS*.

2:30 (86) **D.C. Metz**, R.R. Sheehy, M.T. Close, H.J. Small, J.M. Carrillo, R.M. Overstreet, J.D. Shields, R.F. Hechinger. UNEXPECTED DISCOVERY OF A NEW CILIATE PARASITE IN A WELL-STUDIED POPULATION OF LINED SHORE CRABS.

2:45 (87) **R. Kuchta**, T. Scholz, M. Oros, A. Choudhury. HOW MANY SPECIES ARE CAUSING DIPHYLLOBOTHRIOSIS IN NORTH AMERICA?

3:00 (88) **R.P. Shannon**, M. Bolek. USING GORDIID CYSTS TO DISCOVER THE HIDDEN DIVERSITY, POTENTIAL DISTRIBUTION AND NEW SPECIES OF HAIRWORMS (NEMATOMORPHA: GORDIIDA).

3:15 (89) **S. Brant**, E.S. Loker, V. Tkach, L. Casalins, V. Flores. PHYLOGENETIC PLACEMENT OF A SCHISTOSOME FROM AN UNUSUAL MARINE SNAIL HOST FROM ARGENTINA AND A SECONDARY SWITCH FROM FRESHWATER TO MARINE SNAILS.

3:30 – 4:00 pm **COFFEE BREAK**

4:00 (90) **S.E. Racz**, S.L. Gardner. HYMENOLEPIS WEINLAND, 1858: A PHYLOGENY.

4:15 (91) **T. Ruhnke**. A TAXONOMIC AND SYSTEMATIC ASSESSMENT OF THE TETRAPHYLLIDEAN GENUS *ANTHOBOTHRIUM*.

4:30 (92) † **A. Koontz**, J. Caira. A NEW BATOID-HOSTED CESTODE GENUS, WITH COMMENTS ON ITS PHYLOGENETIC RELATIONSHIPS AND HOST ASSOCIATIONS.

4:45 (93) † **M. Tessler**, M.E. Siddall. HOST AND PARASITE DIVERSITY: MAMMALIAN DIVERSITY FROM LEECH BLOOD MEALS AND TERRESTRIAL LEECH (*HAEMADIPSA*) PHYLOGENETICS.

5:00 (94) † **E.W. Sarvis**, E.T. Ebbs, E.S. Loker, V.V. Tkach, N. Davis, D. Jouet, S.V. Brant. COSMOPOLITAN SPECIES OR CRYPTIC SPECIES COMPLEXES: IS THE ARTERIAL WATERFOWL SCHISTOSOME, *DENTRITOBILHARZIA PULVERULENTA* A WIDESPREAD SPECIES?

2:00-4:45 pm Biochemistry, Physiology, Chemotherapy & Drug Resistance, Immunology, Vector Biology

Location: Yukon

Presiding: **J.F. Hillyer**, Vanderbilt University
J. Mead, Emory University

Time (Abstract No.)

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

2:00 (95) **J.F. Hillyer**, L.T. Sigle, G.P. League. MOSQUITO HEMOCYTE-MEDIATED IMMUNE RESPONSES OCCUR IN AREAS OF HIGH HEMOLYMPH FLOW.

2:15 (96) **D. Larson**, B. Barnes. PARASITE SURVIVAL IN A FREEZE-TOLERANT HOST.

2:30 (97) † **J.E. Igetei**, M. El-Faham, S. Liddell, M. Doenhoff. ANTIGENIC CROSS-REACTIVITY BETWEEN *SCHISTOSOMA MANSONI* AND PEANUT: INDICATION OF SOME SHARED GLYCAN EPITOPES AND IMPLICATIONS FOR THE HYGIENE HYPOTHESIS.

2:45 (98) **S.R. Stahl**, A.B. Taylor, X. Cao, P.J. Hart, S.F. McHardy, R. Tarpley, T.J. Anderson, P.T. LoVerde. SCHISTOSOMICIDAL OXAMNIQUINE DERIVATIVE DRUG ACTIVITY AGAINST ALL THREE HUMAN *SCHISTOSOMA* SPECIES.

3:00 (99) **J. Humphries**, L. Deneckere, B. Harter. IDENTIFICATION OF NUCLEAR FACTOR KAPPAB (NF-KB) BINDING MOTIFS IN *BIOMPHALARIA GLABRATA*.

3:15 (100) **F.O. Akinbo**, R.O. Ibadin, R. Omoregie, S.O. Olotu, I. Agbonile, O.M. Efam. MALARIA IN PSYCHIATRIC PATIENTS.

3:30 – 4:00 pm **COFFEE BREAK**

4:00 (101) **S.D. Zaongo**, D. Ji. IN VITRO OPTIMIZATION OF *NAEGLERIA FOWLERI* AXENIC CULTURE.

4:15 (102) **N.M. Orji**. VARIABILITY OF GIARDIASIS PREVALENCE CAUSED BY ANTHROPOGENIC ACTIVITIES IN FUNDONG HEALTH DISTRICT, CAMEROON.

4:30 (103) **C. Ikpeama**. STUDIES ON THE BIONOMICS OF SANDFLIES (DIPTERA: PSYCODIDAE) IN SOME REMOTE AREAS OF IMO STATE, NIGERIA.

Wednesday Evening, 2016-07-13

7:00 – 10:00 pm Muttart Conservatory

Buses will leave The Westin between 6:45 - 7:00 p.m., and return to The Westin from 9:00 - 10:00 pm. Food and beverage stations, and conservatory access, will be open throughout the event.

Thursday Morning, 2016-07-14

8:00-11:45 am Genomics & Molecular Biology

Location: Alberta

Presiding: **T. Geary**, McGillUniversity
S. Michalski, Univeristy of Wisconsin-Oshkosh

Time (Abstract No.)

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

8:00 (104) † **A. Leveille**, J. Barta. UNEXPECTED DIVERSITY OF ADELEORINID BLOOD PARASITES OF ONTARIO FROGS AND TURTLES DISCOVERED USING MITOCHONDRIAL GENOME SEQUENCES.

8:15 (105) † **S.D. Warring**, M. Bradic, S. Sullivan, J. Carlton. A NOVEL FAMILY OF SMALL RNAS REGULATES GENE EXPRESSION IN THE SEXUALLY TRANSMITTED PARASITE *TRICHOMONAS VAGINALIS*.

8:30 (106) † **J.M. Maritz**, K.H. Rogers, T.M. Rock, N. Liu, S. Joseph, K.M. Land, J.M. Carlton. IDENTIFYING PARASITES IN NEW YORK CITY SEWAGE.

8:45 (107) † **S. Galen**, S. Perkins. MOLECULAR EVOLUTION OF THE MALARIA PARASITES: ASSESSING THE EFFECTS OF NEUTRAL AND ADAPTIVE PROCESSES ACROSS TIME SCALES.

9:00 (108) † **C.D. Keroack**, K.M. Williams, K. Fessler, X. Miller, K. DeAngelis, E. Tsekitsidou, C.M. Velez, M.S. Schwartz, K.G. Anderson, J.Tozloski, S.A. Williams. A NOVEL QUANTITATIVE REAL-TIME PCR DIAGNOSTIC ASSAY FOR SEAL HEARTWORM (*ACANTHOCHEILONEMA SPIROCAUDA*) REVEALS FIRST REPORTED INFECTION IN THE GREY SEAL (*HALICHOERUS GRYPUS*).

9:15 (109) **S.P. Rudko**, N.F. Neumann, P.C. Hanington. A NOVEL DIAGNOSTIC QPCR TEST FOR THE ROUTINE MONITORING OF *ENTEROBIUS VERMICULARIS* IN WASTEWATER.

9:30 (110) **N. Lodh**, S. Soiefer, N. Caro, A. Scott, A. Krolewiecki, C.J. Shiff. DIAGNOSIS OF *STRONGYLOIDES STERCORALIS* SPECIES-SPECIFIC REPEAT DNA IN URINE RESIDUE.

9:45 – 10:15 am **COFFEE BREAK**

10:15 (111) **S. Liu**, D.M. Roellig, Y. Guo, M.A. Frace, K. Tang, L. Zhang, Y. Feng, L. Xiao. REDUCTIVE EVOLUTION OF MITOCHONDRIAL METABOLISM AND DIFFERENTIAL EVOLUTION OF INVASION-RELATED PROTEINS IN *CRYPTOSPORIDIUM*.

10:30 (112) **D.J. Marcogliese**, F. El-Shehabi, K. Boyce, G. McClelland, C. Abbott. A MOLECULAR SURVEY OF ANISAKID NEMATODES FROM MARINE FISHES IN CANADIAN WATERS.

10:45 (113) **J. Sperling**, K. Lucas Silva-Brandao, M. Mendes Brandao, V. Lloyd, S. Dang, C. Davis, F. Sperling, K. Magor. ASSESSMENT OF BACTERIA IN BLACKLEGGED TICKS, *IXODES SCAPULARIS* (ACARI: IXODIDAE).

11:00 (114) **R. Ratnappan**, J. Vadnal, M. Keaney, I. Eleftherianos, D. O'Halloran, J.M. Hawdon. RNAI-MEDIATED GENE KNOCKDOWN BY MICROINJECTION IN THE MODEL ENTOMOPATHOGENIC NEMATODE *HETERORHABDITIS BACTERIOPHORA*.

11:15 (115) **G. Alama-Bermejo**, E. Meyer, S. Atkinson, A.S. Holzer, J. Bartholomew. WEAPONS OF A PARASITE: PROTEASES FROM THE TRANSCRIPTOME OF *CERATONOVA SHASTA* (CNIDARIA: MYXOZOA).

11:30 (116) **H.N. Cinar**, G. Gopinath, D. Choi, A. Im, R. Kim, A. Jang, E. Kim, H. Murphy, A. DaSilva. AMPLICON SEQUENCING OF MITOCHONDRIA GENOME USING NEXT GENE SEQUENCING FOR MOLECULAR CHARACTERIZATION OF *CYCLOSPORA CAYETANENSIS* IN PRODUCE.

8:00-11:45 am Evolutionary Ecology II

Location: British Columbia

Presiding: **K. Lafferty**, US Geological Survey
M. Moser, University of California Berkeley

Time (Abstract No.)

8:00 (117) **C.J. Horn**, L.T. Luong. BIOENERGETIC RESPONSES TO PARASITE EXPOSURE AND INFECTION IN A FRUIT FLY HOST.

8:15 (118) **B.P. Ruehle**. RELATIONSHIP BETWEEN DIVERSITY AND ABUNDANCE OF PARASITES AND REPRODUCTIVE POTENTIAL IN TWO CYPRINIDS WITH DIFFERENT MATING STRATEGIES.

8:30 (109) **B.R. Krasnov**, I.S. Khokhlova, A. Degen, L.J. Fielden. HOST IDENTITY AND FLEA FITNESS: THE EFFECT OF PHYLOGENETIC DISTANCE BETWEEN HOSTS.

8:45 (120) **Z. Song**, H. Proctor. ELUCIDATING MECHANISMS AFFECTING ACANTHOCEPHALAN PREVALENCE IN FRESHWATER *GAMMARUS LACUSTRIS* AMPHIPODS.

9:00 (121) **Z. Zilz**, A.M. Kuris, R. Hechinger. MONTHLY VARIATION OF METACERCARIA ABUNDANCE OF TWO TREMATODE SPECIES IN THE CALIFORNIA KILLIFISH, *FUNDULUS PARVIPINNIS*, IN CARPINTERIA SALT MARSH.

9:15 (122) **K. Jacobson**, L. Weitkamp, D. VanDoornik, A. Aceves, J. Losee, R. Baldwin. TROPHICALLY TRANSMITTED PARASITES REFLECT DIFFERENCES BETWEEN NATURAL ORIGIN AND HATCHERY PRODUCED JUVENILE PACIFIC SALMON IN FRESHWATER, ESTUARINE AND MARINE HABITATS.

9:30 (123) **S. Woodman**, C. Goater. FLOWER CHOICE OF *DICROCOELIUM*-INFECTED ZOMBIE ANTS.

9:45 – 10:15 am **COFFEE BREAK**

10:15 (124) **R. Donnelly**, J. Detwiler. TESTING FOR CRYPSIS WITH INTEGRATIVE TAXONOMY IN A NORTH AMERICAN ECHINOSTOME TREMATODE.

10:30 (125) **G. Sandland**, J.P. Peirce. LIFE-HISTORY RESPONSES OF AN INVASIVE SNAIL (*BITHYNIA TENTACULATA*) AND ITS TREMATODE PARASITE (*SPHAERIDIOTREMA PSEUDOGLOBULUS*) DURING A SIMULATED OVERWINTERING PERIOD.

10:45 (126) **M.A. Gordy**, J. Koprivnikar, L. Kish, V.K. Phillips, M. Tarrabain, P.C. Hanington. VARIATION IN DIVERSITY AND COMMUNITY STRUCTURE OF SNAILS AND DIGENEANS IN CENTRAL ALBERTA LAKE ECOSYSTEMS.

11:00 (127) **C. Goater**. DECOMPOSING ATTACHMENT AND DETACHMENT BEHAVIOURS OF *DICROCOELIUM*-INFECTED ZOMBIE ANTS.

11:15 (128) **V.M. Vidal Martinez**, A.C. Wunderlich. PARASITES AS BIOINDICATORS OF ENVIRONMENTAL DEGRADATION IN LATIN AMERICA.

11:30 (129) **H. Proctor**. DO FEATHER MITES COMPETE FOR SPACE ON THEIR HOSTS?

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

Location: Yukon

Presiding: **R. Blaylock**, University of Southern Mississippi
J. Camp, Purdue University

Time (Abstract No.)

8:30 (130) **M. Batista Heitor Carneiro**, A. Romano, N. Doria, D. Sacks, N. Peters. INFLAMMATORY MONOCYTES, NOT TISSUE MACROPHAGES, ARE THE PREFERRED HOST CELL DURING THE EXPANSION PHASE OF INFECTION WITH THE OBLIGATE INTRACELLULAR PARASITE *LEISHMANIA MAJOR*.

8:45 (131) **A.D. Hernandez**, K. Philhower, D. Hoffman, M. Deganich. MACROPARASITE COMMUNITIES IN THE FISHES OF SACONY CREEK, PENNSYLVANIA.

9:00 (132) **H. Coatsworth**, P. Caicedo, G. Winsor, C. Ocampo, C. Lowenberger. FROM PHENOTYPE TO GENOTYPE: CREATING RESISTANT *AEDES AEGYPTI* TO PREVENT DENGUE TRANSMISSION.

9:15 (133) **G. Ahmad**. GENE SILENCING OF A 65 KDA CYSTEINE PROTEINASE OF *TRICHOMONAS VAGINALIS* INVOLVED IN CYTOTOXICITY OF THIS PARASITE USING A BIODEGRADABLE NANOPARTICLES LOADED WITH SMALL–INTERFERING RNA.

9:30 (134) **M. Haque**, K. Koski, M.E. Scott. MATERNAL PROTEIN DEFICIENCY AND NEMATODE INFECTION CAUSE DIFFERENTIAL EXPRESSION OF THE GENES FOR GROWTH AND PROTEIN BIOSYNTHESIS IN THE FETAL MOUSE BRAIN.

9:45 – 10:15 am **COFFEE BREAK**

10:15 (135) **J.M. Lovell**, K. Wyutyi, B. Springall, L.L. Da Silveira, Jr., A. McElwain. COMPARATIVE HISTOPATHOLOGY OF TREMATODE (DIGENEA) INFECTIONS IN THE GONAD OF FRESHWATER SNAILS (GASTROPODA, PLEUROCERIDAE) FROM RICE CREEK, NEW YORK.

10:30 (136) **K.L. Weinersmith**, S.M. Liu, A.A. Forbes, S.P. Egan. TALES FROM THE CRYPT: A PARASITOID CHANGES EMERGENCE BEHAVIOR IN A CRYPT-FORMING GALL WASP.

10:45 (137) **L.N. Allison**. EVALUATING THE EFFECT OF MALARIA PARASITES ON LIVER ENZYMES AMONG CHILDREN BETWEEN (5-10) YEARS OLD.

11:00 (138) **A. McElwain**, S.A. Bullard. PATHOGENICITY OF LARVAL NEMATODES (NEMATODA) INFECTING THE FOOT OF *VILLOSA NEBULOSA* (BIVALVIA, UNIONIDAE) FROM TERRAPIN CREEK, ALABAMA.

11:15 (139) **R.A. Cole**. HEPATIC AND INTESTINAL CAPILLARIASIS IN COMMON GOLDENEYE (*BUCEPHALA CLANGULA*), BARROW'S GOLDENEYE (*B. ISLANDICA*) AND BUFFLEHEAD (*BUCEPHALA ALBEOLA*) DUCKS HEAVILY INFECTED WITH *BARUSCAPILLARIA OBSIGNATA* (TRICHINELLOIDEA, CAPILLARIIDAE) FROM HANFORD, WASHINGTON.

8:30-10:00 am Poster Display Boards delivered

Location: Manitoba

Authors may set up posters during this time.

Thursday Afternoon, 2016-07-14

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

Location: Manitoba

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

CELL BIOLOGY

(140) **S.D. Warring**. PROMOTING PROTISTS ON SOCIAL MEDIA PLATFORMS.

CHEMOTHERAPY AND DRUG RESISTANCE

(141) **D.D. Aguiar**, M. Moscardini, E. Morais, R. De Paula, P. Ferreira, A. Afonso, S. Belo, W. Cunha, V. Rodrigues, L.G. Magalhães. CURCUMIN INDUCES APOPTOSIS AND OXIDATIVE STRESS IN *SCHISTOSOMA MANSONI* ADULT WORMS.

(142) **M. Moser**, C. Bidlow, C. Bulman, J. Sakanari. METALLOPROTEASE INHIBITORS AS POSSIBLE LEADS TO IDENTIFY DRUGS TO TREAT LYMPHATIC FILARIASIS AND OTHER PARASITIC ROUNDWORM INFECTIONS.

(143) **C. Bulman**, C. Bidlow, P. White, L. Chappell, A. Yang, W. Yang, W. Sullivan, J. Sakanari. SEARCHING FOR GOLD: EFFECTS OF AURANOFIN ON ADULT *BRUGIA PAHANGI* IN VITRO.

EVOLUTIONARY ECOLOGY

(144) **E.O. Campbell**, L. Luong. MITE CHOICE GENERATES SEX AND SIZE BIASED INFECTION IN *DROSOPHILA HYDEI*.

(145) **W. Preisser**, J. Light. HELMINTH FAUNA OF CRICETID RODENTS IN TEXAS AND PRELIMINARY INSIGHTS INTO PARASITE LATITUDINAL GRADIENTS.

(146) **C.J. Brianik**, R.L. Grunberg, J. Lovy. MACROPARASITE COMMUNITIES IN ANADROMOUS AND LANDLOCKED ALEWIVES (*ALOSA PSEUDOHARENGUS*) IN NEW JERSEY.

(147) **R. Bhaduri**, P. Valentich-Scott, M. Hilgers, R. Singh, M. Hickman. IS SIMULTANEOUS COMMENSALISM AND PARASITISM POSSIBLE? THE CASE OF THE BIVALVE *KURTIELLA PEDROANA* AND THE SAND CRAB *EMERITA ANALOGA*.

GENOMICS AND MOLECULAR BIOLOGY

(148) **S.A. Sullivan**, P.L. Sutton, S. Tachibana, Z. Luo, J.W. Barnwell, D.J. Conway, P.C. Divis, B. Singh, K. Tanabe, J.M. Carlton. GENOMICS AND GENETIC DIVERSITY OF THE MONKEY MALARIA PARASITE *PLASMODIUM CYNOMOLGI*.

(149) **A. Babyak**, J. Hurley, M.S. Tucker, D.E. Kyle. EXAMINATION OF POLYMORPHISMS IN ARTEMISININ-RESISTANT *PLASMODIUM FALCIPARUM*.

(150) **N.M. Dinguirard**, U.R. Bickham-Wright, K.K. Geyer, K.F. Hoffmann, T.P. Yoshino. EPIGENETIC MODULATION OF TRANSCRIPT AND PROTEIN EXPRESSION IN THE *BIOMPHALARIA GLABRATA* EMBRYONIC (BGE) CELL LINE BY SCHISTOSOME LARVAL PROTEINS.

(151) **N. Salcedo**, C. Lowenberger. FILLING IN THE GAPS OF THE IMD IMMUNE PATHWAY OF THE KISSING BUG *RHODNIUS PROLIXUS*.

(152) C. Keroack, **K. Williams**, **K. Fessler**, E. Tsekitsidou, K. DeAngelis, M. Xela, S. Williams. ANALYSIS OF SEAL HEARTWORM (*ACANTHOCHEILONEMA SPIROCAUDA*) AND IDENTIFICATION OF UNKNOWN HARBOR PORPOISE (*PHOCOENA PHOCOENA*) PARASITES USING MOLECULAR TECHNIQUES.

HOST-PARASITE INTERACTIONS

(153) **S.G. Sapp**, S.B. Weinstein, C.S. McMahan, S. Handali, M.J. Yabsley. DIFFERENTIAL *BAYLISASCARIS PROCYONIS* INFECTION DYNAMICS AND SURVIVAL IN FOUR SPECIES OF DEER MICE (*PEROMYSCUS* SSP.).

(154) **J. Munoz**, G. Mayer. PREVALENCE AND GENOTYPE OF *TOXOPLASMA GONDII* AND *GIARDIA DUODENALIS* IN DOGS FECES COLLECTED FROM NEW YORK CITY PARKS.

(155) **F.F. Tei**. EVIDENCE OF *CRYPTOSPORIDIUM* SPP IN THREE BIVALVE SPECIES COLLECTED FROM ORCHARD BEACH, NEW YORK.

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Location: Saskatchwan

Presiding: **R. Cole,** USGS, National Wildlife Health Center

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John M. Hawdon
Henry Baldwin Ward Medal

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

Location: Saskatchwan

ASP AWARDS

ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: **R.A. Cole,** US Geological Survey

The recipient of the 2016 New Investigator Award is **Stephen Greiman**, Univeristy of New Mexico.

Dr. Stephen Greiman
Ashton Cuckler New Invesitgator Award

WILLIS A. REID JR. STUDENT RESEARCH GRANTS

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

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

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ASP BUSINESS MEETING

Presiding: **M.E. Siddall**, American Museum of Natural History

Thank you for attending this year's ASP meeting and have a safe trip home.
*See you **June 28-July 1, 2017** at our next meeting in **SAN ANTONIO, TEXAS**.*

Abstract Listings

(1)

FEATHER MITE ABUNDANCE VARIES BY ECOLOGICAL CONTEXT, BUT SYMBIOTIC NATURE OF MITE-HOST RELATIONSHIP DOES NOT DIFFER IN TWO WARBLER SPECIES

A.E. Matthews, Arkansas State University
J.L. Larkin, Indiana University of Pennsylvania
D.W. Raybuck and **M.C. Slevin**, Arkansas State University
S.H. Stoleson, Forestry Sciences Laboratory, United States Department of Agriculture Forest Service Northern Research Station
T.J. Boves, Arkansas State University

Birds are hosts to a variety of ectosymbionts, including feather mites (Astigmata: Analgoidea, Pterolichoidea). Feather mites are obligatory ectosymbionts that inhabit the small spaces between barbules on bird feathers and primarily feed on the oily secretions from the uropygial gland, which are distributed throughout the feathers by the host through a grooming process called preening. Feather mites may influence individual host condition and fitness, but little is known about the nature and variability of this symbiotic system: is it parasitic, mutualistic, or commensal? We aimed to test the hypotheses that individual traits (such as sex and age) and ecological context can explain the variability of abundance and effects of mite infestations on host fitness (reproductive and survival). We focused on two closely related (Parulidae), but ecologically and distributionally distinct, populations: the Cerulean Warbler (*Setophaga cerulea*), an open-cup canopy nester, and the Prothonotary Warbler (*Protonotaria citrea*), an understory cavity nester. We captured, took morphometric measurements (for use in a body condition index), color-banded, and quantified feather mite abundance (using photographs) on individuals. We then monitored uniquely banded individuals and their nests to determine reproductive output and annual survival. Feather mite abundance differed by species, but we found no indication that abundance was related to an individual's body condition, number of fledglings, or nest survival for either species. Results that relate annual survival to feather mite abundance are pending until the 2016 breeding season. These results suggest that although a pattern appears to exist in relation to feather mite abundance and ecological context, this pattern does not seem to extend to differential effects on host fitness.

(2)

DISTRIBUTION AND REPRODUCTIVE STRATEGIES OF *GYRINICOLA BATRACHIENSIS* (OXYUROIDEA: PHARYNGODONIDAE) AND THEIR FUNGAL SYMBIONTS IN TADPOLE STAGES OF FIVE SPECIES OF ANURANS

C.C. Pierce and **M.G. Bolek**, Oklahoma State University

In total, 89 tadpoles of five anuran species were examined for the presence of *Gyrinicola batrachiensis* from Oklahoma. Infection by *G. batrachiensis* occurred in tadpoles of *Acris blanchardi*, *Hyla chrysoscelis*, *Pseudacris clarkii*, and *Rana sphenocephala*. Tadpoles of *Gastrophryne olivacea* were not infected with *G. batrachiensis*. Population structure, defined as prevalence, mean abundance, and mean intensity varied among tadpoles of different amphibian species and was determined by developmental period of tadpole hosts and different reproductive strategies of *G. batrachiensis*. *Gyrinicola batrachiensis* observed in all ranid tadpoles and *P. clarkii* tadpoles confirmed to the didelphic haplodiploidy and monodelphic parthenogenetic reproductive strategies, respectively. *Gyrinicola batrachiensis* infecting tadpoles of *R. sphenocephala* contained both males and didelphic females with thick shelled and thin shelled eggs; whereas *G. batrachiensis* infecting tadpoles of the hylid *P. clarkii* contained only monodelphic females

with thick shelled eggs and no male nematodes. In contrast, tadpoles of the hylids *A. blanchardi* and *H. chrysoscelis* contained both male and female *G. batrachiensis*; however, females only contained thick shelled eggs, suggesting an intermediate reproductive strategy. Additionally, 90% of the nematodes recovered from tadpoles were covered with filamentous flocculent material growing from the cuticle, resembling trichomycete fungi. Of those, the filamentous fungus was distributed on the anterior (35%) and posterior (58%) regions of the cuticle of nematodes in the vicinity of the excretory pore and the anus and tail, but less often on the mid-body region of the cuticle (7%) of nematodes. Similar filamentous organisms have been described growing on nematodes collected from the hindguts of other ectothermic herbivorous hosts such as millipedes and turtles. While no sign of pathogenicity has been noted for either the hosts or the nematodes infected with fungi, the symbiotic nature and role of these microorganisms merits further investigation.

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(3)

A NOVEL TOLL-LIKE RECEPTOR INFLUENCES COMPATIBILITY BETWEEN *BIOMPHALARIA GLABRATA* (GASTROPODA) AND THE HUMAN BLOOD FLUKE *SCHISTOSOMA MANSONI* (DIGENEA)

E. Pila, **M. Tarrabain**, **A. Kabore** and **P. Hanington**, School of Public Health, University of Alberta

The digenean trematode *Schistosoma mansoni* is one of the causative agents of human schistosomiasis, a chronic devastating disease that affects over 260 million people worldwide. To complete its life cycle, *S. mansoni* must undergo larval development in the gastropod *Biomphalaria glabrata*, making it an important model for studying the intra-molluscan aspects of the parasite life cycle and a possible target for disease control purposes. Compatibility between *B. glabrata* and *S. mansoni* is determined in part by the snail immune response but very few immune factors have been identified and functionally characterized in the snail to date. Here, we present the functional report of a snail Toll-like receptor (BgTLR) which we demonstrate as being an important snail immune receptor in the response against *S. mansoni*. BgTLR was identified as part of a peptide screen in which it was found to be more abundant on the haemocytes of *S. mansoni*-resistant strain of *B. glabrata* (BS-90) compared to those of the susceptible strain (M-line). Transcript expression of BgTLR was found to be very responsive in BS-90 snails when challenged with *S. mansoni*, increasing 27 fold relative to β-actin (non-immune control gene); whereas expression in susceptible M-line snails was not significantly increased. Knockdown of BgTLR in BS-90 snails via targeted siRNA oligonucleotides was confirmed using a specific anti-BgTLR antibody and resulted in a significant alteration of the resistant phenotype, yielding patent infections in 43 % of the normally resistant snails, which shed *S. mansoni* cercariae one week before the susceptible controls. Our results represent the first functional characterization of a gastropod TLR, and demonstrate that BgTLR is an important determinant of infection outcome following *S. mansoni* challenge.

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(4)

INCREASED INFECTION OF PRESCHOOL CHILDREN WITH SOIL-TRANSMITTED HELMINTHS DURING EXPOSURE TO AGRICULTURE DIMINISHES IMPROVEMENTS OF AN AGRICULTURAL INTERVENTION ON PRESCHOOL CHILD GROWTH IN RURAL PANAMA

R. Krause, Canadian Mennonite University

Soil-transmitted helminth (STH) infections and undernutrition often co-occur in rural areas of developing countries that are dependent on subsistence agriculture. Improvements in agricultural production may improve child diets and nutritional intakes, but our previous work has shown that children's exposure to increased intensification of agricultural practices increases STH infections. The objective of our study was to examine whether increases in STH infections may help to explain the lack of evidence of improvements in child growth resulting from many agricultural interventions despite improvements in diet. In this

longitudinal study, we examined the co-occurring STH infection impacts and nutritional benefits of subsistence agriculture on preschool child height-for-age (HAZ) using, as a case study, communities involved in the *VERASAN* agriculture-based food security intervention of the Panama Ministry of Health in rural Panama. Data from stool samples, anthropometry (HAZ) and questionnaires about socio-economic, nutritional and agricultural characteristics of households were combined in multivariate models of HAZ. We showed that improvements in household food security and diversity of diets were positively associated with preschool child HAZ, but that exposure to agriculture and increased infections with hookworm were negatively associated with HAZ. Our results suggest that increased STH infections due to child exposure to agriculture may diminish the positive nutritional gains made through increased food security and dietary diversity of preschool children in agriculture-intensive households. This demonstrates that agricultural interventions must be not only nutrition-sensitive, but also infection-sensitive, if improvements in child growth are to be attained.

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(5)

HOST LIFE HISTORY TRAITS PREDICT THE PROBABILITY OF AVIAN MALARIA INFECTION IN THE BRAZILIAN AMAZON

J. Bell, University of North Dakoa
A. Fecchio and **J. Weckstein**, Drexel University
V. Tkach, University of North Dakota

Host life history traits have been shown to affect the prevalence of avian malaria (*Haemoproteus* and *Plasmodium*). To understand avian malaria transmission risk in highly diverse Amazonian bird communities we analyzed four of these traits: 1) nest height, 2) nest type, 3) foraging height, and 4) flocking. These traits are potentially associated with host-vector encounter rates, and encompass the life history variation among Amazonian birds. We collected and screened for avian malaria, 1757 individual bird blood samples from six areas of endemism in Amazonia: Belém (323 samples), Guiana (178), Imerí (164), Inambari (419), Rondônia (573), and Tapajós (100). Generalized linear mixed models were used to identify which combination of host life history traits and geographic factors (area of endemism) most accurately predicted the probability of an individual bird being parasitized by either *Haemoproteus* or *Plasmodium*. Host phylogeny was included as a nested random effect to test for non-independence due to host phylogenetic constraints. Area of endemism was the only significant predictive factor in the original models. Thus, to explore the ability of host life history traits to predict infection probability, each area of endemism was analyzed separately. Each area of endemism differed in which life history traits served as significant predictors. For *Haemoproteus*, nest height (Guiana, Rondônia), foraging height (Rondônia), and flocking (Belém) were found to significantly predict the probability of infection, whereas for *Plasmodium* nest type (Inambari), foraging height (Guiana, Imerí) and flocking (Belém) were significant predictors. None of the life history traits could predict infection probability in Tapajós and host phylogenetic constraints varied between areas of endemism. Thus, in the hyperdiverse Amazon life history traits play a role in avian malaria distribution. However, the overriding effect of area of endemism indicated that biogeographical patterns in Amazonia can affect not only host communities but also their parasites.

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(6)

IMPROVING ESTIMATES OF WILDLIFE DIET: INTEGRATING PARASITES AND STABLE ISOTOPE ANALYSIS

C. Li and **J. Detwiler**, University of Manitoba

Wildlife diet provides information on foraging which is one of the most fundamental behaviors of animals and provides information on movement patterns and habitats that sustain populations. Common

approaches for estimating diet are stomach content and stable isotope analysis, yet both have their limitations including providing only a snapshot of the diet and requiring many untested assumptions related to prey consumption and tissue turnover, respectively. Thus, an additional tool is needed to better estimate animal diets in space and time. Parasites, such as many trematodes, are trophically transmitted and can therefore serve as indicators of ecosystem health because their presence within a host is a record of even a very brief visit to a particular location. In this study, we are testing the hypothesis that stable isotope analysis and trematode parasites can be used as complementary tools to study the diet composition of muskrats. Muskrats are thought to be primarily herbivorous, but occasionally eat animal prey. They are also hosts to several different trematode parasites. From three wetlands in Manitoba, stable isotope data were collected from the muscle tissue of muskrats (n=38) and their potential plant (n=33) and animal prey (n=9). In addition, trematode diversity and intensity was assessed for all muskrats. Preliminary stable isotope analysis suggested that muskrat diet varied by location and season (spring, fall). Overall, there was more overlap between the stable isotope signatures of plant and muskrats compared to the animal prey suggesting that aquatic plants constituted a more significant proportion of the diet relative to animal prey such as snails. Thus, we predict that more plant-encysting trematodes should be recovered from muskrats compared to trematodes transmitted from second intermediate hosts. We will discuss the results of a regression analysis that will reveal the relationship between estimates of diet from individual muskrats (via stable isotopes) and parasite factors (species diversity and intensity).

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(7)

MORPHOLOGICAL SPECIALIZATION FOR ATTACHMENT BY POLYSTOMES (MONOGENEA: POLYSTOMATIDAE)

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Polystomatid flatworms (Monogenea: Polystomatidae) comprising 25 genera infect the Australian lungfish, the African common hippopotamus, lissamphibians and freshwater turtles with the far majority known from anuran hosts followed by freshwater turtles. Within the diversity of hosts and sites on hosts polystomes developed a wide array of attachment specializations. Larval sclerites consisting of 16 marginal hooklets ensure a firm grip on the host allowing the larvae to attach and develop while feeding on either mucus or blood of the host. Haptoral suckers develop and in some instances large hooks known as hamuli are present. In some polystomes elaborate skeletal elements are present within haptoral suckers. Through enzymatic digestion we revealed these skeletal elements and conducted scanning electon microscopy. The results and evolutionary significance will be discussed.

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(8)

WHAT'S ON YOUR MIND: INFECTION OF THE SUB-OESOPHAGEAL GLAND OF ANTS INFECTED BY METACERCARIAE OF *DICROCOELIUM DENDRITICUM*

D. Colwell, Agriculture and Agri-Food Canada
F. Leggett, University of Alberta
C. Goater and **B. van Paridon**, University of Lethbridge

Formicid ants develop a form of lock-jaw while infected with metacercariae of the trematode *Dicrocoelium dendriticum*. Infected ants are temporarily trapped on plants where they are susceptible to being eaten by herbivores that are then likely to become definitive hosts. Following ingestion of cercariae by an ant (*Formica aserva*), one of the cercaria migrates to the sub-oesophageal ganglion (SEG), where it becomes enclosed. Our molecular sequencing data has confirmed that metacercariae in the SEG and in the haemocoel are *D. dendriticum*. The nature of the metacercariae/SEG interface has been examined using light microscopy and confocal scanning microscopy. The larva in the SEG is much smaller and does not become encysted as do the other metacercariae in the ant that are infective to the definitive host.

However, the larva in the SEG does become encased within the neural tissue and seems to be at least partially enveloped by this tissue. There does not appear to be any host encapsulation response within the neural tissue as is seen in the crop during the migration of ingested cercariae. A description of the morphology of host and parasite tissue involved in this iconic host manipulator is provided.

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(9)

DNA SEQUENCING REVEALS UNEXPECTED VARIATION IN FIRST INTERMEDIATE HOST SPECIFICITY IN ECHINOSTOME TREMATODES

P. Selseleh, **T. Chakraborty**, **L. Eliuk** and **J. Detwiler**, University of Manitoba

Elucidating parasite life cycles can be difficult and time-consuming due to their complex nature. Larval and adult stages can have different sets of characters so that the link between them is not always clear. Also, completing the life cycle in the laboratory can be nearly impossible or difficult to do depending upon the potential hosts. In comparison, DNA sequencing is an objective and easy method that improves the accuracy of parasite identification. Linking DNA sequences from larvae and adults not only completes life cycles, but also promotes more accurate estimates of host specificity and geographic distribution. Echinostome trematodes are a species-rich group that infects a wide array of wildlife such as mammals, birds, and amphibians. The variation in host specificity among echinostome species suggests they may be a model system to test hypotheses about the influence of geography and hosts on speciation. However, host specificity and life cycles are not known or may be inaccurate due to the presence of cryptic species. To address these problems, adult and larval stages were collected from muskrats and several freshwater snail species from six wetland sites in Southern Manitoba. All parasites (58 adults and 52 rediae) were sequenced at the ND1 gene, which can distinguish lineages and species of echinostomes. Phylogenetic analysis showed that *Echinostoma trivolvis* lineages A and C were the only observed parasites in muskrats and that at least five echinostome species occurred in snails: *E. trivolvis* lineages A and C, *Echinostoma revolutum*, *Echinoparyphium* lineage 2, and *Echinoparyphium* sp. Surprisingly, *E. trivolvis* lineage C was recovered from *Helisoma trivolvis* snails in Manitoba, which was previously reported only from *Lymnaea elodes* snails in Minnesota. More extensive field and laboratory studies will suggest how geographic, ecological, and physiological factors shape first intermediate host specificity.

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(10)

A FLY ON THE CAVE WALL: USING BAT FLIES (STREBLIDAE) TO UNDERSTAND HOST BAT DISPERSAL

K. Speer, Richard Gilder Graduate School, American Museum of Natural History

Mammalian dispersal can be difficult to quantify, especially when migration is rare or started occurring recently. Estimating these rare or recent events requires sampling from many individuals and loci, which can be difficult to achieve. Because host-specific parasites track the evolution of their hosts and rapidly accumulate mutations, they can act as a high resolution marker of host population dynamics. We studied the connectivity between populations of two bat species (*Tadarida brasiliensis* and *Erophylla sezekorni*) across the Bahamas. However, the signal of population structure we detected in these species may be the result of rare dispersal or dispersal that started occurring recently, rather than reflecting low dispersal ability between islands. To assess rare or recent dispersal of *E. sezekorni*, we developed 9 microsatellite loci to genotype their associated bat flies (*Trichobius frequens*), which are obligate, blood-feeding ectoparasites of bats. Our data suggest that *T. frequens* exhibits greater population structuring in The Bahamas than *E. sezekorni* and has smaller population sizes. This data could suggest that bats are not able to easily disperse between islands of the Bahamas, or it may indicate that bat flies do not always stay attached to their host during nightly foraging events that may result in inter-island dispersal. This work provides the first microsatellite primers for the family Streblidae and the first genetic assessment of the connectivity between populations of bat flies.

(11)

RELATIVE COMPATIBILITY OF *SCHISTOSOMA MANSONI* WITH *BIOMPHALARIA SUDANICA* AND *B. PFEIFFERI* FROM KENYA AS ASSESSED BY PCR AMPLIFICATION OF THE *S. MANSONI* ND5 GENE IN CONJUNCTION WITH TRADITIONAL METHODS

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S. Zhang, Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico
M.W. Mutuku and **G.M. Mkoji**, Center for Biotechnology Research and Development, Kenya Medical Research Institute (KEMRI)
E.S. Loker, Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico, Parasitology Division, Museum of Southwestern Biology, University of New Mexico

Two important African snail hosts for *Schistosoma mansoni* are *Biomphalaria sudanica* from large habitats like Lake Victoria, and *B. pfeifferi* from streams and small impoundments throughout the African tropics. Preliminary evidence from Kenya suggests *B. sudanica* from Lake Victoria is less likely than *B. pfeifferi* from neighboring streams to support patent infections of *S. mansoni*. To assist in monitoring the fate of *S. mansoni* in snails, a sensitive and specific PCR assay targeting the NADH dehydrogenase subunit 5 (*ND5*) mitochondrial gene of *S. mansoni* was developed to supplement traditional methods to assess schistosome-snail compatibility. The *ND5* PCR assay was found to be sensitive (> 0.1 fg *S. mansoni* genomic DNA) and will amplify a signal from *S. mansoni* but not from related *Schistosoma spp.* or from snail species. The PCR assay can detect *S. mansoni* infections in snails exposed to one miracidium for one day. Lab-reared *B. sudanica* and field-derived *B. pfeifferi* were exposed to single *S. mansoni* miracidium infections and at several time points (1, 2, 4, 8, 16, 24 and 40 days post-exposure (dpe), examined for the presence of *S. mansoni*. Depending on the age of infection, snails were dissected and/or shed for cercariae prior to undergoing DNA extraction for use in the ND5 PCR assay. Snails negative upon dissection or shedding were also examined with the PCR assay. Additionally, *B. sudanica* and *B. pfeifferi* were collected from field locations in Kenya and tested with the PCR assay. The number of positive snails in the PCR assay at 1-4 dpe was higher in *B. pfeifferi* than *B. sudanica*, but not significantly so (p=0.052). From 8-24 dpe, more *B. pfeifferi* harbored successfully developing parasites (positive by both dissection and PCR) than did *B. sudanica* (p=0.008). At 40 dpe, more *B. pfeifferi* than *B. sudanica* shed cercariae or harbored dissection positive/PCR positive infections (p=<0.001). Both immature and failed (dissection negative but PCR positive) *S. mansoni* infections could also be detected in naturally infected snails of both species. Although both *B. sudanica* and *B. pfeifferi* supported full development of *S. mansoni*, *B. pfeifferi* was more compatible, with significantly more dissection positive/PCR positive or shedding infections, and significantly fewer failed infections (dissection negative/PCR positive). This confirms the relatively lower compatibility of *B. sudanica* with *S. mansoni* in Kenya and suggests the factors responsible for incompatibility and how they might affect transmission of *S. mansoni* in habitats like Lake Victoria deserve additional study. This research was supported by NIH P30 GM110907, R01 AI101438 grants and Gates Grand Challenges Award.

(12)

ECOLOGICAL EPIDEMIOLOGY OF EMERGING LIVER FLUKE, *DICROCOELIUM DENDRITICUM*, IN OREOHELID LANDS SNAILS IN CYPRESS HILLS PARK, ALBERTA

Z.W. Dempsey, University of Lethbridge

The emergence of parasites into novel geographical areas and novel host populations appears to be on the rise. Many such emergence events are associated with negative consequences on host individuals and populations. The lancet liver fluke was introduced from central Europe into North America in the 1950's

and is now common and abundant in grazing mammals that share pasture in Cypress Hills Park, Alberta. However, it's life cycle and its utilization of intermediate host communities is unknown in this region. I used molecular diagnostic tools on samples of sporocyst tissue, combined with standard host surveys, to confirm that *D. dendriticum* utilizes Oreohelid land snails as first intermediate host. The phylogeography of Oreohelid snails in this region is complex, involving at least 3 independent genetic lineages. All three are susceptible to this invasive trematode. Prevalence of infection within monthly samples of *O. subrudis* ranged between 5-30% between May-October, 2015 with maxima occurring in mid summer. Some infected snails also contained developing embryos, indicating that trematode-induced sterilization is not absolute in these terrestrial, long-lived, viviparous snails. These results indicate that for this emerging parasite, the complex community of oreohelid land snails is responsible for the transmission of cercariae into Formicid ants.

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(13)

UNDERSTANDING EFFECTS OF TREMATODE-INFECTION ON TEMPERATURE SELECTION IN TADPOLES

S.Y. Wang and **G.J. Tattersall**, Brock University
J. Koprivnikar, Ryerson University

Many ectotherms have been shown to exhibit a behavioural fever, where they preferentially select warmer temperatures in response to pathogens. These 'feverish' temperatures have an adaptive value by increasing survival of infected animals. While much of this research has been conducted with injection by killed bacteria or viruses, consequences of parasitic infection are unclear. Given recent amphibian declines, the aim of this study was to understand how trematode infection may impact temperature selection in a model system, *Lithobates sylvaticus* (wood frog) tadpoles and the highly pathogenic *Ribeiroia ondatrae*. 96 tadpoles were exposed to a dose of 25 trematodes or sham-infected with water. At one, two, and three days post-exposure, tadpoles were placed in either a thermal gradient that ranged from 15 to 35°C or in a constant gradient where water was at room temperature. Tadpoles behaviourally selected their preferred temperature by swimming over a four hour period with their position captured via webcam every 20 seconds. Tadpoles in the thermal gradient had a significantly different distribution than those in the constant gradient, indicating they responded to temperature. Linear mixed modeling showed that both exposure to parasites and elapsed time in the experimental apparatus were significant in explaining temperature selection for tadpoles in the thermal gradient condition. However actual individual infection intensity did not significantly explain temperature selection, nor did any other factors. These results suggest that tadpole thermoregulatory behaviour may differ depending on whether they are simply exposed to parasites or if they are actually infected. Short term consequences from trematode exposure that affect temperature selection may cause long term repercussions in tadpoles since body temperature plays a large role in ectothermic growth.

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(14)

EFFECT OF CONTRIBUTING RISK FACTORS ON THE PREVALENCE OF *TOXOPLASMA GONDII* INFECTION IN THE SERA OF PREGNANT AND NON-PREGNANT WOMEN AT NISHTAR HOSPITAL, MULTAN, PAKISTAN

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Toxoplasma gondii infections are widely prevalent in humans and other domestic animals that may cause devastating consequences to neonates. The present study was planned to look into the seroprevalence of toxoplasmosis within pregnant and non-pregnant women in relation to pets and other contributing social and cultural risk factors at Nishtar Hospital, Multan. The 403 sera samples collected from pregnant (with abortion history n=35 and without history of abortion n=197) and non-pregnant women (with reproductive problems n=58 and without reproductive problems n=113) were assayed for *T. gondii* antibodies by a commercially available ELISA (anti-*T. gondii* IgG Human *in vitro* ELISA kit; Abcam®, UK). The prevalence rate to *T. gondii* in pregnant subjects with and without abortion history and non-pregnant women with and without reproductive disorders was 45.71% (16/35), 14.72% (29/197), 25.86 %(15/58) and 9.73% (11/113), respectively. Statistically, no significant variance ($P > 0.05$) was found in the prevalence to *T. gondii* antibodies in between both pregnant and non-pregnant subjects. However, a significant change ($P < 0.05$) was found among pregnant subjects with and without abortion history. The overall prevalence observed in both pregnant and non-pregnant women was 17.61% (71/403). There was a significantly higher ($P < 0.05$) prevalence of *T. gondii* in the age group 26-30 years old (22.22%) while no significant difference was recorded among different ethnic groups. Pet ownership was discerned to be a significant ($P < 0.05$) risk factor, associated with the of *T. gondii* infection. Seropositivity to *T. gondii* was highly associated with the type of residence, marriage category and source of drinking water with statistical significance ($P < 0.05$).

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(15)

PARASITE ASSOCIATED MORTALITY IN SHORTNOSED (*CHASIMISTES BREVIROSTRIS*) AND LOST RIVER SUCKERS (*DEKTISTES LUXATUS*)

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Shortnosed (*Chasimistes brevirostris*) and Lost River Suckers (*Dektistes luxatus*) are endemic to the Upper Klamath Basin of Southern Oregon and Northern California. Populations of these fishes have been dwindling since the 1960's and both species where listed to as endangered in 1988. Poor recruitment of juvenile fish is thought to be a major cause for their demise and in this study we investigate if parasites are a contributing factor. In the summers of 2013 and 2015 we conducted histopathological examinations of age 0 and age 1 suckers, as well as other species of fish in the lake. The most prevalent infections were trematode metacercariae (*Bolbophorus* in the skin and muscle, *Posthodiplostomum* in the viscera and brain and *Ichthyocotylurus* in the heart). rDNA sequence obtained from cercariae shed by 7 snail species revealed 21 cercariae species, 7 which should infect fish (species in the genera *Allassogonoporus, Clonorchis, Diplostomum, Ichthyocotylurus, Petasiger* and *Posthodiplostomum* or family *Echinostomatidae*). However, to date we have not matched any of these with the metacercariae that we have collected. While the metacarcarial infections were most common, the most severe infection was *Contracaecum* L3 larvae in the heart. rDNA ITS1 sequencing showed that the *Contracaecum* species most closely matched *Contracaecum multipapillatum*. We are currently evaluating the host, temporal and geographic distribution of these parasites using a historical collection of 20,000 suckers spanning 13 years of monthly summertime collections.

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(16)

DEVELOPMENT OF SARCOCYSTIS ISOLATED FROM A COOPER'S HAWK (*ACCIPITER COOPERI*) AND A RED-SHOULDERED HAWK (*BUTEO LINEATUS*) IN CELL CULTURE

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We are interested in understanding the diversity of *Sarcocystis* species that use birds of prey as intermediate and definitive hosts. We report isolation of *Sarcocystis* species from the feces of a Cooper's hawk (*Accipiter cooperi*) and a Red-shouldered hawk (*Buteo lineatus)* and their development in cell cultures. Both birds had been admitted to the Carolina Raptor Center for treatment and were euthanized because of poor prognosis. The intestinal tracts were removed and examined for parasites by making several direct smears and examining them with light microscopy. *Sarcocystis* oocysts/sporocysts were present in both birds. Sporocysts were subjected to in vitro excystation and inoculated on to African Green monkey kidney cells. Developmental stages were observed 34 days PI in cultures from the Cooper's hawk and 39 days PI in cultures from the red-shouldered hawk. Subcultures of merozoites were done and the 2 *Sarcocystis* isolates were maintained by subculture and stocks frozen in liquid nitrogen. Transmission electron microscopy demonstrated that the parasites developed directly in the host cell cytoplasm, that development was by endopolyogeny, that merozoites lacked rhoptries, and that they contained all organelles typical of *Sarcocystis* merozoites. Supported by grant # 1505407 from the NSF to ACR and by an IRC grant from Virginia Tech to DSL.

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(17)

QUANTIFYING THE BARRIERS AND BRIDGES TO INTERSPECIFIC TRANSMISSION IN A COMMON HOST-SYMBIONT SYSTEM

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Most parasites use multiple host species, and these host species vary in their ability to acquire and transmit infection. Three types of host species should be particularly important to community-level parasite transmission: (1) host species that maintain a high prevalence of infection, (2) host species that are highly abundant, and (3) host species that are highly infectious when they get infected. However, few studies have empirically quantified which host species characteristics are responsible for variability in interspecific transmission. Using a combination of field surveys, laboratory experiments, and mathematical modeling, we quantified the relative importance of host density, host infestation prevalence, and transmission success to interspecific transmission of a symbiotic oligochaete (*Chaetogaster limnaei*) that is directly transmitted among aquatic snail hosts. In the field, interspecific *Chaetogaster* transmission rates were very low between *Physa gyrina* snails and *Helisoma trivolvis* snails. Contact rate experiments and models demonstrated that low transmission success during *Physa-Helisoma* contacts was the most plausible cause of the observed transmission barrier, rather than low *Physa-Helisoma* contact rates or low *Physa* infestation prevalences. Correspondingly, in our laboratory transmission experiments, *Chaetogaster* transmission success from *Physa* to *Helisoma* was almost zero. Surprisingly, this was caused by strong host preferences, where *Chaetogaster* from field *Physa* preferred laboratory *Physa* and *Chaetogaster* from field *Helisoma* preferred laboratory *Helisoma*. Therefore, we found that an abundant, resilient host species with a high prevalence of infestation – a host species that was predicted to be a superspreading species - was a poor conduit for interspecific transmission due to strong host preference by the symbiont. Despite significant bridges for interspecific transmission, a single barrier has seemingly divided this multi-host system into two single host systems.

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(18)

CYTAUXZOON FELIS INFECTIONS IN BOBCATS, DOMESTIC CATS, AND TICK VECTORS IN THE SOUTHERN REGION OF ILLINOIS

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Cytauxzoon felis is an intraerythrocytic Apicomplexan parasite of felines in the southeastern United States. Infection in domestic cats (*Felis catus*) can result in the highly fatal cytauxzoonosis. Bobcats (*Lynx rufus*) are believed to be 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*, and the current understanding of the distribution of the parasite in tick vectors is based on the screening of 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 objectives: i) to determine the prevalence and parasitemia of *C. felis* in bobcats and domestic cats and determine the prevalence in questing tick vectors, and ii) to compare the genetic diversity of *C. felis* among different hosts. We screened tissues of 150 bobcats, 218 ticks (117 *A.* americanum, 101 *D.* variabilis), 12 domestic cats suspected to suffer from cytauxzoonosis, and 28 asymptomatic domestic cats for the presence of *C. felis* using polymerase chain reaction (PCR). Bobcats from Illinois showed a prevalence of 70%, whereas ticks had a prevalence of 15.6% with no difference between species. Eleven cases of cytauxzoonosis were confirmed in domestic cats and 9 of 28 (32.1%) of asymptomatic domestic cats were positive for *C. felis*. 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. Future research must address the role of domestic cats as reservoirs of this pathogen, the identification of foci of the disease and the effects of chronic infection in bobcats.

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(19)

RESERVOIR COMMUNITIES AND THE MAINTENANCE OF WHITE SPOT SYNDROME VIRUS IN THE NORTHERN GULF OF MEXICO

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White spot syndrome virus (WSSV) can infect almost any decapod crustacean and is a primary impediment to crustacean aquaculture. It was first reported in the U.S. in 1995 and has persisted in U.S. coastal waters since 2005. In the southern U.S., where interest in the farming of crayfish, blue crabs, white shrimp, spiny lobster, and freshwater prawns is increasing, WSSV is likely to impede the industry. We aimed to survey the distribution of WSSV among wild native crustaceans in MS and LA and quantify the transmission among those hosts and farmed hosts to assist in managing the virus's impact on U.S. aquaculture. From 2013-2015 we found WSSV in the blue crab, *Callinectes sapidus* (8%); purple marsh crab, *Sesarma reticulatum* (10%); Gulf mud fiddler crab, *Uca longisignalis* (50%); sand fiddler crab, *U. panacea* (11%); mudflat fiddler crab, *U. rapax* (23%); spined fiddler crab, *U. spinicarpa* (36%); red-jointed fiddler crab, *U. minax* (23%); squareback marsh crab, *Armasus cinereum* (27%); daggerblade grass shrimp, *Palaemonetes pugio* (9%); and Gulf white shrimp, *Litopenaeus setiferus* (20%). In controlled experiments, we observed 100% mortality in the commonly cultured *L. vannamei*, the three penaeid shrimp species native to the Gulf of Mexico (white shrimp, brown shrimp (*Farfantepenaeus aztecus*), and pink shrimp (*F. duorarum*)), and blue crabs. Mean time to death following inoculation was 51.8 h. A metacommunity model comprising multiple species distributed among multiple spatially discontinuous habitat patches was developed to assess the role of reservoir hosts in maintaining the virus in the community. The matrix model includes Susceptible hosts, Infected living hosts, Free virus, and Dead infected hosts. Maintenance of WSSV in reservoir hosts appears to depend on the mean value of the important parameters contributing to the basic reproduction number, R_o. WSSV may be maintained in a region even though the R_o is less than one for some of the species. WSSV will be maintained in those species by spill-over from those species with R_os greater than unity.

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(20)

ADVANCES TOWARD LARGE SCALE PRODUCTION OF *ACANTHACHEILONEMA VITEAE*

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University of Wisconsin Oshkosh

The NIH/NIAID Filariasis Research Reagent Resource Center (FR3) began distributing the filarial nematode *Acanthacheilonema viteae* to its users in 2011. This paper reports ongoing efforts to optimize the life cycle of *A. viteae* and its vector *Ornithodoros tarakovskyi* to meet increasing user demand. We have increased our *A. viteae* L3 yields from 14 L3/tick (n=475) to 142 L3/tick (n=56) by feeding only adult female ticks on gerbils with microfilaremia of approximately 200 mf/uL blood. Similarly, the median recovery of adult *A. viteae* from hamsters has risen from 49 (IQR=7.5-96.5, n=16) to 100 (IQR=80-133, n=17) after increasing the number of subcutaneous injections used during infection from one to two. Meta-analysis of laboratory data followed by an experimental trial demonstrated that worms isolated in RPMI-1640 in preparation for transplant into a new host failed to reproduce *in vivo*, as opposed to those isolated in Hanks' Balanced Salt Solution. Preliminary observations from an ongoing trial demonstrate the value of using the fecundity of cultured adult female worms to predict success of parasite transplant into recipient gerbils. Cultured adult females that individually shed less than 7 mf in a 4-day period in culture reproduce poorly when co-transplanted with males (resulting in 34 and 57 mf/20 uL blood at 30 dpi; n=2) as compared to females that shed more than 34 mf in 4 days (resulting in 176 and 180 mf/20 uL blood at 30 dpi, n=2). A related preliminary study suggests that culture-derived mf are immediately infective for ticks, based on observations using 4-day old mf reconstituted in rabbit blood and delivered via an artificial membrane feeding system. The mf were fed to ticks at 247 mf/20 uL rabbit blood, and at 30 dpi ticks were dissected to reveal 82% prevalence of infection (n=11) with mean intensity of 84 ± 65 L3s/tick (n=9). These ongoing modifications have made significant improvements to the propagation of this filarial nematode, an organism with fascinating biology that is available for no cost to researchers worldwide through FR3.

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(21)

BLENDING TEACHING AND RESEARCH IN A DOG TAPEWORMS STUDY

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Learning parasitology laboratory can be quite monotonous and mundane when the entire laboratory consists of making observations of prepared slides. To cultivate a bit more interest in learning parasitology laboratory, the laboratory was combined with a research project discovering gastrointestinal parasites in dogs in Forsyth County, NC. It is common for dogs to acquire parasitic intestinal infections throughout their lifespan. Parasites have the ability to affect dog in many ways that result in mild conditions such as diarrhea or more serve cases that can lead to death. The purpose of the classroom laboratory experiment was to assess the prevalence of gastrointestinal parasites in dogs stool samples collected in Forsyth County. In addition, surveys were collected from the dog owners to assess the habits of the dog and the owner in caring for the dog. Fresh fecal samples in formaldehyde were concentrated by centrifugation and examined by light microscopy. We also took part of the fresh samples and isolated DNA. The DNA samples were used to assess various parasites by PCR. Here we show that 74% of the dogs studied in Forsyth County had tapeworms.

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(22)

SUBCLINICAL BAYLISASCARIASIS AND ASSOCIATED RISK FACTORS IN WILDLIFE REHABILITATORS FROM THE UNITED STATES AND CANADA

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Baylisascaris procyonis is an emerging zoonotic ascarid of raccoons (*Procyon lotor*) in North America, Europe, and East Asia. Severe neurologic disease has been documented in >130 species, including humans. Nearly all diagnosed human baylisascariasis cases have been fatal or resulted in permanent neurologic sequellae. In recent years, several new cases have been diagnosed which could be due to increased awareness or incidence. Human cases generally are diagnosed in children who likely ingest large numbers of eggs; however, ingestion of low numbers of eggs may only result in mild disease. Currently, knowledge of baylisascariasis in adults is limited. We hypothesized that healthy adults may be exposed to *B .procyonis* due to accidental ingestion of low numbers of eggs, and that wildlife rehabilitators may represent an at-risk cohort due to frequent contact with raccoons and/or their feces. We enrolled 347 wildlife rehabilitators from the United States and Canada, administered a questionnaire to assess risk factors, and collected blood samples. Antibodies were detected using a *Baylisascaris*-specific, recombinant-antigen based immunoblot. Twenty-four participants (7%) were positive for antibodies to *B. procyonis*, 16 (67%) of which were active raccoon rehabilitators, and 22 (92%) of which reported a history of general raccoon contact. Significant risk factors for seropositivity included practicing rehabilitation in the Western region and/or areas of very high (>50%) *B. procyonis* prevalence in raccoons and failure to always wash hands after contact with live raccoons or feces. In summary, antibodies to *B. procyonis* were detected in healthy adult wildlife rehabilitators, indicating the occurrence of subclinical/covert baylisascariasis. Wildlife rehabilitators and other individuals with raccoon contact should be aware of this occupational hazard and be advised to use personal protective equipment appropriately to reduce the risk of exposure, especially those located in high-risk regions. Additional studies are needed to assess the seroprevalence and epidemiology of subclinical baylisascariasis in the general population.

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(23)

THE LIFE CYCLE OF *HAEMATOLOECHUS FLOEDAE* HARWOOD, 1932 (DIGENEA: PLAGIORCHIIDAE)

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The *Haematoloechus* – ranid frog model system has been used to test evolutionary hypotheses regarding host specificity. *Haematoloechus floedae* was first described from bullfrogs (*Rana catesbeiana*) collected in the vicinity of Houston, Texas, but later was interpreted as a junior synonym of *H. varioplexus*. *Haematoloechus floedae* also has been considered a junior synonym of *H. breviplexus*. Recent molecular evidence and morphological distinctions indicate that *H. floedae* is a valid species that infects bullfrogs in the southern United States, and at least 4 other ranid species in Mexico and Central America. The potential for misidentification of *H. floedae* as *H. breviplexus* might resolve an apparent discrepancy in the life cycle. The planorbid snail, *Gyraulus similaris,* serves as a first intermediate host for *H. breviplexus* collected from *R. pretiosa* in Idaho, but successful infections of *H. breviplexus* from Texas were reported in a species of *Ferrissia*, an ancylid snail, and not in *Gyraulus*. Ancylid snails from a pond in South Carolina were observed to shed cercariae consistent with those of *Haematoloechus*. Exposure of libellulid and odonate naiads to these cercariae resulted in the recovery of encysted metacercariae from the branchial basket of the odonates, which produced an infection of adult worms identified as *H. floedae* when fed to bullfrogs. In addition, a second cercaria consistent with *Haematoloechus*, but smaller than that of *H. floedae* and exhibiting different behavior, has been observed being shed from ancylids from the same pond.

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(24)

DISTRIBUTION OF LOIASIS INFECTION IN EHIME MBANO AND EZINIHITTE MBAISE LOCAL GOVERNMENT AREAS OF IMO-STATE NIGERIA

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A survey on the epidemiological mapping of loiasis infection in two Local Government Areas of Imo-State (Ehime Mbano and Ezinihitte Mbaise) Nigeria was carried out between November 2014 and October 2015. The aim of this study was to determine the prevalence/intensity of *Loa loa* using RAPLOA, a rapid assessment procedure for loiasis. A total of 835 inhabitant age 15 years and above were involved in this study. 139 (17%) reported a history of eyeworm. This was not significant (P>0.05). 130 (16%) reported a history of calabar swelling. Of the two local government areas sampled, Ehime Mbano had highest prevalence rate for eyeworm and calabar swelling respectively. The comparative influences of age, sex and occupation on the infection rate of the infected were also evaluated. Infections were higher among the females, for both eyeworm (18.2%) and calabar swelling respectively. The overall peak infection of (22%) was observed among the 41-50 years age group and lowest in the 15-19years age group. The infection prevalence rate varied among different occupational groups with farmers having the highest prevalence with (20%) and students having the least with (8.2%). The overall results obtained indicated that loiasis endemicity was below the WHO 40% standard.

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(25)

HYMENOLEPIASIS IN INSTITUTIONALIZED ROMANIAN CHILDREN

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The prevalence of intestinal parasitic infections was investigated in a Romanian Children Care Unit. Stool examinations were performed using the iodine staining for the identification of protozoan cysts and the Willis-Hung method for the identification of helminth eggs. We investigated 88 institutionalized children aged 2 to 14 years.Parasitic infections were identified in 47 cases (53%). *Hymenolepis nana* (25%), *Giardia lamblia* (23.1%), *Blastocytis hominis* (6.8%), *Entamoeba coli* (4.5%), *Ascaris lumbricoides* (4.4%), and *Trichuris trichiura* (2.3%) were diagnosed. We have determined associations of two (21.3%) and more than two parasites (8.5%) among the infected children; of the 22 with hymenolepiasis, 14 (63%) had multiple parasitic infections.Clinical and laboratory examinations were conducted to investigate the presence of symptoms and eosinophilia in patients with parasitic infections. Diarrhea (38.3%), weight loss (46.8%), abdominal pain (21.3%), nervous disorders (34%), cutaneous manifestations (27.6%), fever (8.5%) and respiratory infections (65.9%) were reported in the infected children. Eosinophilia was noted in 28 (59%) of the 47 patients with parasitosis. High eosinophil values were mostly observed among those diagnosed with helminth infections. *Hymenolepis nana* was reported with an increased frequency among Romanian institutionalized children. The majority of patients with hymenolepiasis were diagnosed with multiple parasitic infections.

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(26)

DETECTION OF LYMPHATIC FILARIASIS USING CLINICAL EXAMINATION AND IMMUNOCHROMATOGRAPHIC CARD TEST AND FILARIASIS RELATED KNOWLEDGE, ATTITUDES AND PERCEPTION AMONG THREE ETHNIC GROUPS IN BENUE STATE, NIGERIA

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Mapping distribution of lymphatic filariasis (LF) is a prerequisite for planning National Elimination Programmes. Little is known of the distribution of the disease in Benue State, Nigeria, and its current importance as a public health problem. Epidemiological mapping was undertaken to determine the prevalence of lymphatic filariasis using immunochromatographic tests to detect circulating filarial antigen (CFA). All volunteers were examined for the clinical manifestations of the disease. A total of 845 persons were examined with 264 (31.2%) testing positive for CFA. Infections were significantly higher in males

(X2 = 7.02, df = 1, P < 0.05). Hydrocoele was seen in 53 (6.28%) persons while lymphoedema was seen in 16 (1.94%) female participants. These manifestations increased with age. Antigenaemia prevalence based on ICT card test ranged from 0% to55.8% in selected LGAs. Pearson correlation analysis showed a weak positive association between ICT rates and hydrocoele prevalence (r = 0.367, P < 0.016). On the other hand, correlation analysis showed a strong positive association between hydrocoele and lymphoedema rates (r = 0.847, P < 0.207). There was a significant difference in ethnic perception of the cause of the disease, with 61.8% of the Igede respondents attributing the cause of the disease to stepping on charm compared to 47.1% and 36.8% of the Tiv and Idoma respondents respectively (X^2 = 6.71, df = 2, P < 0.05). Only 19.5% of the Igede respondents correctly ticked mosquitoes as the cause of the disease compared to 36.2% and 56.6% of the Tiv and Idoma respondents respectively (P < 0.05). The Igede ethnic group appears to be more superstitious in their beliefs and perception. Several areas of community misconceptions, lack of knowledge or erroneous beliefs and practices, were identified in this study. The communities' capacity to protect themselves is hindered by a lack of understanding of the causes, symptoms, transmission route, prevention and treatment of the disease.

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EPIDEMIOLOGY OF CO-INFECTION OF INTESTINAL PARASITES AND TUBERCULOSIS IN BENUE STATE, NIGERIA

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Co-infection with TB and intestinal parasites is exacerbating an already precarious health profile of Africans. This study was designed to determine the prevalence of intestinal helminthes infections in active tuberculosis patients and their healthy household contacts and to assess its association with active TB in an areas endemic for both types of infections. Faecal samples of participants were examined for intestinal parasites using faecal concentration technique and the Ziehl-Nelseen's staining technique was adopted for sputum smear microscopy to determine TB infection. Of the 2,519 participants investigated, 998 (39.6%) were positive for intestinal parasites, 445 (17.7%) were positive for TB while 210 (8.3%) had both TB and intestinal parasites. Intestinal parasite infection amongst TB patients was 38.4% while the 790 out-patients examined had 41.9% infection with parasitic helminthes. The prevalence of intestinal parasites in the apparently healthy community members was 40.3%. The prevalence of intestinal parasites is significant in all the study groups with (= 157.84 df = 4 and P<0.05). The overall prevalence of tuberculosis was 17.6%, out of this number, 112 (25.16%) were scantly infected, 160 (35.95%) had light infection (1+), 134 (30.11%) were moderately infected (2+), while 39 (8.76%) had heavy infection. The prevalence of intestinal parasites in patients with severe TB infection was 51.3%. Statistical analysis showed that the burden of TB was significant in all the LGAs surveyed (P < 0.01). Prevalence of co-infection with PTB and intestinal parasites were significant in the seven local government areas studied (P<0.05). The prevalence of co-infection ranged from 43.13% to 51.49% depending on the severity of TB. *Entamoeba histolytica*, hookworm, *Strongyloides stercoralis* and *Ascaris lumbricoides* were the most predominant intestinal parasites identified in PTB patients. This study reveals a high prevalence of intestinal parasites, TB and the co-infection of both in Benue State. Our findings justify the urgent need to include routine deworming in DOT strategy and mass drug administration to treat apparently health community members.

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(28)

DOES CHEMOTHERAPY HAVE A FUTURE IN PARASITE CONTROL?

W.C. Campbell, Drew University

It seems inevitable that chemotherapy will continue, at least in the near-term, to be a significant factor in the control of infectious diseases. The emergence of drug resistance will, perhaps inevitably, continue to reduce the effectiveness of new drugs. Efforts to thwart resistance should continue, but there are also other areas that might profitably be re-examined. They include (a) methods of new-drug discovery; (b)

selection of parasite life-cycle targets; (c) epidemiological determinants of effectiveness in large-scale control programs; and (d) the economic, managerial, psychological, and political ramifications of drug discovery and of drug utilization.

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(29)

THE E-WORD: IS MALARIA ERADICATION A REALISTIC GLOBAL GOAL?

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In 2007, Bill and Melinda Gates surprised the malaria community by urging its members to develop a plan to eradicate malaria. The response was visceral and immediate and since then plans have been adopted by many countries around the globe. Armed with long lasting insecticidal nets (LLINs) to prevent mosquitoes biting, and new artemisinin-based combination therapies (ACTs) to kill the *Plasmodium* parasite in the human host, there has been renewed vigor and coordination. However, almost a decade later since the Gates' call-to-arms, how realistic *is* malaria eradication and how much has it advanced? With reports of a quiescent stage of *Plasmodium falciparum* having evolved in parts of Southeast Asia to evade the effects of the short-acting artemisinin-based drugs, and with other less-studied species such as *Plasmodium vivax* potentially vacating the niche left by falciparum malaria, is malaria eradication a realistic global goal?

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(30)

MAYBE THERE IS REASON FOR OPTIMISM FOR LONG TERM MDA EFFECTIVENESS?

F. Richards, The Carter Center, Atlanta, Georgia

Ivermectin is being used in mass drug administration (MDA) programs where the objective is to provide chemotherapy to entire communities. It is the community, not an individual, that is the public health practitioner's patient. If the 'community diagnosis' is for treatment, then all eligible people are offered MDA. If the community is compliant with treatment (meaning all those offered treatment accept it—'good' coverage) then there is a very good chance in some systems that very quickly transmission will be dramatically reduced. If the patient is to be cured once and for all, then infection transmission interruption must be the goal, and the patient becomes not just the community, but a larger circumscribed region we call a 'transmission zone.' The ability to pass on resistance genes may or may not be enhanced by MDA, depending on the innate characteristics of the infectious agent and its transmissibility. The emergence of drug resistance is a function of these complex factors. I am optimistic that ivermectin resistance will not become an issue for many decades. I believe that the experience with other vector borne helminthic infections, with similar transmission dynamics to onchocerciasis, supports that optimism. So, our window of opportunity may be more widely open than many might believe to eliminate this parasite once and for all.

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IF YOU THINK YOU WANT TO SAVE THE SALMON, OR THE WHALES…, OR REALLY JUST GO FLY FISHING?

K. Jacobson, NOAA Fisheries, Northwest Fisheries Science Center

The National Oceanic and Atmospheric Administration (NOAA), it's not just about the weather, weather, weather. NOAA Fisheries "provides science-based conservation and management for sustainable fisheries

and aquaculture, marine mammals, endangered species, and their habitats." The science is applied. It is "guided by two core mandates—to ensure the productivity and sustainability of fisheries and fishing communities through science-based decision-making…, and to recover and conserve protected resources including whales, turtles, and salmon". There are research opportunities in 20 different science laboratories throughout the United States and U.S. territories. Each regional science center and their laboratories address specific regional habitat issues and focal species. We are working on emerging issues that include climate change (okay, so some of it is about the weather), ocean acidification, and invasive species. We work closely with scientists from state governments and academia to help inform policy makers. Career opportunities exist for next generation scientists with broad skill sets.

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(32)

I'M FROM THE GOVERNMENT AND I'M HERE TO HELP

K.D. Lafferty, U.S. Geological Survey, UC Santa Barbara

I am a senior ecologist with the US Geological Survey USGS. You know USGS for our maps and earthquake predictions, but the USGS is also the nation's leading natural science organization. The USGS mission is to serve the information needs of the U.S. Department of Interior, which includes the National Park Service, the Fish and Wildlife Service, The Bureau of Land Management, the Bureau of Indian Affairs, and the Bureau of Ocean Energy and Management. Our scientists focus on issues related geology, water, and biology. We also have a strong mapping division. For instance, I was hired as a marine ecologist, not a parasitologist. But we do have a National Wildlife Health Center in Madison Wisconsin, a Fish Health center in Leetown, and the Western Fisheries Research Center in Seattle that employ parasitologists. And we have several researchers like myself that study infectious diseases in a range of species. A good way to end up working for USGS is to get into federal service as a student, whether as a volunteer or an employee. Regardless, the jobs are competitive, so a good CV with strong publications is helpful, as is experience with applied research.

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PARASITOLOGY IN INDUSTRY

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Parasite control and prevention remains a major source of revenue for the animal health industry; pharmaceutical products are still the predominant instruments used to maintain the health of livestock and companion animals. The evolution and spread of drug resistance has complicated the landscape of parasite control, leading to increased investment in parasitology research in this industry. Countering that trend is the seemingly unceasing consolidation of the animal health sector; only a handful of companies maintain research programs in parasitology. Contract research organizations (CROs) have developed to fill some of the gaps in parasitology research, particularly in the area of target animal testing and field trials. Parasitologists capable of working with multiple in vitro and in vivo systems for relevant parasite groups are in demand, as are those who can participate in development and registration studies related to parasite control. On the human health side, many major pharmaceutical companies have recently committed significant resources to global health, opening a need for parasitologists capable of understanding parasite models of relevance for human health indications. Rapid consolidation changes in the pharmaceutical/biotechnology industry have markedly changed working conditions and the demand for long-term research groups and projects. Parasitologists with multi-disciplinary training, including the ability to work with animal models of parasitism, are most likely to find career opportunities in industry.

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(34)

BAYLISASCARIS PHYLOGENETICS: ASSESSING SPECIES VALIDITY

L.E. Camp and **S. Nadler**, University of California-Davis

The genus *Baylisascaris* was created by Sprent in 1968 to include seven nematode parasites of carnivorans that were previously classified as *Ascaris* or *Toxascaris*. Three species have been added to the genus since it was described. Even though there are ten *Baylisascaris* species in different hosts, most research focuses on the parasite in raccoons, *B. procyonis*, or raccoon roundworm. Raccoon roundworm is a common, highly prevalent parasite in raccoons throughout North America, but distinguishing this parasite from other *Baylisascaris* species is difficult. Due to high morphological similarity at all life stages, *Baylisascaris* species are often identified by host of origin. I will describe a molecular phylogenetic approach for resolving relationships among the parasites in the genus, and determining if species in raccoon, skunk, bear, and Tasmanian devil hosts are valid.

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(35)

A REVIEW OF *SALSUGINUS SECULUS* (PLATYHELMINTHES: MONOGENEA) IN THE WESTERN MOSQUITOFISH (GAMBUSIA AFFINIS) FROM TEXAS

G. Vasquez and **N.J. Negovetich**, Angelo State University

Western mosquitofish (*Gambusia affinis*) is cosmopolitan in warmer climates and can serve as a host for a number of parasites. The gill monogeneans from this host are especially interesting because of the very low species diversity that has been reported in the literature. In the United States alone, only a single species, *Salsuginus seculus* (Mizelle and Arcadi), is reported from the gills of fish collected across the country. To assess the validity of a single species on the gills of *G. affinis*, fish were collected from 11 geographically-distant aquatic systems in Texas and surveyed for monogenean infections. The gill monogeneans were then subjected to morphological and molecular analyses. Preliminary analyses suggest that more than one species of monogenean may be infecting the gills of *G. affinis* in Texas. Morphologically, most of the monogeneans resemble *S. seculus*, but parasites from a few locations exhibit anatomical differences that do not conform to the description of *S. seculus*. They are smaller in overall size and differ in their opisthaptor, including the size of the hamuli and shape of the haptoral bars. Sequence analysis on these parasites is on-going and will further clarify the identification of the monogeneans infecting the gills of the western mosquitofish.

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(36)

GENETIC DIVERSITY AND CRYPTIC SPECIES OF THE *ECHINOSTOMA TRIVOLVIS* SPECIES COMPLEX FROM CENTRAL NEW YORK MUSKRATS

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C. Kline, Hamilton College

Members of the trematode family Echinostomatidae exhibit a broad definitive host range that includes a variety of mammals and birds and are increasingly being used in ecological studies. Species boundaries have been difficult to define morphologically in this group, and molecular evidence has suggested that many species exist as cryptic species complexes. We used the mitochondrial DNA locus ND1 and the ribosomal DNA locus ITS to explore cryptic species and genetic diversity in the *Echinostoma trivolvis* species complex in muskrats (*Ondatra zibethicus*) from NY state. Over 30 individual trematodes were sequenced for both loci from 28 muskrats trapped at 7 localities. We found 2 out of the 3 *E. trivolvis* lineages reported previously from muskrats in VA (lineages a and b) but found further substructure in the

dominant lineage b. Further understanding of cryptic species diversity in *E. trivolvis* will inform future studies of ecology, epidemiology and host specificity.

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(37)

DOES SIZE MATTER? TAPEWORM FAUNAL DIVERSITY AND HOST SIZE IN THE MANGROVE WHIPRAY FROM THE SOLOMON ISLANDS AND AUSTRALIA

K.S. Herzog and **K. Jensen**, University of Kansas

Since its description by Macleay in 1883, only three tapeworm species have been reported to parasitize the mangrove whipray, *Himantura granulata*. These are the rhinebothriideans *Rhinebothrium himanturi* and a presumably new species referred to as *Rhinebothrium* sp. by Williams (1964) and the trypanorhynch *Prochristianella clarkeae* reported by Schaeffner and Beveridge (2012). Elasmobranch collection efforts in the Solomon Islands and Australia from 1997 to 2012 yielded ten specimens of *H. granulata*, all of which were examined for tapeworms. Standard morphological methods were used, including light and scanning electron microscopy and histological sectioning. Molecular sequence data were also generated for the D1-D3 gene regions of 28s rDNA for a subset of species. Morphological and molecular data indicate that at least 31 species of tapeworms parasitize *H. granulata* in these localities: two species of *Acanthobothrium*, seven species of *Anthocephalum*, one species of *Caulobothrium*, five species of *Rhinebothrium* (including *R. himanturi* and *R.* sp.), two species from one novel rhinebothriidean genus, six species of *Polypocephalus*, three species from two novel lecanicephalidean genera, and five species of trypanorhynchs (including *P. clarkeae*). The majority of these 31 species appear to be new to science. Of the ten specimens of *H. granulata* examined, six were small immature rays (disk width <35 cm) and four were large mature rays (disk width >100 cm), presenting the unique opportunity to assess differences in tapeworm faunal diversity between two host size classes. Not unexpectedly, host size appears to play an important role, as conspicuous disparities in tapeworm faunal diversity at the specific, generic and ordinal levels were noted between the two host size classes. Ultimately, a combination of variation in both host diet and habitat use between different size classes, as well as the specificity of larval tapeworms within their intermediate hosts, will likely be necessary to explain these differences.

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(38)

EXAMINING THE NOVEL INTERNAL ANATOMY OF AN ENIGMATIC TAPEWORM USING TRANSMISSION ELECTRON MICROSCOPY

K.A. Gallagher, **J.N. Caira** and **M. Cantino**, University of Connecticut

This study examined the bizarre internal anatomy of *Litobothrium aenigmaticum*, an enigmatic tapeworm that parasitizes pelagic thresher sharks in Taiwan and Mexico. Molecular data strongly support placement of this species within *Litobothrium* despite the substantial morphological differences seen between it and its congeners. Whereas typical members of the genus bear a scolex that consists of an apical sucker and cruciform pseudosegments, *L. aeigmaticum* lacks both of these features and instead bears a dome shaped scolex proper and elongate cephalic peduncle. Furthermore, examination of *L. aenigmaticum* with light microscopy revealed the presence of four novel tissue types within the scolex and sublateral paired ducts that run through the length of the body. The function of these structures was previously unknown. The present study used transmission electron microscopy (TEM) and histological staining and light microscopy to examine the internal anatomy in further detail. Three specimens were stained with 1% osmium tetroxide and embedded in epoxy resin for TEM. Two specimens were embedded in paraffin and serially sectioned for light microscopy. Each structure and tissue examined using light microscopy was stained using both hematoxilyn and eosin and the periodic acid-schiff protocol. TEM revealed that the sublateral paired ducts are surrounded by flames cells and associated collecting ducts,

suggesting that the sublateral ducts are excretory in nature. TEM also revealed the presence of a complex of 11, rather than 4, distinct tissues within the medulla of the scolex. The 11 tissues were distinguished and characterized based on cell size, nucleus size, cytoplasm to nucleus ratio, presence/absence of organelles, and presence/absence and nature of vesicles and/or inclusions. Each of the 11 tissues was found to contain electron dense vesicles; three tissues also contained electron lucent inclusions. The presence of these features suggests these tissues are producing some sort of secretory product. Light microscopy revealed that at least some regions of all 11 tissues were PAS positive and thus indicating the presence of glycoproteins. The secretory products of at least some of the anterior most tissues appear to be released through an aperture and its surrounding pores located at the apex of the scolex. Some evidence that the products of a subset of the more posterior tissues may be released through the tegument was also observed. While attached to the spiral intestine, individuals of this tapeworm species have been found to be surrounded by a papilla of host tissue. Our results indicate that this papilla surrounds only the portions of the scolex containing the 11 tissues. This result leads us to suspect that the products of these tissues may be eliciting an inflammatory reaction that induces the host mucosa to produce the papilla. However, further investigation is necessary if we are to fully understand the interactions among the many different tissues, the movement and release of their products, and the roles these products play in the biology of this unusual tapeworm species.

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(39)

MONOZOIC TAPEWORMS OF FRESHWATER FISHES IN NORTH AMERICA: AN UPDATE AND PERSPECTIVES

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A. Choudhury, Division of Natural Sciences, St. Norbert College
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Systematic research on caryophyllideans, the only monozoic group of 'true' tapeworms (Eucestoda), in the Nearctic region began with Hunter's (1927) monograph and was most intensive in the 1960's and 1970's. Since then, only two North American caryophyllideans have been described. This long period of neglect is unfortunate, because caryophyllideans represent an interesting model for studies of unusual molecular and cytogenetic phenomena, cryptic species diversity, and phenotypic plasticity. To date, as many as 60 species of caryophyllidean tapeworms have been described from catostomid and cyprinid fishes. However, most of them were studied only by traditional morphology-based taxonomic methods and molecular data are mostly lacking. Recently, a research project on the North American caryophyllideans has been initiated, with the main aim of providing a critical overview of their species composition, classification, host specificity, geographical distribution and phylogenetic relationships. Based on morphological and molecular data, five Nearctic species previously placed in *Monobothrium* were transferred to the originally monotypic *Promonobothrium*. In addition, two new species of *Promonobothrium* were described from *Ictiobus bubalus* and *Ictiobus niger* in Mississippi, and from *Erimyzon oblongus* in North Carolina, respectively. During a recent survey of the helminth parasites in Oregon, the common Palaearctic fish parasite, *Caryophyllaeides fennica*, was found for the first time, which represents evidence of a relatively uncommon amphi-Pacific distribution of the caryophyllidean tapeworms. The actual species diversity of North American freshwater fish parasites is likely to be grossly underestimated. Integrative taxonomy should be used to unravel the actual species diversity and host specificity of these and other North American fish tapeworms. *This study was supported by the Grant Agency VEGA (No. 2/0159/16) and Slovak Research and Development Agency (No. APVV-15-0004).*

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(40)

CESTODE FAUNA OF THE GIANT FRESHWATER WHIPRAY COMPARABLE TO THAT OF ITS MARINE RELATIVES

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

A total of seven species of dasyatid stingrays (Myliobatiformes) are characterized as freshwater obligate, including the giant freshwater whipray (*Himantura polylepis*), comprising at least three separate incursions into freshwater habitats. However, a tolerance of estuarine environments has been suggested for *H. polylepis*. Seven individuals of this species were collected between 2003 and 2008 at two sites in Borneo (five from the Kinabatangan River [Malaysia] and one from Tarakan [Indonesia]) and examined for lecanicephalidean cestodes. Cestode specimens were prepared for morphological examination following standard techniques; for select taxa, molecular sequence data were generated to confirm species boundaries. Collectively, these hosts were parasitized by eight species of lecanicephalidean cestodes: three new species of *Tetragonocephalum*, three new species of *Polypocephalus*, and one species each of two as of yet undescribed genera. This brings the total number of reported cestodes from *H. polylepis* to 18 species in nine genera of four orders. No cestode data exists for any of the other six species of freshwater dasyatids. Of the nine total genera parasitizing *H. polylepis*, one is unique while seven are collectively also found parasitizing its closest marine relatives, *H. granulata* and *Urogymnus asperrimus* 1. In contrast, the South American freshwater potamotrygonids are parasitized by a total of seven genera; three of these are unique to potamotrygonids while only three others are shared with its closest marine relative, *H. schmardae*. The similarity of the cestode assemblage of the giant freshwater whipray and its marine relatives supports this stingray venturing into higher salinity habitats, and suggests that it may in fact be a euryhaline species.

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UNEXPECTED TAPEWORM FORAYS INTO SKATE HOSTS

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

Elasmobranchs of the order Rajiformes (i.e., skates) host a diversity of tapeworm higher taxa. While some of these taxa appear to have diversified exclusively within their skate hosts, recent surveys have revealed the presence of other seemingly unrelated lineages as part of the parasite faunas of skates. Three such taxa are addressed here. The yellownose skate, *Dipturus chilensis,* was found to host tapeworms morphologically consistent with members of the order Phyllobothriidea, typically found parasitizing shark and ray hosts. The smooth skate, *Malacoraja senta*, and the shorttail fanskate, *Sympterygia brevicaudata*, were found to host *Zyxybothrium kamienae* and a novel member of the rhinebothriidean family Escherbothriidae, respectively. This study focuses on the morphology and phylogenetic affinities of these tapeworm lineages in order to better understand the composition and evolution of the parasite assemblages of these host species. Specimens of all three cestode lineages were prepared for morphological examination using both light and scanning electron microscopy (SEM). Sequence data for the 28S rDNA locus (D1-D3 region) were generated for specimens of all three cestode lineages. Phylogenetic analyses of these sequences and comparable data of extensive generic representation across elasmobranch-hosted cestode taxa were performed under both Maximum Likelihood and Bayesian Inference optimality criteria. Trees resulting from these analyses placed *Z. kamienae* in a clade with the electric ray-hosted genus *Pentaloculum* and an undescribed genus parasitizing the collared carpetshark. Proglottid and scolex morphology of *Z. kamienae* support these findings. Phylogenetic affinities of the phyllobothriidean species from *D. chilensis* based on molecular data, however, do not fully agree with the relationships suggested by the morphological features observed. Although SEM revealed the presence of neck scutes, suggesting affinities with the other scute-bearing phyllobothriidean taxa, sequence data suggest affinities with phyllobothriideans hosted by sharks that lack neck scutes. In the case of the cestode taxon from *Sympterygia brevicaudata*, while its scolex morphology resembles that of members of the rhinebothriidean family Rhinebothriidae, closer examination revealed the presence of conspicuous bothridial apical suckers, a feature seen in members of the family Escherbothriidae, all of which parasitize stingrays. In fact, results of the phylogenetic analyses support placement of this taxon within the Escherbothriidae. The close affinities of all three of the disparate tapeworm lineages with taxa parasitizing

elasmobranchs other than skates provide strong evidence that the processes responsible for the parasite assemblages observed in each of these host species include not only diversification within individual host species, but also host-switching events.

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CHARACTERIZATION OF CARBOHYDRATE STRUCTURES THAT TRIGGER REPLICATION IN *CRYPTOSPORIDIUM*

A.L. Edwinson, North Dakota State University

Cryptosporidiosis, a diarrheal disease caused by the protozoan parasite *Cryptosporidium*, can become chronic and life threatening in malnourished and immunocompromised individuals. There is no vaccine and no effective treatment for populations most at risk of severe disease. Previous work has shown that host glycoproteins and the carbohydrate galactose n-acetyl-galactosamine (Gal-GalNAc) trigger the transformation of invasive *Cryptosporidium* sporozoites to replicative trophozoites. The present work aimed to determine how trophozoite development is affected by the structure and spatial presentation of carbohydrates on glycoproteins. Isolating and experimentally manipulating the carbohydrate presentation of native host glycoproteins can be difficult, so our approach was to use synthetic glycoprotein mimetics which allow carbohydrate structure and spatial presentation to be controlled with nanoscale precision. Trophozoite development and replication was triggered when *Cryptosporidium* sporozoites were exposed to a solution of synthetic glycoproteins displaying the carbohydrates Gal-GalNAc or Gal, but not rhamnose. In other experiments, sporozoites were exposed to varying carbohydrate structures and densities displayed on synthetic glycoproteins grafted onto a glass slide in a microarray. Trophozoite development was greatest following sporozoite interactions with synthetic glycoproteins displaying high densities of Gal or GalNAc. In contrast, non-glycoprotein associated carbohydrates, such as rhamnose, were poor triggers of trophozoite development at the same densities. These data are consistent with previous reports that Gal-GalNAc is targeted by *Cryptosporidium* sporozoites during invasion of host cells, and they suggest that transformation to a replicative mode is intimately associated with the invasion process.

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TOXOPLASMA GONDII AFFECTS TRANSLATION INITIATION IN MACROPHAGES BY TARGETING THE MTORC1 AND MNK1/2 PATHWAYS

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Toxoplasma gondii, the etiological agent of toxoplasmosis, is an obligate intracellular parasite that infects about a third of the human population. Although the infection remains usually asymptomatic, reactivation of encysted parasites poses a threat to immunocompromised individuals (AIDS, chemotherapy). Also, congenital toxoplasmosis can lead to miscarriage or severe birth defects. In order to replicate within infected cells, *T. gondii* must acquire nutrients from its host (amino acids, polyamines, cholesterol, etc.). In addition to scavenge nutrients, *T. gondii* targets numerous signaling pathways and affects transcription of several genes involved in immune functions to gain an advantage over its host. Despite the fact that subversion of host metabolism and transcriptional regulation have been extensively studied, knowledge on translational control, specifically via the mTORC1 and Mnk1/2 pathways, by *T. gondii* is lacking. Here, we aim to determine whether the parasite affects these pathways to modulate mRNA translation (protein synthesis) in infected macrophages. Bone-marrow-derived murine macrophages (BMMF) were inoculated with either type I (virulent) or type II (avirulent) *T. gondii* strains, and the phosphorylation status of translational regulators was assessed by Western blotting. We observed a sustained phosphorylation of the translation repressor 4E-BP1 (inactivation) and the ribosomal protein S6 (activation). In contrast, we

detected a decreased phosphorylation of Mnk1 and the translation initiation factor eIF4E. Polysomal profiling analyses revealed a higher polysome-to-monosome ratio in *T. gondii*-infected BMMF, indicative of an overall increase in the rate of translation. RNAseq analysis of the highly translated mRNAs (polysome-associated) and the total input material will allow us to distinguish transcripts regulated at the level of translation versus transcription. Ultimately, characterizing the translatome of *Toxoplasma*-infected immune cells will help identify metabolic and immune functions subverted through translational control.

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(44)

SCREENING OF ETHANOL EXTRACT OF *COMBRETUM RACEMOSUM* AND *EUPHORBIA HIRTA* LEAVES FOR POSSIBLE ACTIVITY ON *TRYPANOSOMA BRUCEI* BRUCEI INFECTED MICE

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Enrichment of medicinal plants with biologically active compounds which induce various chemo-therapeutic effects has made a good turn and philosophy in the science of pharmacology. In the light of the popular notion of the use of *Combretum racemosum* and *Euphorbia hirta* as potent ethnopharmaceutical botanicals, the trypanocidal activity of the ethanol leaf extracts of the plants against *Trypanosoma brucei brucei* which was induced in Swiss albino mice was assessed. The animals were inoculated intraperitoneally (IP) with trypanosome load of 10^6, and were then kept under standard conditions for 10 days to enable circulation and reproduction of the parasite within them. Parasitaemia level was detected and analyzed via microscopy. Both plants proved positive by overall reduction in the mean parasitaemia level as the days progressed at concentrations of 50,100 and 200mg/kg body weight respectively. Acute toxic dose for analysis of the high dose extract toleration was also checked by a 1000mg/kg administration of the extracts, while diminazene aceturate, a standard trypanocidal drug was used as control. *Combretum racemosum* exhibited its best trypanocidal activity at the 200mg/kg concentration, and *Euphorbia hirta* was at its best at 50mg/kg. Following the administration of diminazene aceturate (control) the parasites were cleared within four days of administration. The results derived were confirmed with statistical analysis using SPSS 16 software at $p<0.05$, and posits the possible utilization of these extracts of *C. racemosum* and *E. hirta* as trypanocidal agents.

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(45)

ALTERATIONS TO NEURONAL ACTIVITY AS A FUNCTION OF METACERCARIAE INFECTION INTENSITY

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Eye infecting metacercariae can alter a fish's ability interact with its environment, such as impeding predator avoidance or limiting foraging ability. Less is understood on how infection by such parasites may alter the physiological regulatory factors of the host. The interactions of light with anatomical structures such as the suprachiasmatic nuclei (SCN), penial gland, and retina, are fundamental in hormonal regulation, and the presence of parasites in or around those tissues may alter key components of melatonin production and circadian timing. Fish infected with a higher intensity of metacercariae of the eye fluke *Tylodelphys* sp. exhibit a reduced threat response to a light stimulus. As the amount of retinal obstruction associated with *Tylodelphys* sp. infection is independent of the number of metacercariae present, the observed lack of response is likely the result of a cumulative diffusion of light through the bodies of the metacercariae. If true, the number of metacercariae within the eye of the host should influence the amount of light reaching the retina, and the SCN via the retinohypothalamic tract, altering hormonal and neuronal regulation. To verify this, we analysed the level of neuronal activity of fish

exposed to a flashing light stimulus. An immunohistochemical analysis was performed on cryosectioned brain tissue, using the c-fos protein for an assessment of neuronal activity. By assessing the level of c-fos in the brains of fish with varying levels of infection, we aimed to determine if neuronal activity is reduced in the optic lobes as a result of visual obstruction by the parasites. Our results provide a mechanistic link between infection and behavioral alterations in the host.

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ACUTE PHASE RESPONSE DURING THE COURSE OF INFECTION IN *TRYPANOSOMA CARASSII* INFECTED GOLDFISH (*CARASSIUS AURATUS* L.)

N. Kovacevic, University of Alberta

The acute phase response (APR) is a key component of innate immunity. It is a rapid sequence of systemic and physiological changes in response to any inflammation, infection or trauma. Its induction is characterized by a significant change in the blood composition of acute phase proteins (APPs), whose various roles are known to play a crucial role in immune responses, pathogen elimination and restoration of homeostasis in higher vertebrates. However, in lower vertebrates such as fish, the function of APP orthologos has not been fully elucidated. *Trypanosoma carassii* is an extracellular protozoan parasite infecting a variety of economically important fish including our model organism, the goldfish (*Carassius auratus* L.). In aquaculture settings, prevalence of *T. carassii* infection can reach 100%, resulting in significant morbidity and mortality. We characterized the APR in goldfish infected with *T. carassii*. Quantitative expression analysis revealed significant changes in a panel of APPs assessed in the kidney, liver and spleen of goldfish during the course of infection. Two major APPs, C-reactive protein (CRP) and Serum Amyloid A (SAA), were significantly up-regulated during the infection, and consequently chosen for further investigation by generation of recombinant proteins. SAA mRNA were positively correlated to parasitemia in the kidney and spleen, but not liver. Recombinant goldfish CRP (rgfCRP) enhanced complement-mediated killing of trypanosomes *in vitro,* and addition of immune serum to cultures enhanced effects

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EXPRESSION OF THIOESTER-CONTAINING PROTEINS IN THE SNAIL *BIOMPHALARIA GLABRATA* IN RESPONSE TO MICROBIAL CHALLENGE

J. Marquez, **C.E. Montelongo**, **G. Overcast** and **M.G. Castillo**, New Mexico State University

The snail *Biomphalaria glabrata* is an important intermediate host for the parasite *Schistosoma mansoni*, the cause of human schistosomiasis. Previous studies have reported different levels of snail resistance and susceptibility to infection by this parasite. Some of these differences are inherited and associated with the modulation of immune components. Our laboratory has recently identified six immune-related transcripts that code for members of the thioester-family of proteins (TEPs), including homologues for alpha-2-macroglobulin (A2M), CD109, insect thioester-containing proteins (iTEPs), and complement component C3. The goal of this study was to determine the expression pattern of these transcripts in *B. glabrata* tissues, and to determine if they are modulated in response to microbial challenge. For this purpose, *B. glabrata* snails from two strains (susceptible-BB02; and resistant-BS90) were exposed to microbial immune challenge by injecting live bacteria (*Escherichia coli*, *Micrococcus luteus*) and yeast (*Saccharomyces cerevisiae*), followed by TEPs-expression analysis by amplification methods (qPCR) and *in situ* hybridization. Preliminary results from semi-quantitative PCR indicate that *B. glabrata* snails respond differentially to each microbial challenge. In addition, resistant and susceptible strains appear to differentially modulate TEPs too, depending on the specific microbial challenge given. The highest increase in transcript expression was found to be in response to the Gram negative bacteria *E. coli*. In this treatment group, the TEP with highest expression was A2M in resistant (BS90) snails, while TEP-3

showed the highest expression in susceptible (BB02) snails when compared to buffer-only injection. Regardless of strain, *E. coli* caused the highest change in expression of C3-1 in both resistant and susceptible snails when compared to the buffer-only control. Further experiments are being performed to confirm these results by qPCR and to compare them to changes in TEPs expression due to *S. mansoni* exposure.

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(48)

AMPHIBIAN TRYPANOSOMES FROM NORTH CENTRAL OKLAHOMA: MORPHOLOGY, MOTILITY, AND PHYLOGENETIC RELATIONSHIPS.

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

From May-August 2014-2015, 200 amphibians from 5 families and 9 species were examined for *Trypanosoma* spp., leeches and leech hematomas. Of those, only bullfrogs (*Rana catesbeaiana*) and southern leopard frogs (*Rana sphenocephala*) were infected with *Trypanosoma* spp., but no leeches or leech hematomas were observed on any of the amphibians examined. Five species/morphotypes of trypanosomes infected adult southern leopard frogs and 4 species/morphotypes of trypanosomes infected adult bullfrogs. All five trypanosome morphotypes conform to previous descriptions of (1) *Trypanosoma ranarum*, (2) *Trypanosoma rotatorium*, and (3) *Trypanosoma chattoni*. Both leeches and hematophageous dipterans have been reported as vectors for amphibian trypanosomes. To evaluate how and when frogs become infected with trypanosomes, we sampled for potential leech and dipteran vectors and examined tadpoles, newly metamorphs and adult southern leopard frogs for trypanosome infections. One species of leech (*Placobdella rugosa*), two species of mosquitoes (*Culex erraticus*, and *Uranotaenia sapphirina*) and biting midges, *Forcipomyia* spp., were collected as potential vectors of frog trypanosomes. However, both trypanosome prevalence and morphotype richness increased as frogs aged being 0 in tadpoles, 9% and 0.09 + 0.3 in newly metamorphs and 59% and 1 + 1.2 in adult leopard frogs, suggesting that frogs become infected with trypanosomes via a dipterans after metamorphoses. Among trypanosome morphotypes, video-microscopy revealed distinct differences in trypanosome motility in frog blood plasma. Trypanosome morphotypes also separated into distinct groups based on morphological measurements. Additionally, the 18s rRNA gene of each morphotype was sequenced and aligned with previously sequenced anuran trypanosome 18s rRNA genes, and a phylogeny was created using a maximum likelihood framework. Phylogenetic analyses reinforced morphological identification of *T. ranarum*, but some morphotypes remain ambiguous, possibly representing new species of trypanosomes infecting amphibians in Oklahoma.

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DO ECTOPARASITE INFRACOMMUNITIES OF COASTAL BIRDS FOLLOW THE METABOLIC THEORY OF ECOLOGY?

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Energetic models can be powerful tools that increase our understanding of the condition of individual animals and their populations. These models track energy inputs (e.g., dietary consumption) and energy outputs (e.g., metabolic rate). For birds, energy output is most frequently associated with thermoregulation, foraging, and breeding activities. However, parasitism may also account for a substantial proportion of energetic losses. Here we use the Metabolic Theory of Ecology to examine the abundance and potential impacts of ectoparasites on coastal birds. We use scaling relationships between metabolic rate and body size for both hosts and parasites to predict the maximum density of ectoparasites that an individual bird can support. We compare these theoretical maximums to observed densities of

mites and lice of birds collected in California estuaries. We initially predicted that ectoparasite density would increase with host body mass to the 5/12 power because space (host surface area) not energy supply, limits ectoparasite abundance; however, preliminary results suggest energy is more important and ectoparasite density scales closer to 3/4. We also use metabolic scaling to evaluate the possible energetic impacts that different ectoparasite groups have on their hosts.

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MAXIMIZING THE OUTPUT: COLLECTING AND FIXATION OF QUALITY HELMINTH SPECIMENS IN THE FIELD

V. Tkach, University of North Dakota

Collecting parasitological materials poses many of challenges. One of them is the ability to obtain necessary collecting permits and arrange other associated permissions and logistics. The next one is the collecting specimens in the field. Whether it is done close to home or in a remote location on the other end of the world, it is rarely easy. If a researcher overcomes these two major hurdles and has collected animals, the scientific output from these specimens needs to be maximized. Each group of hosts has a different fauna of potential parasites (this presentation will be mostly devoted to helminths) that may inhabit various organs and tissues, surprisingly many of them outside of the most commonly examined organ, namely the intestine. It is important to know where and how to look. And even if we have successfully done all of the above and found the worms, all this hard work and future outcomes depend on our ability to properly fix the specimens. While doing this, we should keep in mind the need for quality specimens for morphological studies (e. g., traditional identification and descriptions, SEM, TEM, histology), and molecular work using a multitude of techniques and approaches. Can we do it all considering usually limited time and resources? Unfortunately the answer is frequently no. If we cannot do it all what is the acceptable level of compromise? Unfortunately, the importance of the fixation quality is frequently underestimated in various studies, from molecular to ecological. Somewhat artificial separation of parasite ecology from parasite taxonomy and systematics is partly to blame. The presentation will include discussion of some of the most useful helminth fixation techniques as well as some of the pluses and minuses of alternatives. The good news is that most of these techniques are not difficult and easy to follow. They only need to be implemented and used on a regular basis by researchers working in various sub-fields of parasitology.

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A TOTAL EVIDENCE APPROACH TO THE IDENTIFICATION AND DESCRIPTION OF HELMINTHS

J.N. Caira, Board of Trustees Distinguished Professor, University of Connecticut

As Parasitologists we, perhaps more than any other group of biologists, are well aware of the vast amount of diversity that remains to be discovered and described globally. Modern methods have provided access to new and exciting sources of data to help inform the identification and description of new taxa. These methods have had an impact on fieldwork for they mandate collecting strategies that allow a diversity of preservatives beyond formalin (e.g., ethanol, RNAlater, etc.) to be employed in the field for both host and parasite identifications and description. Host (or host images) and parasite specimens and their associated data (both morphological and molecular) must be explicitly linked and publicly available. However, given that above all else *stability* is the hallmark of good taxonomy, in order to serve future generations of Parasitologists effectively, these methods must be employed in a consistent and complimentary fashion. It is key to avoid the temptation of *replacing* characterizations of species based on previous methods (e.g., light microscopy) with those based on the newest available methods (e.g., sequence data) alone, and instead to work to expand characterizations to include data from new sources—for new methods will continue to emerge and this strategy will facilitate comparisons required to confirm

taxonomic novelty into the future. In terms of molecular methods now employed in helminth identification and taxonomy, sequence data from ribosomal genes (rather than the barcoding gene COI) have proven to be extremely informative and in many cases are largely congruent with morphological assessments of species boundaries. The power of such data has grown in proportion to the library of confirmed species for which comparable data are available. Sequence data for these loci are now routinely employed to aid in the identification of larval stages, thereby helping to correlate larval and adult morphologies and assemble food webs. Nonetheless, the search continues for additional loci. As whole genome sequencing becomes more tractable and affordable, one can foresee the day when descriptions of novel species might include whole genome data. But, proper vouchering is essential. Other recently developed sources of data, such as those from Transcriptomics and Proteomics have yet to be employed in the identification and description of helminths—both of which may be eclipsed by other yet-to-be developed sources of data.

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HISTOLOGY AND FISH PARASITE SURVEYS

M.L. Kent, Oregon State University

Over the last decade we have used histology to complement traditional tissue wet mount examinations in parasites surveys of fishes. Histology is advantageous because it allows for the examination of multiple parasites without a priori designations, concomitantly providing important information on associated pathological changes to the host. Histology also allows for detection of certain developmental stages of parasites not seen in wet mounts and determination of the precise tissue location of certain of small parasites (e.g., intracellular parasites). Histology was more sensitive than wet mounts for detecting ova of blood flukes in coho salmon *Oncorhynchus kisutch* smolts. Moving on to adult Chinook salmon *Oncorhynchus tschawytscha*, we found that histology was much more sensitive for detecting presporogonic forms of *Ceratonova shasta* and *Parvicapusula minibicornis*. We also discovered a new microsporidium in the intestinal epithelium similar to *Enterocytozoon*. Consistent with the genus, the spores are very tiny and would not have been seen in wet mounts. In collaboration with Dr. Lafferty and colleagues in Santa Barbara, we examined several estuarine fishes using histology. Most notably was a common and severe kidney infection by *Chloromyxum kurisi* in topsmelt *Atherinops affinis*. Extremely few spores are produced, and hence the infection would have likely not been detected by wet mounts. Most recently, we are examining endangered suckers and cyprinids from Klamath Lake, Oregon. Here we discovered an undescribed *Unicauda* sp. (Myxozoa), which produces few spores and only develops in the blood vessels walls of the kidney. Again, it would have been very difficult to discern this location in tissue wet mounts. One negative aspect of histology is that is less sensitive for larger parasites (e.g., helminths) as a much smaller amount of tissue is used, and intact worms are usually not available for precise identifications. Therefore, one method is not better than the other, so we recommend including both in fish parasite surveys.

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ARCHIVING PARASITES IN SCIENTIFIC COLLECTIONS – SPECIMENS, DATA, AND THE BIOREPOSITORY

A.J. Phillips, Department of Invertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, D.C.

The fieldwork was a success. The data gathering and analyzing the results took longer than expected. Writing and revising produced a solid manuscript. Getting the email from the journal editor that your manuscript has been accepted makes all of the long hours and hard work worth it. But now, what are you expected to do with the specimens that are the foundation of your soon-to-be published study? For this

talk, I will discuss the basics of archiving parasite specimens in permanent scientific collections, the importance of data management, and ensuring that your specimens were acquired and transported legally. I will also discuss the role of the biorepository for frozen tissues or organisms in preserving specimens for future work using the Biorepository at the National Museum of Natural History as an example. By archiving specimens and corresponding data in a scientific collection, the specimens upon which your work is based will be useful for researchers in expected or unexpected ways for decades to come.

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GENOMICS METHODS FOR PARASITOLOGY

S.L. Perkins, **M. Zilversmit** and **J. Foox**, American Museum of Natural History

Genome sequencing offers parasitologists an enormous wealth of information to better understand the evolution of these organisms. The recent lowered cost of high-throughput sequencing combined with an increased accessibility to genomics technology and bioinformatics has made the incorporation of genomic data easier and thus more prevalent in our field. There are multiple challenges, however, that parasitologists often face when conducting genomic and/or transcriptomic work, such as a poor ratio of parasite DNA to host DNA, genome composition biases, and lack of available reference genomes. These challenges can thwart genomics studies across the pipeline, including introducing complications in sequencing itself, quality control, and assembly. Several strategies to mitigate some of those challenges have been developed, however. These include *in vitro* methods to deplete host DNA via selective DNA extraction methods as well as post-sequencing *in silico* bioinformatic filters. Strategies for best practices in terms of sample collection for genomic work will also be presented.

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(55)

ECOLOGICAL METHODS FOR PARASITOLOGY

K.D. Lafferty, US Geological Survey

Disease ecologists ask questions based on epidemiological theory, such as how parasites affect host populations and communities and how host populations, communities and the abiotic environment affect parasite transmission, distribution, and spread. Know that theory before doing fieldwork. When planning an ecological study, first identify the statistical replicate. More replication leads to statistical power, and it is better to sample many hosts poorly than few hosts well. For instance, to understand how host size relates to parasitism, one needs many individuals. More challenging are questions where the replicate is a host population. Hypothesis testing is most efficient when replicates represent a wide range of the independent variable and covariates are controlled for. Furthermore, ecological studies aim to put these replicates in a natural context through random or systematic sampling or with field experiments. Finally, the ecological effect size is as important as the statistical significance. Before collecting/processing, be sure to have permits, safety protocols, and a consistent process. Processing hosts for parasites requires metadata and systematic quantification. Typical summary statistics include abundance data, prevalence, and intensity (see Bush et al. 1997). Above all, keep your eyes open and expect the unexpected.

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ASSESSMENT OF HELMINTH COMMUNITIES IN NORTHERN BOBWHITES FROM SOUTH TEXAS

S.A. Shea, **A.M. Fedynich**, **L.A. Brennan** and **D.B. Wester**, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville

This study was initiated to examine helminths of northern bobwhites (*Colinus virginianus*) at the infracommunity and component community level and evaluate various intrinsic and extrinsic factors that may influence host-helminth system dynamics. One hundred and twenty-four bobwhites were obtained from South Texas during the 2014–2015 hunting season and examined for helminth parasites. Four species of nematodes, 1 acanthocephalan (cystocanth), and 2 cestode species were found at the component community level; however, infracommunities consisted of up to 3 species. The heteroxenous cecal nematode *Aulonocephalus pennula* dominated numerically (6,651 individuals, 99% of all nematode individuals, averaged 67 worms per infected host, and occurred in 80% of the sample). Prevalence and intensity of *A. pennula* did not vary significantly by host age, sex, their interaction, or body weight. The remaining species rarely occurred (<25% prevalence) and contributed few individuals (70 worms). At the infracommunity level, *A. pennula* occurred in 19 bobwhites that were also co-infected with 2–3 helminth species. However, only 2 cestode species were found within the same microhabitat indicating that co-occurrence within the same feeding guild was rare, which minimized resource and interference competition. This study presents insight on a host-helminth system that is species-poor and numerically dominated by a single nematode species occurring in northern bobwhites within South Texas.

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RNA-SEQ RESPONSES OF FIELD-DERIVED SPECIMENS OF THE AFRICAN SNAIL *BIOMPHALARIA PFEIFFERI* TO INFECTION WITH THE HUMAN PARASITE, *SCHISTOSOMA MANSONI*

S.K. Buddenborg and **S. Zhang**, University of New Mexico
G.M. Mkoji, Kenya Medical Research Institute
E.S. Loker, University of New Mexico

Biomphalaria pfeifferi is likely one of the primordial hosts for *Schistosoma mansoni*, exhibits extraordinary compatibility with this parasite, and currently transmits more cases of *S. mansoni* than any other snail species due to its widespread distribution across Africa. Ironically, we still know relatively little at the molecular level regarding the responses of *B. pfeifferi* to infection with *S. mansoni*. To redress this shortcoming, we have undertaken Illumina HiSeq transcriptomics of the following triplicate samples of *B. pfeifferi* from Kenya: uninfected snails, snails exposed for 1- or 3-days (20 miracidia/snail), and snails with naturally-acquired shedding *S. mansoni* infections. We deliberately emphasized field-collected snails exposed to human-derived parasites as the most natural study system. *Schistosoma mansoni* reads were first filtered out and will be the topic of a separate study. Then, a *de novo B. pfeifferi* transcriptome was assembled from over a half billion paired-end reads. Transcripts were annotated using protein and nucleotide databases (including the *B. glabrata* genome database) with an emphasis on immune and stress responses, and reproduction. Expression analyses showed an increase in the total number of *B. pfeifferi* transcripts significantly up- or down-regulated at 1- and 3-days post exposure relative to shedding snails. Inhibitory neuropeptides like ovipostatin and developmentally regulated albumen gland protein were up-regulated especially in shedding snails, suggesting that host castration is not merely a passive response to diminished energy supplies. The absence of expression of sex pheromones may be related to the strong self-fertilizing preferences of *B. pfeifferi*. Fibrinogen-related proteins (FREPs) showed complex patterns of responses but one, FREP4, was consistently up-regulated, serving as a reliable marker of infection. Many of the features most responsive to infection are unknowns. Additional features will be discussed to help reveal other interactions taking place in these snails taken straight from a natural transmission focus.

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SURPRISING EVOLUTIONARY PATTERNS IN COCCIDIA INFECTING *APODEMUS* AND ARVICOLID HOSTS

J. Kvicerova
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Recent studies have shown that host switching is much more frequent evolutionary event than was originally believed, and it constitutes an important driver in evolution of host-parasite associations. We analyzed phylogeny and population genetics of an extensive sample, from a broad geographic area, for commonly occurring parasites of the genus *Eimeria* within the abundant rodent genera in Europe - *Apodemus*, *Microtus* and *Myodes* - using two molecular markers. Morphology of the obtained eimerians matched the five described species/morphotypes, corresponding to the specific lineages in the phylogenetic tree. Some of the lineages comprised samples from various localities across Europe and displayed a capability to infect several host species, whereas others were restricted to a particular host species or region. However, the most important finding was a repeated occurrence of recent host switches among closely related genetic lineages of *Eimeria* which may become rapidly fixed. This phenomenon, proved by several different methods, applied particularly to switches of eimerians from the *Apodemus flavicollis*/*Apodemus sylvaticus* to *Apodemus agrarius* hosts. We showed that genetic differentiation and isolation between *A. flavicollis*/*sylvaticus* and *A. agrarius* faunas was a secondary recent event and did not reflect host-parasite coevolutionary history. Rather, it provided an example of rapid ecology-based differentiation in the parasite population. This work was supported by grants P505/12/1620, P506/14-07004S (Czech Science Foundation) and APVV-14-0274 (Slovak Research and Development Agency).

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USING MORPHOLOGICAL AND MOLECULAR DATA TO IDENTIFY A *NEOECHINORHYNCHUS* SP. (PHYLUM: ACANTHOCEPHALA) INFECTING A NEW SNAIL HOST (*HELISOMA TRIVOLVIS*)

R.W. Koch, **R.P. Shannon**, **K.D. Gustafson** and **M.G. Bolek**, Oklahoma State University

As adults, acanthocephalans are parasites of vertebrate hosts but use arthropods as intermediate hosts. Additionally, some species of acanthocephalans use an additional paratenic host in the life cycle, usually a vertebrate host, where the juvenile acanthocephalan encysts and survives without further development. However, freshwater snails have occasionally been reported as paratenic hosts for acanthocephalans (*Neoechinorhynchus* spp.) which infect freshwater turtles as definitive hosts and ostracods as intermediate hosts. In a snail survey in Stillwater, Payne Co., Oklahoma, we found juveniles of a *Neoechinorhynchus* sp. encysted in a freshwater snail (*Helisoma trivolvis*). Prevalence in the spring, fall, and winter was 20% (n = 25), 1% (n = 200) and 1.5% (n = 200), respectively. To identify this acanthocephalan to species we amplified 1600 base pairs of the 18S rRNA gene. Using available sequences on GenBank we were able to match this juvenile *Neoechinorhynchus* sp. from a snail host to a previously reported sequence for *Neoechinorhynchus pseudemydis* (99.3% base pair match). To further identify the snail *Neoechinorhynchus* sp. and because few sequences for turtle acanthocephalans are available on GenBank, we collected a red-eared slider turtle from Stillwater, OK and recovered adult female *Neoechinorhynchus emydis* which were identified based on egg morphology. We amplified 1600 base pairs of the 18S rRNA gene from a single female *N. emydis* and found it to be genetically identical (100% base pair match) to the sequence of the juvenile *Neoechinorhynchus* sp. recovered from snails. These results indicate that *H. trivolvis* is a new snail host for *N. emydis*. More importantly, juveniles from snail hosts suggests that they are much larger than previous reports of *Neoechinorhynchus* spp. from ostracod hosts, suggesting that worms grow in snail hosts which may have important implications on establishment and survival as adults in turtle definitive hosts.

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EVALUATION OF ANTI-MALARIAL AND ANTIOXIDANT ACTIVITIES OF ETHANOLIC LEAF EXTRACT OF *VERNONIA AMYGDALINA* DELILE ON MICE INFECTED WITH *PLASMODIUM BERGHEI*

I.C. Mgbemena and **R.C. Asianuba**, Federal University of Technology, Owerri

Ethanolic extract obtained by 72 hours maceration with constant shaking using GLF shaker was evaluated for antimalarial, antioxidant activities, acute toxicity (LD_{50}), phytochemical constituents. Mice (20 -32g) infected with 1×10^7 *P.berghei* were used to test the suppressive and curative antiplasmodial activities through oral administration. The antioxidant activity of the extract at various concentrations was evaluated *in vitro using* 1, 1-diphenyl-2-picrylhydrazyl (DPPH) free radical and hydrogen peroxide scavenging ability assays, DPPH effect of the extract showed concentration dependent increase in its percentage scavenging activity. At the highest concentration (500µg/ml), the percentage inhibition of *V. amygdalina* was 68% which was not comparable to 92% of ascorbic acid (standard). Also, the extract at highest concentration scavenged 49.6% and ascorbic acid scavenged 91% of H_2O_2 at the same concentration. Percentage suppression of parasites at 150mg/kg was 63.7% and 77.0% at 300mg/kg while chloroquine at 10mg/kg gave 81.7% suppression of parasitaemia in early malaria infection. V. *amygdalina* extract at the same doses (150mg/kg and 300mg/kg) exhibited significant ($P<0.0001$) and dose related increase in parasitaemia suppression (66.2% and 75.8% respectively) in the curative model which was very close to 78.4% suppression caused by chloroquine (10mg/kg). Also, the two doses of the extract caused significant ($P<0.0001$) reduction of parasite load in established malaria infection. Preliminary phytochemical studies revealed the presence of alkaloids, flavonoids, saponins, tannin, sterol, phlobatanin, C. glycosides and phenol. The LD_{50} test caused no death in mice treated with oral administration of *V. amygdalina* extract up to highest dose (3200mg/kg/b/wt). Oxidative stress of the mice was accessed using catalase, gluthathione reductase and malondialdehyde (MDA). The result obtained showed significant increase ($P<0.0001$) in level of glutathione reductase but significant ($P<0.0001$) decrease in catalase activity and malondialdehyde level of all the extract and chloroquine treated groups when compared to the negative control group. However, ethanolic leaf extract of *Vernonia amygdalina* has demonstrated a potent antimalarial and antioxidant activities and is safe up to a dose of 3200mg/kg.

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PLANKTON-PARASITOID INTERACTIONS: A WINDOW INTO WITHIN-HOST DYNAMICS

T.E. Stewart and **C.E. Cáceres**, University of Illinois at Urbana-Champaign

Parasites are regulated by extrinsic (outside of the host) and intrinsic (within-host) processes. For many natural systems, we have substantially increased our understanding of how ecological factors can facilitate or limit parasitism. However, the within-host processes that govern a parasite's establishment, development, and reproduction are often unknown. Hosts have evolved a series of traits to defend against parasites, but how important are these defenses for regulating host-parasite interactions? The zooplankton, *Daphnia dentifera,* and its fungal parasitoid, *Metschnikowia bicuspidata*, provide an ideal system for assessing the consequences of host defenses for infection outcomes. *Metschnikowia bicuspidata* are transmitted to *D. dentifera* through the environment: the fungus possesses free-living spores that reside in the water column and infect filter feeding *D. dentifera*. These spores must be ingested to infect their hosts, and the feeding rate of *D. dentifera* has been historically linked with its rates of infection. However, variation in *D. dentifera* infection rates is not sufficiently explained by feeding rate alone, which raises the question of whether post-exposure defenses contribute to the success or failure of *M. bicuspidata* infections. Disentangling exposure from susceptibility in this system requires an

understanding of the within-host events that define the *D. dentifera-M. bicuspidata* interaction. I first resolved the within-host life cycle of *M. bicuspidata* by exposing *D. dentifera* to a high spore dose, culling individuals daily for ten days, and describing the progression of infection. This project revealed five discrete fungal stages that occur after host exposure and before host death. Next, I assessed whether exposed *D. dentifera* can clear *M. bicuspidata* infections, and whether they vary in their capacity to do so. I exposed ten genotypes of *D. dentifera* to high spore doses of *M. bicuspidata* and culled individuals daily for ten days to stage their infections. Using Markov models, I then evaluated genotype-specific transition rates from each fungal stage to the uninfected class. Results of this project suggest that *D. dentifera* can prevent infections with a robust gut barrier, can clear early fungal stages with an activated cellular response, and that host genotypes vary strongly in these abilities.

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ANCHORING *PLASMODIUM FALCIPARUM* EXPORTED PROTEINS TO ERYTHROCYTE CYTOSKELETON AND UNDERSTANDING THEIR FUNCTION

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G.K. Kilili, Food and Drug Administration
D.J. LaCount, Purdue University

Plasmodium falciparum, which causes the deadliest form of malaria, extensively modifies the host red blood cell (RBC). The RBC cytoskeleton is a prominent target for remodeling, resulting in changes in RBC deformability, shape and surface properties. These changes in the infected RBC (iRBC) are attributed to the actions of hundreds of proteins that are exported by the parasite to the iRBC. However, the molecular interactions of these exported proteins are largely undefined. To determine which exported *P. falciparum* proteins target the RBC cytoskeleton, we carried out a large-scale screen to identify the parasite proteins that bind to inside-out vesicles (IOVs) prepared from uninfected RBCs. The screen identified 47 parasite proteins that bind to IOVs. We then used complex purification plus mass spectrometry and split-luciferase assays to identify the specific RBC cytoskeletal proteins that bind to the exported *P. falciparum* proteins. Twenty-one pairs of novel parasite-RBC cytoskeletal protein-protein interactions were identified, of which six were found in both assays. Twelve out of 21 interactions have been confirmed by affinity purification using *E. coli*-expressed parasite proteins. We found four parasite-exported proteins that share the MESA erythrocyte cytoskeleton-binding (MEC) motif all target the same region of the RBC cytoskeletal protein ankyrin; in each case the motif was sufficient for the interaction with ankyrin. Experiments in progress are designed to confirm additional interactions in pull-down assays, study localization of the interacting parasite proteins and assess the role of these proteins in parasite multiplication and host cell remodeling.

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TEMPORAL AND SPATIAL INFECTION PATTERNS OF TUNA BLOOD FLUKES *CARDICOLA* SPP. IN POLYCHAETE INTERMEDIATE HOSTS AT A TUNA FARM IN JAPAN

S. Shirakashi, **K. Tani**, **K. Ishimaru** and **T. Honryo**, Fisheries Laboratory, Kindai University
H. Uchida, Kushimoto Marine Park
K. Ogawa, Meguro Parasitological Museum

Aporocotylid (sanguinicolid) blood flukes, also known as fish blood flukes, comprise over 130 nominal species, representing one of the largest trematode groups in fish. However, their lifecycle and general biology/ecology are poorly known especially for the marine species. Recently, extensive studies on marine aporocotylids have been conducted as they can cause serious problems in aquaculture. Among them, *Cardicola* spp. are receiving special attention due to their impacts on tuna farming industries around the world. To date, 3 species of tuna-infecting *Cardicola* species have been described; namely *Cardicola*

forsteri, Cardicola orientalis and *Cardicola opisthorchis*. We have confirmed the infection of all of the three species in farmed Pacific bluefin tuna in Japan. These blood flukes reside in the heart or gill blood vessels and produce numerous eggs which block the gill capillaries, causing tuna to suffocate to death. Juvenile tuna are especially prone to the infection and large mortalities may occur unless farmers conduct oral treatment of Praziquantel. Recently, we have identified two terebellid polychaetes as the intermediate hosts for *C. orientalis* and *C. forsteri* in a tuna farm in Japan. To understand the general infection pattern of the blood flukes in their intermediate host, we conducted monthly samplings to monitor their infections for 1 year between January 2015 and January 2016. Terebellids polychaetes were collected from various points around the tuna cages such as floats, ropes, cage frames, sediments and bottom substrates. Terebellids form nests on sessile organisms or hard materials such as sponges, ascidians, barnacles and bivalve shells that are grown or accumulated around the farming cages. Terebellids were individually isolated and checked under a dissecting scope for the presence of sporocysts in their body cavity. We have checked a total of 9,850 terebellids and found over 700 infected individuals. Majority of the infected terebellids were *Nicolea gracilibranchis,* the intermediate host of *C. orientalis*. This species was the most common polychaete in the study area and they are most frequently collected from ropes and floats. However, the infection prevalence at those two points was considerably different, over 10% at ropes and less than 0.5% at floats. Moreover, both the density and infection prevalence of *N. gracilibranchis* on the ropes tended to be higher at the depth up to 4m. On the other hand, we have found a total of only 7 individuals of infected *Neoamphitrite vigintipes,* the intermediate host of *C. forsteri* during 1 year sampling. Almost all of them were found in the sediments accumulated on the bottom floor of culture cages. These results indicated that specific biotic/abiotic characteristics strongly influence the population density of each terebellid species and also their infection by the blood flukes. The *C. orientalis* infection in *N. gracilibranchis* showed a clear temporal pattern. The prevalence increased from January (0.9%) to April (16%), then rapidly declined after the peak in July (19%) when juvenile tuna are transferred from hatcheries to the culture cages. No infected terebellids were found in November and December, but re-appeared in January of following year. This suggests *C. orientalis* has an annual cycle of development in the intermediate host. However, precise development speed of the *C. orientalis* in the intermediate host and general biology/ecology of the *N. gracilibranchis* remain unknown.

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COMPARATIVE PHYLOGEOGRAPHY OF NORTH AMERICAN PIKA PARASITES: UNRAVELING A HISTORY DRIVEN BY CLIMATE CHANGE

H. Toman, Northern Michigan University

The geographic movement and genetic evolution of parasites and their hosts have varying degrees of concordance or independence. Molecular investigations into co-distributed, host specific parasite lineages provide a unique opportunity to elucidate the factors that contribute to a parasite's phylogeographic history, and assessment of independent parasite lineages allows general histories to be distinguished from taxon-specific patterns. Nearctic pikas (genus *Ochotona*) and their endoparasitic helminths provide an excellent study system to investigate these interactions. American pikas have a narrow temperature tolerance, so have experienced historical range fluctuations in response to climatic oscillations. This has produced five major lineages distributed throughout the mountain systems of the American West. Parasites have been thoroughly sampled across this host's range and we investigate two major lineages, the tapeworm genus *Schizorchis*, and the nematode subgenus *Labiostomum* (*Eugenuris*). We see that both include species with concordant distributions, yet are not concordant with pika lineages. We use multi-locus datasets to uncover the timing and order of population level diversification within species of these two genera relative to the geographic placement of major host lineages. Hypothesis testing was conducted using the Approximate Bayesian Computational (ABC) method, with parameterization of the priors done using LAMARC and *Beast. Further analyses include Bayesian skyline plots to assess demographic change over time relative to glacial cycles and host demography. The results of these analyses can provide us with better models to predict future parasite shifts due to anthropogenic effects as well as climate change.

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EFFECTS OF HAIRWORM INFECTION (NEMATOMORPHA: GORDIIDA) ON CRICKET REPRODUCTIVE OUTPUT

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B. Hanelt, University of New Mexico
M.G. Bolek, Oklahoma State University

Freshwater gordiids have complex life cycles that include multiple hosts. During infection of the definitive arthropod host, gordiids reside in the hemocoel of their arthropod hosts and rely on the host's fat body for growth and development. Within the arthropod host, gordiids begin development from a microscopic larva and grow to a length of over two meters for some species. As a result, very little energy, in the form of fat body remains and most female arthropod hosts experience inhibition of egg production as a result of the infection. At the end of their parasitic phase, gordiids manipulate the behavior of their terrestrial arthropod hosts to enter aquatic habitat where adult worms emerge from the host. More importantly, unlike most parasites, the odd life cycle of gordiids with a parasitic phase in a terrestrial host and a free-living aquatic stage which leaves its host, suggests that female arthropod definitive hosts which survive worm emergence may be capable of producing eggs post-infection. The focus of this investigation was to evaluate post-parasitism production of eggs and oviposition behavior in the female house cricket (*Acheta domesticus*). To test the production of eggs after infection, four week old female house crickets were fed aquatic snails containing cysts of *Paragordius varius*. Once worms emerged from their cricket hosts, crickets were sequestered into individual containers and checked daily for additional worm emergence. Upon death, necropsy was performed to check for additional worms which may have not emerged, and the production eggs by the cricket host. Our results indicated that crickets infected with hairworms experience inhibition of egg production but some were capable of producing eggs post infection (up to 18%) and some crickets were able to produce eggs while harboring an additional latently developed hairworm. This work is the first to examine egg production post-parasitism in *Acheta domesticus* infected with *Paragordius varius*.

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IVERMECTIN AND FILARIAE: THE DAWN OF UNDERSTANDING

T.G. Geary, Institute of Parasitology McGill University

Perhaps the most prominent aspect of the use of ivermectin as an anthelmintic has been in the control of filariases, especially heartworm infections and onchocerciasis. Studies in whole parasites have revealed that ivermectin has little activity on these clade III nematodes in culture; unlike GI nematodes and the free-living species *C. elegans*, ivermectin does not affect the motility of adults or microfilariae at pharmacologically-relevant concentrations. Recent work indicates that exposure to the drug may block the ability of microfilariae to evade host immune responses. How ivermectin causes long-term cessation of microfilarial production by adult females after a single dose is now beginning to come to light. An avenue of current research in this regard is the possibility that ivermectin causes prolonged pharyngeal paralysis in adult filariae, preventing the acquisition of iron for heme biosynthesis and larval development. Despite the historic importance of ivermectin in filarial chemotherapy, much remains to be learned about how it works.

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EX UNO PLURES: SPECIES RECOGNITION AND DIVERSIFICATION OF FRESHWATER *BOTHRIOCEPHALUS* SPECIES IN NORTH AMERICAN FRESHWATER FISHES

A. Choudhury, St. Norbert College

Species recognition in parasites becomes challenging in the face of cyrptic diversity and host-induced morphological variablity. Integrative taxonomy, which makes use of molecular, morphological, and other biological characteristics has already caused extensive revision of several taxa. It is also likely that true diversity in many groups of parasites is underestimated. Here, we examine these phenomena involving species recognition in a case study of the genus *Bothriocephalus*, a lineage widely distributed in Nearctic freshwater fishes. Of the several nominal species, 1, *B. cuspidatus*, has been considered a highly variable species and appears to have three disparate principal hosts or host clades: its type host, walleye (*Sander vitreus*), goldeye (*Hiodon alosoides*) and *Lepomis* sunfishes, mainly pumpkinseed, *L. gibbosus*. Morphological and molecular studies using existing and freshly collected material from these hosts, as well as others (rock bass, *Ambloplites rupestris*, and darters, *Etheostoma* spp.), when integrated with host-associations and biogeography, allow us to recognize at least 5 distinct biological and evolutionary entities (arguably species). Historical records - mainly in the form of museum depositions - when rev-examined in the light of new information, provide a fuller understanding of the consistency and geography of these host-parasite associations.

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PALEOPARASITOLOGY: A WINDOW TO THE PAST FOR APPRECIATION OF HOST-PARASITE RELATIONS IN SPACE AND TIME

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Paleoparasitology is the study of parasitism in animal and human host populations based on the occurrence of diagnostic indicators of infection preserved in the fossil record. Historically the field traces its origins to the recovery of eggs in the tissues of mummified human remains associated with Egyptian tombs of the 12th millennium BC. The adoption of diagnostic methods developed in veterinary and clinical parasitology stimulated descriptive studies of the health and hygiene of prehistoric human populations based on analysis of sediments and preserved feces from residential sites. Studies in the ensuing years included description of host-parasite relationships from extinct animal species and provided a foundation for exploring issues of broad epidemiologic interest to understanding the distribution of parasitic infections in human populations. The adoption of immunologic assay and molecular based diagnostic methods hold the promise of increased sensitivity and specificity for detecting parasitic infections in samples that are otherwise hidden from microscopic examination. The combination of increasingly sophisticated diagnostic methods and interpretive paradigms reinforce the relevance of paleoparasitology to inform on timeless epidemiological processes such as the translocation of parasites to new environments and enhanced transmission opportunities for new host populations that arise from globalization

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PARASITISM OF INVASIVE AND NATIVE SPECIES: EVALUATION OF ENDOHELMINTHS IN ROCK BASS AND SMALLMOUTH BASS FROM ALGONQUIN PARK LAKES

F. Zahlan and **J. Koprivnikar**, Ryerson University

Exotic and invasive species often differ in their parasite fauna compared to native hosts within their introduced range. This can have important consequences for their establishment success, but also for local transmission dynamics. We examined 112 invasive rock bass (*Ambloplites rupestris*) and 59 native

smallmouth bass (*Micropterus dolomieu*) from 8 different lakes in Algonquin Park, ON, Canada to evaluate their endohelminth parasites. Our results indicate that smallmouth bass are not only more likely to be infected with trophically transmitted parasites such as cestodes and acanthocephalans than rockbass, but also have a higher infection intensity and greater diversity of endohelminths. There was no significant difference between the two fish species with respect to non-trophically transmitted trematode metacercariae. Along with host size, fish diet and habitat use will be discussed to demonstrate how the ecology of different species influences their probability of infection and endohelminth communities. As environmental perturbations such as climate change alter ecosystems, and species continue to shift their ranges, this may have important consequences for host-parasite interactions and their broader ecological communities.

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PARASITE EVOLUTION: HERITABLE VARIATION IN INFECTION STRATEGY IN A FACULTATIVE PARASITE

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Facultative parasites express variation in life-history strategies – they can persist in a free-living state or engage in host exploitation. Generally, such phenotypic variation is generated by genetic variance and/or environmental variance. Here, I investigated the heritability of variation in infectivity by performing artificial selection on the parasitic mite, *Macrocheles muscaedomesticae*. While free-living, mites feed on nematodes but will parasitize insect hosts under certain conditions. Selective breeding involved exposing a *Drosophila* host to a mite while controlling for environmental variation. Mites that attached were selected to seed the 'infectious' lines and mites that did not attach were selected to generate 'non-infectious' lines. Control lines were maintained in parallel without imposing selection. While the response to selection (slope) was significantly different from 0 in both selection lines, the attachment rates were not significantly different from the controls among lines selected for low infectivity. Lines selected for increased attachment showed significant divergence from the control lines. The rapid positive response to selection suggests that infection strategy is heritable in this system. In other words, variation in infectivity in the mite population is due to genetic variation among individuals in that population. Determining the heritability of parasite infection strategy is fundamental to understanding the evolution of parasites from free-living organisms.

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SHOULD I STAY OR SHOULD I GO: INFECTION PLASTICITY IN THE FACULTATIVELY PARASITIC MITE *MACROCHELES SUBBADIUS*

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When presented with a host, the mite *Macrocheles subbadius*—a facultative parasite—may either take or forego the opportunity to engage in parasitism/phoresy. It is unclear what factors underlie this variation; however, it seems likely that certain environmental factors play a role. This seems likely because *M. subbadius* typically occupies ephemeral and patchy habitats from which phoresy—despite the associated risks—often represents the most reliable means of dispersal. We hypothesized that environmental indicators of habitat degradation like low food availability and overcrowding act as cues that increase the tendency of individual mites to attach to a host. This hypothesis was tested by way of a factorial experiment in which mites were reared in food-scarce and/or crowded conditions and were subsequently assayed for attachment to the natural host, *Drosophila nigrospiracula*. We also examined potential maternal effects by assaying the offspring for host attachment. Preliminary results suggest that exposure to food scarcity positively influences host attachment in individual mites but not their offspring—which in turn suggests that host attachment is a phenotypically plastic trait in *M. subbadius*. These results could

have bearing on the larger question of how obligate parasites evolve from free-living ancestors as facultative parasites represent an obvious evolutionary "stepping-stone" between these two life history strategies; in particular, they could help illustrate the importance of phenotypic plasticity in the evolution of obligate parasitism.

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ROAD SALT REDUCES LARVAL AMPHIBIAN PARASITE AVOIDANCE BEHAVIOUR BUT NOT RESISTANCE TO INFECTION

D. Milotic and **J. Koprivnikar**, Ryerson University

Road salt is used heavily in North America, and has various effects on aquatic organisms, but has never been considered in the context of host parasite-interactions. This is important because increases in salinity have the potential to stress organisms, which can lower their immunocompetence, activity, and competitive ability. This has been demonstrated in larval amphibians as well as other freshwater animals. The objectives of this study were: 1) to determine if road salt affected the susceptibility of larval *Rana sylvatica* (wood frogs) to infection by the trematode *Ribeiroia ondatrae*, and, 2) if road salt exposure affected tadpole parasite avoidance behaviour. Twenty tadpoles were exposed to each of three treatments (0, 400 and 800 mg/L of commercial road salt) for two weeks. After twelve days, we exposed the tadpoles to 20 cercariae each and recorded their behaviour before and after the addition of parasites. At the end of the experiment, we quantified tadpole growth, anti-parasite behaviour (activity in the presence of cercariae), developmental stage, individual infection status, and number of parasite cysts. We found that road salts do not have a significant effect on the growth of wood frog tadpoles, or on their infection status, cyst abundance, or cyst intensity. However, there was a marginally insignificant overall effect on anti-parasite behaviour as there was a strong trend for *R. sylvatica* in the lowest salt concentration to show increased activity when cercariae were present compared to the higher salt concentrations. In particular, there was a significant difference between activity in the 0 mg/L and 400 mg/L concentrations, and a marginally insignificant difference between the 0 mg/L and 800 mg/L concentrations. These activity differences were not observed in the absence of parasites. Our results suggest that intermediate levels of road salt, which easily encompass concentrations found in nature, may have an impact on amphibian anti-parasite behaviour, and perhaps to other natural enemies as well. Further studies are needed to investigate how various amphibian and parasite species might be affected by road salts, including at higher concentrations and in the presence of other interacting factors.

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DENSITY AND COMPLEXITY OF AQUATIC VEGETATION DOES NOT AFFECT LARVAL AMPHIBIAN PARASITISM

M. Milotic and **J. Koprivnikar**, Ryerson University

Macrophytes can have a great influence in aquatic ecosystems, such as providing refuges for larval or juvenile animals from predators, and may also act in a similar role for other natural enemies such as parasites. Previous studies examining the structural complexity of aquatic environments suggest this might affect the host-finding success of free-swimming trematode cercariae. Alternatively, this could influence host anti-parasite behaviours, such as detection or escape. Macrophytes can range from high to low density, and can be structurally complex (many leaflets) or simple (few broad leaves). The purpose of our experiment was to examine whether the structural complexity of aquatic vegetation affects larval amphibian infection by the trematode *Ribeiroia ondatrae*. We used four treatments (five replicates each) representing combinations of two main components of structural complexity in aquatic plants: low density/low complexity, low density/high complexity, high density/low complexity, and high density/high complexity. Each replicate contained five *Rana sylvatica* tadpoles in a tub containing plastic vegetation corresponding to the treatment to which 100 *R. ondatrae* cercariae were added and allowed to remain

for 2 hours. Tadpoles were then preserved for later quantification of their infections, mass, and developmental stage. We found that neither vegetation density nor complexity had a significant effect on host infection status or number of cysts within our model system. Further studies are needed to explore how structural complexity in natural systems can affect host-parasite interactions, especially when considering the introduction of invasive species which can cause massive physical alterations of ecosystems.

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POPULATION DYNAMICS AND PHYLOGEOGRAPHY OF A BERINGIAN CESTODE, *AROSTRILEPIS MACROCIRROSA*

S.R. Gallagher and **K.E. Galbreath**, Northern Michigan University

Historical episodes of climate change caused distinct patterns of dispersal and differentiation in mammals across the Holarctic. Understanding of these patterns can be strengthened by examining histories of associated parasites, which were influenced by host population events. For example, northern red-backed voles (*Myodes rutilus*) and the tapeworm *Arostrilepis macrocirrosa* share a complex history of dispersal and differentiation across Beringia, the land bridge that periodically connected Eurasia and North America. Previous work has demonstrated that populations of *M. rutilus* were isolated in separate Beringian and central Asian refugia during past glacial periods. Subsequently, vole lineages underwent geographic range shifts as some populations retracted while others expanded. This study investigates patterns of intraspecific diversity within *A. macrocirrosa* to quantify the consequences of climate-mediated host history for parasite populations. We have acquired 160 tapeworm specimens representing 31 localities and used a multi-locus phylogeographic approach to resolve geographic patterns of genetic structure. As detected for the host, we show support for refugial isolation between parasite populations in Beringia and central Asia. Additionally, we have support for recent population expansions in both parasite lineages similar to that of the host. However, we did not detect evidence of historical geographic shifts by *A. macrocirrosa* that were congruent with those inferred for the host. These partially incongruent histories suggest that though major vicariant events associated with refugial isolation may have structured host and parasite populations similarly, additional factors caused host and parasite populations to follow semi-independent trajectories when environmental barriers were released.

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(75)

PARASITE-MEDIATED HABITAT USE BETWEEN CONGENERIC ISOPODS

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Parasite-mediated competition can be an important force shaping community structure. Closely related species are often susceptible to the same parasites, yet the prevalence and virulence of the infection may vary among host species. The freshwater isopods *Austridotea annectens* and *A. lacustris* are both hosts to the trematode *Maritrema poulini*, yet there is a substantial difference in prevalence (100% versus 50%, respectively) and intensity (25.1 versus 5.0, respectively) between host species. Additionally, it is uncommon to find the two isopods in the same microhabitats when field sampling, despite the species having similar ecological requirements. The spatial segregation of the isopod hosts and the large differences in parasite abundance between host species suggest an interaction between infection and habitat selection. If *M. poulini* impacts the two hosts differently, infection may be mediating habitat use. On the contrary, if differences in microhabitat use changes exposure to parasites, it may explain observed differences in parasite abundance. The effects of parasitism on host competition and habitat use were examined in laboratory trials containing varying proportions of experimentally infected and uninfected isopods. Groups of both isopod species were placed in aquaria containing rocky and sandy substrate to simulate natural conditions. Location of individual isopods was recorded after one week and dissections were performed to assess parasite presence and abundance. Differences in habitat use were observed within/between species when parasites were present in neither, only one, or both species. *Maritrema poulini* may mediate the interaction between the two hosts, altering the strength and/or direction of interspecific competition, resulting in altered habitat distribution. As

the sandy substrate leaves isopods at a greater risk of predation, *M. poulini* infection may alter induce higher predation rate of one host over the other via parasite-mediated competition.

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A PARADIGM SHIFT: SYNTHESIS AND FUTURE DIRECTIONS FOR TREMATODE SOCIALITY

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Until recently, when considering trematode parthenitae, one did not imagine colonies with a reproductive division of labor. Some parasitologists still envision that all redial infections are merely self-sustaining infrapopulations that consist of individuals of varying levels of maturity (Galaktionov et al. 2015). However, several lines of evidence support the existence of complex sociality in some trematode species in their mollusk first intermediate hosts. As in other complex animal societies, trematode individuals live in colonies characterized by a high degree of cooperative organization, and have morphologically and behaviorally distinct reproductive and non-reproductive castes. Although non-reproducing individuals might have other roles, a major role is defense—that is, they are soldiers. Here we present the extent of the evidence for trematode sociality. A non-reproductive soldier caste has now been documented for fourteen trematode species from different trematode families, geographic regions, and host species. Further, ten species lack soldiers, and present a population structure consistent with that of differing maturation. Literature evidence of life histories of several other species suggests that both patterns are widespread. We review and synthesize what is known regarding the ecology and evolution of trematode sociality, and argue that trematode parthenitae are often more than merely a self-sustaining population: they form colonies and some species exhibit a reproductive division of labor. Finally, we discuss the implications of this paradigm and future research directions.

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BIOTIC DIVERSITY AND HUMAN SCHISTOSOMIASIS TRANSMISSION IN WESTERN KENYA

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Recent studies emphasize the importance of understanding the dynamics of the aquatic phases of human schistosomiasis transmission, particularly because mounting evidence suggests that many years of annual praziquantel treatments may achieve only limited reductions in schistosomiasis prevalence or in schistosome genetic diversity. Also, disease ecologists have gained an increased appreciation for the importance of understanding the biotic context in which disease transmission occurs. In west Kenya, we study *Schistosoma mansoni* in stream habitats where it is transmitted by *Biomphalaria pfeifferi*. During our bi-monthly surveys, we collect data on water temperature, water velocity, pH, absolute and relative snail densities, and prevalence of larval trematode infections. We are interested in understanding how transmission is influenced by 1) climatic factors, 2) the diversity of snail species present, and 3) the diversity of trematode species dependent on *B. pfeifferi* for their development. Our data suggest that snail species diversity changes with time with lower diversity correlated with an increased abundance of *B. pfeifferi*. The prevalence of *S. mansoni* changes markedly with time and is positively correlated (R^2= 0.683) with *B. pfeifferi* abundance. Other trematodes also commonly infect *B. pfeifferi*. For example, almost twice as many snails are infected with amphistomes as with *S. mansoni* (625 vs. 342 infections, respectively), and even though both amphistomes and *S. mansoni* infections are common, only 3 double infections have been noted, significantly fewer than expected by chance ($p < 0.008$). We have also pieced together a dominance hierarchy among the trematode species infecting *B. pfeifferi*, and a previously-undescribed echinostome is the most dominant species. We will continue our field surveys in association

with lab experiments to pin down specific aspects of transmission biology, including mechanisms underlying interactions between schistosomes and other trematodes. Supported by NIH R01 AI 101438, and a Gates Grand Challenge grant.

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INDEPENDENT ORIGINS OF PARASITISM IN ANIMALIA

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Parasite species comprise nearly half of animal life, yet the number of transitions to parasitism and their potential for associated adaptive radiations remain unresolved. Based on a comprehensive survey of the animal kingdom we find that parasitism has independently evolved approximately 223 times in just 15 phyla with the majority of identified independent parasitic groups occurring in the Arthropoda, at or below the level of Family. And, although metazoan parasitology is dominated by the study of helminthes, only 20 percent of independently derived parasite taxa belong to those groups, with numerous transitions also seen in Mollusca, Rotifera, Annelida, and Cnidaria. Parasitism is almost entirely absent from deuterostomes, and although worm-like morphology and host associations are widespread across Animalia, the dual symbiotic and trophic interactions required for parasitism may constrain its evolution from antecedent consumer strategies such as generalist predators and filter feeders. In general, parasitic groups do not differ from their free living relatives in their potential for speciation. However, the ten largest parasitic clades contain 90% of described parasitic species, or perhaps 40% of all species. Hence, a substantial fraction of animal diversity on Earth arose following these few transitions to a parasitic trophic strategy.

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PARASITE EFFECTS ON FRESHWATER SNAIL, *ELIMIA LIVESCENS* ELEMENTAL CONTENT AND METABOLISM

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Parasites are present in every ecosystem, but their effects on ecosystem functioning are largely unexplored. Ecological stoichiometry uses the mass balance of elements to predict 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 1) the carbon (C), nitrogen (N), and phosphorus (P) content of parasitic trematodes and their intermediate host, the freshwater snail *Elimia livescens*, and 2) the parasites effects on nutrient recycling and metabolism. 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 and parasitized snails would recycle N and P slower, but maintain faster metabolic rates. Snails (13.1 to 23.2 mm) were collected from the White River in east-central Indiana and dissected to separate snail tissue (foot and gonad) from trematode sporocyst, rediae, and cercariae. Trematode tissues contained lower C:P and N:P (more P per unit C and N) than the snail tissues. Snail gonadal tissues more closely resembled the elemental content of parasite tissues, although P content was 13% higher in the gonad than the trematode tissues. Phosphorus recycling rates were slower in parasitized snails, but parasites did not affect N recycling. Parasitized snails maintained faster metabolic rates than non-parasitized snails. However, the species of parasite did not affect metabolic rate. Parasitized snails with smaller biomass had slower metabolic rates than the non-parasitized snails, but maintained faster metabolic rates than non-parasitized snails at larger biomasses. Together, this elemental imbalance between parasite and host, and the altered metabolic rate of infected snails may lead to parasite effects on nutrient dynamics and energy flow in stream ecosystems.

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PATTERNS IN PARASITE INFRAPOPULATION ENERGY USAGE

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The energetic equivalence rule (EER; Damuth, 1981) stipulates that population energy usage is invariant of an organism's body size due to thermodynamic constraints. A slope of 0.75 defines the logarithmic relationship between population density of a species and its body size in free-living animals. However, the EER has been infrequently applied to host-parasite systems. Parasitism is the most common consumer strategy on Earth, and the exclusion of parasites has been a challenge to many ecological rules. We aim to evaluate if the EER, an interspecific power law, would also describe intraspecific patterns in parasite infrapopulations. We applied the EER to natural parasite populations in freshwater ecosystems in New Jersey during preliminary studies to identify the factors that cause parasites to deviate from the EER. Data on parasite infections were collected from various host species, including 3 invertebrates (*Gammarus fasciatus*, *Pleurocera virginica*, *Libellula* sp.) and 4 vertebrates (*Fundulus diaphanus*, *Lepomis macrochirus*, *Micropterus salmoides, Umbra pygmaea*). In total we recovered 13 species of parasites for our analyses including: 3 protozoans, 4 trematodes, 1 tapeworm, 1 nematode and 4 acanthocephalan species. Log-linear models were constructed to describe the interspecific, species wide, relationship between parasite density and host body size. In our interspecific analyses, we initially used maximum parasite density as the dependent variable, and found that it was related to host body size by a slope of -0.82, which is higher than expected by the EER. A reanalysis of our data using mean density, which is more commonly used in ecological models, lowered the slope to -0.71. However, maximum density was a better fit for our data (max density: $R^2 = 0.81$, $P < 0.0001$; mean density: $R^2 = 0.56$, $P = 0.003$). In the intraspecific, species-specific analyses, we found each parasite species deviated substantially from the predicted value of the EER. The species-specific slopes formulated from our analysis ranged from -0.56 (*Eustrongyloides* sp.) to -1.26 (*Neoechinorhynchus cylindratus*) and even resulted in a positive value of 4.25 (*Posthodiplostomum minimum*). We suggest that although the EER may replicate large-scale patterns in nature, it may not accurately reflect conditions at local scales, and it does not describe patterns within parasite infrapopulations.

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HELMINTH COMMUNITY STRUCTURE IN TWO SPECIES OF ARCTIC BREEDING WATERFOWL

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Wildlife health is inextricably tied to climate. Changes in environmental factors, such as precipitation and temperature, affect the life cycles and transmission dynamics of infectious agents and have been associated with the geographic spread of many endemic and emerging diseases. Climate change is occurring approximately twice as fast in the Arctic than the rest of the globe. Consequently, changes in Arctic parasite communities may have severe repercussions for wildlife and human hosts. Migratory waterfowl (Anseriformes) are known hosts for numerous parasite species and act as vectors for parasite movement across expansive geographic areas. This study investigated the gastrointestinal helminth communities of two species of avian herbivores, Pacific black brant (*Branta bernicla nigricans*) and greater white-fronted geese (*Anser albifrons*), breeding in Arctic and subarctic Alaska to examine species, age, sex, and location variation in helminth species prevalence, intensity, abundance, and richness. Adult and juvenile Pacific black brant (n=84) and greater white-fronted geese (n=58) were collected from Arctic and subarctic (Pacific black brant only) Alaska July-August, 2014. Eleven helminth species were identified and all geese were infected with at least one helminth. All helminth species were found in 1) both host species, suggesting broad host susceptibility, 2) both age classes, suggesting parasite transmission occurs at high latitudes, and 3) all helminth species except one (i.e., *Epomidiostomum crami* was present only in the Arctic sites) were found at all sites, indicating suitable transmission conditions for a broad suite of helminths across a large latitudinal gradient. Our study provides baseline information on helminth

community structure, infection rates, and local transmission at high latitudes that is important for understanding wildlife community health and can be used as a comparison for future work as climate, parasite, and host distributions change.

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LIFE IN A DISH: OPTIMIZATION OF AN IN VITRO SYSTEM FOR TREMATODE PARTHENITAE

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A greater numbers of species of marine trematodes known to parasitize the snail *Cerithidea californica* have recently been shown to possess characteristics indicative of complex social organization. However, much is still unknown about the complex sociality and interspecific interactions of these species. Many questions into these areas of research could be further progressed through the availability of an *in vitro* cultivation system for trematodes. Currently, the only successful, long term *in vitro* system is a freshwater one generated by co-cultivating trematodes and embryonic cells from the snail *Biomphalaria glabrata* (*Bge* cells). This system is unable to support marine trematodes because they require a saline environment that would kill the *Bge* cells. Recent research into marine trematode *in vitro* cultures has utilized osmolarity adjusted Leibovitz' medium L-15, with very limited long-term success (35-60 days). The purpose of this study is to generate an *in vitro* system capable of sustaining normal development and activity of parthenitae. To evaluate our system, the survivorship of the trematode *Himasthla* sp. B (HIMB) was evaluated both quantitatively and qualitatively under two main experimental treatments i) coculture with *Bge*-cells and ii) *Bge*-conditioned marine media. To determine survivorship, parthenitae were counted and classified as either alive or dead based on tegument integrity, movement, and shape. Video footage was used in blind trials to qualitatively gauge parthenitae activity *in vitro*. Our results indicate that trematode parthenitae can survive for extended periods of time *in vitro* (>35 days*)* when *Bge* media is used. Based on our findings, parthenitae in *Bge* media are more active, maintain body integrity, and potentially continue to grow and reproduce. It is anticipated that *Bge*-conditioned marine media will allow improved growth and development of marine trematode species compared to Leibovitz' medium L-15 previously used in culture of marine trematodes.

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IMPACT OF AGRICULTURAL RUNOFF AND COAL MINE EFFLUENCE ON MINNOW INTESTINAL PARASITES

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Parasitic communities are an overlooked aspect of freshwater ecosystem function. Minnow intestinal parasite communities can be useful indicators of ecosystem health, because parasites often require multiple hosts throughout their life cycle. This study investigated the relationship between macroparasite prevalence and common water pollution sources in Appalachian waterways. We examined intestinal parasites in minnows from Eastern Kentucky streams polluted with agricultural runoff, straight pipe sewage, and coal mine drainage. Six streams were selected, two of relatively good water quality, and four that were considered impaired by multiple inputs. Minnows collected from these streams, and their intestinal parasite communities, were analyzed for diversity and abundance. Diversity of both minnows and their parasites was analyzed using inverse Simpson Indices. We found that parasite diversity and mean intensity of parasites varied with sources of pollution. Coal mine effluent appeared to have the strongest impact on parasite community composition. Digeneans and nematodes were absent entirely from the three streams in an area strongly influenced by coal mine drainage. The relationship between Kentucky Index of Biotic Integrity (KIBI) and parasite diversity was not significant. This could be due to the inverse relationship between Simpson Indices of minnows and parasites or it could show that parasite communities are better indicators of stream health.

Parasite diversity provided a good indicator of potential ecosystem level effects, over a long term, of multiple pollutants. This provides us with some evidence that parasite diversity should potentially be incorporated into assessments of stream health.

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TRANSBERINGIAN BIOGEOGRAPHY OF A HOLARCTIC TAPEWORM SPECIES COMPLEX

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The Bering land bridge connected Eurasia and North America during glacial maxima in the Quaternary and facilitated the exchange of species between these continents. Phylogeographic investigations of mammalian histories are revealing the direction and timing of this intercontinental exchange. For example, studies investigating arvicoline rodents (e.g., *Myodes*, *Microtus*, *Lemmus*) have revealed deep and shallow colonization events across Beringia, with complex histories of expansion, contraction, and diversification. These northern rodents are parasitized by the Holarctic cestode genus *Arostrilepis*. Here we examine the biogeographic history of *Arostrilepis* in light of hypotheses for transberingian dispersal by its rodent hosts. Using specimens previously collected from across the Holarctic, a nuclear and mitochondrial DNA sequence data set was assembled. Biogeographic analyses were performed based on multi-locus species trees for these loci generated using the coalescent based program *BEAST. These phylogenies suggest multiple Nearctic colonizations by *Arostrilepis* species; with patterns indicating that *Arostrilepis* colonized the Nearctic both simultaneously with multiple host genera, and sequentially in association with temporally distinct waves of host dispersal. Our data also reveal unexpected levels of new *Arostrilepis* diversity (as many as 15 deeply divergent and previously unrecognized genetic lineages) across the Holarctic, but especially in the northwestern United States. These results highlight the complex history of faunal assembly associated with Beringian mammal-parasite assemblages.

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A FORAY INTO THE GENETICS OF THE SUPER-DIVERSE GENUS *GYRODACTYLUS*

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For fishes, parasites represent a major selective force, capable of facilitating trophic interactions, causing population crashes and driving host evolution. The viviparous genus *Gyrodactylus*, comprised of an estimated 20,000 species, has been especially pathogenic, causing considerable economic losses globally from parasite-induced mortality in both cultured and wild fish. Despite this, relatively little work has been done on their genetics and the genus is still lacking mitochondrial and microsatellite markers, which can aid in population and phylogenetic study. Here, we use traditional molecular approaches as well as high-throughput sequencing to delve into the genetics of this super-diverse genus in an attempt to better understand the population biology, co-phylogeography and phylogenetic relationship of select Canadian species.

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UNEXPECTED DISCOVERY OF A NEW CILIATE PARASITE IN A WELL-STUDIED POPULATION OF LINED SHORE CRABS

D.C. Metz, Scripps Institution of Oceanography
R.R. **Sheehy** and **M.T. Close**, Radford University
H.J. Small, Virginia Institute of Marine Science

J.M. Carrillo and **R.M. Overstreet**, University of Southern Mississippi
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Our recent surveys at Carpinteria Salt Marsh (Santa Barbara Co., CA) revealed that lined shore crabs (*Pachygrapsus crassipes*) were commonly infected by a previously unreported parasitic ciliate. This discovery was a surprise: these crabs have been examined for parasites for over 15 years at this and other localities. To better understand this parasite, we examined methods of detection, infection prevalence, cell morphology, DNA-sequence based phylogenetic relationships, host pathology, and possible transmission routes. Unstained smears of hemolymph drawn from live crabs permitted simple and rapid identification of infected crabs, revealing 13.0% prevalence (9.0-18.5%, 95% CI, n = 193). Morphological analysis and phylogenies constructed from ITS1 and ITS2 sequences placed the ciliate in the Order Apostomatida. However, the parasite did not group with known genera and lied basal to all other apostomatidans. Histological comparisons of healthy and infected crab tissues revealed unusually extensive ciliate-caused pathology. We could not generate experimental infections from a variety of lab and field techniques. This, combined with the ciliate's placement within the Apostomatida, indicate that crab molting may play a role in parasite transmission. However, prevalence increased in injured crabs, alternatively suggesting that infection is facilitated by crab fighting or failed bird predation. The results indicate that this ciliate represents a new genus, and perhaps a new family. The sudden emergence of a novel, easily-detectable parasite at such a well-studied locality suggests that the ciliate has recently increased in abundance or recruited to Carpinteria Salt Marsh. The parasite's geographic range and ecosystem impacts are not yet known.

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HOW MANY SPECIES ARE CAUSING DIPHYLLOBOTHRIOSIS IN NORTH AMERICA?

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Human diphyllobothriosis is a well-known food-borne disease. Originally, only one species, *Diphyllobothrium latum*, was recognized in humans, but as many as 13 other species of broad fish tapeworms have subsequently been reported from human infections. In North America, diphyllobothriosis is not very common, unlike some regions of Europe or Far East Asia; there are only a few human cases every year and at least 6 species have been reported from humans in North America. *Diphyllobothrium latum* is widely distributed in northern boreal regions, mainly in Canada in North America with exception of North Pacific coast and in a variety of larger lakes in Europe and Russia. The freshwater fishes such as perch, pike, ruff, burbot, walleye, and sauger serve as a source of infections. *Diphyllobothrium dendriticum* occurs circumboreally and uses salmonids and coregonids as second intermediate hosts. Until now, human cases caused by this species have been reported only from Lake Baikal, Alaska, and northern Canada. Another species that was misidentified as *D. latum* is *D. nihonkaiense*, previously reported almost exclusively from Far East Asia, but recently found also on the North Pacific coast of North America. The source of infections is Pacific salmon, which are most commonly consumed raw or undercooked as sushi, sashimi or ceviche. Pacific salmon are exported fresh (on ice) from Alaska or Canada to various destinations. Most of the recent cases in North America seem to have been caused by this species. The remaining species, i.e. *D. alascense*, *D. dalliae*, and *D. ursi*, have been reported only from Alaska and Canada, based on pioneer research of the late R. Rausch. However, the validity of these species from the subarctic should be confirmed. To conclude, globalization of fish markets and travelling seem to contribute to the increasing risk of (re-) emergence of human diphyllobothriosis worldwide. *This study was partly supported by the Czech Science* Foundation (project no. P506/12/1632) and Grant Agency VEGA (No. 2/0159/16) and Slovak Research and Development Agency (No. APVV-15-0004).

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USING GORDIID CYSTS TO DISCOVER THE HIDDEN DIVERSITY, POTENTIAL DISTRIBUTION AND NEW SPECIES OF HAIRWORMS (NEMATOMORPHA: GORDIIDA)

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One reason for the lack of knowledge on the diversity and distribution of hairworm species is the lack of reliable ways to collect adult free-living worms over large geographical areas. However, a recent study indicates that cyst stages of hairworms may be the most commonly encountered gordiid life stages in the environment and our previous work indicates that cyst stages can be used in generic and/or clade gordiid identification. These discoveries have given us the ability to investigate the biodiversity and distribution of these cryptic species of parasites. In this study, we sampled aquatic snails for the presence of hairworm cysts from 46 streams in Payne Co., Oklahoma. Using this modified survey procedure, gordiid cysts were found at 70 % (32/46) of sites examined throughout Payne Co., Oklahoma. Based on cyst morphology and/or arthropod host infections, we were able to identify three morphological types of gordiid cysts including *Paragordius*, *Gordius*, and *Chordodes*/*Neochordodes*. Using our gordiid cyst presence data in conjunction with environmental layers for Payne Co., Oklahoma, we developed an ecological niche model (ENM) using Maxent to identify areas suitable for snail infections with gordiids. The ENM for Payne Co., Oklahoma successfully predicted all presence localities of gordiid in snails over a geographical area of 1,810 km^2. Using this information along with sampling for adult free-living worms during peak emergent times in ENM predicted areas allowed us to discover a new species of gordiid. To our knowledge, this is the first ecological niche model attempted on such a small geographical scale (county level) that recovered known locations successfully. Our field data and ecological niche model clearly indicate that gordiid cysts are extremely common in the environment and this sampling technique can be useful in discovering new species of gordiids, even in relatively well sampled areas for these cryptic parasites.

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PHYLOGENETIC PLACEMENT OF A SCHISTOSOME FROM AN UNUSUAL MARINE SNAIL HOST FROM ARGENTINA AND A SECONDARY SWITCH FROM FRESHWATER TO MARINE SNAILS

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In the blood fluke family Schistosomatidae, marine snails are well known as intermediate hosts. Eight families of marine snails have thus far been reported to host schistosomes across the world, most of which have been implicated in human cercarial dermatitis outbreaks. As part of our larger effort to better define the species diversity and biology of schistosomes we searched in the marine pulmonate snail *Siphonaria lessoni* for a schistosome species previously described from southern Argentina. Additionally, gulls (*Larus dominicanus*) collected from a different project locality (inland Argentina) were examined since they are known to frequent intertidal regions. Schistosome sporocysts were found in *S. lesson,* and a small schistosome adult fragment was retrieved from a gull. The molecular phylogeny revealed that the specimens grouped together, suggesting they are conspecifics. However, these samples did not group with the marine snail-transmitted schistosome clade comprised of *Austrobilharzia* species at the base of the family tree. Rather, they were closely related to a few other marine schistosomes contained within the larger more recent avian schistosome clade that is otherwise comprised of several genera and species using freshwater snail hosts. This is the third molecularly-based record of a marine schistosome species

that groups within this large recent clade; the first was of cercariae from the marine snail *Haminoea japonica* and the second was of a worm from a penguin in South Africa. In addition, unknown schistosome samples from gulls from Ukraine also group with these three marine samples, both defining a newly-recognized marine clade of schistosomes, and strongly suggesting there was likely a single switch back to marine snails from freshwater snails. Also, unlike the large-bodied basal marine schistosomes in *Austrobilharzia* or *Ornithobilharzia,* the worms comprising the newly-recognized marine clade are long and thin, a feature they share with the many freshwater snail-based species in this large clade of avian schistosomes.

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HYMENOLEPIS WEINLAND, 1858: A PHYLOGENY

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The phylogenetic relationships of several species of *Hymenolepis* s. str. were inferred using both morphology and molecules. Several species of 'New World' and cosmopolitan *Hymenolepis* were studied, including two new undescribed *Hymenolepis* species, *H. citelli*, *H. diminuta*, *H. geomydis*, *H. pitymi*, *H. robertrauschi*, *H. scalopi*, *H. tualatinensis*, and *H. weldensis*. Outgroup taxa include *Rodentolepis microstoma* and *Taenia pisiformis*. 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 these data and results showed a general convergence in topologies.

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A TAXONOMIC AND SYSTEMATIC ASSESSMENT OF THE TETRAPHYLLIDEAN GENUS *ANTHOBOTHRIUM*

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The tetraphyllidean genus *Anthobothrium* is one of the oldest cestode genera of elasmobranch fishes. *Anthobothrium* has a long and complicated taxonomic history, with 47 species associated included in it. The genus was erected by van Beneden (1850) for *A. cornucopia*. Over the next century and a half, 46 species have been added. Ruhnke and Caira (2009) noted that *Anthobothrium* was most certainly a polyphyletic taxon, and that of the 43 species historically associated with it, only eight species were consistent in morphology with the type species. Recent analysis of the literature facilitated by the existence of the Global Cestode Database revealed the following for the 47 *Anthobothrium* species records: one is referred to the Diphyllobothriidea, eight to the Phyllobothriidea, four to the Proteocephalidea, 22 to the Rhinebothriidea, and 12 to the Tetraphyllidea. In terms of taxonomic status, eight records refer to valid species of *Anthobothrium*, 15 are synonyms, 19 are *incertae sedis*, two are *species inquirenda*, two are *nomina dubia*, and one is a homonym. The phylogenetic position of *Anthobothrium sensu stricto* was considered by Caira et al. (2014) to be problematic, with the position of *Anthobothrium* being labile in position depending on analysis, but weakly allied with *Megalonchos*. Recent morphological and molecular investigation has revealed at least 12 new species of *Anthobothrium* and several of these taxa are in some stage of being formally described. Given that species of *Anthobothrium* are found in carcharhinid, sphyrnid and triakid sharks, the known diversity of the genus may only be a fraction of the actual diversity.

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A NEW BATOID-HOSTED CESTODE GENUS, WITH COMMENTS ON ITS PHYLOGENETIC RELATIONSHIPS AND HOST ASSOCIATIONS

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Recent work aimed at formally resolving the controversial identity of the shark-hosted genus *Carpobothrium* has paved the way for formal erection of the superficially similar, yet taxonomically distinct, batoid-hosted genus preliminarily referred to in recent molecular phylogenetic works as New genus 9. Extensive collecting efforts targeting cestodes from a diversity of batoid hosts throughout Borneo and Australia have yielded material of multiple new species belonging to this new genus. In the short term, the new genus is established based on 3 novel species found parasitizing the stingrays *Himantura uarnacoides* Bleeker, 1852 and *Himantura pastinacoides* Bleeker, 1852, and the guitarfish *Rhina ancylostoma* Bloch and Schneider, 1801 as its type. Light microscopy, histological sections, and scanning electron microscopy were used to characterize and describe all three novel species. Using these insights a generic diagnosis was generated. Members of the new genus resemble *Carpobothrium* in their possession of bothridial pouches, but differ from the latter genus substantially in their possession of conspicuous apical suckers and marginal loculi on their bothridia, and in multiple features of their proglottids. Sequence data generated for the D1-D3 region of the 28S rDNA gene were used to explore the phylogenetic relationships among members of the new genus and members of other potentially closely related genera, including two species from the genus *Carpobothrium*. Phylogenetic analyses of the sequence data confirmed (i) morphological species boundaries for the new genus, (ii) phylogenetic distance between species of *Carpobothrium* and species from the new genus, and (iii) that both *Carpobothrium* and the new genus remain members of the wildly polyphyletic “Tetraphyllidea”. The trees from these analyses were compared with existing host trees, and co-phylogenetic assessed.

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HOST AND PARASITE DIVERSITY: MAMMALIAN DIVERSITY FROM LEECH BLOOD MEALS AND TERRESTRIAL LEECH (*HAEMADIPSA*) PHYLOGENETICS

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Throughout their broad range in southerly Asia, terrestrial leeches in the genus *Haemadipsa* are well known as bothersome blood feeding ectoparasites. Recently, their thirst for blood has become a boon for surveys of southern Asian vertebrate biodiversity as DNA sequencing of their blood meals is starting to become an effective vertebrate survey method. However, this developing approach has yet to incorporate information on the leeches themselves, let alone to determine the diversity of the leeches reviewed in this type of work. This study focuses on two goals: 1) to explore the blood meal DNA technique across a large sample from throughout Cambodia and in both Yunnan and Hainan provinces in China while considering parasite identity, and 2) to assess the phylogenetic relationships and diversity of *Haemadipsa* throughout its range. Hundreds of leeches were collected and individually had DNA from their gut contents extracted and amplified for the vertebrate mitochondrial 16S ribosomal RNA gene. DNA sequences were used to positively identify a broad array of vertebrates, including primates, rodents, ungulates, carnivores, bats, and birds. Terrestrial leech hosts were then assessed for host specificity. Leeches from these previously unsampled areas, as well as samples from much of the range of *Haemadipsa* were then incorporated into the largest genus level phylogeny conducted for this group, with over four times the number of specimens reviewed and using a four gene dataset with both nuclear (18S and 28S rRNA) and mitochondrial (cox1 and cox3) data. Knowledge of vertebrate host and leech parasite and their interactions will become critical for the future conservation of both these groups.

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COSMOPOLITAN SPECIES OR CRYPTIC SPECIES COMPLEXES: IS THE ARTERIAL WATERFOWL SCHISTOSOME, *DENTRITOBILHARZIA PULVERULENTA* A WIDESPREAD SPECIES?

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Parasites of migratory birds are fascinating topics of investigation for evolutionary and ecological questions regarding host-parasite interactions. Molecular studies of trematodes in waterbirds have identified species that are distributed across the migratory range of a group of bird host, as well as species that are geographically or host restricted. Questions remain for those species reported as cosmopolitan. Are they geographically isolated and complexes of cryptic species, and/or are they truly widespread and homogenized by gene flow? A recent study found that *Trichobilharzia querquedulae* was cosmopolitan, in a small but widespread clade of ducks. Other species of *Trichobilharzia* appear to be more geographically constrained. Thus, *T. querquedulae* represents the first report of a cosmopolitan avian schistosome confirmed by genetic data and the first to exhibit trans-hemispheric gene exchange. The arterial dwelling *Dendritobilharzia pulverulenta* is the only other schistosome species that has been reported as cosmopolitan in waterfowl. The goal of this project is to determine genetically if the specimens we have collected and identified as *D. pulverulenta* represent a single, widely distributed species, and/or a complex of species. Specimens were collected from North America, South Africa, France and New Zealand, from snails and from waterfowl. Gene regions of 28S, cox1 and ITS1 were sequenced. The molecular evidence supports two clades of *Dendritobilharzia*, one that includes samples from around the world, and a second thus far only from North America. Currently it is unclear if specimens from the two groups can be distinguished morphologically. The two clades are not obviously differentiated with respect to definitive or intermediate host use, habitat use within the definitive host, and they overlap geographically. The clade identified as bonafide *Dendritobilharzia pulverulenta* may prove to be cosmopolitan, but there are additional putative species found in the same species of waterfowl. How they have diverged genetically remains a topic for further inquiry.

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MOSQUITO HEMOCYTE-MEDIATED IMMUNE RESPONSES OCCUR IN AREAS OF HIGH HEMOLYMPH FLOW

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Mosquitoes respond to infection by mounting robust cellular and humoral immune responses. These responses are mediated in part by hemocytes, which are immune cells that circulate (circulating hemocytes) with the hemolymph (mosquito blood) and also attach to tissues (sessile hemocytes). In this project we assessed whether immune activity by sessile hemocytes is increased in areas of high hemolymph flow and found that this is indeed the case. In adult mosquitoes, for example, infection induces the aggregation of phagocytic hemocytes in the periostial regions of the heart. The periostial regions are located in the anterior portion of abdominal segments 2-7, and surround the points of hemolymph entry into the mosquito's primary circulatory organ: the heart. Hemolymph flow across the six periostial regions is asymmetric, and phagocytic hemocytes preferentially aggregate in the periostial regions that receive the most hemolymph flow. In larvae, however, the periostial regions do not serve as locations where hemolymph enters the heart, and thus, few hemocytes are located in these regions. Instead, hemolymph enters the heart through the posterior incurrent openings, which are located in the 8th abdominal segment and are surrounded by respiratory structures called tracheal tufts. In larvae,

hemocytes naturally associate in high numbers with the tracheal tufts, where they phagocytose and melanize invading pathogens. Thus, although the pattern is different in adults and larvae, in both life stages the immune activity of sessile hemocytes is highest in areas of high hemolymph flow.

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PARASITE SURVIVAL IN A FREEZE-TOLERANT HOST

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Parasite winter survival is dependent on host overwintering adaptations. Wood frogs (*Lithobates sylvaticus*) in the Arctic and Subarctic are adapted to survive up to 7 months frozen down to -18°C. To survive freezing wood frogs synthesize glucose and urea as cryoprotectants in high concentrations. These same cryoprotectants may influence parasite survival during freezing within hosts. We examined whether a parasitic trematode metacercariae, *Ribeiroia ondatrae*, could survive freezing within the freeze-tolerant wood frog and if metacercariae survival was dependent on host physiological responses to freezing. We exposed 107 tadpoles to 30 cercariae each. Metamorphosed frogs were divided into three groups: unfrozen control, single freezing event, or repeated freeze-thaw. Prior to freezing, we necropsied 10 frogs from each group and found no significant difference in parasitism. Control wood frogs (n=22) were held for two weeks at 2°C. Single freezing event wood frogs (n=26) were cooled from 2°C to -6°C over 12 hours, nucleated with ice at -1.5°C, and then held for two weeks at -6°C. Wood frogs experiencing repeated freeze-thaw (n=29) were cooled over 12 hours from 2°C to -6°C, nucleated with ice at -1.5°C, and then warmed over 12 hours to 2°C; this cycle was repeated twice before wood frogs were then held at -6°C for two weeks. Freezing significantly impacted parasite survival. Wood frogs averaged 18.7±2.7 motile metacercariae prior to freezing and there was no change in the unfrozen control group after 2 weeks. No parasites from the single freezing group survived while parasite survival was 23% in the freeze-thaw group. Survival was dependent on the pattern of freezing and cryoprotectant production of a host. Parasite survival had a positive linear relationship with host cryoprotectant production. Our results demonstrate how overwintering physiology of a host can detrimentally affect parasites and how parasites may use host physiological responses to winter to survive low temperatures.

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ANTIGENIC CROSS-REACTIVITY BETWEEN *SCHISTOSOMA MANSONI* AND PEANUT: INDICATION OF SOME SHARED GLYCAN EPITOPES AND IMPLICATIONS FOR THE HYGIENE HYPOTHESIS

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Chronic infection with *S. mansoni* and atopy to allergens often show a negative correlation. Reasons for this are still relatively unclear. Here, the antigenic cross-reactivity between *S. mansoni* and peanut was investigated to seek explanations for the above phenomenon. Molecules in an aqueous extract of peanuts were separated in 1-D SDS-PAGE and probed with anti-*S. mansoni* egg (SmSEA) IgG antibodies from two different rabbits in immunoblots. Several molecules in peanut were antigenically cross-reactive to a similar degree with both antisera, of which a pair of molecules at ~30 kDa was investigated further. Purification of the lower band and analysis in tandem mass spectrometry (MS) showed they had a significant peptide match for the peanut (*Arachis hypogaea*) allergen Ara h 1. Rabbit anti-SmSEA IgG antibodies that were cross-reactive with Ara h 1 were acid-eluted and used to probe electroblots of SmSEA to identify reactive egg antigens. A pair of egg antigens of ~40 kDa and another antigen of ~100 kDa was recognized by the purified antibodies and these bands appeared homologous with, respectively, *S. mansoni* egg antigens IPSE/alpha-1 and kappa-5 detected in immunoblots with monospecific sera. Alignments of the amino acid sequences of Ara h 1 and the two putative antigenically cross-reactive egg antigens revealed a low peptide sequence identity of 3.5% with IPSE/alpha-1 and 9.8% with kappa-5. However, incubation of nitrocellulose

paper (NCP) carrying electrophoresed peanut and SmSEA antigens in sodium metaperiodate solution prior to probing with the rabbit anti-SmSEA antisera or with acid-eluted anti-SmSEA antibodies that were cross-reactive with Ara h 1, revealed that most of the antigenic cross-reactivity was periodate-sensitive, indicating that cross-reactive carbohydrate determinants (CCDs) may be involved in this cross-reactivity phenomenon. These findings are novel and could provide an explanation for the inverse relationship observed between infection with *S. mansoni* and allergies.

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SCHISTOSOMICIDAL OXAMNIQUINE DERIVATIVE DRUG ACTIVITY AGAINST ALL THREE HUMAN *SCHISTOSOMA* SPECIES

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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*. We employ an iterative process of using structural data to inform chemical synthesis of derivatives, which are then tested *in vitro*. The most efficacious derivatives and then soaked into SULT crystals and the process repeated. Using this iterative process, we have discovered an OXA derivative (CIDD790) that is effective against *S. mansoni* (100% killing), *S. haematobium* (40% killing) and *S. japonicum* (80% killing). CIDD 790 in an early *in vivo* pilot study in a murine model of *S. mansoni* has demonstrated significant killing.

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IDENTIFICATION OF NUCLEAR FACTOR KAPPAB (NF-κB) BINDING MOTIFS IN *BIOMPHALARIA GLABRATA*

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The freshwater snail *Biomphalaria glabrata* acts as an intermediate host to the parasite *Schistosoma mansoni*, one of several species that cause the debilitating disease schistosomiasis in humans. Several studies have demonstrated that the transcriptome profile of *B. glabrata* changes following exposure to *S. mansoni*, yet very little is known regarding the regulation of gene expression in this species. Nuclear factor kappaB (NF-κB) homologues have been identified in *B. glabrata* however their role in regulating gene expression in this species has not been extensively researched. The aims of this study therefore were: 1) to identify NF-κB binding sites (κB motifs) upstream of putative immune-related genes in *B. glabrata*, and 2) examine these sites via electrophoretic mobility shift assays (EMSAs). Several different κB motifs were predicted upstream of *B. glabrata* genes. Furthermore, the Rel homology domain (RHD) of a *B. glabrata* NF-κB was shown to recognize and bind predicted κB motifs in EMSAs.

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MALARIA IN PSYCHIATRIC PATIENTS

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Malaria has been associated with mental disorders including asymptomatic *Plasmodium falciparum* infection. However, no study has looked at the prevalence of asymptomatic malaria among out-patients of a mental health institution. Hence, this study was conducted. Thick blood films were made from blood specimens taken from 400 subjects consisting of 300 mentally ill patients and 100 apparently healthy non-mentally ill subjects. The thick blood films were used for malaria diagnosis, and the remaining blood samples were used for haemoglobin estimation using standard techniques. Information on gender, age, marital status and occupation were obtained for the mentally ill patients. Mental illness was significantly associated with asymptomatic malaria (OR=4.750 95% CI=1.850, 12.196; P=0.0002). Among the mentally ill, asymptomatic malaria was significantly associated with anaemia (OR=17.458 95% CI=8.711, 35.349; P<0.0001). Mentally ill patients 61 years and above had a significantly (P<0.0001) higher prevalence of asymptomatic malaria. Gender, marital status and occupation of the mentally ill patients did not significantly affect the prevalence of asymptomatic malaria (P>0.05). An overall prevalence of 20% of asymptomatic malaria was observed among the mentally ill and measures to eliminate asymptomatic malaria and associated sequelae among the mentally ill are advocated.

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IN VITRO OPTIMIZATION OF *NAEGLERIA FOWLERI* AXENIC CULTURE

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Naegleri fowleri is a single cell parasite responsible of primary amebic meningoencephalitis. The *in vitro* axenical culture of the parasite was demonstrated and is an alternative to *in vivo* researches which are much expensive with sometimes ethical issues. The lack of paper presenting such type of culture at different set of temperature motivated this study. Also, we have investigated to see whether we can optimize the parasite growth by modifying two media recently used. The Nelson and Modified PYNFH medium were selected for the axenic culture of the Taiwan CDC clinical strain at 25, 37 and 43°C. Nelson medium supplemented with 1% peptone (N+pep), Modified PYNFH medium without peptone (PYNFH-pep), yeast extract (PYNFH-yext), folic acid (PYNFH-folac), and yeast nucleic acid (PYNFH-yna) were also prepared. After 96 hours of incubation, we found that 37 and 43°C were suitable temperatures for *N. fowleri* culture and temperature such as 25°C inhibits it proliferation. At 25, 37 and 43 °C, the highest trophozoite densities per 100 µm² observed in the Nelson medium and the modified PYNFH medium were respectively 13.5 ± 0.70 versus 12 ± 2.83, 139 ± 8.49 versus 101 ± 43.84 and 23.5 ± 2.12 versus 62.5 ± 10.6. In both medium the log phases were equal to 48h at 25°C and 72h at 37 and 43°C. After modification, at 25, 37 and 43°C the highest trophozoite densities per 100 µm² observed in N+pep and PYNFH-yext were respectively 50.5 ± 6.36 versus 58 ± 1.41, 2550 ± 494.97 versus 2100 ± 141.42 and 1735 ± 21.21 versus 1800 ± 14.14. The PYNFH-folac and PYNFH-yna had comparable results as both exhibited intermediate growth profiles and their highest cell densities were 23.5 ± 0.71 versus 13.5 ± 0.71 at 25°C, 708 ± 11.31 versus 800 ± 70.71 at 37°C and 399.5 ± 60.1 versus 664 ± 50.91 at 43°C. Finally, the PYNFH-pep exhibited the lowest growth profile with a highest cell density equal to 9 ± 1.41 at 25°C, 108 ± 7.07 at 37°C and 169 ± 15.55 at 43°C. In addition, no stationary phase was observed in N+pep, PYNFH-yext, PYNFH-folac, after 96 hours of incubation except for the PYNFH-yna at 25°C. We concluded that *N. fowleri* growth is temperature and medium dependent. Moreover, we suggested that yeast extract, folic acid and yeast nucleic acid had a negative effect on peptones or liver hydrolysate when mixed together. Therefore, to improve the *N. fowleri* in vitro culture, we recommend the N+pep or PYNFH-yext.

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VARIABILITY OF GIARDIASIS PREVALENCE CAUSED BY ANTHROPOGENIC ACTIVITIES IN FUNDONG HEALTH DISTRICT, CAMEROON

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Giardia intestinalis is a flagellate intestinal parasite considered one of the most prevalent protozoa infecting human worldwide. It is most common in developing countries of the tropics where its transmission by inappropriate water source, or cross contamination through flies, food, legal tenders and feacal-oral routes has been recorded. Accordingly this cross sectional study on the variability of giardia prevalence, related to anthropogenics, community setting, age grouping, gender, zoonotic risk factors in the transmission of giardia was carried out in the Fundong Health district of Cameroon. Out of the eleven Health Areas of the District, eight communities were randomly selected by secret ballot, for the study. 645 stool samples were collected from individuals of age between 2 and 70 years old of whom 312 were male and 333 were females. Socioeconomic data was collected through the issue of questionnaire and stools samples were processed using direct wet mount of salina/eosine microscope techniques proceeded by Ridley modified formal ether centrifuge concentration technique for the identification of *Giardia lamblia*. Results showed a significant prevalence rate of 102 out of 645 (16 %) globally. Prevalence comparatively increased from the urban (02.9 %) through periurban (8.8%) to the rural areas (18.6%), with poor sanitary conditions, showing a significant level of association between the community setting of the people and the prevalence of giardia. ($P > 0.05$), with chi-square as the statistical tool. Anthropogenically the percentage frequency of giardiasis varied significantly on the bases of the activities and occupation of the sampled individuals. Variation on prevalence based on occupation was, Farmers (40.1%), grazers (4.9%), officers (0.9%), traders (2.9%), students (9.8%), pupils (40.1%). Comparative prevalence based on other risk factors such as water resources, sanitation and age grouping showed a statistically significant relationship between such parameters and giardia prevalence ($P > 0.05$). Conclusively *Giardia lamblia* is still a public health problem endemic here and stems from native unhygienic socio-cultural attitudes with water resources. Also the dynamics of transmission is most probably through anthroponotic, which is human to human directly or indirectly through contamination of food. Health education on these routes of transmission, sanitation, improvement on portable water management and provision of bore holes should be considered as recommended strategies to combat the problem.

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STUDIES ON THE BIONOMICS OF SANDFLIES (DIPTERA: PSYCODIDAE) IN SOME REMOTE AREAS OF IMO STATE, NIGERIA

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Studies were carried out between June 2013 and May 2014 to estimate the relative abundance, biting rates and spatial variation in the biting densities of sandflies in some part of remote areas of Imo State, Nigeria. Sticky traps with light and human baits were used to collect sandflies. Sticky trap captures with lights were carried out between 18.00hrs and 21.00hrs, once a month for a period of one year while fly catches using human baits were carried out between 7.00hrs and 19.00 hours twice a month for one year. A total of 2, 254 flies were captured to estimate the seasonal relative abundance while 781 flies were caught using human baits to calculate the biting rates. More flies were caught during the raining season (1793), accounting for 79.5% than during the dry season (461). There was a significant variation ($P< 0.05$) in the seasonal abundance. Flies showed a seasonal, punctual and peripheral pattern of distribution. Daily biting cycle showed a peak during the late afternoon and evening of the raining season between 13.00hrs and 19.00hrs, the highest monthly biting rate (MBR) of 2,025 was recorded in June 2013. An improved understanding of sandfly ecology, distribution and biting activities should facilitate the implementation of control strategies of sand fly vectors of leishmaniasis.

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UNEXPECTED DIVERSITY OF ADELEORINID BLOOD PARASITES OF ONTARIO FROGS AND TURTLES DISCOVERED USING MITOCHONDRIAL GENOME SEQUENCES

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Adeleorina (Apicomplexa) includes heteroxenous blood parasites that infect vertebrates globally. *Hepatozoon* spp. and *Haemogregarina* spp. commonly parasitize erythrocytes of poikilotherms. Differentiating morphologically similar intraerythrocytic parasites is challenging; finding the definitive host and nature of sporogony is problematic. Sequencing (principally nuclear 18S and ITS rDNA) has been helpful for differentiating some adeleorinids but many questions remain. Mitochondrial sequences are reliable species-level markers for other coccidia (e.g. DNA barcoding using partial mtCOI sequences); lack of primers and no closely related reference sequences prevented the use of mitochondrial sequences for differentiation of these blood parasites. Analysis of the mt genome of a *Hepatozoon* sp. suggested that the mtCOIII locus was suitable for differentiating *Hepatozoon* species. To test this, DNA was extracted from blood of infected Green frogs (*Lithobates clamitans*), bullfrogs (*L. catesbeianus*) and northern leopard frogs (*L. pipiens*). A ~660bp region of the mtCOIII gene was amplified and PCR products sequenced. Sequences (n=23) matched *H. catesbianae* (n=10) and *H. clamatae* (n=9), but 4 were a novel genotype in leopard frogs. PCR and sequencing of overlapping fragments generated complete mt genomes of *H. clamatae* (6377 bp) and the unnamed *Hepatozoon* sp. (6315 bp); the 3 *Hepatozoon* species infecting local frogs had mt genomes with pairwise genetic distances of 1.2% to 1.7%. All were circular-mapping genomes with identical genome contents and arrangement. A partial mt genome (~3kb to date) was obtained from *Haemogregarina balli* by PCR amplification of DNA from infected blood of snapping turtles (*Chelydra serpentina*). A single adeleorinid parasite was assumed to be present based on intraerythrocytic gamonts but sequencing uncovered mt genome divergence not reported previously for any single apicomplexan parasite. Either this parasite has multiple divergent mt genome copies or the number of *Haemogregarina* spp. present in the blood of this host have been grossly underestimated.

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A NOVEL FAMILY OF SMALL RNAS REGULATES GENE EXPRESSION IN THE SEXUALLY TRANSMITTED PARASITE *TRICHOMONAS VAGINALIS*

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Trichomonas vaginalis is the causative agent of trichomoniasis, the most prevalent non-viral sexually transmitted infection world-wide, causing ~270 million new infections annually. A draft assembly of its ~160 Mb genome is predicted to encode ~100,000 genes, including ~40,000 transposable elements (TEs) in ~ 10 families. This is the largest TE colonization observed in a parasite, and appears to have occurred recently, with many TE families still maintaining the protein machinery necessary for their transposition. We previously analyzed 19 TE loci in a global population of 94 *T. vaginalis* isolates and found TE insertions to be highly variable, with most existing at low population frequencies and some correlating with reduced or abolished expression of flanking *T. vaginalis* genes (Bradic, Warring, *et al.,* Mobile DNA, 2014). Here we expand our work to characterize how the expression of TEs is regulated on a genome-wide scale. We generated RNA-Seq datasets for the reference *T. vaginalis* strain G3, characterizing both the mRNA and small RNA populations. Mapping both data sets to the *T. vaginalis* reference genome enabled us to compare the density of mapped reads at TE genes and *T. vaginalis* genes, revealing that TE genes are under-represented in the mRNA of *T. vaginalis* and likely targeted for silencing by an epigenetic mechanism. At the same time, we identified a novel species of small RNA that map to these repressed TE genes and may be responsible for their silencing. Interestingly, these TE-associated small RNAs also map to many *T. vaginalis* genes flanking TE insertions, and thus may be responsible for the reduced gene

expression observed for these genes as well. We show that the *T. vaginalis* small RNAs share some similarities with PIWI-associated small RNAs expressed in metazoans, although the *T. vaginalis* proteins required for small RNA biogenesis appear divergent from the PIWI clade. Our results raise intriguing questions as to the role TEs may play in shaping *T. vaginalis* genome evolution and the diversity of small RNA pathways in general.

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IDENTIFYING PARASITES IN NEW YORK CITY SEWAGE

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Protists are important components of terrestrial and aquatic environments, as well as animal and human microbiomes. Their relationships with metazoa range from mutualistic to parasitic and zoonotic (*i.e.*, transmissible between humans and animals), and they can cause significant morbidity particularly where contact between host and reservoir species is increased. Despite their ecological and economic importance little is known about the diversity, incidence, or emergence of parasites -- or protists in general -- in urban environments. The 7,400-mile combined sewer system of New York City (NYC) collects human and animal waste, street runoff and groundwater, providing an ideal system to study these microbes. First we developed wet-lab protocols for detecting protists in sewage samples. We investigated the utility of two widely used variable regions of the 18S rRNA marker gene by amplifying and sequencing them from 16 species of protist including *Cryptosporidium parvum*, *Giardia intestinalis*, *Toxoplasma gondii* and several species of trichomonad. Our results show that both 18S rRNA regions are effective at identifying protists and can be used together to provide an accurate picture of diversity. Next, assisted by the NYC Department of Environmental Protection, we collected 17 raw sewage samples four times within 12 months from 14 NYC wastewater treatment plants representing all five NYC boroughs. Deep amplicon sequencing generated from both 18S rRNA regions of the four time point sewage samples, revealed diverse microbial communities dominated by free-living environmental protists, and lower numbers of human associated taxa. Zoonotic protists were found in all samples, such as *Blastocystis hominis* and multiple species of trichomonad, which in one case composed ~60% of the taxa present. Abundance of these parasites varies significantly both spatially and temporally suggesting that spikes could reflect changes in disease incidence in the source population. This study provides a baseline for further investigation of zoonotic protists in urban environments.

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MOLECULAR EVOLUTION OF THE MALARIA PARASITES: ASSESSING THE EFFECTS OF NEUTRAL AND ADAPTIVE PROCESSES ACROSS TIME SCALES

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The malaria parasites (order Haemosporida) represent a compelling system with which to study the interaction of molecular evolution and life history. Recent phylogenetic hypotheses have revealed that the malaria parasites have likely undergone multiple shifts in key life history traits across the evolutionary history of this group, encompassing changes in host cell environment, life cycle, and metabolism. It is unclear, however, how these shifts among life history characters are associated with neutral and adaptive

molecular evolution of malaria protein-coding genes. To investigate molecular evolutionary processes across the phylogeny of malaria parasites, we studied neutral and adaptive evolution of 21 nuclear and two mitochondrial protein-coding genes for a diverse array of malaria taxa representing 54 species and 9 genera. We sought to test for the effects of mutation bias (a putatively neutral process) and natural selection (an adaptive process) on patterns of molecular variation across protein-coding genes within the malaria parasites. We found that the evolution of nucleotide base composition bias carries significant phylogenetic signal with a Brownian motion model providing the best fit to the evolution of this trait, and that multiple lineages have independently evolved extreme adenine-thymine composition biases upwards of ~80% (*Haemocystidium*, *Haemoproteus,* and *Plasmodium*). We found that mutation bias has also had a profound impact at the protein level, as evidenced by extreme codon usage and amino acid composition biases across malaria taxa. Purifying selection was pervasive across all nuclear loci that we studied, though diversifying selection was detected at a proportion of codon positions for 17 of 21 nuclear genes. We also tested for signatures of diversifying selection on specific branches of the malaria phylogeny, focusing on the internal branches within which shifts in life history traits occurred. We found largely idiosyncratic patterns of positive selection across branches of the malaria phylogeny; though there was evidence that positive selection was elevated on internal relative to external branches. Overall, mutational bias and natural selection have interacted to drive the evolution of malaria protein-coding genes, though according to different processes – mutational bias appears to be the result of a neutral process that is manifest in a pervasive manner over long time scales, while natural selection has driven adaptive change of a small subset of codon positions that was likely ephemeral in nature.

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A NOVEL QUANTITATIVE REAL-TIME PCR DIAGNOSTIC ASSAY FOR SEAL HEARTWORM (*ACANTHOCHEILONEMA SPIROCAUDA*) REVEALS FIRST REPORTED INFECTION IN THE GREY SEAL (*HALICHOERUS GRYPUS*)

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Marine mammals are a diverse and rather evolutionarily unique group of organisms, characterized by their ancestors' transition from land to sea life (Foote, 2015). Pinnipeds, unlike cetaceans, live a more amphibious lifestyle. This unique adaptation not only poses evolutionary pressures onto pinnipeds, but also onto the parasitic fauna they host (Leidenberger, 2007), ensuring relationships with unique parasitic species. This study focuses on the phocid seal heartworm species *Acanthocheilonema spirocauda*. Although its molecular characterization is limited, *A. spirocauda* infects a variety of phocid seals. The parasite does not have a preferred host species among seals, having been reported in harp seals, harbor seals, ringed seals, and hooded seals (Lehnert et al., 2015; Leidenberger et al., 2007; Measures et al., 1997). To date, seal heartworm has never been reported in the grey seal (*Halichoerus grypus*) (Lehnert et al., 2015; Leidenberger et al., 2007; Measures et al., 1997). Seal heartworm is a filarial parasite, and as such is believed to be transmitted through an insect vector. The proposed vector for seal heartworm is *Echinophthirius horridus*, the seal louse. Seal lice are known to parasitize a wide array for phocid seal species. With the advent of climate change, disease burden is expected to increase across terrestrial and marine mammals (Harvell et al., 2002). Indeed, increased prevalence of seal heartworm has been reported in harbor seals (Lehnert et al., 2015). With this increase in prevalence, the need for improved, rapid, and cost effective diagnostics for treatment and surveillance is paramount. Proper treatment, management, and control of infectious disease in any system relies on sensitive, reliable, and rapid diagnostics with extreme organism specificity to guide proper clinical management (Banoo et al., 2008; Caliendo et al., 2013). Molecular diagnostics has rapidly expanded as the optimal diagnostic tool, quickly outcompeting traditional approaches such as blood smears (Alhassan et al., 2015; Banoo et al., 2008; Edvinsson et al., 2006; Mejia et al., 2013; Papaiakovou, 2014; Pilotte et al., 2016; Powers, 2004; Ricciardi and Ndao, 2015). Here we present the first *A. spirocauda*-specific rapid diagnostic (quantitative real time PCR), based on highly repetitive genomic repeats identified using whole genome sequencing and subsequent bioinformatic analysis. These genetic elements are often what would be considered non-functional "junk" DNA, Because these regions are non-coding, they are not subjected to equal

conservative evolutionary pressure as coding DNA regions, making them highly variable and typically species-specific (Pilotte et al., 2016). This diagnostic is capable of detecting parasite DNA in blood samples, lice samples, and whole worm extracts. Using this assay we provide evidence for the first reported case of seal heartworm in a grey seal.

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A NOVEL DIAGNOSTIC QPCR TEST FOR THE ROUTINE MONITORING OF *ENTEROBIUS VERMICULARIS* IN WASTEWATER

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Wastewater reuse seeks to alleviate stress on freshwater ecosystems by recycling treated or partially treated wastewater. Many municipalities worldwide are adopting planned reuse strategies; however, biological indicators vary between regions depending on the health and disease prevalence of the source population. Bacterial and viral indicators of treatment efficacy are common. Overlooked are helminthic worms, despite the importance of environmental reservoirs in the transmission of many parasitic species. In North America, while only certain populations—notably rural, first nations, traveller, or immigrant populations are more likely to harbor such infections, in the context of wastewater reuse, a single worm infection yielding thousands of infectious worm ova per day may constitute a health risk for certain reuse applications. Our study has two aims; to design a specific quantitative molecular diagnostic test for *Enterobius vermicularis* and to monitor parasite levels in wastewater influent and effluent. Our second aim is to assess the efficacy of *E. vermicularis* as a surrogate pathogen used to study the fate of other pathogens in a specific environment. Ova are expected to settle out of the water matrix and into the biosolid phase during the sedimentation phase of treatment; however, this is largely dependent on the size, shape, and physicochemical properties. We hypothesize that *E. vermicularis* is an effective surrogate as it represents a breadth of smaller, lighter helminth ova that are capable of aerosolization. We are monitoring *E. vermicularis* presence in wastewater influent and effluent using a highly sensitive diagnostic qPCR assay. In addition to this detection test, we have also developed qPCR inhibition controls, and have a parasite lysis control using the muskrat trematode *Echinostoma caproni*. We find consistent levels of the parasite in wastewater influent, and find that the parasite persists through to discharge. This data will be used to perform a quantitative microbial risk assessment.

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DIAGNOSIS OF *STRONGYLOIDES STERCORALIS* SPECIES-SPECIFIC REPEAT DNA IN URINE RESIDUE

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Recent work indicates that the prevalence of *Strongyloides stercoralis* infection is underestimated and of growing concern for immunosuppressed individuals. Most infections remain asymptomatic and difficult to identify. Standard parasitological tests of *S. stercoralis* rely on time-consuming culture based protocol to identify larvae in the stool. Although highly specific, this approach suffers from low sensitivity as larvae are produced sporadically. This may also be the case when fecal specimens are used for detection of parasite DNA. While antibody base detection methods can be sensitive, these can be problematic for the identification of ongoing infections. We have previously demonstrated that species-specific DNA can be

detected in the urine of patients infected with *Schistosoma haematobium* or *S. mansoni* and that this approach is useful even when eggs cannot be detected in urine or feces, respectively. We have adapted these methods for detection of *S. stercoralis* DNA from urine samples. Fresh urine from infected and control individuals were collected locally and in Northern Argentina. The urine was filtered through filter paper, dried and individually sealed with desiccant and mailed for analysis. The DNA was extracted from filter papers and used to amplify a 125 base pair *S. stercoralis* repeat sequence using species-specific primers by PCR. The PCR products were visualized on agarose gel and sequenced to verify the repeat and to determine any sequence variation. The results from the urine analysis were compared to the outcome of standard parasitological analysis from the same individuals. Of the 100 urine samples analyzed, 52 were concordant (24 were positive in both feces and urine and 28 were negative for feces and urine), 41 were positive in the urine but negative in the feces and 7 were positive in the feces and negative for the urine analysis. The results suggest that detection of species-specific repeat DNA, which passed in the urine, could significantly enhance sensitivity for the identification of asymptomatic individuals infected with *S. stercoralis*.

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REDUCTIVE EVOLUTION OF MITOCHONDRIAL METABOLISM AND DIFFERENTIAL EVOLUTION OF INVASION-RELATED PROTEINS IN *CRYPTOSPORIDIUM*

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The switch from photosynthetic or free-living predating to parasitic life strategies by apicomplexans is accompanied with a reductive evolution of genomes and a loss of many energy metabolic capabilities. *Cryptosporidium* spp. are extreme examples of reductive evolution among apicomplexans, with losses of both the mitochondrial genome and many metabolism pathways. Our current observations on reductive evolution are largely based on comparative studies of divergent microorganisms. In this study, we conducted a comparative genomic analysis of several *Cryptosporidium* species to infer the reductive evolution of metabolism pathways and differential evolution of invasion-related proteins within the apicomplexan lineage. In energy metabolism, Cryptosporidium species differ from each other mostly in mitochondrial metabolic pathways. Comparing to *C. parvum* and *C. hominis*, *C. andersoni* possesses more aerobic metabolism and a more conventional electron transport chain, whereas *C. ubiquitum* has further reductions in ubiquinone and polyisprenoid biosynthesis and has lost both the conventional and alternative electron transport systems. Regarding invasion components, similar to *C. hominis*, a reduction in the number of genes of secreted MEDLE and insulinase-like proteins in the subtelomeric regions of chromosomes 5 and 6 was also observed in *C. ubiquitum* and *C. andersoni*; whereas, mucin-type glycoproteins associated with host cell adhesion and invasion are highly divergent between the gastric *C. andersoni* and intestinal *Cryptosporidium* species. Thus, rapidly evolving mitochondrial metabolism and secreted invasion-related proteins could be involved in tissue tropism and host specificity in *Cryptosporidium* spp. The progressive reduction in mitochondrial metabolism among *Cryptosporidium* species could be a model for fine-scale studies of reductive evolution within apicomplexans

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A MOLECULAR SURVEY OF ANISAKID NEMATODES FROM MARINE FISHES IN CANADIAN WATERS

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Larval anisakid nematodes in marine fishes pose cosmetic and potential health risks to consumers. Large-scale surveys and monitoring efforts typically involve coarse identifications to genus and species based solely on visual inspections without the aid of magnification. Yet the genera *Anisakis*, *Pseudoterranova* and *Contracaecum* are all composed of cryptic species whose larvae cannot readily be identified to species without the use of biochemical or molecular techniques. However, few nematodes from Canadian waters to date have been sequenced to determine specific identity and species composition may be incompletely known from these waters. We performed large-scale molecular surveys on nematodes from different fishes collected in Atlantic and Pacific waters off Canada using the internal transcribed spacer region (ITS1 and ITS2) and the barcoding region of the mitochondrial cytochrome oxidase 1 gene to discriminate among taxa. The species *Anisakis simplex* (*sensu stricto*), *Pseudoterranova decipiens* (*sensu stricto*), *Contracaecum osculatum* A, *Contracaecum osculatum* B, and *Contracaecum osculatum* (*sensu stricto*) were sequenced from fishes collected in Atlantic waters. The species *A. simplex* (*s. s.*), *Anisakis pegreffi*, and *C. osculatum* A were sequenced from fishes collected in Pacific waters. Of these species, the occurrence of *C. osculatum* (*s. s.*) in the northwestern Atlantic, as well as *A. pegreffi* and *C. osculatum* A in the northeastern Pacific oceans, represent new locality records and significant range extensions from their previously known distributions. Error rates in identifications based on coarse visual surveys will be presented and discussed.

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ASSESSMENT OF BACTERIA IN BLACKLEGGED TICKS, *IXODES SCAPULARIS* (ACARI: IXODIDAE)

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The blacklegged tick, *Ixodes scapularis*, is already known to vector numerous diseases, including Lyme disease, and yet new and potentially pathogenic components of its microbiome continue to be discovered yearly. Comprehensive surveys of the bacterial associates of this tick are now possible using high throughput sequencing of 16S rRNA gene fragments amplified using universal primers. However there is little agreement on which fragment of 16S provides the best information, and no comparative assessments for tick bacterial communities. Our study compares short reads of all nine 16S variable regions, using Ion Torrent semiconductor sequencing for 23 ticks that were surface cleaned before DNA extraction. Bacterial sequence variation was assessed at a local and a commercial facility, using three independent library preparations covering different sets of variable regions and five specimens in common among them. We conclude that DNA sequence from multiple 16S regions is required to reliably describe the breadth of bacterial communities associated with individual ticks. The dominant phyla in our consensus data were Proteobacteria, particularly *Rickettsia*, and when present, spirochetes of the genus *Borrelia*. Diversity estimates were consistent from two different sequencing facilities and when analyzed with multiple bioinformatics pipelines. Inclusion of null environmental control samples help to provide baseline information for potential DNA contamination during the extraction process. Consistent assessment of the number, identity and proportions of bacterial taxa associated with *I. scapularis* will provide a foundation for understanding the roles of geographic variation and interaction effects in the regional disease risks presented by these ticks.

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RNAI-MEDIATED GENE KNOCKDOWN BY MICROINJECTION IN THE MODEL ENTOMOPATHOGENIC NEMATODE *HETERORHABDITIS BACTERIOPHORA*

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Parasitic nematodes (PN) continue to plague humans, placing considerable burden both on human health and on agricultural production. Current control strategies are limited to periodic de-worming of infected individuals, which is limited by rapid re-infection rates and the development of drug resistant worm populations. There are currently no vaccines available against PNs. Identification of new drug targets and vaccine antigens will require a better understanding of the PN infective process. The obligate requirement for vertebrate host has hampered investigations of the molecular mechanisms of infection. *Heterorhabditis bacteriophora* is an entomopathogenic nematode that allows simultaneous monitoring of infection processes and host immune function, and offers potential as a tractable model for PN infections. The obligatory dauer infective stage makes this species more suitable as a model than *C. elegans*, and the ability to culture the complete life cycle on plates permits investigation of molecular events that are inaccessible in vertebrate hosts. However, the molecular tools required to investigate gene function and infection mechanisms are lacking for this species. We report the first use of RNA interference (RNAi) in a parasitic nematode by microinjection. Double stranded RNA of 4 genes (*cct-2*, *nol-5*, *dpy-7*, and *dpy-13*) was injected into the gonad of adult *H. bacteriophora* hermaphrodites. RNAi phenotypes were scored in the F1 progeny on the fifth day post-injection, and knockdown of gene-specific transcripts was quantified with real-time quantitative RT-PCR. Significant variability in phenotypic expression was seen, ranging from 2-60% of the progeny showing the expected phenotype, depending on the targeted gene. Transcript levels of each gene were reduced significantly in worms expressing the knock down phenotype, but the magnitude of the reduction was also variable, suggesting a threshold transcript level above which the nematodes appear phenotypically wild type, and that this level may vary significantly across different genes.

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WEAPONS OF A PARASITE: PROTEASES FROM THE TRANSCRIPTOME OF *CERATONOVA SHASTA* (CNIDARIA: MYXOZOA)

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Proteases are important components of parasite virulence. These proteolytic enzymes are considered virulence factors due to their essential roles during invasion, migration and nutrition of a parasite. The myxozoan *Ceratonova shasta* is an intestinal parasite of cultured and wild salmonid fishes in the rivers of the Pacific coast of North America. *C. shasta* has host-specific genotypes with different degrees of virulence, quantified as different rates of mortality and proliferation in the fish host. We extracted RNA from intestines and ascitic fluid of salmonids infected with single *C. shasta* genotypes: genotype I in Chinook salmon, genotype IIC in coho salmon and genotype IIR in rainbow trout. cDNA libraries were sequenced on two lanes of Illumina HiSeq 2000/3000. These yielded 119 and 778 million raw reads respectively. To control for host transcript contamination, we mapped raw reads against *C. shasta* and rainbow trout genomes using Gmapper and sorted as more likely belonging to the parasite or to the host. Parasite: host reads ratios ranged from 1/20 to 2/3. Separate transcriptomes were assembled for *C. shasta* and for the host using the *de novo* assembler Trinity. Contigs were annotated using UniProt, Gene Ontology and NCBI taxonomy databases. Gene mining allowed identification of numerous cysteine proteases (cathepsins L, Z) and zinc-dependent metallopeptidases (belonging to M3, M13, M24, M41

families) transcripts. We designed specific PCR primers and confirmed the presence of these proteases as transcripts expressed in ascites and intestine samples. We used qPCR to examine differential expression of transcripts during parasite development in the fish host. We hypothesize that cysteine cathepsins L, Z and zinc metallopeptidades contribute to parasite pathogenicity by destruction of the host extracellular matrix, to facilitate migration of *C. shasta* in the gut, as reported in other parasite groups. *C. shasta* proteases are candidates for development of chemotherapeutants against this parasite in aquaculture systems.

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AMPLICON SEQUENCING OF MITOCHONDRIA GENOME USING NEXT GENE SEQUENCING FOR MOLECULAR CHARACTERIZATION OF *CYCLOSPORA CAYETANENSIS* IN PRODUCE

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Cyclospora cayetanensis is a coccidian parasite causing large outbreaks in different countries. In the U.S. these outbreaks affected 1481 person from 2013 to 2015. Outbreak investigations are hampered by the absence of molecular epidemiological tools for epidemiologic traceback analysis. Because of the unculturable nature of this organism it is not possible to enrich produce samples contaminated with *C. cayetanenesis* to facilitate the detection of the parasite using gold standard laboratory techniques such as microscopy. Furthermore, difficulties in the recovery of the oocysts from produce, and limitations in efficient DNA extraction due to resistant oocyst wall structure, make it even harder to generate enough DNA templates for robust amplification of large DNA fragments, for traditional sequencing analysis. In different apicomplexan parasites multicopy organellar DNA such as mitochondrion genomes have been used for detection and genetic traceback analysis. *C. cayetanensis* mitochondrial genome is 6274 bp long, and appears to exist in concatemeric arrays. We PCR amplified the whole mitochondrial genome in two overlapping amplicons from genomic DNA extracted from cilantro spiked with *C. cayetanensis* oocysts. DNA sequence libraries of the gel purified amplicons were prepared using NuGEN technologies, Ovation Ultralow System library kit, and sequenced using MiSeq. Sequence reads were assembled by mapping onto a reference mitochondrial genome of *C. cayetanensis,* using CLC Genomics WorkBench, and Geneious programs. This approach allowed us to sequence complete mitochondria genomes from produce samples contaminated with *C. cayetanensis* oocysts. Our method will facilitate the application of genomics tools to link *C. cayetanensis* identified in clinical and food samples during outbreak investigations.

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BIOENERGETIC RESPONSES TO PARASITE EXPOSURE AND INFECTION IN A FRUIT FLY HOST

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Parasites affect host physiology and populations in numerous ways including through increased mortality, decreased fecundity, and changes to host behavior. Central to many such changes is the effect of parasitism on the energy budgets of hosts. These include the energetic costs of resistance and the metabolic effects of the parasite (e.g. blood feeding) on the host. Studying these metabolic changes and their wider effects on host populations is the domain of ecological physiology. Studies have shown ambiguous relationships between host metabolic rate and infection, depending on the system and the conditions under which measurements were obtained. We seek to elucidate the interactions between parasitism, host activity, and host respiration. We use a fly-mite system, *Drosophila hydei* infected by *Macrocheles muscaedomesticae*. Mites attach to hosts as a means of moving between habitats and simultaneously feed on hemolymph. Previously, we showed that mite infection reduces flight endurance

of *D. hydei*. Here, we aim to measure the energetic costs associated with parasite avoidance, infection, and sustained flight. Flies exhibit continuous locomotor activity, bursts of flight, and reflex movements in response to contact by mites. These behavioral defenses against mite attachment are likely energetically costly. We also hypothesize that the energy penalty of flight following infection will be larger than the effects of parasitism or flight alone. We use flow through respirometry to measure the metabolic rate of individual flies under different conditions. Results suggest that the interaction between flight and infection status are nonadditive. Additionally, mere exposure to mites increased the resting metabolic rate of flies compared to unexposed flies. By accounting for these bioenergetic changes, we can develop a bottom up picture of how parasites affect host metabolism, energy flow, and population dynamics.

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RELATIONSHIP BETWEEN DIVERSITY AND ABUNDANCE OF PARASITES AND REPRODUCTIVE POTENTIAL IN TWO CYPRINIDS WITH DIFFERENT MATING STRATEGIES

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Parasitic organisms can affect ecosystems by driving population dynamics of the hosts and influencing community interactions. Reproductive efforts of the host species can be affected due to parasite-induced alterations. The effects of parasites on the reproduction of their host was investigated by calculating Shannon's diversity, Simpson's diversity, species richness, parasite abundance, and the gonadosomatic index of the host. Parasite communities of two host species were investigated, *Cyprinella venusta* and *Notropis volucellus,* which have varying reproductive strategies. Fish were collected from a single site on the Paluxy River, TX from May-September in 2014 and 2015, and returned to the lab to measure parasite abundance, diversity and host reproductive potential. Our results revealed significant differences in parasite diversity between the two species, but not between males and females within the species. Additionally, we recorded a significant, positive correlation between the gonadosomatic index and total number of helminth parasites in *C. venusta* but not *N. volucellus*. The results indicate a potential difference between the two species in terms of parasite abundance during the breeding season.

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HOST IDENTITY AND FLEA FITNESS: THE EFFECT OF PHYLOGENETIC DISTANCE BETWEEN HOSTS

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Among multiple host species that a parasite is able to exploit, a principal and auxiliary host can be distinguished. We studied feeding and reproductive performance of two flea species (a host specific *Parapulex chephrenis* and a host generalist *Xenopsylla ramesis*) exploiting nine host species in the laboratory and asked if flea fitness, as measured by various feeding and reproductive parameters, is affected by a host species identity and its phylogenetic relatedness to the principal host species. In general, feeding and reproductive performance of fleas differed among hosts. Fleas did not always take larger blood meals from a principal than from an auxiliary host; and feeding performance on an auxiliary host was not correlated negatively with phylogenetic distance of this host from the principal host. In some cases, fleas fed better on hosts that were phylogenetically distant from their principal host. However, energy expenditure for blood digestion was lowest when a flea fed on either its principal host or on a host that was phylogenetically most distant from it. When all auxiliary hosts were considered, there was no significant relationships between reproductive performance of fleas exploiting an auxiliary host and phylogenetic distance between this host and the principal host. However, when the analyses were restricted to auxiliary hosts belonging to the same family as the principal host, offspring production in an auxiliary host decreased significantly with an increase in phylogenetic distance between the auxiliary and

principal hosts. Furthermore, fleas not only produced more eggs when exploiting principal hosts, they also spent less energy for production per egg. In addition, *P. chephrenis* produced larger eggs after exploiting auxiliary hosts, while the opposite was true for *X. ramesis*. Association between offspring quality and phylogenetic distance of the maternal host from the principal host of a flea was found in *X. ramesis* (but not *P. chephrenis*) with new imagoes being larger if their maternal hosts were phylogenetically distant from the principal host. We conclude that among-host variation in parasite performance may result from interplay of several factors including co-occurrence between hosts, susceptibility of a host to parasite attacks, species-specific level of immunocompetence of a host and the level of host specificity of a parasite.

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ELUCIDATING MECHANISMS AFFECTING ACANTHOCEPHALAN PREVALENCE IN FRESHWATER *GAMMARUS LACUSTRIS* AMPHIPODS

Z. Song and **H. Proctor**, University of Alberta

Understanding factors that determine parasite prevalence is a central interest in parasitology. In freshwater ecosystems, parasite prevalence in a waterbody can be influenced by colonization times for host and parasite, waterbody size and environmental conditions, or host abundance. However, empirical evidence remains scarce regarding how these biotic and abiotic factors interact to influence parasite prevalence in natural host-parasite systems. We use a waterfowl-*Gammarus*-Acanthocephala system to test the effects of waterbody age and size, water quality variables, waterfowl richness, and *Gammarus* abundance on acanthocephalan prevalence in the *Gammarus* intermediate host. Our results show that water body age, waterfowl richness and salinity had strong positive correlations with acanthocephalan prevalence. Surprisingly, acanthocephalan prevalence was negatively affected by water body size and not significantly influenced by *Gammarus* abundance. These results provide evidence that amount of time available for colonization by intermediate hosts and parasites, richness of final hosts, and salinity can affect prevalence of freshwater parasites.

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MONTHLY VARIATION OF METACERCARIA ABUNDANCE OF TWO TREMATODE SPECIES IN THE CALIFORNIA KILLIFISH, *FUNDULUS PARVIPINNIS*, IN CARPINTERIA SALT MARSH

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We investigated seasonal changes in parasite abundance for the metacercariae of two species of digenean trematodes, *Euhaplorchis californiensis* and *Renicola buchanani*, in the California killifish, *Fundulus parvipinnis*, the most abundant fish in many southern California estuaries. One of the parasites, *E. californiensis*, is known to modify the behavior of its host in an intensity dependent fashion, increasing trophic transmission to predators. Parasite abundance was quantified, for fish of a wide range of sizes, monthly from the Carpinteria Salt Marsh, Santa Barbara County, California, from April 2012-March 2013. The abundance of parasitism was examined considering the seasonal timing of cercaria shedding, seasonal changes in the fish population demography, and disproportionate predation of highly infected hosts. Seasonal changes in fish population size structure were consistent with those described elsewhere. A generalized linear model taking into account month, fish size (total length), fish sex, and all interactions, was the best predictive model for both *E. californiensis* and *R. buchanani* abundance. As predicted, mean abundance of both parasites always increased with host size and was higher in summer and fall than in winter and spring months. This information on the seasonality of two parasites of a very common fish adds temporal dynamic information to the otherwise relatively well-studied Carpinteria Salt Marsh food web.

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TROPHICALLY TRANSMITTED PARASITES REFLECT DIFFERENCES BETWEEN NATURAL ORIGIN AND HATCHERY PRODUCED JUVENILE PACIFIC SALMON IN FRESHWATER, ESTUARINE AND MARINE HABITATS

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R. Baldwin, Alberta Environment and Parks

Differences in the behavior and ecology between natural-origin and hatchery salmon indicate what extent hatchery salmon may serve as surrogates for natural-origin fish. Trophically transmitted parasites extend diet history in fish beyond documenting prey items in stomachs, and we have shown they can reflect ocean conditions and effects of diversity of diet on growth and condition of juvenile Pacific salmon in the ocean. In previous studies, results also suggested differences in parasite communities between hatchery and natural origin juvenile salmon. A subsequent comparison between hatchery and natural origin Mid/Upper Columbia River Chinook salmon (*Oncorhynchus tshawytscha*) from the lower Columbia River estuary (2007-2011) indicated a trend for natural origin fish to harbor more freshwater (50% vs. 14%) and marine (50% vs. 35%) parasites than hatchery fish, suggesting that juvenile hatchery Chinook salmon may not be consuming prey at the same rate, or diversity, as natural origin fish during river and estuarine emigration. In May 2015 we focused on collecting juvenile Chinook salmon off the mouth of the Columbia River to compare natural origin to hatchery produced juveniles after they just entered the ocean. The majority of parasites recovered were intestinal. Despite small sample sizes of unmarked Chinook salmon, the difference in intestinal parasites between marked (hatchery) and unmarked fish was unequivocal with a mean abundance of total intestinal parasites in unmarked salmon of 39.9 compared to only 3.8 from marked fish. Species richness was also different: a mean of 2.2 in unmarked to 0.6 in marked Chinook salmon. Other differences and the utility of parasites as biological markers in juvenile salmon will be discussed.

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FLOWER CHOICE OF *DICROCOELIUM*-INFECTED ZOMBIE ANTS

S. Woodman and **C. Goater**, University of Lethbridge

Larvae of the lancet liver fluke, *Dicrocoelium dendriticum*, cause infected ants (*Formica* spp.) to leave the warmth and protection of their nests and to cling to adjacent plants throughout the evening hours. When temperatures exceed 18C the following day, they detach from the plant and return to their nests. They repeat this behaviour day after day, often returning to the same plant. It is unknown whether infected ants demonstrate preferences to particular sympatric plants or if they can distinguish between familiar and unfamiliar plants. We evaluated flower choice of infected and uninfected worker ants that were provided paired combinations of novel, familiar, and artificial inflorescences within replicated, sealed chambers placed outdoors. The placement of the chambers was alternated between cool and warm microsites to control attachment and detachment behaviours. Our results showed that only ants that harboured at least one larval fluke in their brains attached to one of the flowers. Thus, uninfected ants were never observed clinging to flowers. Infected ants demonstrated a significant preference for familiar versus unfamiliar flowers and the magnitude of the preference increased over the duration of the trials. However, there was no significant preference for one flower over another when both flowers were novel. These findings demonstrate that infected ants prefer clinging to familiar flowers and that they tend to avoid novelty. Our follow-up experiments are designed to evaluate the mechanism underlying such choices, and to determine the extent to which such choices influence rates of metacercariae transmission.

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TESTING FOR CRYPSIS WITH INTEGRATIVE TAXONOMY IN A NORTH AMERICAN ECHINOSTOME TREMATODE

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More cryptic species (morphologically indistinguishable, yet genetically distinct) of trematodes have been found than in any other helminths. This high rate may be due to a lack of morphological divergence amongst sibling species or the lack of detailed morphological assessments. To resolve this issue, taxonomic studies should integrate data on morphology, host specificity, geography and genetics. Our study focuses on the cryptic nature of *Echinostoma trivolvis*, which may be a North American trematode species complex comprised of lineages A, B, and C. This suggestion was based primarily on differences in genetics and first intermediate host specificity, and did not include detailed morphological analysis. To more fully understand their biology, we used integrative taxonomy to determine whether or not *E. trivolvis* is a cryptic species complex consisting of three separate species. Adult worms (n=924) were collected from muskrats (n=49) from four locations in Manitoba and Ontario. A total of 58 worms were genetically identified using partial ND1 sequences and then a subset (n=30) were measured at 41 morphological features. In addition, 22 museum specimens identified as *E. trivolvis* were measured and combined into an analysis with the Canadian specimens. Two clustering analyses performed on 29 and 18 adult characters tested whether there were any morphological differences between and within lineages. Phylogenetic and network analyses found that 57 individuals were *E. trivolvis* C, and only one was *E. trivolvis* A. Lineage A was the most genetically distinct, while B and C were sibling lineages. Clustering analyses indicated that within Manitoba, lineage C and A were morphologically distinct from each other as well as from most museum vouchers. However, due to a lack of diversity in Manitoba, and the inability to obtain genetic sequences from museum specimens, we could not determine if B and C were cryptic sibling species. Overall, our study suggests divergence according to genetics and morphology, and the role of geography and definitive host use in parasite speciation.

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LIFE-HISTORY RESPONSES OF AN INVASIVE SNAIL (*BITHYNIA TENTACULATA*) AND ITS TREMATODE PARASITE (*SPHAERIDIOTREMA PSEUDOGLOBULUS*) DURING A SIMULATED OVERWINTERING PERIOD

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Seasonal infection patterns can have important consequences for parasite transmission and the subsequent emergence of wildlife disease. The invasive snail, *Bithynia tentaculata,* harbors a number of parasite species (including *Sphaeridiotrema pseudoglobulus*) which have been implicated in thousands of waterfowl deaths throughout the upper Mississippi River (UMR). Unfortunately, little is known about snail and parasite dynamics within this region, particularly during winter. To begin addressing this shortcoming, we conducted a 10-week laboratory experiment looking at the effects of simulated overwintering on both *B. tentaculata* and *S. pseudoglobulus* life histories. Experimentally infected and control snails were randomly assigned to one of two environmental chambers. One of the chambers was maintained at 20 C whereas the second was programmed to undergo a simulated period of overwintering. On a weekly basis, snail activity and parasite reproduction (shedding) were assessed. There was an overall reduction in *B. tentaculata* activity with decreasing temperature; this pattern was similar across infection treatments. Survival did not differ between infected and uninfected hosts after simulated overwintering. In terms of *S. pseudoglobulus*, cercarial shedding not only varied based on temperature, but also on whether infected snails were entering into, versus emerging from, simulated winter. Together these results may help to explain field based-patterns of infection in *B. tentaculata* throughout the winter period in the UMR.

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VARIATION IN DIVERSITY AND COMMUNITY STRUCTURE OF SNAILS AND DIGENEANS IN CENTRAL ALBERTA LAKE ECOSYSTEMS

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The geographic distribution of digenean trematodes is reliant upon the presence of compatible snail hosts within the environment to maintain their life cycles, as snails are obligate, first intermediate hosts. However, there are many environmental and ecological factors that can play key roles in shaping snail-digenean community structure in addition to host presence. For most digeneans, a part, or all of their life cycle takes place within an aquatic environment. Thus, factors that can alter the aquatic environment, whether natural or anthropogenic, can have impacts on their success and the resulting community structure. To understand these potential impacts on community structure, it is first necessary to have a record of natural variations across the landscape. In Alberta, there are very few records of snail-digenean associations available. To understand the structuring forces of snail-digenean communities within Alberta, a comprehensive, three-year (2013-2015) survey was conducted across six lakes to gather information on species presence and distributions, host-parasite associations, and water and habitat quality. Snails were collected from 11 sites on a biweekly basis and inspected for patent digenean infections. Water and habitat quality data was recorded at each collecting point. Both morphological and molecular methods were used to identify snail and trematode species. In total, 18,130 snails were processed for digenean infections. From 5 snail intermediate hosts, over 39 digenean species have been recovered, representing exceptional regional diversity. To begin to assess the role of environmental and ecological factors on community structure, models have been used to derive key factors and test their influences on the resulting communities. Overall, this survey contributes new information towards digenean-snail compatibility, life cycles, distributions, and potential environmental impacts that may affect them in Northern lake ecosystems.

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DECOMPOSING ATTACHMENT AND DETACHMENT BEHAVIOURS OF *DICROCOELIUM*-INFECTED ZOMBIE ANTS

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The modified behaviour of formicid ants infected with metacercariae of the lancet liver fluke, *Dicrocoelium dendriticum*, is an iconic example of adaptive host manipulation by parasites. Our observations of marked infected ants have confirmed that infected ants are chauffeured from their nests onto flower petals, where they remain attached with their mandibles during the evening. These 'clingers' detach when temperatures rise the next day. However, this attachment/detachment pattern is only observed for ants marked in mid-summer and later. Those marked earlier in summer attach to plants, but do not detach. We evaluated the consequences of attachment/detachment on the mortality of infected and uninfected ants in temperature-controlled cabinets. At 10 and 15C, ants remained attached to their plants for at least 5 days, confirming the pattern we observed in the field. Yet even at these low temperatures, the mortality of infected clingers was significantly higher than controls. At 20, 25, and 30C, mortality of infected clingers could exceed 95%, and mortality was always higher than in the controls. These results show that attachment behaviour is best interpreted as a parasite adaptation to increase rates of transmission to mammalian grazers. But detachment behaviour likely reflects a compromise between host

and parasite interests to reduce their mutual risk of desiccation-induced mortality. Decomposing zombie behaviour into its fundamental components will help in our aim to uncover underlying mechanisms.

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PARASITES AS BIOINDICATORS OF ENVIRONMENTAL DEGRADATION IN LATIN AMERICA

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Unregulated economic growth in Latin America has resulted in environmental degradation, including the release of toxic compounds to the environment. One strategy to understand and prevent the outcomes of this harmful environmental degradation is the use of bioindicators. These are free-living or parasite species that respond to habitat alterations with changes in their numbers, physiology or chemical composition. The aim of this review was to determine whether there is evidence of a significant parasite response to environmental damage in Latin America. We collected 27 papers published between 2003 and 2015 and conducted a meta-analysis to test the null hypothesis that there is no significant overall effect of environmental insults on parasites. The meta-analysis showed a low but still significant negative mean overall effect (-0.221; 95% CI: -0.241 to -0.200; $P < 0.0001$). However, the magnitudes and directions of the significant effects varied widely. These results suggest that different groups of parasites have distinct responses to various environmental insults and that the groups should be separately analysed after the accumulation of a sufficient number of studies. For future studies on this topic in Latin America, we suggest: 1) using field and experimental approaches to determine the response of parasites to environmental degradation; 2) using an interdisciplinary approach, including different type of biomarkers in both parasites and individuals hosts, to generate long-term data sets in polluted and reference areas; 3) conducting studies on parasites as accumulation bioindicators.

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DO FEATHER MITES COMPETE FOR SPACE ON THEIR HOSTS?

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Parasites and other symbionts often appear to be restricted to particular microhabitats on or in their hosts. A basic question is whether site-restriction is influenced by current competition among different parasite species occupying that host individual. Feather mites (Acariformes: Analgoidea, Pterolichoidea) inhabit all parts of the plumage of birds, including downy feathers and the flat vanes of the flight feathers. Most birds host at least two species of vane-dwelling mites. In this talk I present recent research on three bird-mite systems (two passerine and one seabird host) testing for evidence of competition for space or food on the flight feathers. Results show very strong microhabitat partitioning among co-existing mite species on flight feathers, but little evidence that the presence of mites of one species influences location of individuals of the other species. Stable-isotope and gut-content analyses indicate that mites on the seabird host consume similar foods. Site-specificity on host feathers may be a result of the Ghost of Competition Past.

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INFLAMMATORY MONOCYTES, NOT TISSUE MACROPHAGES, ARE THE PREFERRED HOST CELL DURING THE EXPANSION PHASE OF INFECTION WITH THE OBLIGATE INTRACELLULAR PARASITE *LEISHMANIA MAJOR*

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Leishmaniasis is neglected tropical disease of growing global importance. *Leishmania major*, a causative agent of cutaneous leishmaniasis, is an obligate intracellular parasite that is transmitted to the skin of a mammalian host via an infected sand fly bite resulting in the formation of a cutaneous lesion. Following transmission, parasites predominantly infect neutrophils followed by a transition to secondary phagocytic cells within which they establish chronic infection. Tissue macrophages are thought to be the major secondary target cell for *L. major*. Employing needle challenge with *L. major*-RFP parasites and CX_3CR1-eGFP knock-in reporter mice we found that $CD64^+Ly6C^+CX_3CR1^+CCR2^{+/int}$ inflammatory monocytes, not tissue resident cells, are the predominant secondary target cell for *L. major* and the host cell during parasite expansion. At later time points following needle or sand fly transmission infected cells were heterogeneous but the majority maintained expression of multiple markers of inflammatory monocytes. Isolation of *in-vivo* infected monocytes revealed that these cells are permissive for parasite replication. Human primary monocytes were also found to be a viable host for *L. major*. In contrast to primary infection, following challenge at a secondary site in mice with a healed but chronic primary infection, inflammatory monocytes were activated by the adaptive immune response, and the predominant effector cell mediating parasite clearance. Our observations suggest that, contrary to convention, *Leishmania* preferentially infect inflammatory monocytes and prevents the maturation of these cells rather than directly infecting mature tissue resident antigen presenting cells. These observations have implications for treatment and effective vaccination against this neglected tropical disease.

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MACROPARASITE COMMUNITIES IN THE FISHES OF SACONY CREEK, PENNSYLVANIA

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The study of parasite assemblages is useful in improving the resolution of food webs describing trophic interactions in aquatic communities. Parasites are also useful as bioindicators because they respond to habitat alterations through changes in their physiology, behavior or number. Yet, surprisingly, there are still relatively few studies that include parasites in food webs or that explore their utility as bioindicator species. This study provides the first description of the helminth parasite community that cycles through the fishes of Sacony Creek in Berks County, Pennsylvania. The Sacony Creek is a 28-km tributary of the Maiden Creek, which drains into the upper Schuylkill River basin, and is part of the drinking water sources for over 1.5 million people residing in the City of Philadelphia. We sampled fish from two sites along the Sacony in August 2015 using a seine for 1 hour at each site along a 100-150 m transect, and necropsied fish to identify and count the helminth parasites on or in their bodies. Some of the most common fish sampled included white sucker, blacknose dace, johnny darter, creek chub, brown trout and bluntnose minnow. So far, the list of parasites infecting some of these fishes includes leeches, nematodes, acanthocephalans, tapeworms and flukes. Preliminary results indicate that the number of parasite species infecting fish is lower near forested headwaters than along a stretch downstream from agricultural and urban areas, suggesting that changes in parasite species richness could be a useful bioindicator of anthropogenic disturbance. Furthermore, the majority of parasites found thus far are transmitted trophically using fish as either definitive or intermediate hosts, and better understanding their life cycle will undoubtedly help improve the resolution of the food web in this creek. Finally, the most abundant fish species appears to have the most diverse parasite community, and this suggests that these fish may play a central role in the flow of parasites (and energy) through the food web. Long-term monitoring of helminth parasites communities across the different tributaries of the watershed will help reveal

variabilities in the relative strength of the interactions across the biogeographic landscape of hosts and parasites.

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FROM PHENOTYPE TO GENOTYPE: CREATING RESISTANT *AEDES AEGYPTI* TO PREVENT DENGUE TRANSMISSION

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Dengue viruses infect 400 million people annually, and are transmitted by mosquitoes, especially *Aedes aegypti*. There are currently no vaccine or treatment options available. Despite *A. aegypti* being the most important vector species, approximately 30% of feral *A. aegypti* in Cali, Colombia are refractory to Dengue through midgut factors. We used RNA-sequencing and microarray analyses to identify putative pro- and anti-viral genes via differential expression in the midguts of susceptible (Cali-S) and resistant (Cali-R) mosquitoes after feeding on blood, or blood containing Dengue. Putative pro-viral genes were knocked down in susceptible mosquitoes using RNAi, and these mosquitoes were subsequently fed on blood containing Dengue, and the resultant phenotype was assessed. Modifying gene expression demonstrated our ability to flip the phenotype in *A. aegypti*, with the possibility of modifying the genotype using gene editing techniques. Such approaches provide a novel and ecologically stable control mechanism for limiting the transmission of Dengue, and conceivably other flaviviruses such as Yellow Fever, and Zika.

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GENE SILENCING OF A 65 KDA CYSTEINE PROTEINASE OF *TRICHOMONAS VAGINALIS* INVOLVED IN CYTOTOXICITY OF THIS PARASITE USING A BIODEGRADABLE NANOPARTICLES LOADED WITH SMALL–INTERFERING RNA

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Trichomonas vaginalis is a flagellated parasitic protozoan that infects the human uronogenital tract. The disease is called trichomonasis which is sexually transmitted and can occur almost exclusively in women with male rarely exhibiting the symptoms of the disease. Trichomonaisis is responsible for the number one nonviral sexually transmitted disease worldwide. It is estimated that there are some 250 million new cases of trichomonasis around the world and some estimates indicate about 9 million new cases occur in the United States every year. The symptoms of the disease trichomonasis include pneumonia, bronchitis, oral lesions, preterm delivery, low birth weight and predisposition to AIDS infection and cervical cancer. Standard treatment for trichomonasis is commonly with metronidazole. Unfortunately, metronidazole–resistant *T. vaginalis* has been implicated in an increasing number of refractory cases. The failure of metronidazole regimens to cure *T. vaginalis* infection is of great concern because metronidazole is currently the only FDA approved drug for the treatment of trichomonasis in the United States. Clearly alternative curative therapies are very much needed, considering increasing global infection rates, pregnancy complications and increased susceptibility to human immunodeficiency and other sexually transmitted diseases, make it of paramount importance to look other ways of effective treatment in order to curb the menace of trichomonasis among our young women. *T. vaginalis* cysteine proteases have been related to nutrient uptake, immune evasion and virulence properties including cytoadherence. Adherence to the epithelial cells of the urogenital tract is an essential process in the establishment of *T. vaginalis*

infection. This process of adherence is specifically mediated by a group of adhesion proteins. It has been shown that proteases play a significant role in the adhesion to Hela cells and also to the vaginal epithelial cells. RNA interference mediated by siRNA is a promising approach for prevention and treatment of human diseases and is moving rapidly from basic science to clinical application. In the present investigation we designed siRNA specific for CP65 protease gene of *Trichomonas vaginalis*, encapsulated these siRNA in FDA approved nanoparticles and tested the efficacy of the our small interfering RNA loaded on biodegradable nonoparticles in vitro on the co-culture of *Trichomonas vaginali* and *HeLa* cells. The results thus obtained from these experiments have opened the door to test this method of siRNA delivery and gene silencing in an animal model of *Trichomonas vaginalis*.

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MATERNAL PROTEIN DEFICIENCY AND NEMATODE INFECTION CAUSE DIFFERENTIAL EXPRESSION OF THE GENES FOR GROWTH AND PROTEIN BIOSYNTHESIS IN THE FETAL MOUSE BRAIN

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Background: Maternal dietary protein deficiency and nematode infection during early pregnancy have negative impacts on both maternal placental gene expression and fetal growth in the mouse. Here we used next generation RNA sequencing to test our hypothesis that maternal protein deficiency and/or nematode infection alter the expression of genes in the developing fetal brain. Methods: Outbred pregnant CD1 mice were used in a 2x2 design with two levels of dietary protein (sufficient [24%] and deficient [6%]) and two levels of infection (sham and *Heligmosomoides bakeri*). Pregnant dams were euthanized on gestation day 18 to harvest the whole fetal brain. Five fetal brain samples from each treatment group were analyzed using RNA Hiseq sequencing. The raw RNA-seq FASTQ files were aligned to the reference genome to get BAM files and HTSeq was used to count the number of expressed transcripts. Differential expressions of genes were determined by DESeq2 package in R. Results: In response to maternal *H. bakeri* infection, a total of 14 fetal brain genes including genes related to skeletal muscle development were differentially expressed. In response to maternal protein deficiency, only serine protease 22 was differentially expressed in fetal brain. Of interest, nematode infection in protein deficient, but not sufficient, dams was associated with differential expression of 14 genes of the fetal brain, including methionine tRNA synthetase, methionyl aminopeptidase type 1D and eukaryotic translation initiation factors 4E binding protein-1, which are involved in protein biosynthesis and protein modification pathways. Among infected dams, protein deficiency was associated with differential expression of 6 fetal brain genes including growth hormone gene. Conclusion: The study indicates that maternal malnutrition and nematode infection have a significant role in fetal brain gene expression, which may affect growth and development.

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COMPARATIVE HISTOPATHOLOGY OF TREMATODE (DIGENEA) INFECTIONS IN THE GONAD OF FRESHWATER SNAILS (GASTROPODA, PLEUROCERIDAE) FROM RICE CREEK, NEW YORK

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North America contains 703 species of freshwater snails (Gastropoda) in 16 families, but 74% this biodiversity is imperiled or extinct. Population declines may be due to physical changes to habitats, contaminants, and or competition with introduced species. However, the potential role of metazoan

parasites is poorly understood. To that end, we are conducting a comparative histopathological study of trematodes infecting freshwater snails in Rice Creek (Lake Ontario tributary), New York. Snails were collected by hand while snorkeling, and identified to the lowest taxonomic rank possible in the laboratory. We collected a total of 130 snails of four species representing Pleuroceridae, which we refer to as sp. 1 (n = 56), sp. 2 (n = 40), sp. 3 (n = 20), and sp. 4 (n = 14) from collections made in June and July 2015. Cercariae were obtained through shedding, heat-killed at 60 C, and fixed in 10% formalin. A tissue sample from each snail, and a subset of 20 cercariae were fixed in 95% ethanol for DNA sequencing. We observed four trematode species based on cercaria morphology, which were refer to as cr. 1 (monostome), cr. 2 (leucochloridium or mutabile), cr. 3 (vivax), cr. 4 (haplosplanchnid). Among the sampled snails, prevalence ranges are as follows: cr. 1, 0–64%; cr. 2, 0–5%; cr., 3 0–3%; cr. 4, 7–25%. However, prevalence of each infection is likely higher as we sometimes observed underdeveloped trematodes in histological sections. Among infected snails, gonad typically appeared to be replaced by sporocysts or redia, and cercaria with the exception of an occasional focus of reduced or compressed testicular or ovarian acini. While morphological differences between trematode species were apparent, damage associated with each trematode species was histologically similar, and cellular responses to infections were not observed.

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TALES FROM THE CRYPT: A PARASITOID CHANGES EMERGENCE BEHAVIOR IN A CRYPT-FORMING GALL WASP

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Parasites can manipulate the phenotype of their hosts to benefit the parasite. However, actual tests of the adaptive value of parasite-associated phenotypic changes in hosts are rare. The host in this system is *Bassettia pallida,* a cynipid wasp, which itself is a parasite of the sand live oak (*Quercus geminata*). *B. pallida*,induces its host to form a “crypt” in which the wasp undergoes larval development and subsequently emergences as an adult. Prior to emergence, the adult *B. pallida* chew their way out of the crypt, which produces distinctive emergence holes in the tree branch. We observed that many of these wasps fail to successfully emerge, and plug their incomplete emergence hole with their head prior to dying. Tree dissection of branches where this “head-plugging” behavior was observed revealed that plugged holes contained a developing parasitoid larva that had consumed much of its *B. pallida* host. We hypothesize that this head-plugging behavior benefits the parasitoid, since it may be unable to burrow through the crypt wall, wood, and bark, and thus needs its host to create an emergence hole in order for the parasitoid to successfully exit the crypt. We also hypothesize that plugging the incomplete emergence hole benefits the parasitoid, as an unplugged hole may result in abiotic conditions within the crypt that are not conducive to parasitoid survival. Here we will discuss four aspects of our current work in this system. First, we will discuss molecular, morphological, and natural history evidence that the parasitoid is a previously unidentified member of the genus *Euderus* [Hymenoptera: Eulophidae]. Second, we present observational data comparing the characteristics of holes drilled by *B. pallida* that subsequently emerged successfully, and holes drilled by *Euderus*-infected *B. pallida* that failed to emerge completely. Third, we discuss preliminary data from the manipulative experiment aimed at quantifying the fitness benefit of “head-plugging”. Finally, we present field and museum data to explore the geographic distribution of this phenomenon.

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EVALUATING THE EFFECT OF MALARIA PARASITES ON LIVER ENZYMES AMONG CHILDREN BETWEEN (5-10) YEARS OLD

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In spite of threats posed by malaria to public health, specific records on effects of *Plasmodium* species on liver (hepatic) enzymes of inhabitants of Owerri, Imo State have not received wide reports and documentation. Accordingly, the present study sought to evaluate the effects of malaria parasites on liver enzymes among children between the ages of 5 – 10 years in the Owerri metropolis. A total of 80 blood samples were collected from 80 children of the stated age consisting of 40 males and 40 females. The blood samples were collected employing the vein puncture technique, the samples were tested for malaria parasite (M P). The malaria parasite count (level of parasitaemia) was done by microscopic examination of slides stained with giemsa while the liver enzymes were assayed by standard biochemical methods. The malaria parasite status and density were correlated with the values of the following enzymes; alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphates (ALP) and lactate dehydrogenase (LDH). The results showed that there was a positive relationship between the level of the enzymes (ALT and AST) and the malaria parasite. Out of 80 children tested for malaria, 49 (61.3%) were infected (72.5% males and 77.5% females). 48.9% had low (+) parasitaemia, 26.5% moderate (++) parasitaemia, 18.4% severe (+++) parasitaemia and 6.1% no malaria parasite (control). The mean test values of ALT and AST are 55 and 50 respectively and these are higher than the normal values of the control test due to severe malaria attacks. There was no significant effect of the low (+) and moderate (++) malaria parasite on the liver enzymes. ALP and LDH were not affected by the parasites. A liver enzymes test is therefore recommended for effective diagnosis of severe malaria in children for improved treatments to ensure hepatic integrity and save lives in the study area.

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PATHOGENICITY OF LARVAL NEMATODES (NEMATODA) INFECTING THE FOOT OF *VILLOSA NEBULOSA* (BIVALVIA, UNIONIDAE) FROM TERRAPIN CREEK, ALABAMA

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The inland waters of North America historically contained 305 nominal species of freshwater mussels (Bivalvia, Unionoida) in two families (Unionidae = 300 spp.; Margaritiferidae = 5 spp.). However, approximately 70% of these species are imperiled. A recent review regarding parasites and diseases of freshwater bivalves revealed that the biodiversity and pathogenicity of metazoan parasites of mussels is poorly understood. While characterizing the tissues of *Villosa nebulosa* towards the development of a histological atlas for freshwater mussels, we observed filiform nematodes infecting the foot. Although free-living nematodes are common inhabitants of aquatic habitats, and although there are many records of histozoic nematodes from marine bivalves, there are few observations of parasitic nematodes from freshwater bivalves. From a sample of 43 *V. nebulosa* (24–51 mm shell length) sampled from Terrapin Creek, Alabama in May 2010, August 2011, July 2012, May 2013, and July 2014, nematodes were observed in 32 individuals (prevalence = 74%). This sample comprises 14 mussels sampled for histology, and 29 that were sampled to obtain worms for a diagnosis. Uninfected foot consists of bundles of myofibers that become branched and interwoven in the ventral tip of the foot. Infections ranged from a small number of isolated worms threaded through the myofibers, to a larger, irregular mass consisting of 100 or more individuals. Infections characterized by a seemingly low number of worms exhibited a small, localized gap surrounding each worm. Foot infected with a larger mass of worms exhibited severed or compressed myofibers. However, a cellular response to these infections was not observed. Since these worms damage pedal musculature, we speculate that these parasites may limit pedal extension and retraction such that mussels may be more vulnerable to predation or to scouring water currents.

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HEPATIC AND INTESTINAL CAPILLARIASIS IN COMMON GOLDENEYE (*BUCEPHALA CLANGULA*), BARROW'S GOLDENEYE (*B. ISLANDICA*) AND BUFFLEHEAD (*BUCEPHALA ALBEOLA*) DUCKS HEAVILY INFECTED WITH *BARUSCAPILLARIA OBSIGNATA* (TRICHINELLOIDEA, CAPILLARIIDAE) FROM HANFORD, WASHINGTON

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In January, 2015, six common goldeneye ducks (*Bucephala clangula*), one Barrow's goldeneye duck (*B. islandica*) and one bufflehead duck (*Bucephala albeola*) were found dead in a pond at the 200 Area of the Hanford Site (former nuclear site) in Washington State and submitted for necropsy. On gross examination, birds were adults in fair to emaciated body condition characterized by low to no subcutaneous, visceral or epicardial fat and moderate to severe pectoral muscle atrophy. Significant internal findings included multifocal to coalescing slightly raised yellow foci on the surface of the liver that extended into the hepatic parenchyma on cut section. Coelomic hemorrhage was present in all birds, and in one bird there were multiple intestinal adhesions centered around a large blood clot. On histopathology, the liver had multifocal to coalescing areas of necrosis with intralesional nematodes consistent with capillarid-type nematodes. The nematodes were also present within the intestinal lumen and lamina propria. Parasitological exams of the complete gastrointestinal tracts from two common goldeneye ducks and a 5 cm subsample of small intestine from one common golden eye duck found greater than 3000, 9000 and 221 *Baruscapillaria obsignata*, respectively. Morphological identification was corroborated by sequencing analysis of the 18S rRNA gene from nematodes collected from the gastrointestinal tracts. Microbiological culture and virus isolation was negative for pathogenic agents. This is the first report of disseminated *B. obsignata* infection associated with hepatitis.

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PROMOTING PROTISTS ON SOCIAL MEDIA PLATFORMS

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Microscopic unicellular life forms are intrinsic members of every ecosystem on Earth. They inhabit the soil, air and water all around us, and reside on and in our bodies. Despite this, most people have never seen unicellular life forms, and the terms protist, eukaryote and prokaryote sound erudite and esoteric. But unicellular organisms are intrinsically fascinating and visually stunning; they are architects, builders, travellers, parasites, hunters, scavengers and prey; they have sex lives and mating rituals; they build communities and they go it alone. They are as complex in terms of behavior and lifestyle as plants and animals, yet they do it all within the confines of one cell. For the past year I have been collecting water samples from urban locations in and around New York City and documenting the protists and bacteria I find living within. I post pictures and video of the organisms to an Instagram account called @pondlife_pondlife. The account's following has grown ~10,000 people, and has been featured in The Atlantic magazine. Each post is accompanied with a description of what the organism is and what it is doing. The project is intended to be educational, inspirational and visually stunning. I want to make these organisms accessible to a general audience with the intention of encouraging wonder, interest and adventure in protists and bacteria, and increasing familiarity with microbes, cells and evolutionary biology. So far my project has been limited to free-living species that inhabit our urban environments, but there is much scope for extending the project to document parasites, symbionts and extremophiles. By documenting these organisms in ways that are appealing and accessible to a non-scientific audience, we could help people to understand the importance and identity of unicellular life, the process of evolution and our own cellular origins.

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CURCUMIN INDUCES APOPTOSIS AND OXIDATIVE STRESS IN *SCHISTOSOMA MANSONI* ADULT WORMS

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The induction of apoptosis is an interest therapeutic approach for drug development that yet needs to be more explored for helminthic parasites. The effect of curcumin (CUR), a biologically active compound extracted from rhizomes of *Curcuma longa*, has been shown activity *in vitro* and *in vivo* against *Schistosoma mansoni*. In addition, studies have been associating CUR to the induction of the generation of reactive oxygen species (ROS) in several cancer cell lines and also on leading to cell apoptosis. In the present study, the effect of CUR was evaluated on apoptosis induction and oxidative stress on *S. mansoni* adult worm pairs. Results from viability assays showed that CUR causes a significant reduction in viability of male and female parasites at concentration 25 μM in 24 hours. Also, adult worms incubated at 50μM of CUR showed typical apoptosis morphological such as vacuoles formation, swelling and disruption of mitochondrial membrane and chromatin condensation. To understand the effect of CUR on *S. mansoni* adult worms, different apoptotic parameters were determined. Our results strongly suggest that CUR induced DNA damage and fragmentation, and increased the expression of transcripts of *SmCaspase 3/7* and the caspase 3 activity in female and male worms. Interestingly, the effects on apoptotic parameters were higher in female worms than male worms. The superoxide anion level and different antioxidant enzymes were also evaluated to explore further the mechanism of the death of the parasites. There was an increased in the superoxide anion level as well as in the Superoxide Dismutase activity (SOD) and a decrease in the Glutathione - S -Transferase (GST), Glutathione reductase (GR) and Glutathione peroxidase (GPX) enzymes activities which lead to proteins oxidation of in female and male adult worms incubated with CUR. Our study suggests that CUR generates oxidative stress followed by apoptotic- like event in female and male *S. mansoni* adult worms leading to their death.

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METALLOPROTEASE INHIBITORS AS POSSIBLE LEADS TO IDENTIFY DRUGS TO TREAT LYMPHATIC FILARIASIS AND OTHER PARASITIC ROUNDWORM INFECTIONS

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Lymphatic filariasis (elephantiasis) is a disease caused by the parasitic nematodes *Wuchereria* and *Brugia*. Over 120 million people worldwide are infected, a majority of whom are in impoverished countries, and more than 1.1 billion people are at risk of infection (WHO, 2016). This classifies the disease as a Neglected Tropical Disease by the World Health Organization. Adult worms can live in lymphatic tissue for serval years and prolonged exposure can cause tissue swelling, pain, and enlarged limbs. It is the adult stages of the worm that are responsible for the disease, not the larval stages. Proteolytic enzymes are present inside *Bruiga* and are critical for the molting process. The focus of this study was to identify a compound or drug that could inhibit the adult worm's proteolytic enzymes as a lead to possible treatment options. Results showed that the metalloprotease inhibitor, 1,10-Phenanthroline (1,10P) killed adult *Bruiga pahangi* within 48 hours at 24 μm. 1,10P also inhibited protease activity in *Brugia* lysate by 30% compared to the control lysate. Drugs that are metalloprotease inhibitors that are already in use by

humans were assayed with adult *B. pahangi* in vitro for 5 days at 100 µm: Lisinopril, Luteolin, Captopril, Alendronate, Verapamil, Ivermectin, Doxycycline, Tetracycline, and 4,7-Dimethyl-1,10-Phenanthroline. IC50s for luteolin, 1,10P, and 4,7-Dimethyl-1,10-Phenanthroline were 32 µm, 15 µm, and 7 µm respectively. To determine if metalloproteases were also important to the survival of other parasitic nematodes, *Anisakis*, which is related to *Ascaris,* was used to see if metalloprotease inhibitors that can kill *B. pahangi* adult worms could kill other roundworms that pose a serious threat to human health. Luteolin and 1,10P inhibited the motility of *Anisakis* L3 by 85% and 90%, respectively, compared to their controls. The results of this study suggest metalloprotease inhibitors may be useful in developing effective drugs against adult *Bruiga* worms and other parasitic roundworms. A continuation of this project would incorporate other ascarid nematodes and hookworms.

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SEARCHING FOR GOLD: EFFECTS OF AURANOFIN ON ADULT *BRUGIA PAHANGI* IN VITRO

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River blindness and lymphatic filariasis are two neglected tropical diseases that combined affect millions of people throughout the developing world. Current mass drug administration programs rely on drugs that primarily target the microfilariae that are released from adult female worms. Adult worms (macrofilariae) live for several years and females release millions of microfilariae throughout the course of infection. Thus, to stop transmission of the microfilariae and shorten the time to elimination of these diseases, a safe and effective macrofilaricidal drug is critically needed to kill adult worms. Previously we identified auranofin, a gold containing drug, as a lead macrofilaricidal candidate that kills adult *Brugia pahangi* and *Onchocerca ochengi* female worms *in vitro* and significantly decreases worm burden in *B. pahangi* infected gerbils. The purpose of this study was to measure the amount of auranofin that is taken up by adult *Brugia* females *in vitro* and determine what exposure levels are necessary to kill worms *in vivo*. By analyzing the levels of auranofin in worms, we hope to make predictions as to how much drug is needed to treat patients. Our studies showed that 1 uM of auranofin is needed to kill adult female *Brugia* in 6 days *in vitro* and these worms have gold levels of ~20 nM. Treatment with 1 uM auranofin also decreased titers of the endosymbiont, *Wolbachia*, by 84% in 24 hrs. Given that the $T_{1/2}$ of auranofin in humans is 17-25 days after taking a single 6 mg dose and gold levels in plasma are ~0.5 to 1 uM for up to 3 weeks, it is possible that this dose may be sufficient to kill worms in patients treated with this dose. This study will further our understanding of the PK profile in filarial worms and help us determine the drug levels necessary to cure human infections. In our next *in vivo* study, we plan to measure gold levels from worms extracted from animals dosed with the human equivalent amount of auranofin to determine if the values obtained *in vitro* translate to those *in vivo*.

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MITE CHOICE GENERATES SEX AND SIZE BIASED INFECTION IN *DROSOPHILA HYDEI*

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Heterogeneities in parasite infection among conspecific hosts often manifest as sex- or size-biased infections, which are typically attributed to differential host susceptibility and exposure. Since parasite fitness is often tied to host quality, host preference by parasites is likely to be under strong selection. We test the hypothesis that host preference is sufficient to generate variability in infection rate among conspecifics. Specifically, we ask whether the mite *Macrocheles muscaedomesticae* is able to discriminate between *Drosophila hydei* hosts of different sex and size, while explicitly accounting for the potential

confounding effects of these two factors. Our results indicate a preference for female hosts, but this preference appears to be driven by size and not sex *per se*. When differences in body size were controlled for the sex-biased infection disappeared. Mites presented with the choice of two female flies of disparate sizes were more likely to select the larger host. Across the distribution of fly body weight in this study, mites preferentially attached to flies of intermediate size. This study provides evidence that mite choice for certain host types can play an important role in parasite transmission, even in the absence of differential susceptibility or exposure among hosts.

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HELMINTH FAUNA OF CRICETID RODENTS IN TEXAS AND PRELIMINARY INSIGHTS INTO PARASITE LATITUDINAL GRADIENTS

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Parasitic helminth records from rodents in Texas are sparse and often decades old, representing a large gap in our knowledge of the helminth diversity in Texas. We aim to address these missing data by providing updated biodiversity surveys of the parasitic helminths of cricetid rodents from multiple localities in Texas. Not only will these surveys increase our knowledge of the biodiversity and natural history in these regions, these data will also contribute to understanding the latitudinal diversity gradient of parasitic helminths of rodents, including the effects of various abiotic and biotic factors on parasite species richness patterns. Cricetid rodents were collected from multiple counties in southern, central, and eastern Texas, humanely euthanized, and dissected for internal parasite collection. Helminths were quantified, preserved, and morphologically identified using standard techniques. During dissection, data on host factors, including weight, sex, length, and reproductive status, were collected from each rodent. Environmental factors, including latitude, longitude, habitat type, and average temperature, were recorded for each trapping locality. We analyzed host and environmental factors with parasite species richness and species counts at both intraspecific and between locality scales.Preliminary results from these analyses will be presented along with insights into how these data integrate into the study of the North American latitudinal diversity gradient of parasitic helminths.

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MACROPARASITE COMMUNITIES IN ANADROMOUS AND LANDLOCKED ALEWIVES (*ALOSA PSEUDOHARENGUS*) IN NEW JERSEY

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The Alewife, *Alosa pseudoharengus*, is a species of river herring that naturally has an anadromous life history. Following introduction into Lake Hopatcong, NJ over 150 years ago, derived landlocked (LL) Alewife populations have become established. These fish populations experience disparate life histories and encounter different abiotic and biotic conditions throughout their lifespan, and we expect this recent alteration in host life history to shape the present macroparasite assemblage infecting these fish. In this study we compare the macroparasite communities in migratory and LL Alewives to investigate the influence of host life history on the assembly of parasite communities. We predict that parasite assemblages infecting LL population will contain fewer parasite species and experience lower infection levels when compared to the migratory population. To test our prediction, we collected and necropsied 40 adult LL Alewives from Lake Hopatcong and 14 migratory Alewives from the Maurice River, NJ. Adult LL Alewives were considerably smaller than migratory forms with a mean fork length of 9.3 ± 0.12 cm and weight of 12.3 ± 0.53 g, compared to 24.3 ± 0.29 cm and 239 ±7.2 g for migratory fish. Our results found contrasting parasite communities in the two life history forms. In total two parasitic species were found in the LL population and overall infection was low with a prevalence of 5%, with one unidentified nematode

and one unidentified tapeworm species found in separate fish. In contrast the natural, migratory population harbored more parasites and contained four species which included two genera of nematodes, *Anisakis* sp., *Hysterothylacium* sp., and 2 genera of acanthocephalans, *Acanthocephalus* sp. and *Echinorhynchus* sp. The most common parasite *Hysterothylacium* sp. had an overall prevalence of 71.4% and mean intensity of 14.1± 3.40, while *Anisakis* sp. had a prevalence of 35.7% and an intensity of 11.6 ± 3.35. Acanthocephalan infection was low with an overall prevalence 7.1% for both species and intensity of *Acanthocephalus* sp. was one and *Echinorhynchus* sp. four. There is a discrepancy in parasite species and infection levels between these two Alewife populations and we believe this is due to host life history. Our findings demonstrate the importance of alterations in host ecology on the assembly of parasite communities.

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IS SIMULTANEOUS COMMENSALISM AND PARASITISM POSSIBLE? THE CASE OF THE BIVALVE *KURTIELLA PEDROANA* AND THE SAND CRAB *EMERITA ANALOGA*

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Simultaneous commensalistic and parasitic relationships between one symbiont and its host are exceedingly rare in nature. Here we present a case of such occurrence involving a clam *Kurtiella pedroana* (Bivalvia: Galeommatoidea) and the sand crab, *Emerita analoga* (Decapoda: Hippidae) from Monterey Bay, California, USA. Galeommatoideans are known commensals of various invertebrates, including crustaceans. The sand crab is an abundant decapod inhabiting sandy beaches of the Pacific coast of North and South America and often harbors various commensals and parasites. Preliminary laboratory analysis revealed the presence of a previously undocumented bivalve associated with *E. analoga*; this mollusk was identified as *K. pedroana*. Therefore, the present study was undertaken to examine the distribution and abundance of the clam *K. pedroana* in relation to this host species. Of the 520 crabs examined, 26 (5.0%) had ectocommensal bivalves attached either inside their brachial chambers or on their pereopods, and 15 (2.88%) harbored them inside their hemocoel. Mean intensities of infections of ectocommensal and endoparasitic bivalves were 1.19 and 1.20, respectively. Host size ranged from 10.07–29.60 mm; only females measuring >17.23 mm harbored these clams. The ectocommensals were attached to their hosts using byssal threads; however, these structures were notably absent in the endoparasitic bivalves. Such example of transition from ectocommensal to endoparasitic lifestyle offers an exceptional opportunity for studying preadaptation and host–symbiont relations, and warrants further investigation. This discovery is the first known record of a bivalve serving both as an ectocommensal as well as an endoparasite concurrently in a crustacean host.

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GENOMICS AND GENETIC DIVERSITY OF THE MONKEY MALARIA PARASITE *PLASMODIUM CYNOMOLGI*

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Plasmodium cynomolgi, a malaria parasite of Asian Old World monkeys, is the sister taxon of the common human malaria parasite *Plasmodium vivax*, with which it shares many phenotypic characteristics, such as formation of a dormant liver stage and a preference to invade reticulocytes. We sequenced genomes of three *P. cynomolgi* strains and identified genome-wide SNPs, microsatellites, and copy number variations (CNVs), providing a first overview of genetic variation in the species. CNVs in multigene families appear to distinguish strains within species as well as differences between *P. cynomolgi* and two other members of the monkey malaria clade, *P. vivax* and *P. knowlesi*. To better sample its genetic diversity, we subsequently developed a panel of *P. cynomolgi* microsatellite markers and genotyped 11 *P. cynomolgi* laboratory strains and 18 field isolates from Sarawak, Malaysian Borneo. We found diverse genotypes among most of the laboratory strains, though two nominally different strains were found to be genetically identical, We also investigated sequence polymorphism and copy number variation in two erythrocyte invasion gene families, the reticulocyte binding protein and Duffy binding protein genes, and found strain-specific complementarity in copy number of two RBP genes. We expect our MS panel and findings to be useful tools for future investigation of this model parasite for human malaria.

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EXAMINATION OF POLYMORPHISMS IN ARTEMISININ-RESISTANT *PLASMODIUM FALCIPARUM*

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Plasmodium falciparum has developed resistance to multiple antimalarial drugs and recently artemisinin resistance has emerged in Southeast Asia. Single nucleotide polymorphisms (SNPs) in the propeller domain of the kelch gene on chromosome 13 (K13) correlate with artemisinin resistance, defined by reduced drug susceptibility and delayed parasite clearance. Previously, whole-genome sequencing of an African strain resistant to 2400 ng/ml artemisinin (D6.QHS2400) identified a K13 SNP (E208K) upstream from the propeller region and SNPs in other genes that may correlate with resistance. A subsequent study found the E208K SNP was not associated with resistance but a SNP (N139I) in gene PF3D7_0307600 (on chromosome 3) may be implicated in resistance. We investigated if K13 propeller SNPs of importance and the SNP in PF3D7_0307600 may exist in D6 lines, other *in vitro* drug selected lines from Asia (W2, TM91c235), and isolates from Thailand and Senegal that exhibit reduced artemisinin susceptibility. Complete K13 and a portion of PF3D7_0307600 were PCR amplified from each strain and sequenced. Results from K13 sequencing identified polymorphisms upstream of the kelch propeller region. A single Asparagine (N) insertion was identified after residue 142 in all D6 parent/resistant parasites but insertions were not found in three Senegal isolates. A tandem NN insertion was identified in all parasites of Asian origin (W2, TM91c235 parent/resistant lines, TM90c2a). A SNP (K189T) was found in D6 parent/resistant lines and Senegal isolates P11.02 and P51.02. Senegal isolate P26.04 had a different SNP at the same position (K189N). Results from PF3D7_0307600 sequencing detected the N139I SNP only in resistant D6 lines and it arose prior to exposure to 80 ng/ml QHS pressure. A novel SNP at S170N was also identified in Senegal isolates P51.02 and P26.04. These findings give insight into the genetic diversity of polymorphisms in reported areas of resistance and possible strain-specific markers. Further study is needed to elucidate their relationship with emerging artemisinin resistance.

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EPIGENETIC MODULATION OF TRANSCRIPT AND PROTEIN EXPRESSION IN THE *BIOMPHALARIA GLABRATA* EMBRYONIC (BGE) CELL LINE BY SCHISTOSOME LARVAL PROTEINS

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Previous studies have shown that proteins released *in vitro* by *Schistosoma mansoni* miracidia during transformation to the primary sporocyst stage (larval transformation proteins or LTP) can influence both gene and protein expression in blood cells (hemocytes) from the snail intermediate host *Biomphalaria glabrata*. However, to date, the mechanisms underlying LTP-mediated regulation of host cell expression and the larval proteins responsible for initiating/signaling these molecular interactions are unknown. Because of the difficulties inherent in manipulating snail hemocytes under culture conditions, we are currently using the *B. glabrata* embryonic (Bge) cell line as an *in vitro* cell model to investigate possible epigenetic linkages, via methylation and/or acetylation, between LTP exposure and snail cell gene/protein expression. At the transcript level, significant increases in relative expression of Bge cell DnMT1 (DNA (cytosine-5-)-methyltransferase 1) and MBD2/3 (methyl-CpG-binding domain protein 2/3) were observed after 24 hr of LTP exposure (PE). At the protein level, we used an anti-acetylated (Ac) lysine antibody to evaluate the effects of LTP-exposure (2-, 4-, 24-hr) on cellular protein acetylation. LTP-treatment resulted in the appearance of new/enhanced Ac-proteins of approximately 25-30, 40, and 50 kDa at all time-points PE compared to non-exposed Bge cells. Overall our findings strongly implicate LTP in influencing gene, and subsequent protein, expression through DNA/protein epigenetic mechanisms. Proteomic analyses are currently being used to identify both the putative initiating LTPs and acetylated Bge cell target proteins.

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FILLING IN THE GAPS OF THE IMD IMMUNE PATHWAY OF THE KISSING BUG *RHODNIUS PROLIXUS*

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Rhodnius prolixus is a hemathophagous hemipteran insect that has served for decades as a model organism for the study of insect physiology. *R. prolixus* also is a major vector of *Trypanosoma cruzi*, the etiological agent of Chagas disease that kills 45,000 people annually and affects over 8 million people worldwide. The genome of *R. prolixus* was published recently with ~15,500 putative protein-coding genes. Many immune-related pathways such as the Toll and JAK-STAT pathways were conserved as expected. Keyey components of the highly conserved IMD immune pathway, however, were not detected, an observation shared with the Pea aphid (*Acyrthosiphon pisum*) and the bedbug (*Cimex lectularius*). Despite this modified pathway, effector immune genes normally regulated by the IMD pathway are expressed. Whether the IMD pathway functions through novel proteins linking existing IMD pathway components, through functional redundancy of existing proteins, or through a non-canonical pathway is unknown. We have initiated studies to identify and evaluate the role of hypothetical *R. prolixus* genes based on homology with elements of the canonical IMD pathway present in other insects to fill in the gaps of the IMD pathway and our knowledge of invertebrate immunity.

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ANALYSIS OF SEAL HEARTWORM (*ACANTHOCHEILONEMA SPIROCAUDA*) AND IDENTIFICATION OF UNKNOWN HARBOR PORPOISE (*PHOCOENA PHOCOENA*) PARASITES USING MOLECULAR TECHNIQUES

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Smith College

Seal heartworm (*Acanthocheilonema spirocauda*) is a filarial parasite of phocid seals, mainly the harbor seal (*Phoca vitulina*). Seal heartworm has been reported in several phocid seal host species, and is distributed throughout the Northern hemisphere (Measures et al. 1997). Clinical manifestations are very similar to that of classic dog heartworm, including respiratory and cardiac complications (Daily, 2001). To date, seal heartworm is believed to be restricted to only phocid hosts, and has only been observed in particular species (Leidenberger, 2007). Our initial molecular results, based on single gene barcodes, suggest that seal heartworm, or an extremely close relative, is capable of infecting the common harbor porpoise (*Phocoenca phocoena*), a species that has never been reported to harbor the parasite (Leidenberger, 2007). To generate definitive identifications, recent work has focused on isolating and amplifying full mitochondrial genomes (mtDNA). Thus far, we have amplified and sequenced genomes from representative samples of two strongyliid lungworms: *Halocercus delphini, Otostrongylis circumlitis,* as well as *A. spirocauda* using long PCR. Recently, we have also sequenced and annotated three mtDNA from the unknown porpoise parasites using low-coverage massively parallel sequencing. These mitochondrial genomes have enabled better, but not definitive, identification of seal heartworm in the harbor porpoises, as the mtDNA gene arrangement is usually indicative of species (Moore, 1995). Additionally, we have sequenced the full genome of *A. spirocauda* and developed a simple quantitative PCR diagnostic assay that is extremely specific to seal heartworm and is able to distinguish between heart and lungworms. These data combined have allowed us to identify these porpoise parasites.

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DIFFERENTIAL *BAYLISASCARIS PROCYONIS* INFECTION DYNAMICS AND SURVIVAL IN FOUR SPECIES OF DEER MICE (*PEROMYSCUS* SSP.)

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Baylisascaris procyonis, the raccoon roundworm, is a zoonotic helminth that causes fatal larva migrans in many mammalian and avian species. White-footed mice (*Peromyscus leucopus*) are commonly found infected with *B. procyonis* in nature, as such likely serving an important role in the parasite's ecology. Although infection has been reported in other *Peromyscus* species, no data are available on differences in susceptibility. We compared survival and infection dynamics of *B. procyonis* in *P. leucopus, P. maniculatus, P. californicus,* and *P. polionotus,* which are native to varying habitat types and regions with variable prevalence of *B. procyonis* in raccoons. Groups of six captive-bred mice of each species were inoculated *per os* with one of three doses (~10, ~50, or ~500) of *B. procyonis* eggs. Animals were monitored twice daily for behavioral abnormalities, and were euthanized at the onset of severe neurologic symptoms or at 45 days post inoculation if clinically normal. Larvae were recovered from muscle and viscera separately by artificial digestion and enumerated and from the brain by microscopic examination. Humoral response to infection was assessed with a novel ELISA based on a recombinant *B. procyonis* antigen. The high dose was uniformly fatal for all species, while the medium dose group mortality ranged from 50-83% across species. Only one *P. maniculatus* was euthanized in the low-dose group. Survival analysis revealed that *P. leucopus* demonstrated greater survival compared to the other species. No statistically different survival rates were noted among the other species. Significantly more larvae were recovered from *P. leucopus* viscera and *P. maniculatus* brains. Serologic analysis also suggests differences

in seroconversion and antibody concentrations across species. In conclusion, we found differences in *B. procyonis* infection dynamics and survival across several closely related *Peromyscus* species. Further work is needed to understand the implications of this differential survival on the role of different *Peromyscus* spp. in the natural history of *B. procyonis*.

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PREVALENCE AND GENOTYPE OF *TOXOPLASMA GONDII* AND *GIARDIA DUODENALIS* IN DOGS FECES COLLECTED FROM NEW YORK CITY PARKS

J. Munoz and **G. Mayer**, Manhattan College

Toxoplasma gondii and *Giardia duodenalis* produce major diseases in both humans and domestic animals. The occurrence of human intestinal protozoan parasites in domestic dogs in the United States is not well-documented. The goal of this study was to determine the prevalence and genotypes of *T. gondii* and *G. duodenalis* among dogs in New York City. Fecal matter from 120 dogs (*Canis lupus familiaris*) from 3 New York City parks, West Central Park in Manhattan, Van Cortland Park in the Bronx and Prospect Park in Brooklyn, were collected from November 2013 to March 2014. The samples were analyzed by a polymerase chain reaction-based assay. Three-percent of the samples tested positive for *T. gondii*, while 15% were positive for *G. duodenalis*. PCR-RFLP of *T. gondii*-positive samples revealed genotypes I, and III, while sequence analysis of the *G. duodenalis*-positive samples indicated that 94.1% of the dogs were infected with the zoonotic assemblage A. Surprisingly, all the dogs tested negative for *Neospora caninum*. Further studies are needed to determine the prevalence of zoonotic protozoan parasites in domestic dogs and the potential for transmission to humans.

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EVIDENCE OF *CRYPTOSPORIDIUM* SPP IN THREE BIVALVE SPECIES COLLECTED FROM ORCHARD BEACH, NEW YORK

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Bivalve mollusks obtain nutrients by filtering the aquatic environment. Bivalves are typically bottom-dwellers or spend their lives attached to substrates. Mussels and oysters are a common part of our diet. Recently, bivalves have been shown to be infected with the human intestinal parasite of the genus *Cryptosporidium,* which causes cryptosporidiosis in humans and other vertebrates. Therefore, bivalves could be useful as bio-indicators for detecting *Cryptosporidium* in aquatic environments. The goal of this study is to determine the prevalence of *Cryptosporidium* from mollusks of New York City using a polymerase chain reaction (PCR)–based assay. Four bivalve species, namely *Mytilus edulis, Mya arenaria, Geukensia demissa* and *Crassostrea virginica* were collected at low tide from Orchard beach New York in September 2014. For this study, we have focused on *Mytilus edulis*, *Mya arenaria*, and *Geukensia demissa*. We found that the prevalence of *Cryptosporidium* in *Mytilus edulis* was 1% (1/97), and 16% (7/44) in *Geukensia demissa*. Surprisingly, 50% (4/8) of the collected specimens of *Mya arenaria* tested positive for *Cryptosporidium* DNA. Our data indicates that *Mya arenaria* would be the best bio-indicator for *Cryptosporidium*.

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PARASITE FAUNA OF *OCTOPUS MAYA* OF THE YUCATAN PENINSULA

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Octopus maya is an endemic octopus species found off the coast of the Yucatán Peninsula, México; it is one of the most important fisheries in the Gulf of México and the Caribbean Sea. In general, the parasite-fauna of cephalopods in México is little known. In this study we present, data on the parasite-fauna of *Octopus maya* from eight localities in the north of the Yucatán Peninsula. A total of 1,202 octopuses were cought and necropsied between August 2009 and June 2010 searching for parasites. Twenty taxa were recorded as parasites from all octopuses examined: seven were cestodes, eight digeneans, three nematodes, one copepod and one coccidian. All taxa are new records for this host species, as well as all locations represent new geographical distribution. The gills and the intestine were the micro-habitats where the highest numbers of taxa were found. More than half of the parasites (13 taxa) found in *O. maya* infect it via feeding habits, although a high number of taxa colonize via active transmission (nine). Cestoda and Digenea were the taxonomic groups with the largest number of taxa found in *O. maya*. *Prochistianella hispida* showed the highest prevalence and mean abundance values in the localities where it was presented. This work represents the first study on the parasite-fauna of any cephalopod species present in México.

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SEX RATIOS OF RARELY OCCURRING NEMATODES IN BOBWHITES AND SCALED QUAIL

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Hypotheses regarding nematode reproduction strategies predict that sex ratios at the component population level will be female biased when prevalence and mean intensity are low and approach 1:1 when prevalence and mean intensity increase. However, reproduction occurs at the infrapopulation level. To learn more about sex ratios at the component and infrapopulation level, we examined sex ratios of nematodes that rarely occurred (<30% prevalence) in 128 northern bobwhites (*Colinus virginianus*) collected in the Rolling Plains of Texas, 333 northern bobwhites collected in South Texas, and 170 scaled quail (*Callipepla squamata*) collected in West Texas. Three species were found from the Rolling Plains: *Tetrameres pattersoni* (24% prevalence, n = 118 individual worms), *Cheliospirura spinosa* (14%, n = 54), and *Gongylonema phasianella* (10%, n = 19); three species were found from South Texas: *Oxyspirura petrowi* (8%, n = 144), *T. pattersoni* (7%, n = 65), and *Dispharynx nasuta* (<1%, n = 25); two species were found from West Texas: *Procyrnea pileata* (27%, n = 87) and *Tetrameres* sp. (2%, n = 3). In this presentation, we report our results and discuss the impact of our findings on productivity and ultimately the persistence of these rarely occurring helminth species within quail host populations.

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CHARACTERIZATION OF HOST CELL AND PARASITE TRANSCRIPTOME IN *C. PARVUM* INFECTED MICE

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Cryptosporidium is an apicomplexan pathogen that causes the diarrheal illness cryptosporidiosis. Currently, no effective treatments are available for immunocompromised individuals and no vaccine exists. While gene expression of *C. parvum* in infected host cells has been shown, sequencing data

available to identify differential gene data in vivo is limited. Identification of host-parasite gene expression could provide insights to host-parasite interactions. We employed Next Generation RNAseq (Illumina HiSeq) to deep sequence the small intestine transcriptome and of the parasite of infected C57 black 6 mice (5 control; 5 infected at 24 hours and 5 infected at 48 hours) to identify novel transcripts, corresponding to different stages of infection. The RNA samples were processed for high-throughput sequencing according to standard Illumina protocols. Samples were barcoded and 4 samples were multiplexed in a single lane on an Illumina sequencing flow cell for paired end sequencing on an Illumina HiSeq 1000 machine. An alignment was performed with the *C. parvum* IowaII reference strain using the CryptoDB database and the STAR aligner tool. We found that 1.15 to 1.7% of the mappable sequences were of parasite origin. We were able to detect 98% of parasite genes (approximately 3600) at some level. Pathogen transcript depth ranged from 10-15 to >10,000 read counts. Host cell genes associated with metabolism, innate immunity and inflammatory responses were differentially expressed in infected mice. As expected genes involved in the expression of translation (ribosomal RNA,) and metabolic genes such as those used in glycolysis were highly expressed. Interestingly, a major surface protein was the third most highly expressed protein among all parasitic transcripts. Our findings should aid in providing a better understanding of the pathology and host immune response to *C. parvum* infections.

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INTESTINAL HELMINTHIASIS AMONG INMATES OF OWERRI PRISONS, IMO STATE

A.U. Allison, Imo State University, Owerri Imo State
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A study on intestinal helminthiasis among inmates of Owerri prison was undertaken with the approval of the prison authorities and informed consent of the inmates. Faecal samples were collected and examined using the wet film preparations and formol-ether concentration techniques. Of the 300 inmates examined, 240 (80.0%) were infected. Four parasites, namely *Ascaris lumbricoides* (32.0%), hookworm (23.3%), *Taenia solium* (16.7%), and *Strongyloides stercoralis* (8.0%) were detected. Mixed infections were also encountered, with the combination of *A. lumbricodes* and hookworm occurring highest (2.7%). In terms of gender, more female inmates (86.6%) were infected than male inmates (79.26%). The age group of 18-27 years recorded the highest rate of infection (31.3%). The study showed high endemicity of intestinal parasites, attributed in large part to poor sanitary conditions, poor personal and community hygiene, and a lack of education. To control the further spread of infections, providing proper sanitary conditions, educating the inmates on how to maintain personal hygiene, a reduction in the number of inmates per cell, and mass treatment of inmates is recommended.

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COMPARISON OF INFECTION PREVALENCE AND HISTOLOGICAL RESPONSE TO *SCHISTOSOMA MANSONI* IN STRAINS OF *BIOMPHALARIA GLABRATA* WITH DIFFERING VOLUMES OF HEMATOPOIETIC TISSUE

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The Salvador (BS-90) strain of *Biomphalaria glabrata*, which is resistant to infection with *Schistosoma mansoni*, has a significantly more hematopoietic tissue (HT) and higher numbers of circulating hemocytes than 2 schistosome-susceptible (M-line) strains, BRI-M (obtained from the Biomedical Research Institute, Bethesda, MD in February 2014) and USF-M (maintained at the University of San Francisco since 2000). The BRI-M strain, in turn, has significantly more HT than the USF-M strain, despite similar circulating hemocyte concentrations. The questions addressed in this study were: (1) is susceptibility to infection different in the 2 “susceptible” M-line strains, and (2) how does hemocytic reaction against sporocysts compare among the 2 susceptible M-line strains and the resistant Salvador

strain? Juvenile snails were individually exposed to miracidia of *S. mansoni*, and infection prevalences as well as tissue responses in all 3 strains were assessed. Among the 2 susceptible strains, infection prevalences were significantly higher in USF-M than in BRI-M snails, and although no tissue responses occurred in the former strain, many encapsulated sporocysts occurred in BRI-M snails by 9 DPE. In comparison, most Salvador snails remained uninfected following challenge with miracidia and histologically showed rapid destruction and almost complete elimination of sporocysts by 9 DPE. Thus, although no causal relationship can be inferred, a higher volume of HT in *B. glabrata* is associated with a lower prevalence of infection with *S. mansoni* and a stronger tissue response against sporocysts.

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THE ENDOGENOUS GROWTH FACTOR GRANULIN INDUCES RESISTANCE AGAINST *SCHISTOSOMA MANSONI* INFECTION IN THE GASTROPOD *BIOMPHALARIA GLABRATA*

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Schistosomiasis, a chronic, devastating disease caused by parasitic flatworms of the genus *Schistosoma*, affects over 260 million people worldwide especially in tropical and sub-tropical regions. Schistosomes must undergo their larval development within specific species of snail intermediate hosts, a trait that is shared among almost all digenean trematodes, presenting an opportunity for studying the intra-molluscan development of schistosomes and utilizing the snail as a possible target for schistosomiasis control efforts. While it is well supported that the snail immune cells (haemocytes) are important for protecting against schistosome infection, nothing is known about endogenous control of haemocyte development in any gastropod model. Here, we present the functional report of *B. glabrata* granulin (BgGRN), an endogenous snail growth factor. This granulin was identified as part of a peptide screen of snail haemocyte surface proteins that differed in abundance between the *S. mansoni*-resistant (BS-90) and susceptible (M-line) strains of *B. glabrata*. BgGRN transcript expression was found to be responsive in both BS-90 and M-line snails when challenged with *S. mansoni*, increasing 39 and 16 folds respectively relative to β-actin (non-immune control gene). Injection of recombinant BgGRN induced haemocyte proliferation in both snail strains, particularly of the adherent subset that participates in the anti-digenean response. Proliferation of adherent haemocytes in M-line snails prior to *S. mansoni* challenge resulted in significant increases in the abundance of this subset in the circulation and led to a reversal of the highly susceptible phenotype, yielding 54 % reduction in infections. This represents the first functional characterization of an endogenous growth factor of any gastropod mollusc, and is also the first gain-of-resistance study in a snail-digenean infection model using a defined factor to induce snail resistance to infection.

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PRESENCE OF HUMAN INTESTINAL PARASITES IN OYSTERS (*CRASSOSTREA VIRGINICA*): TEMPORAL TREND IN PREVALENCE AND GENOTYPE

S.M. Kowalyk and **G. Mayer**, Manhattan College

Bivalves, such as the Atlantic oyster, are excellent bio-indicators of marine environments. By filter feeding, these organisms often ingest various pollutants and parasites, providing an overall picture of the health of a marine habitat. *Toxoplasma gondii, Cryptosporidium parvum,* and *Giardia lamblia* are intestinal protozoan parasites that can lead to serious complications in immunocompromised individuals. Surprisingly, *T. gondii, C. parvum*, and *G. lamblia* have been found recently in many marine organisms. The goal of this study is to determine the prevalence of *T. gondii, C. parvum,* and *G. lamblia* in oysters. Oyster samples were collected from Orchard Beach in New York in the fall of 2014 and 2015 during low tide. Tissues were harvested from the oysters prior to DNA isolation. To determine whether the collected

samples were infected with *T. gondii*, *C. parvum,* and *G. lamblia,* a polymerase chain reaction (PCR) was performed using primers specific to those parasites. We found that none of the tested samples from 2014, 0/10, were positive for *T. gondii* or *C. parvum*. However, a 60% prevalence of *G. lamblia* was found in the samples. It was determined that the *G. lamblia*-positive samples were of the assemblage A genotype. In contrast, an 89% prevalence of *G. lamblia* DNA was found in the samples collected in 2015, indicating approximately a 50% increase in prevalence of *G. lamblia* from 2014 to 2015 in the oyster samples. Additionally, it was found that the *G. lamblia* samples were once again of the assemblage A genotype. We will be screening for *C. parvum* and *T.* gondii in the samples collected in 2015. The results indicate that Atlantic oysters are excellent bio-indicators of human intestinal parasites.

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DOSE-DEPENDENT MORTALITY OF PHYSA SNAILS TO THE HAIRWORM *PARAGORDIUS VARIUS*

F.T. Nguyen and **B. Hanelt**, University of New Mexico

The freshwater hairworm (Phylum Nematomorpha) life cycle involves 2 hosts. The paratenic host becomes infected with cysts in aquatic environments and includes snails; the definitive terrestrial insect host becomes infected by consuming the paratenic host containing cysts. Although the impact of hairworms on their definitive host has been studied, their impact on the paratenic host has not. Previous studies have shown that 40% of aquatic snails are naturally infected with cysts. Furthermore, it has been shown that snails can be superparasitized by other parasites in addition to hairworms. To examine the impact of hairworms on snails, we examined 1) the effect of the intensity of *Paragordius varius* (20, 50, 100, 500 cysts/snail) on the survival of laboratory-reared *Physa sp.* snails, and 2) the survival of field-collected *Physa acuta* infected and uninfected with an echinostome trematode. In the first experiment, we found that increasing cyst intensity correlated with increased snail mortality, with up to 45% mortality in snails infected with 500 cysts. In experiment 2, we found that mortality with 500 cysts increased to near 100% in snails without existing trematode infections and 80% with existing trematode infections. These data suggest that the presence of hairworms in aquatic environments may act as important drivers of selection. In addition, infection with trematodes appears to provide the snails with a protective effect.

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NEW DISTRIBUTION RECORDS AND REVIEW OF THE GENUS *HEPATOZOON* (APICOMPLEXA: ADELEORINA) INFECTING NORTH AMERICAN ANURANS

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

Of all the studies on anuran parasites, the apicomplexan protists have been largely ignored. Of those, the adeleorine coccidia are perhaps the most poorly studied group of parasites of anurans. Within the adeleorine, the genus *Hepatozoon* Miller, 1908 has been documented in the erythrocytes of frogs worldwide. Of the five North American *Hepatozoon* species infecting anurans, *H. catesbianae* (Stebbins, 1903) and *H. clamatae* (Stebbins, 1905), have been reported on multiple occasions infecting bullfrogs (*Rana catesbianae*) and green frogs (*Rana clamatans*) in Eastern North America. However, no accounts exist for these two species west of Illinois. The two species are morphologically similar, yet they can be distinguished by the effect of the gametocyte on the host erythrocyte nucleus. Infections with *H. clamatae* distort and fragment the anuran erythrocyte nucleus; whereas *H. catesbianae* infections do not. In a survey of blood protozoans of nine species of amphibians from Teal Ridge Wetland, Stillwater, Oklahoma, *Hepatozoon* gametocytes were found in (2/70) *Rana sphenocephala* and (2/28) *Rana catesbeiana* by examination of Giemsa stained blood smears with a compound light microscope. Ten *Hepatozoon* gametocytes infecting erythrocytes were measured from each infected individual and compared to previously reported morphometric data for all North American species of *Hepatozoon* infecting anurans.

Additionally, the 18s rRNA and ITS-1 genes were sequenced from two heavily infected individuals. Sequences obtained in this study were aligned with available sequence data for *Hepatozoon* spp. on GenBank and a phylogeny was created using a maximum likelihood framework. The *Hepatozoon* sp. found in this study was morphologically similar to both *H. catesbianae* and *H. clamatae*, however the host erythrocyte nucleus was not distorted or fragmented. Based on this characteristic and a close phylogenetic association to previously reported *H.* cf. *catesbianae* sequences, we report a new locality for *Hepatozoon* cf. *catesbianae* in Oklahoma, extending the known range for the species by at least 1800 km.

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OBSERVATIONS ON THE LIFE HISTORY OF *GORDIUS* CF. *ROBUSTUS* (NEMATOMORPHA: GORDIIDA) FROM OKLAHOMA. IS THIS THE FIRST DOCUMENTED SEMI-TERRESTRIAL HAIRWORM LIFE CYCLE?

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B. Hanelt, University of New Mexico
M.G. Bolek, Oklahoma State University

Freshwater gordiids have complex life cycles which include multiple hosts and a free-living aquatic phase. In North America one of the most commonly encountered gordiid species is *Gordius robustus*. However, a recent molecular study indicates that *Gordius* cf. *robustus* is comprised of at least 8 different species, and little is known about the general biology and life cycles of these species. To increase our knowledge on the biology of this newly discovered complex of gordiids, we investigated the seasonal occurrence, morphology, and life history of *Gordius* cf. *robustus* from Oklahoma. Adult hairworms were collected in puddles from lawns and road gutters in Stillwater, Payne County, Oklahoma. Habitats were surveyed throughout the year, but all free-living worms were found during rain events from November 2014-March 2016. Although hundreds of worms could be observed during rain events, no arthropod hosts were ever observed. In the laboratory, after mating, females laid eggs which contain a double membrane. Larval morphology was characteristic for the genus *Gordius*. Although egg strings were never observed in the field, surveys of earthworms and land snails indicated that they were commonly infected with *Gordius* type cysts suggesting that gordiid larvae also occur in a terrestrial environment. Additionally, scanning electron microscopy observations of *G.* cf. *robustus* from Oklahoma indicate that although the cuticle is variable among individual worms, this species is distinct in its morphology from other described North American species in the genus *Gordius*. From these observations, we hypothesize that this species may represent the first documented hairworm with a semi-terrestrial or terrestrial life cycle.

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NATURAL AND EXPERIMENTAL INFECTIONS OF *DAUBAYLIA* SP. IN *HELISOMA TRIVOLVIS* AND OTHER FRESHWATER SNAILS

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Nematodes in the genus *Daubaylia* are known to parasitize planorbid snails and can exhibit major effects on snail survival and reproduction. As a result, they have been implicated as biocontrol agents for disease-vector snails, specifically for *Biomphalaria glabrata*, which is a major vector of *Schistosome* spp. However, little is known about *Daubaylia* spp. in nature, their host specificity, and their effects on various snail hosts. In the field, we surveyed *Helisoma trivolvis* snails for *Daubaylia* sp. infections. In the laboratory, we exposed individual snails from four species of laboratory-reared snails (*B. glabrata, H. trivolvis, Physa acuta, and Stagnicola elodes*) to freshly-shed *Daubaylia* sp. nematodes from wild-caught *Helisoma trivolvis* snails. Additionally, in aquaria, we exposed the same snail species to *H. trivolvis* snails that were presently shedding *Daubaylia* sp. nematodes. Based on those results, we exposed individual

snails (laboratory-reared *B. glabrata* and *H. trivolvis*) to 0, 5, 10, 20, or 40 nematodes and recorded prevalences, infection intensities, and host snail survival. Our results indicate that *Daubaylia* sp. is specific to planorbid snails. Host survival decreased with increasing nematode exposure dose. Lastly, *Daubaylia* sp. tended to successfully reproduce in snails when snails were given lower nematode exposure doses whereas fewer worms were observed in snails given higher nematode exposure doses. This suggests there is either completion among worms or the host is negatively affected in such a way that higher infections reduce habitat quality for the nematodes.

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MOLECULAR AND MORPHOLOGICAL IDENTIFICATION OF LARVAL ECHINOSTOMES IN THE MUD SNAIL, *ILYANASSA OBSOLETA*, AND RIBBED MUSSEL, *GEUKENSIA DEMISSA*, IN A DELAWARE SALT MARSH

A.M. Barse, **M.A. Moran** and **R.S. Scheibner**, Salisbury University
H.H. Wirshing and **A.J. Phillips**, The Smithsonian Institution

Our aim is to elucidate the life cycle of an echinostome trematode in a Delaware salt marsh in southeastern Rehoboth Bay (38°37'43"N, 75°4'19"W) where the echinostome *Himasthla quissetensis* has been recorded in the mud snail, *Ilyanassa obsoleta*, at >50% prevalence. We hypothesized that the next host here is the ribbed mussel, *Geukensia demissa*, where we observed 100% prevalence of echinostome metacercariae. To confirm this, we collected rediae from snails and metacercariae from mussels, identified the parasites using morphological evidence, and tested these identifications using DNA barcoding. Morphologically the parasites match published descriptions of *H. quissetensis* (Echinostomatoidea: Himasthlidae) (in agreement with previous snail host-parasite studies). Additional echinostome larvae were collected and sequenced for a partial mitochondrial CO1 and a partial nuclear 28S rDNA locus. Analysis of the sequencing results indicate: (1) COI was amplified from the host and not the parasite, incidentally confirming our host species identifications; (2) 28S was amplified from the echinostome, and a phylogenetic analysis grouped most rediae and one metacercaria together in a clade, suggesting that these samples are the same trematode species utilizing the mud snail and the ribbed mussel as intermediate hosts; and (3) a BLAST search in GenBank revealed that the 28S sequences are most similar to sequences of species in Philophthalmidae, not Himasthlidae. The result that the echinostome larvae are not *Himasthla* is surprising and casts doubt on species identifications made by previous researchers. The most recent work on phylogenies of these trematodes purports that there are 11 philophthalmid genera, but only three of these are represented by sequences published in GenBank. Further study of morphology will be necessary to resolve the lack of agreement between our morphological and molecular identifications. Future efforts will focus on collecting echinostome adults from the definitive hosts (gulls), and fully elucidating the life cycle of this enigmatic echinostome.

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PREVALENCE OF *TRYPANOSOMA CRUZI* IN WILD MAMMALS FROM THE SOUTH COAST OF JALISCO, MEXICO

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The southern coast of Jalisco has high ecosystem diversity and consequentially high species richness. Of the 18 vector species of *Trypanosoma cruzi* reported in Mexico, 8 are found in Jalisco with an overall infection prevalence of ~53%. Unfortunately, little is known regarding the enzootic circulation of *T. cruzi* in wild mammal communities. Humans are at a high risk of *T. cruzi* infection due to their close contact

with wild mammals and the construction of houses that increases contact between vectors, reservoirs and humans. Our objective is to determine the prevalence of infection in different groups of mammals that are important in terms of the number of species and high populations in Jalisco: rodents and bats (n=136 and n=125 individuals respectively). These animals live in close proximity to humans, often sharing their houses. The use of molecular techniques including PCR and sequencing allows us to determine more accurately the prevalence of infection, identify important reservoirs and vectors involved in the transmission cycle, the phylogeny of T. cruzi strains, and the implications for human infections. The human communities that live near the coast of Jalisco are among the poorest in the State and are reported to have high prevalences of infection, and available data are likely underestimates. Identifying the major mammalian reservoirs, the principal vector species, and the regions with highest risk of infection are essential to develop long term control strategies to reduce transmission in domestic, peri-domestic and wild environments.

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PREVALENCE OF SARCOCYSTIS OOCYSTS AND SPOROCYSTS IN THE INTESTINES OF RAPTORS FROM NORTH AND SOUTH CAROLINA

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Little is known about the diversity of *Sarcocystis spp* infecting raptors. Birds of prey can be definitive hosts and pass oocysts of some species while they can also serve as intermediate hosts and have sarcocysts in their muscles. The intestinal tracts from 19 raptors (3 red-tailed hawks (RTH), 4 red-shouldered hawks (RSH), 2 Cooper's hawks (CH), 2 Eastern screech owls (ESO), 6 barred owls (BO), 1 great horned owl (GO), and 1 turkey vulture (TV) were collected from terminally ill or patients that were euthanized because of they could not be rehabilitated and released at the Carolina Raptor Center. The intestines were collected at necropsy, placed in plastic bags, and refrigerated at 4 °C until they were examined microscopically for parasites. Multiple mucosal smears were made from 3 to 6 sections of intestinal tract and examined as fresh preparations for parasites. Fluke eggs were seen in 5 raptors (RTH, 2 RSH, CH & ESO) while adult flukes were seen in 2 BO. Capillarid eggs were seen in 4 raptors (RSH, RTH and 2 BO) and spirurid eggs were seen in a RSH. Twelve (63%) of the 19 samples (2 RTH, 2 RSH, 2 CH, 4 BO, 1 TV, and 1 ESO) contained oocysts/sporocysts of *Sarcocystis* species. Intestines from the 9 of the 12 *Sarcocystis* infected raptors were processed using commercial bleach and the sporocysts stored at 4 °C for use in in vitro studies. The ESO and 2 of the BO had very few sporocysts and their samples were not collected. Infectivity of sporozoites obtained from excysted sporocysts is currently being examined using African Green monkey kidney cell cultures. So far, we have been successful in growing and maintaining *Sarcocystis* from a CH and RSH in cell culture. We observed limited growth of *Sarcocystis* from a RTH but could not maintain the parasite in vitro. We are currently collecting merozoites of the 2 isolates to obtain DNA to characterize by phylogenetic analysis. Supported by grant # 1505407 from the NSF to ACR and by an IRC grant from Virginia Tech to DSL.

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EXAMINATION OF A NEW SPECIES OF RHINEBOTHRIIDEAN CESTODE FROM *DASYATIS MARGARITELLA* (PEARL STINGRAY)

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This study of a new species of rhinebothriidean cestode is part of a world-wide survey of parasites, including cestodes, from elasmobranchs. 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 the

spiral intestines of several specimens of *Dasyatis margaritella* in Senegal. Unique characteristics for this species were identified using methods such as light microscopy, line drawings, and scanning electron microscopy (SEM). Through analysis using these methods it was observed that the septa and loculi pattern set the species apart. The new species possesses a single loculus followed by a row of four loculi in the anterior region, unlike any of its congeners. Distribution of microtriches also sets the species apart from its congeners. Spinitriches on the distal bothrideal surface are unevenly distributed within the anterior loculi. While filitriches are found on the entirety of the proximal bothridial surface, spinitriches are restricted to a narrow band on the posterior half. The unique arrangements of septa enable distinction of this new species from one other species known from the Eastern Atlantic. 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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TRUNK SPINES IN CYSTACANTHS AND ADULTS OF *CORYNOSOMA* SPP. (ACANTHOCEPHALA): *CORYNOSOMA CETACEUM* AS AN EXCEPTIONAL CASE OF PHENOTYPIC VARIABILITY

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Adults of the acanthocephalan *Corynosoma cetaceum* attach to the stomach of dolphins using its spiny foretrunk as a disk while the spiny hindtrunk bends to adhere its ventral spines. During attachment two ventral folds of tegument, anterior and posterior, are created, in which spine growth is inhibited to a variable degree, generating an extraordinary phenotypic variability. Inhibition apparently improves attachment performance. However, little is known on how this variability is generated and why it is not found apparently in other *Corynosoma* spp. In this paper we examined the trunk armature of 77 and 388 cystacanth larvae of *C. cetaceum* and *C. australe*, respectively, from fish and over 8,800 adult specimens of *C. australe*, *C. bullosum*, *C. cetaceum*, *C. strumosum*, *C. villosum* and *C. wegeneri* from marine mammals. Cystacanths and adults of *C. cetaceum* exhibited the same range of fold spine variability, suggesting that such variability is generated prior to the adult stage (i.e., before spines are functional) and does not primarily result from phenotypic plasticity. All the *Corynosoma* species created at least the anterior fold as a side-effect of attachment, but it was always spined except in *C. cetaceum*. Females of this species had significantly larger foretrunk and hindtrunk spines than the other species. The exceptional colonization of a harsh microhabitat, the stomach, could have generated a trade-off in *C. cetaceum*, which must bend the trunk to attach (as other *Corynosoma* spp.) but must also produce large spines that, in the folds, presumably are maladaptive and must be reduced.

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THE ALBERTA "RAT KING": AN EXAMPLE OF THE IMPORTANCE OF MOLECULAR METHODS TO INFORM SPECIES IDENTIFICATIONS AMONG LARVAL TREMATODES

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The infamous zygocercous cercariae can be found in nearly every parasitology textbook, depicting the unique aggregating behaviour of these larval digeneans. Commonly referred to as “rat-king” or “Rattenkönig”, these digenean trematode cercariae emerge from their snail intermediate host and begin to attach to each other by the tails, forming an aggregate of many individuals. This behavior is similar to a phenomenon observed in rats, where the tails of multiple rats become intertwined and from which the name “rat king” was derived. Historically, there have been only 11 reports of aggregating cercariae in the literature, of which only 9 can be characterized as zygocercous. This behavior is observed in species of marine and freshwater digenean that have been classified into five different superfamilies based on morphological observations. Only a few of these reports have provided detailed morphological characterizations. No life cycles have yet been described, despite attempts; and until now, no molecular information has been used to classify a zygocercous species. Much of this is not surprising, considering that these aggregating cercariae seem to be quite rare. By chance, in 2015, among collections as a part of a larger survey, zygocercous cercariae were found to emerge from two small Physid snails collected at Buffalo Lake in Alberta. From a combination of morphological and molecular tools, these zygocercous cercariae have, for the first time, been identified beyond the level of superfamily, as a member of the genera *Australapatemon* within the family Strigeidae. The importance of this level of information is that it can guide further investigations into the life cycle of this species. The question that remains, however, is whether or not the aggregating behavior is indicative of a separate species or if it is a trait that appears under unique conditions. Morphological assessments would suggest independent evolution among several superfamilies, but until molecular data can be acquired for more specimens, it is difficult to test this hypothesis.

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* 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
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§§ With Sociedád Méxicana de Parasitología
¶¶ With Parasitology Section, Canadian Society of Zoologists
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