The 83rd Annual Meeting of the American Society of Parasitologists

Rangers Ballpark in Arlington

Six Flags Over Texas

Arlington Trolley

Hilton Arlington
Arlington, Texas
June 27 – 30, 2008

Program & Abstracts

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The American Society of Parasitologists gratefully acknowledges the following for their support and sponsorship of this year's annual meeting.

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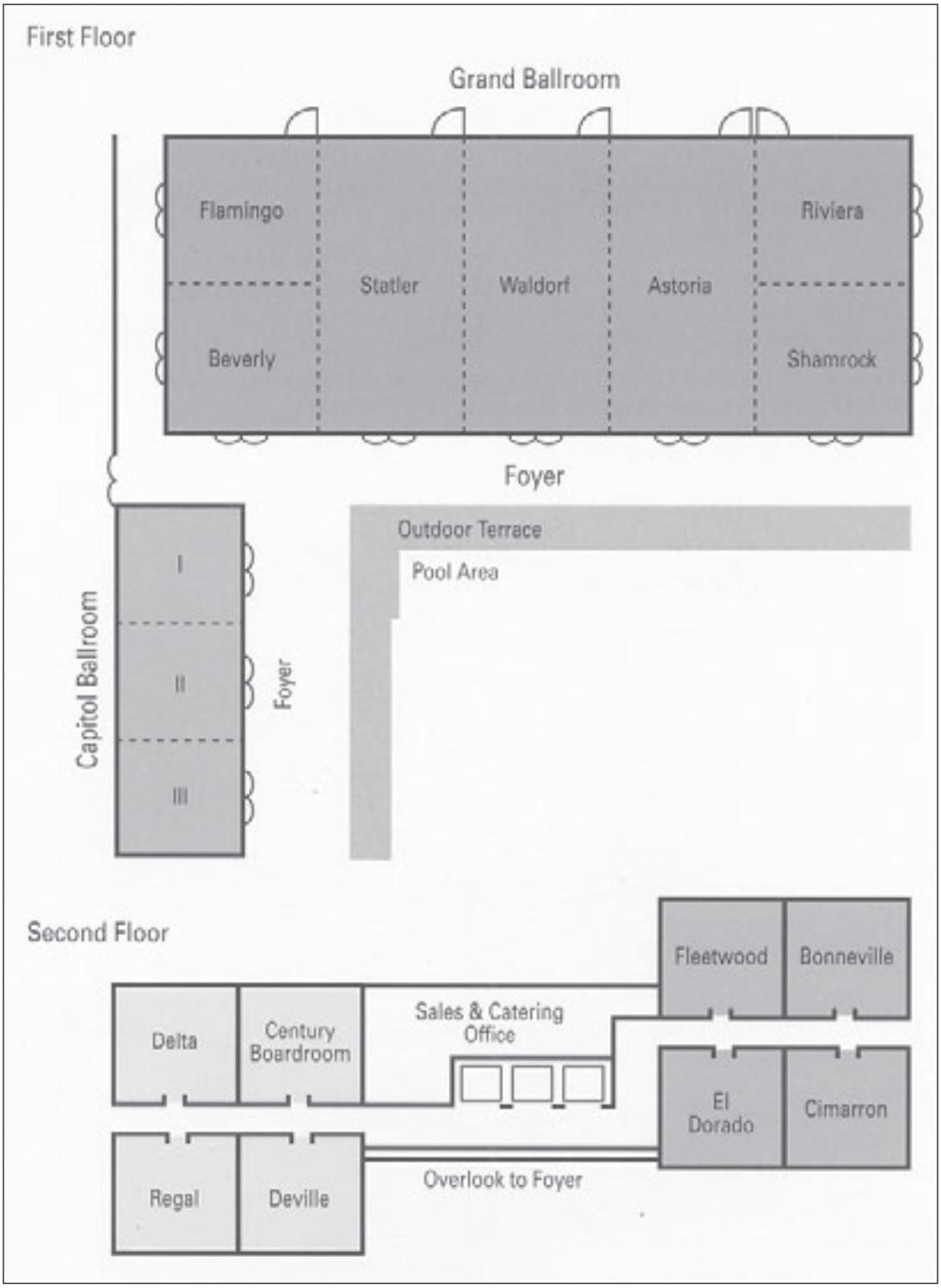
Meeting Rooms

27-30 June, 2008

Day/Times	Activity/Function	Room/Space	Page No.
June 27 (Fri.)			
8:00 a.m.–Noon	ASP Council	**Astoria**	8
1:00–5:00 p.m.	Student Paper Competition-I	**Statler**	8
1:00–3:00 p.m.	Symposium: Population Genetics	**Waldorf**	9
3:00–3:15 p.m.	Coffee Break	**Foyer, Capitol Ballroom**	9
3:15–5:00 p.m.	Life Cycles, Epidemiology	**Waldorf**	10
7:00–10:00 p.m.	Gala Opening Reception	**Pool Area**	10
June 28 (Sat.)			
8:30–10:30 a.m.	ASP President's Symposium	**Statler + Waldorf**	11
10:30–11:00 a.m.	Coffee Break	**Foyer, Capitol Ballroom**	11
11:00 a.m.–Noon	Stoll-Stunkard Lecture	**Statler + Waldorf**	11
1:00–3:30 p.m.	Symposium: Evolutionary Ecology	**Statler**	12
1:00–3:00 p.m.	Student Paper Competition-II	**Waldorf**	12
3:00–5:00 p.m.	ASP Students' Symposium	**Astoria**	13
3:00–6:00 p.m.	Auction Set Up	**Capitol Ballroom (I+II+III)**	13
6:00–7:00 p.m.	Auction preview	**Capitol Ballroom (I+II+III)**	13
7:00–9:00 p.m.	19th Annual ASP Student Auction	**Capitol Ballroom (I+II+III)**	13
June 29 (Sun.)			
8:00–10:00 a.m.	Symposium: Associate Editors	**Statler**	14
9:00–11:30 a.m.	Genetics, Molecular Biology	**Waldorf**	14
10:00–10:15 a.m.	Coffee Break	**Foyer, Capitol Ballroom**	14
8:00–11:45 a.m.	Student Paper Competition-III	**Astoria**	15
10:15 a.m.–12:15 p.m.	40th Coccidiosis Conference	**Shamrock**	16
1:00–2:00 p.m.	ASP President's Address	**Statler + Waldorf**	17
2:00–4:30 p.m.	Taxonomy, Systematics, Phylogeny	**Astoria**	17
2:00–4:30 p.m.	Ecology-I	**Shamrock**	18
3:00–3:30 p.m.	Coffee Break	**Foyer, Capitol Ballroom**	18
3:30–5:00 p.m.	Host-Parasite Interactions	**Statler**	19
3:00–5:00 p.m.	Poster boards delivered, Authors may setup posters	**Capitol Ballroom (I+II+III)**	19
June 30 (Mon.)			
8:00–10:30 a.m.	Symposium: Paleoparasitology	**Statler**	20
8:30–10:30 a.m.	Late Breakers	**Astoria**	20
8:30–10:30 a.m.	Ecology-II	**Waldorf**	20
8:00–10:30 a.m.	Authors complete poster setup	**Capitol Ballroom (I+II+III)**	20
10:30–Noon	Poster Session, coffee, snacks	**Capitol Ballroom (I+II+III)**	21
1:00–1:50 p.m.	H.B. Ward Lecture	**Statler + Waldorf**	24
1:50–2:35 p.m.	Bueding Von Brand Lecture	**Statler + Waldorf**	24
2:35–3:00 p.m.	Coffee Break	**Foyer, Capitol Ballroom**	24
3:00–4:30 p.m.	ASP Awards and Business Meeting	**Statler + Waldorf**	24
24 hours daily	Storage	**Cimarron (2nd floor)**	NA
24 hours daily	Speaker Ready-Room	**Bonneville (2nd floor)**	NA

Floor Plan
Hilton Arlington
Arlington, Texas



For Your Information

Registration: Main Lobby

Friday, June 27, Noon–5:00 p.m.
Saturday, June 28, 8:00 a.m.–5:00 p.m.
Sunday, June 29, 8:00 a.m.–5:00 p.m.

Speaker Ready Room: Bonneville (2nd floor)

Friday, Saturday, Sunday, Monday, 8:00 a.m.–5:00 p.m.

Coffee Breaks: Foyer in front of the Capitol Ballrooms

Friday, June 27, 3:00–3:15 p.m.
Saturday, June 28, 10:30–11:00 a.m.
Sunday, June 29, 10:00–10:15 a.m., 3:00–3:30 p.m.
Monday, June 30, 2:35–3:00 p.m.

Journal of Parasitology Editorial Board Breakfast, Regal (2nd Floor)

Saturday, June 28, 7:00–8:30 a.m.

Poster Session: Capitol Ballroom (I+II+III)

Sunday, June 29

3:00 p.m., Poster boards delivered
4:00–5:00 p.m., Authors can begin to set up their posters

Monday, June 30

8:00–10:30 a.m., All authors please complete setup of your posters
10:30–Noon, All authors please stand by your poster

Opening Welcome Reception: Hotel Pool Area

Friday, June 27, 7:00–10:00 p.m.

Legends of the Game Museum Reception: Texas Rangers Ballpark

Sunday, June 29

5:05 p.m., Texas Rangers *vs.* Philadelphia Phillies
5:15 p.m., Buses leave Hilton parking lot for the Museum
5:30 p.m., Reception (and food) in the Legends of the Game Museum, including tickets and programs to the Rangers/Phillies game and easy access from the Museum into the game.
8:45 p.m., Buses leave Museum/Stadium parking lot for return to Hilton

Late Breakers: Astoria

Monday, June 30, 8:30–10:30 a.m.

This session is specifically designed for brief presentations of important, new data obtained long after the deadline for abstract submission. It should not be abused as a way to give your paper because you "forgot" to meet the abstract deadline. Presentations are restricted to *five* (5) minutes with 5 minutes for discussion. Submit abstracts of 200 words or less prior to the meeting, or at the meeting (check at the Registration Desk in the Hilton), but no later than noon on Sunday, June 29. Bring 20 copies of your abstract for distribution at the Late Breakers session. The list of titles and presenters will be posted on Monday morning outside the Astoria.

Title, abstract, and presenter for "Late Breakers" should be submitted to: Dr. Rich Clopton, P.O. Box 10, Peru State College, Peru NE 68421; 402-872-2284 (Phone), 402-872-2412 (Fax); rclopton@oakmail.peru.edu

A Reminder

Students Sharing Discounted "Quad" Rooms

If you are an ASP student registrant and want to share a discounted room with other ASP student members, but aren't sure how to do this, contact your elected ASP Student Representative, Caroline Fyler at caroline.fyler@uconn.edu

Carrie will help you get organized. Once 3-4 students agree to share a room, one of you must communicate directly with the Hilton and be the responsible person to secure the room with a credit card and pay the bill at checkout (students sharing quads will need to work out their portions of the room cost with each other). Carrie has been in contact with last year's Student Representative, Liz Thiele, who has helped her set up this year's ASP students' message board, so you will be able to communicate with each other and pair up to share rooms. (http://web.isc.purdue.edu/~eathiele/phpBB2)

Transportation Information

Airport

Direct flights on most commercial airlines from anywhere in the world can easily be made to the Dallas/ Fort Worth (DFW) International Airport. Southwest Airline flights also are available, but these arrive at Love Field in Dallas, a 30-minute drive from the Hilton Arlington.

Free Shuttle

The Hilton has a free shuttle bus from DFW (but not from Love Field) to the hotel. When you arrive at DFW, call the main switchboard at the Hilton (817-640-3322). Tell them the gate and terminal of your location and they will send the driver out. You will need to retrieve your luggage at your assigned baggage claim and proceed to the Lower Level. The shuttle is only allowed to pick up passengers on the lowest level.

Super Shuttle

The current rate from Love Field is $26.00 per person for one-way. Download a $2.00-off coupon from the ASP website.

Rental Vehicles: Enterprise Rent-A-Car

ASP has arranged a discount (cars, vans, etc.) for the conference with Enterprise (www.enterprise.com). *Corporate Discount Code:* 09C6599 *Pass Code:* ASP

Vehicles can be rented from DFW or Love Field Airports, or you can save an extra 20% in taxes by having Enterprise deliver your vehicle to you at the Hilton-Arlington. For hotel delivery, group rates, vehicle options, or questions, please contact Trevor Armstrong with Enterprise at 817-244-3526 or trevor.armstrong@erac.com.

Program Schedule for 2008 ASP

† denotes an ASP Student Competition Paper

FRIDAY MORNING, JUNE 27

8:00–Noon ASP COUNCIL MEETING, Astoria

Presiding: S. Nadler, University of California, Davis CA

FRIDAY AFTERNOON, JUNE 27

1:00–5:00 STUDENT PAPER COMPETITION – I, Statler

Presiding: G. Stewart, University of West Florida, Pensacola FL
R.S. Seville, University of Wyoming, Laramie WY

Time	Paper No.	
1:00	1†	*SCHISTOSOMA MANSONI* ISOLATED MUSCLE FIBERS INWARD CURRENTS ARE SENSITIVE TO CLASSICAL VOLTAGE-OPERATED CA^{2+} CHANNEL BLOCKERS AND ARE ENHANCED BY FLATWORM FMRF AMIDE-LIKE PEPTIDES. **E.B. Novozhilova***, **A.P. Robertson**, **H. Qian**, **M.J. Kimber**, **P. McVeigh**, **A.G. Maule,** and **T.A. Day**.
1:15	2†	*ANCYLOSTOMA CANINUM* DAF-16 BINDS TO A CONSERVED DAF-16 FAMILY MEMBER-BINDING ELEMENT. **X. Gao*** and **J. Hawdon**.
1:30	3†	EXTRACTS OF THE BITTER MELON, *MOMORDICA CHARANTIA*, INHIBIT ACTIVATION OF HOOKWORM LARVAE. **K. Batich*** and **J.M. Hawdon**.
1:45	4†	EFFECT OF POST-CYCLIC TRANSMISSION ON MICROHABITAT USE OF *PAULISENTIS MISSOURIENSIS* (ACANTHOCEPHALA) IN CREEK CHUB. **H.A. Robinson*** and **M.A. Barger**.
2:00	5†	CORE-PERIPHERY STRUCTURE IN FOOD WEBS DRIVES PARASITE COMMUNITY ASSEMBLY IN NAÏVE FISH HOSTS. **T.K. Anderson*** and **M.V. Sukhdeo**.
2:15	6†	SEASONAL OCCURRENCE AND POPULATION STRUCTURE OF *DACTYLOGYRUS* SPP. (PLATYHELMINTHES; MONOGENEA) ON NEBRASKA MINNOWS. **A.K. Knipes*** and **J. Janovy Jr.**.
2:30	7†	TEAL (1957) AND ODUM (1957) REVISITED: WHAT IS THE EFFECT OF PARASITISM ON ECOSYSTEM ENERGY FLOW?. **S.E. Lettini*** and **M.V. Sukhdeo**.
2:45	8†	EFFICACY OF FENBENDAZOLE, FORMULATED IN A COMMERCIAL PRIMATE DIET, FOR TREATING SPECIFIC PATHOGEN FREE BABOONS (*PAPIO CYNOCEPHALUS ANUBIS*) NATURALLY INFECTED WITH *TRICHURIS TRICHIURA*. **L.C. Clingenpeel***, **R.F. Wolf**, **S.K. Doan**, **A.N. Jones**, **K.M. Gray,** and **M.V. Reichard**.

00–3:15 **COFFEE BREAK, Capitol Ballroom – Outer Foyer**

15 9† PRE-APPROVED DRUGS AS A SOURCE FOR NOVEL SCHISTOSOMICIDES. **D.S. Ruelas***, **M. Abdulla**, **K. Lim**, **B. Wolff**, **J. Williams**, **A.R. Renslo**, **J.H. McKerrow,** and **C.R. Caffrey**.

30 10† PREVALENCE OF ECTOPARASITES IN FOREST BIRDS ON THE ISLAND OF OAHU. **S.A. Bader***, **K.L. Krend,** and **L.H. Freed**.

3:45 11† PCR ASSAY FOR DETECTION OF *BAYLISASCARIS PROCYONIS* EGGS AND LARVAE. **S. Dangoudoubiyam***, **R. Vemulapalli,** and **K.R. Kazacos**.

4:00 12† CASTRATOR OR CRADLE ROBBER? THE EFFECTS OF A PARASITIC COPEPOD ON ITS NUDIBRANCH HOST. **M. Wolf*** and **C.M. Young**.

4:15 13† THE CHOSEN FROZEN: COLD-TOLERANCE AND SURVIVAL OF *PARAGORDIUS VARIUS* (NEMATOMORPHA: GORDIIDA) LARVAE. **W.E. Doerfert*** and **B. Hanelt**.

4:30 14† AN INTEGRATED CONTROL STRATEGY AGAINST COCCIDIOSIS IN BROILER CHICKENS MAY BENEFIT FROM THE USE OF PROBIOTICS. **J.L. McPherson-Komorowski*** and **J.R. Barta**.

4:45 15† A BIOGEOGRAPHICAL STUDY OF GREGARINES (APICOMPLEXA: EUGREGARINIDA) PARASITIZING *ARGIA* SPP. (ODONATA: ZYGOPTERA). **J.J. Hayes***, **T.J. Cook,** and **R.E. Clopton**.

1:00–3:00 SYMPOSIUM ON POPULATION GENETICS, Waldorf

Presiding: C.D. Criscione, Texas A&M University, College Station TX
N.K. Whiteman, Harvard University, Cambridge MA

Theme: *Population genetics of parasites: From geography to genes.*

Time	Paper No.	
1:00		Welcome and Introduction. **C.D. Criscione**
1:10	16	THE GEOGRAPHY OF HOST-PARASITE COEVOLUTION. **N.K. Whiteman*** (nwhiteman@oeb.harvard.edu), **A.J. Drummond,** and **P.G. Parker**.
1:35	17	MOLECULAR EPIDEMIOLOGY AND LANDSCAPE GENETICS AS TOOLS TO EXAMINE FOCI OF PARASITE TRANSMISSION WITHIN HOST POPULATIONS. **C.D. Criscione*** (ccriscione@mail.bio.tamu.edu), **D. Sudimack**, **J.D. Anderson**, **J. Subedi**, **D.R. Rai**, **R.P. Upadhayay**, **J. Bharat**, **S. Williams-Blangero,** and **T.J.C. Anderson**.
2:00	18	INFERRING TRANSMISSION PATTERNS AND MATING DYNAMICS OF *SCHISTOSOMA MANSONI* USING MOLECULAR MARKERS. **M.L. Steinauer*** (mls1@unm.edu), **B. Hanelt**, **E.L. Agola**, **I.N. Mwangi**, **G.M. Maina**, **D.M. Karanja**, **G.M. Mkoji,** and **E.S. Loker**.
2:25	19	POPULATION GENETICS OF SELECTED LOCI: DRUG RESISTANCE IN MALARIA. **T. Anderson** (tanderso@sfbrgenetics.org).
2:50		Summary and Conclusions. **N.K. Whiteman**

3:00–3:15 **COFFEE BREAK, Capitol Ballroom – Outer Foyer**

3:15–5:00 LIFE CYCLES, EPIDEMIOLOGY, Waldorf

Presiding: S.S. Hendrix, Gettysburg College, Gettysburg PA
J.W. Camp, Purdue University, West Lafayette IN

Time	Paper No.	
3:15	20	*HISTOMONAS MELEAGRIDIS* (TRICHOMONADIDAE; PARABASALA): DIRECT TRANSMISSION IN THE TURKEY HOST WITHOUT THE AID OF VECTORS. **L.R. McDougald***, **A.L. Fuller**, **P.L. Armstrong,** and **J. Hu**.
3:30	21	MOLECULAR INSIGHT INTO HOST SPECIFICITY, LIFE CYCLES AND GEOGRAPHICAL DISTRIBUTION OF THE RHABDIASIDAE (NEMATODA). **V.V. Tkach***, **Y. Kuzmin,** and **S.D. Snyder**.
3:45	22	PREVALENCE OF INTESTINAL PARASITES IN RED SOKOTO (GUDALI) GOATS SLAUGHTERED IN THE GWAGWALADA AREA COUNCIL ABATTOIR, GWAGWALADA, ABUJA, NIGERIA. **H.S. Idris*** and **H. Umar**.
4:00	23	EXPANSION OF *LEYOGONIMUS POLYOON* (CLASS: TREMATODA) INTO THE MISSISSIPPI RIVER. **R.A. Cole***, **J. Sauer**, **J. Nissen,** and **M. Sterner III**.
4:15	24	AN UNUSUALLY SEVERE INFECTION OF *COLLYRICLUM FABA* IN AN AMERICAN CROW, *CORVUS BRACHYRHYNCHOS*. **M.C. Sterner III**.
4:30	25	THE ROLE OF DAMSELFLIES (ODONATA) IN THE TRANSMISSION OF *HALIPEGUS ECCENTRICUS* TO ANURANS. **M.G. Bolek**.
4:45	26	INFECTION OF *BABESIA GIBSONI* IN CONFISCATED PIT BULL TERRIERS. **M.V. Reichard***, **T.J. Yeagley**, **J.E. Hempstead**, **K.E. Allen**, **L.M. Parsons**, **S.E. Little**, **M.A. White,** and **J.H. Meinkoth**.

FRIDAY EVENING, JUNE 27

7:00–10:00 WELCOME RECEPTION, Pool Area

NOTES...

SATURDAY MORNING, JUNE 28

8:30–10:30 ASP PRESIDENT'S SYMPOSIUM, Statler + Waldorf

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

Theme: *Lessons from the tree of life: Illuminating macro-parasite biology through molecular phylogenetic frameworks.*

Time	Paper No.	
8:30		Introduction. **G.D. Cain**
8:40	27	PLANT PARASITISM – EVOLUTION OF NEW UTENSILS FOR EATING VEGAN. **J.G. Baldwin*** (james.baldwin@ucr.edu), **E. Ragsdale,** and **D. Bumbarger**.
9:15	28	PHYLOGENY OF ACANTHOCEPHALANS: INFERRING THE EVOLUTION OF PARASITISM USING NUCLEAR AND MITOCHONDRIAL GENE SEQUENCES. **M. García-Varela**. (garciav@servidor.unam.mx).
9:50	29	THE GENETIC UNDERPINNING OF HIDDEN SYNAPOMORPHIES: EVOLUTION AND DEVELOPMENT IN CESTODES. **P.D. Olson** (P.Olson@nhm.ac.uk).
10:25		Closing comments and questions. **G.D. Cain**

.

10:30–11:00 COFFEE BREAK, Capitol Ballroom – Outer Foyer

11:00–Noon STOLL-STUNKARD LECTURE, Statler + Waldorf

Presiding: D.W. Halton, Queen's University Belfast, UK

Time	Paper No.	
11:00		Introduction of Dr. D.M. MCKAY University of Calgary, Calgary, Alberta, Canada
11:10	30	HEALTH LESSONS FROM ANALYSES OF HELMINTH-RODENT MODEL SYSTEMS. **D. McKay**.

SATURDAY AFTERNOON, JUNE 28

1:00–3:30 SYMPOSIUM ON EVOLUTIONARY ECOLOGY, Statler

Presiding: S.E. Bush, University of Kansas, Lawrence KS
D.H. Clayton, University of Utah, Salt Lake City, UT

Theme: *Evolutionary ecology of host-ectoparasite interactions.*

Time	Paper No.	
1:00		Introduction. **S.E. Bush** and **D.H. Clayton**.
1:10	31	THE EVOLUTION OF INDISCRIMINATION IN ECTOPARASITIC MITES. **M.R. Forbes** (mforbes@connect.carleton.ca).
1:35	32	REGULATION MECHANISMS OF FLEA NUMBERS ON THEIR RODENT HOSTS: ARE FLEAS CONSUMERS OR PREY? **H. Hawlena** (hadashaw@gmail.com).
2:00	33	IMMUNOGENETICS AND IMMUNE DEFENSE AGAINST AN AVIAN ECTOPARASITE. **J.P. Owen** (jowen@wsu.edu).
2:25	34	PARASITE-MEDIATED SEXUAL SELECTION IN THE *DROSOPHILA-MACROCHELES* SYSTEM. **M. Polak** (polak@email.uc.edu).
2:50	35	HOST DEFENSE REINFORCES HOST-PARASITE COSPECIATION. **S.E. Bush*** (sbush@ku.edu) and **D.H. Clayton**.
3:15		Closing comments and questions. **D.H. Clayton** and **S.E. Bush**

1:00–3:00 STUDENT PAPER COMPETITION – II, Waldorf

Presiding: O. Amin, Institute of Parasitic Diseases (IPD), Tempe AZ
A.S. Didyk, University of New Brunswick, Moncton NB, Canada

Time	Paper No.	
1:00	36†	PARASITE INFRACOMMUNITIES WITHIN BLUEGILL (*LEPOMIS MACROCHIRUS*) IN THE RARITAN RIVER, NJ. **C. McCoy*** and **M.V. Sukhdeo**.
1:15	37†	MOLECULAR CLONING AND CHARACTERIZATION OF FOUR NOVEL SCHISTOSOME *a* FUCOSYLTRANSFERASES. **N.A. Peterson***, **D.M. Reinitz,** and **T.P. Yoshino**.
1:30	38†	ASSESSING THE UTILITY OF DEFINED PROBIOTICS DURING LIVE VACCINATION AGAINST COCCIDIOSIS IN BROILER CHICKENS. **J.L. McPherson-Komorowski*** and **J.R. Barta**.
1:45	39†	ORAL TRANSMISSION OF *TRYPANOSOMA CRUZI* WITH OPPOSING EVIDENCE FOR THE THEORY OF CARNIVORY IN THE SYLVATIC CYCLE. **D.M. Roellig***, **A.E. Ellis,** and **M.J. Yabsley**.

2:00 40† FATAL INFECTIONS OF A PROTISTAN AGENT IN SOUTHEASTERN RANID FROG SPECIES. **J.O. Cook*** and **R.M. Overstreet**.

2:15 41† HIRUDINIDAE[3]: TOWARDS A REVISION OF THE WORLD'S MEDICINAL LEECHES. **A.J. Phillips*** and **M. Siddall**.

2:30 42† EVOLUTION OF FEEDING PREFERENCES AND ECOLOGICAL ASSOCIATIONS OF LEECH SPECIES OF *PLACOBDELLA, HAEMENTERIA* AND *HELOBDELLA*. **A.F. Oceguera-Figueroa*** and **M.E. Siddall**.

2:45 43† AMPHIBIAN LUNGWORMS AND PESTICIDES: A BALANCED VIEW OF HOST-PARASITE RELATIONSHIPS AND ECOTOXICOLOGY. **G.J. Langford*** and **J. Janovy Jr.**.

3:00–5:00 ASP STUDENT'S SYMPOSIUM, Astoria

Presiding: **C.A. Fyler**, University of Connecticut, Storrs CT

Theme: *Parasitology: Public awareness through literature, art, and film.*

Time	Paper No.	
3:00		Welcome. **C.A. Fyler**
3:10	44	INFECTIOUS PARASITES AS AMBASSADORS FOR BIOLOGY IN BOOKS, MAGAZINES, NEWSPAPERS, AND BLOGS. **C.W. Zimmer** (carl@carlzimmer.com).
3:35	45	PUBLIC AWARENESS OF PARASITOLOGY THROUGH ART. **W.C. Campbell** (wcampbel@drew.edu).
4:00	46	PUBLIC AWARENESS OF PARASITOLOGY THROUGH FILM. **D. Despommier** (ddd1@columbia.edu).
4:25		Audience questions for the panel of guest lecturers.
4:50		Summary and closing remarks. **C.A. Fyler**.

SATURDAY EVENING, JUNE 28

6:00–9:00 19TH ANNUAL STUDENT AUCTION, Capitol Ballroom

6:00 Auction Items Preview and Libations

7:00 19th Annual Live and Silent Auctions

NOTES...

SUNDAY MORNING, JUNE 29

8:00–10:00 ASSOCIATE EDITORS' SYMPOSIUM, Statler

Presiding: G.W. Esch, Editor, *Journal of Parasitology*, Wake Forest University, Winston-Salem NC

Theme: *Parasite ecology, evolution and genetics—old and new dogma.*

Time	Paper No.	
8:00	47	INTRODUCTION TO SYMPOSIUM: DOGMA IN PARASITE ECOLOGY, EVOLUTION, AND GENETICS. **G.W. Esch** (esch@wfu.edu).
8:20	48	PARASITE BEHAVIOR AND HOST FOOD WEBS: THE WORM'S EYE VIEW. **M.V. Sukhdeo** (sukhdeo@AESOP.Rutgers.edu).
8:50	49	METACERCARIAE, MINNOWS, AND MYTHS: EXPERIMENTAL ECOLOGY OF A HOST/PARASITE INTERACTION. **C.P. Goater** (cam.goater@uleth.ca).
9:20	50	GENETIC DIVERSITY AMONG PARASITIC NEMATODES AND ITS IMPACT ON MOLECULAR EPIDEMIOLOGICAL STUDIES. **D.S. Zarlenga Jr.** (zarlenga@anri.barc.usda.gov).
9:50		Audience questions for the panel of guest lecturers, summary and closing remarks. **G.W. Esch**

10:00–10:15 COFFEE BREAK, Capitol Ballroom – Outer Foyer

9:00–11:30 GENETICS, MOLECULAR BIOLOGY, Waldorf

Presiding: J. Hawdon, George Washington Medical Center, Washington DC
P. Olson, The Natural History Museum, London, UK

Time	Paper No.	
9:00	51	NEUROPEPTIDE IDENTIFICATION IN PHYLUM PLATYHELMINTHES. **P. McVeigh***, **G.R. Mair**, **M. Zamanian**, **E. Novozhilova**, **L. Atkinson**, **M.J. Kimber**, **T.A. Day,** and **A.G. Maule**.
9:15	52	LIGAND-GATED ION-CHANNELS IN THE GENOME OF *HAEMONCHUS CONTORTUS*. **R.N. Beech***, **J. Lian,** and **J. Nabhan**.
9:30	53	SEQUENCE VARIATION IN THE GENOME OF *HAEMONCHUS CONTORTUS*. **R.N. Beech***, **E. Redman**, **K. Mungall**, **M. Berriman,** and **J.G. Gilleard**.
9:45	54	AMIDATING ENZYME —FUNCTIONAL CHARACTERIZATION AND GENE SILENCING IN THE BLOOD FLUKE *SCHISTOSOMA MANSONI*. **L. Atkinson***, **P. McVeigh**, **G.R. Mair**, **N. Marks**, **M.J. Kimber**, **T.A. Day,** and **A.G. Maule**.

10:00–10:15 COFFEE BREAK, Capitol Ballroom – Outer Foyer

10:15 55 A POTENTIAL ROLE FOR *FASCIOLA HEPATICA* CATHEPSIN L IN NEUROPEPTIDE SIGNAL TERMINATION. **A. Mousley***, **L. McGonigle**, **E. Cameron**, **N.J. Marks**, **G.P. Brennan**, **J.P. Dalton,** and **A.G. Maule**.

10:30 56 IDENTIFICATION AND CHARACTERIZATION OF CALCIUM-INTERACTING PROTEINS IN LARVAL *SCHISTOSOMA MANSONI*.. **A.S. Taft*** and **T.P. Yoshino**.

10:45 57 APPLICATION OF RT-PCR TO STUDY *IN VITRO* DEVELOPMENT OF *CRYPTOSPORIDIUM PARVUM* AND ITS VIRAL SYMBIONT CPV. **M.C. Jenkins***, **C.N. O'Brien**, **B. Rosenthal**, **J. Trout**, **J. Karns,** and **R. Fayer**.

11:00 58 MICROSATELLITE VARIATION IN THE SALMONID TREMATODE *CREPIDOSTOMUM FARIONIS*. **W.D. Wilson*** and **T.F. Turner**.

11:15 59 ISOLATION AND IMMUNO-CHEMICAL LOCALIZATION OF *TAENIA SOLIUM* GAP JUNCTIONS. **K.L. Willms***, **R. Zurabian**, **A. Landa,** and **L. Robert**.

8:00–11:45 STUDENT PAPER COMPETITION – III, Astoria

Presiding: J. Milhon, Azusa Pacific University, Azusa CA
S. Patton, University of Tennessee, Knoxville TN

Time	Paper No.	
8:00	60†	PHYLOGENETIC RELATIONSHIPS AMONGST MEMBERS OF THE APICOMPLEXA INFERRED USING A MULTI-GENE AND MULTI-GENOME APPROACH. **J.D. Ogedengbe*** and **J.R. Barta**.
8:15	61†	SNAIL HOST GENETIC DIVERSITY ACROSS SPACE AND TIME. **E.A. Thiele***, **G. Corrêa-Oliveira,** and **D.J. Minchella**.
8:30	62†	FOR THE BUSY PARASITE - SO MANY CHOICES, SO LITTLE TIME: HOST UTILIZATION IN THE FIELD CORRESPONDS WITH LABORATORY 'CHOICE EXPERIMENTS.' **J.T. Detwiler*** and **D.J. Minchella**.
8:45	63†	HETEROGENEITY AMONG PARASITES, NOT HOSTS, CONTROLS VARIATION IN SPECIES RICHNESS. **M.S. Sokolowski***, **T.H. Cribb**, **A.D. Dove,** and **S.B. Munch**.
9:00	64†	THE ROLE OF SPATIAL HETEROGENEITY IN TREMATODE AGGREGATION IN THE MUDSNAIL, *ILYANASSA OBSOLETA*. **W.D. Rossiter*** and **M.V. Sukhdeo**.
9:15	65†	LANDSCAPE AND PARASITE DISTRIBUTION IN WOOD FROGS (*RANA SYLVATICA*). **E.E. Pulis***, **R.A. Newman,** and **V. Tkach**.
9:30	66†	PARASITE ASSEMBLAGES OF THE COMMON GRASS SHRIMP ALONG THE ALABAMA GULF COAST: SEASONAL DISTRIBUTION AND USE AS AN ENVIRONMENTAL INDICATOR. **K.L. Sheehan***, **J. O'Brien,** and **J. Cebrian**.
9:45	67†	MORPHOLOGICAL EFFECTS, PARASITOLOGICAL OUTCOMES, AND TRADE-OFFS OF CONCURRENT *HELIGMOSOMOIDES BAKERI* (NEMATODA) INFECTION AND PREGNANCY IN CD-1 MICE. **M.R. Odiere***, **K.G. Koski,** and **M.E. Scott**.

10:00–10:15 COFFEE BREAK, Capitol Ballroom – Outer Foyer

[8:00–11:45 STUDENT PAPER COMPETITION – III, Astoria, *continued*]

10:15 68† INFECTIONS WITH GEOGRAPHICALLY AND GENETICALLY DIFFERENT STRAINS OF *TRYPANOSOMA CRUZI* IN TWO NORTH AMERICAN RESERVOIR HOSTS INDUCE DISSIMILAR INFECTION DYNAMICS. **D.M. Roellig***, **A.E. Ellis,** and **M.J. Yabsley**.

10:30 69† INTESTINAL HELMINTHS FROM 6 SPECIES OF DOVES RESIDING IN SOUTH TEXAS. **A.J. Smith*** and **A.M. Fedynich**.

10:45 70† DO INSECTICIDES ALTER NATURAL HOST-PARASITOID INTERACTIONS IN *DROSOPHILA*? **N. Milan*** and **T. Schlenke**.

11:00 71† IDENTIFICATION OF HOST DNA AND THE ETIOLOGIC AGENT FOR EPIZOOTIC BOVINE ABORTION IN *ORNITHODOROS CORIACEUS*. **A.K. Long***, **M.B. Teglas,** and **V. Kirchoff**.

11:15 72† MULTIPLE SPECIES OF *PHOREIOBOTHRIUM* FROM THE BLACKTIP SHARK *CARCHARHINUS LIMBATUS*, FROM THE GULF OF MEXICO. **H.L. Owens*** and **K. Jensen**.

11:30 73† THE LECANICEPHALIDEAN FAUNA OF THREE SPECIES OF EAGLE RAYS OF THE GENUS AETOMYLAEUS (MYLIOBATIFORMES: MYLIOBATIDAE). **K.R. Koch*** and **K. Jensen**.

10:15–12:15 40TH COCCIDIOSIS CONFERENCE AND WORKSHOP, Shamrock

Presiding: J.B. Barta, University of Guelph, Guelph, Ontario, Canada
R.S. Seville, University of Wyoming, Laramie WY

Theme: *Taxonomy (α and β) and systematics of the coccidia.*

Time	Paper No.	
10:15		Welcome and Introduction. **J.R. Barta and R.S. Seville**
10:25	74	COCCIDIA FROM MAMMALS: STATUS OF THE TAXONOMY AND METHODS FOR COLLECTION, PRESERVATION, AND SPORULATION OF FECAL STAGES. **R.S. Seville** (SSeville@uwyo.edu).
10:40	75	AMPHIBIAN COCCIDIA: TAXONOMY, HOST SPECIFICITY, ECOLOGY, AND PHYLOGENY. **M.G. Bolek*** (bolekmg@unk.edu), **D.W. Duszynski,** and **S.J. Upton**.
10:55	76	METHODS FOR COLLECTION, PRESERVATION, AND SPORULATION OF SNAKE FECAL STAGES TO HELP RESOLVE WHAT WE STILL DON'T KNOW ABOUT SNAKE COCCIDIA. **S.J. Upton*** (coccidia@ksu.edu) and **D.W. Duszynski**.
11:10	77	COLLECTION, PRESERVATION, AND SPORULATION OF FECAL STAGES FROM BIRDS: CONCEPTS, METHODS AND CHALLENGES. **J.R. Barta*** (jbarta@uoguelph.ca), **J.D. Ogedengbe,** and **J. Cobean**.
11:25	78	THE EMERGING ROLE OF MOLECULAR MARKERS IN COCCIDIAN SPECIATION. **K.B. Miska*** (kmiska@anri.barc.usda.gov), **D. Motriuk-Smith,** and **R.S. Seville**.

11:40 Roundtable Discussion with all participants and audience members: Each presenter, above, will give a status report on the taxonomy for their host group, including how many species named, geographic areas and host groups under-sampled, projections for total species diversity if all were surveyed, research questions ripe for study. Serious questions must be addressed: *a*-taxonomy for the coccidia—what are or should be minimal requirements for a species description?; guidelines for what sequences should be the focus for differentiating similar species from closely related hosts (ITS1 and 2 and others?); can we agree on how different the sequences should be between "species?"; should providing at least one standard sequence be a mandatory requirement for new species descriptions?; what is the future of the Coccidia of the World website and how can we enhance the system to make it more up-to-date, comprehensive and practical?

SUNDAY AFTERNOON, JUNE 29

1:00–2:00 ASP PRESIDENTIAL ADDRESS, Statler + Waldorf

Presiding: G.W. Esch, Wake Forest University, Winston-Salem NC

Time	Paper No.	
1:00		Introduction of Dr. STEVE NADLER University of California, Davis CA
1:10	79	NOTHING SUCCEEDS LIKE EXCESS. S. Nadler.

2:00–4:30 TAXONOMY, SYSTEMATICS, PHYLOGENY, Astoria

Presiding: C.M. Whipps, SUNY-ESF, Syracuse NY
M.L. Steinauer, University of New Mexico, Albuquerque NM

Time	Paper No.	
2:00	80	TWO NEW CESTODE SPECIES FROM THE DWARF WHIPRAY, *HIMANTURA WALGA* (BATOIDEA: DASYATIDAE) FROM BORNEO, WITH COMMENTS ON SITE AND MODE OF ATTACHMENT. **M.E. Twohig***, **J.N. Caira,** and **C.A. Fyler**.
2:15	81	NEW CESTODES FROM FRESHWATER STINGRAYS OF INDONESIAN BORNEO. **J.N. Caira***, **K. Jensen,** and **F.B. Reyda**.
2:30	82	PHYLOGEOGRAPHY OF *RHABDOCHONA LICHTENFELSI* (NEMATODA) AND THE RECENT HISTORY OF FRESHWATER BASINS IN CENTRAL MEXICO. **H.H. Mejía-Madrid***, **E. Vázquez-Domínguez,** and **G. Pérez-Ponce De León**.
2:45	83	TAXONOMIC STATUS, GEOGRAPHIC DISTRIBUTIONS, AND ORIGINS OF HUMAN HEAD AND BODY LICE. **J.E. Light***, **M.A. Toups**, **J.M. Allen,** and **D.L. Reed**.

3:00–3:30 COFFEE BREAK, Capitol Ballroom – Outer Foyer

[2:00–4:30 TAXONOMY, SYSTEMATICS, PHYLOGENY, Astoria , *continued*]

3:30 84 PHYLOGENY AND EVOLUTION OF BAT FLIES (STREBLIDAE, NYCTERIBIIDAE). **K. Dittmar***, **C. Dick**, **B. Patterson,** and **M. Gruwell**.

3:45 85 BLOODSUCKERS AND THEIR BACTERIA: A SYSTEMATIC SYMBIONT SURVEY. **S.C. Watson*** and **M.E. Siddall**.

4:00 86 COMPARATIVE EST LIBRARIES FROM MEDICINAL LEECHES. **M.E. Siddall***, **G. Min**, **S.C. Watson,** and **I.N. Sarkar**.

4:15 87 EVOLUTION OF LIFE CYCLES AND HOST ASSOCIATIONS AMONG THE HYMENOLEPIDIDAE: HOW MANY SWITCHES?. **V.V. Tkach***, **B.B. Georgiev**, and **D.J. Littlewood**.

2:00–4:30 ECOLOGY – I, Shamrock

Presiding: R. Hathaway, Colorado College, Colorado Springs CO
L.F. Mayberry, University of Texas-El Paso, El Paso TX

Time	Paper No.	
2:00	88	MANIPULATION OF HOST FOOD AVAILABILITY AND NUMBER OF EXPOSURES TO ASSESS THE CROWDING EFFECT ON *HYMENOLEPIS DIMINUTA* IN *TRIBOLIUM CONFUSUM*. **A.W. Shostak*** and **J.G. Walsh**.
2:15	89	DISCRIMINATION IN HAWAIIAN STREAMS: NOT ALL HOSTS TREAT *CAMALLANUS COTTI* EQUALLY. **W.F. Font**.
2:30	90	SEASONALITY AND THE LONG-TERM VARIATION OF THE PREVALENCE OF TROPICAL AQUATIC HELMINTH PARASITES. **D. Pech**, **M.L. Aguirre-Macedo,** and **V.M. Vidal-Martínez***.
2:45	91	STRESS, IMMUNITY, AND BLOOD PARASITES (*LEUCOCYTOZOON*, *HAEMOPROTEUS*, AND *PLASMODIUM* SPP.) IN A FREE-LIVING POPULATION OF WHITE-CROWNED SPARROWS (*ZONOTRICHIA LEUCOPHRYS ORIANTHA*) IN COLORADO. **C. Murdock***, **M. Dietz**, **M. Romero,** and **J. Foufopoulos**.
3:00–3:30		**COFFEE BREAK, Capitol Ballroom – Outer Foyer**
3:30	92	TREMATODE COMMUNITIES OF *PYRGOPHORUS CORONATUS* IN 4 WATERBODIES OF YUCATÁN. **M.L. Aguirre-Macedo*** and **A.T. Sabasflores-Díaz De León**.
3:45	93	ANCIENT EGYPTIAN MEDICINE. **O.M. Amin**.
4:00	94	ARABIC MEDICINE. **O.M. Amin**.
4:15	95	INTESTINAL PARASITIC INFECTIONS AMONG SCHOOL CHILDREN IN KOTA KINABALU, SABAH, MALAYSIA. **H. Mahsol*** and **A. Sapaat**.

3:00 — POSTER SET-UP, Capitol Ballroom

Poster boards delivered; authors can begin setup of your posters.

3:30–5:00 HOST-PARASITE INTERACTIONS, Statler

Presiding: J.F. Hillyer, Vanderbilt University, Nashville TN
K. Sapp, High Point University, High Point NC

Time	Paper No.	
3:30	96	METRONIDAZOLE-INDUCED PROGRAMMED CELL DEATH IN *GIARDIA DUODENALIS*. **A.E. Oniku***, **S. Bagchi,** and **T.A. Paget**.
3:45	97	ENDOPARASITIC HELMINTHS AND HOST DISTRIBUTION IN SELECTED POPULATIONS OF MALAGASY LEMUROIDS. **C.T. Faulkner***, **A. Chapman**, **R. Junge**, **G. Crawford,** and **C. Welch**.
4:00	98	MALARIA SPOROZOITE MIGRATION THROUGH THE MOSQUITO HEMOCOEL. **J.F. Hillyer***, **J.G. King,** and **J.D. Glenn**.
4:15	99	TICKS AND TICK-BORNE PATHOGENS AND SYMBIONTS OF BLACK BEARS IN FLORIDA AND GEORGIA. **L.A. Durden***, **T.N. Nims**, **M. Savage,** and **M.J. Yabsley**.
4:30	100	A ROLE FOR ENDOGENOUS NITRIC OXIDE PRODUCTION IN *GIARDIA DUODENALIS*. **S. Bagchi***, **R. Steuart**, **R. Thompson,** and **T.A. Paget**.
4:45	101	PARTIAL PURIFICATION AND CHARACTERIZATION OF EXCRETORY/ SECRETORY (E/S) ANTIGENS OF THE RUMEN AMPHISTOME *GASTROTHYLAX CRUMENIFER*. **M.K. Saifullah***, **G. Ahmad**, **W.A. Nizami,** and **S.M. Abidi**.

SUNDAY EVENING, JUNE 29

5:15 Buses leave for our Reception at the **Legends of the Game Baseball Museum**, part of the Texas Rangers Ballpark in Arlington, just a few blocks from the Hilton-Arlington.

5:30 Reception at the Ballpark and baseball game: Texas Rangers *vs.* Philadelphia Phillies!

NOTES...

MONDAY MORNING, JUNE 30

8:00–10:30 PALEOPARASITOLOGY SYMPOSIUM AND WORKSHOP, Statler

Presiding: K. Reinhard, University of Nebraska, Lincoln NE

Theme: *Archaeoparasitology: Coprolites and mummies: conservation, curation, and methods of analysis.*

Time	Paper No.	
8:00		Welcome and Introduction. **K. Reinhard**
8:10	102	MINIMALLY DESTRUCTIVE UTILIZATION OF MUMMIES IN ARCHAEOHELMINTHOLOGICAL STUDIES. **D.J. Richardson*** (Dennis.Richardson@quinnipiac.edu), **K. Reinhard**, **R. Beckett**, and **G. Conlogue**.
8:30	103	THEORY AND APPLICATION OF MOLECULAR BIOLOGY TO COPROLITES WITH SPECIFIC PARASITE TARGETS. **K. Dittmar*** (kd52@buffalo.edu).
8:50	104	PROBLEMS OF INTERPRETING PREHISTORIC ODDITIES FROM ARID ARCHAEOLOGICAL SITES: TAENIIDS, HYMENOLEPIDIDS, AND FLUKES. **K.J. Reinhard*** (kreinhard1@unl.edu), **A. Araújo**, **M.H. Fugassa,** and **A. Jiménez-Ruiz**.
9:10		Microscopes and coprolites will be available for a hands-on demonstration along with a variety of posters concerning methods and debates. **J. Hawdon** and **C.T. Faulkner** will join the panel as discussants to offer insightful comments and provide some thought-provoking questions.

8:00–10:30 POSTER SET-UP, Capitol Ballroom

All authors please complete setup of your posters.

8:30–10:30 LATE BREAKERS, Astoria

Presiding: R. Clopton, Peru State College, Peru NE

8:30–10:30 ECOLOGY – II, Waldorf

Presiding: H. Eure, Wake Forest University, Winston-Salem NC
M.V.K. Sukhdeo, Rutgers University, New Brunswick NJ

Time	Paper No.	
8:30	105	EARED GREBES: WHERE HAVE ALL THEIR HELMINTHS GONE? **A.S. Didyk*** and **J.R. Jehl Jr.**.
8:45	106	IMPACT OF EUTROPHICATION ON WOOD FROG, *RANA SYLVATICA,* TADPOLES INFECTED WITH *ECHINOSTOMA TRIVOLVIS* CERCARIAE. **L.K. Belden**.
9:00	107	SPECIES RICHNESS IN TREMATODE COMMUNITIES OF SNAIL HOSTS FROM YUCATÁN, MÉXICO. **R. Rodríguez-Olayo***, **N.A. Herrera-Castillo,** and **M. Aguirre-Macedo**.

9:15 108 MODERATE *ECHINOSTOMA TRIVOLVIS* INFECTION HAS NO EFFECTS ON PHYSIOLOGY AND FITNESS-RELATED TRAITS OF LARVAL PICKEREL FROGS (*RANA PALUSTRIS*). **S.A. Orlofske***, **L.K. Belden,** and **W.A. Hopkins**.

9:30 109 A TEST OF THE MICROSATELLITE ANALYSIS OF POOLED *SCHISTOSOMA MANSONI* MIRACIDIA DERIVED FROM NATURALLY-INFECTED PATIENTS. **B. Hanelt***, **M.L. Steinauer**, **I.N. Ndungu**, **G.M. Maina**, **E.L. Agola**, **J.M. Kinuthia**, **G.M. Mkoji**, **D.M. Karanja,** and **E.S. Loker**.

9:45 110 THE VEGETARIAN AND THE BLOOD FEEDER: ALTERNATIVE LIFE CYCLE STRATEGIES OF *MEGALODISCUS TEMPERATUS* IN TADPOLES AND METAMORPHOSED ANURANS. **M.G. Bolek*** and **J. Janovy Jr.**.

10:00 111 LOCAL ADAPTATION: GEOGRAPHIC VARIATION IN TREMATODE RELEASE BY GASTROPOD HOSTS IN RESPONSE TO TEMPERATURE. **J. Koprivnikar*** and **R. Poulin**.

10:15 112 TOXICITY OF METAM SODIUM TO *ASCARIS SUUM* EGGS IN BIOSOLIDS FROM FIVE LOCATIONS. **G.D. Cain**.

10:30–Noon POSTERS, COFFEE, SNACKS, Capitol Ballroom

All authors please stand with your posters from 10:30–Noon.

CHEMOTHERAPY, DRUG RESISTANCE

113 TOXICITY OF AMPHOTERICIN B ON *LEISHMANIA MAJOR* PROMASTIGOTES. **D.R. Bienek***, **P.C. Thomas, M.L. Coen,** and **P.K. Fu**.

114 AN ABCG HOMOLOGUE GENE IN MULTI-DRUG RESISTANT *PLASMODIUM YOELII*. **I. Ferrer- Rodriguez***, **G. Gonzalez Ruiz, B. Gonzalez Vazquez,** and **A.E. Serrano Brizuela**.

ECOLOGY

115 THE OCCURRENCE OF SPECIES OF *TOXOCARA* IN WILD MAMMAL POPULATIONS FROM EGYPT. **N.A. Radwan, A.I. Khalil***, and **R.A. El Mahi**.

116 INFLUENCE OF DIET ON HELMINTH SPECIES RICHNESS IN SOUTH TEXAS DOVES. **A.J. Smith*** and **A.M. Fedynich**.

117 DAY LENGTH, RATHER THAN TEMPERATURE, PREDICTS TRANSMISSION OF A TREMATODE CERCARIA TO AN ESTUARINE SNAIL. **B.L. Fredensborg**.

118 MACROPARASITE COMMUNITY ANALYSES OF PACIFIC SARDINE (*SARDINOPS SAGAX*) POPULATIONS IN THE CALIFORNIA CURRENT SYSTEM. **R.E. Baldwin* and K.C. Jacobson**.

GENETICS, MOLECULAR BIOLOGY

119 GENETIC VARIATION IN RIBOSOMAL INTERNAL TRANSCRIBED SPACER (ITS-1) REGION OF *LEISHMANIA DONOVANI* PROMASTIGOTES OF INDIAN ISOLATES. **S. Thakur***, **S.T. Pasha, V.R. Mittal,** and **A. Rai**.

120 THE WySTEP PROGRAM: TRAINING PRE-SERVICE EDUCATORS TO PRACTICE SCIENCE IN THE SECONDARY SCIENCE CLASSROOM. **S. Jensen*, D. Motriuk-Smith,** and **R.S. Seville**.

121 FUNCTIONAL GENOMIC SCREEN OF EARLY LARVAL *SCHISTOSOMA MANSONI* DEVELOPMENT USING RNA INTERFERENCE. **M.M. Mourao*, N. Dinguirard, G.R. Franco,** and **T.P. Yoshino**.

122 DIFFERENTIATION OF GENE EXPRESSION BETWEEN TACHYZOITES AND BRADYZOITES OF *IN VITRO*-CULTURED *NEOSPORA CANINUM*. **K. Seung-Won, K. Chang-Hee, L. Eun-Hang, C. Se-Eun*, J. Suk-Chan,** and **Q. Dong-Van**.

123 SmZF1, A *SCHISTOSOMA MANSONI* ZINC FINGER PROTEIN, HAS A NUCLEAR LOCALIZATION AND IS ABLE TO ACTIVATE GENE TRANSCRIPTION. **M.G. Drummond, C. Calzavara-Silva, D.S. D'Asolfo, M.M. Mourão*, F.C. Cardoso, M.A. Rajão, E. Gava, N.P. Koritschoner,** and **G.R. Franco**.

124 RECOMBINANT EXPRESSION OF *TOXOPLASMA GONDII* SURFACE ANTIGEN SAG2 IN THE METHYLOTROPHIC YEAST *PICHIA PASTORIS*. **L. Yee Ling*** and **F. Mun Yik**.

HOST-PARASITE INTERACTIONS

125 HYDATIDOSIS IN SOUTH INDIA. **J.M. Varghese*, G.P. Varghese,** and **R.R. Yesudas**.

126 INFILTRATION AND ACQUISITION OF HELMINTHS WITHIN THE INVASIVE CUBAN TREEFROG, *OSTEOPILUS SEPTENTRIONALIS*, IN WEST CENTRAL FLORIDA. **N. Ortega*, W. Price, K. Oliver,** and **T. Campbell**.

127 EXPOSURE TO SNAIL HOST CHEMICAL CUES DOES NOT INDUCE EARLY HATCHING OF *ECHINOSTOMA TRIVOLVIS* MIRACIDIA. **L.K. Belden*, P.D. Widder, L. Fischer, A. Carter,** and **J.M. Wojdak**.

128 EFFECTS OF A PARASITIC LARVAL NEMATODE ON MATING BEHAVIOR IN THE WESTERN MOSQUITOFISH, *GAMBUSIA AFFINIS*. **R. Deaton* and S. Noble**.

IMMUNOLOGY

129 IMMUNODIAGNOSIS OF HUMAN *WUCHERERIA BANCROFTI* INFECTION USING A PAIR OF MONOCLONAL ANTIBODIES AGAINST WORM ANTIGEN. **M.A. Hendawy*, W.A. Mansour, F.M. Salah, I.S. Rabia, N.A. El-Gamal, A.A. El-Bassiouny,** and **Z.A. Demerdash**.

130 DETECTION OF *LEISHMANIA* (*L.*) *CHAGASI* IN CANINE SKIN. **W.A. Starke-Buzetti*, N.G. Queiroz, M.F. Neves, R.D. Viveiros, A.C. Noronha Jr., R.Z. MacHado,** and **T.F. Oliveira**.

LIFE CYCLES, EPIDEMIOLOGY

131 SCHOOL-BASED COMPREHENSIVE INTERVENTION TO PREVENT RE-INFECTION BY *GIARDIA LAMBLIA* AND *ASCARIS LUMBRICOIDES* AMONG TARAHUMARA INDIGENOUS CHILDREN OF NORTHERN MEXICO. **J. Monárrez-Espino*, C. Rocío Pérez Espejo, M. Itzel Loya Montiel, S. Pizarro Chávez, R. Alvarado Rojas, E. Pérez García, A. Balleza Carreón, R. Caballero Hoyos,** and **G. Vázquez Mendoza**.

132 NEUROCYSTICERCOSIS IN SLOVENIA FROM 2001–2007. **J. Logar*, B. Soba,** and **J. Tomazic**.

133 SHEDDING OF OOCYSTS BY DOGS FED DIFFERENT TISSUES FROM NATURALLY *NEOSPORA CANINUM*-INFECTED BOVINES. **G.T. Cavalcante*, R.M. Monteiro, R.M. Soares, S.M. Nishi, F.A. Neto,** and **S.M. Gennari**.

134 ONE CASE OF FELINE LEISHMANIOSIS IN BRAZIL. **K.D. Bresciani*, A.C. Serrano, V.M. Lima, F.L. Bonello, R.O. Vasconcelos, E.S. Savani, S.R. D'Auria,** and **C.M. Nunes**.

135 FREQUENCY AND INTENSITY OF GASTROINTESTINAL HELMINTHS IN DOMESTIC CATS FROM BRAZIL. **K.D. Bresciani*, M.N. Ishizaki, C.N. Kanetouky, T.R. Montano, S.H. Perri, R.O. Vasconcelos,** and **O.A. Nascimento**.

136 PARASITIC FREQUENCY AND INTENSITY OF GASTROENTERIC HELMINTHS IN DOMESTIC DOGS IN BRAZIL. **K.D. Bresciani*, M.N. Ishizaki, C.N. Kaneto, T.P. Montano, S.H. Perri, R.O. Vasconcelos,** and **A.A. Nascimento**.

137 NATURAL INFECTION WITH *CRYPTOSPORIDIUM GALLI* IN CANARIES (*SERINUS CANARIA*), IN A COCKATIEL (*NYMPHICUS HOLLANDICUS*), AND IN LESSER SEED-FINCHES (*ORYZOBORUS ANGOLENSIS*) FROM BRAZIL. **M.V. Meireles*, D.C. Simões, A.A. Nakamura,** and **R.G. Antunes**.

138 COMPARISON BETWEEN FOUR COPROPARASITOLOGICAL TECHNIQUES FOR THE EFFICIENCY IN THE DIAGNOSIS OF HELMINTHS EGGS OR PROTOZOA OOCYSTS IN CATS. **É.D. Ribeiro, A.F. Amarante, A.C. Serrano, C.V. Taparo, R.F. Nunes, M.N. Ishizaki,** and **K.D. Bresciani***.

139 OCCURENCE OF *TOXOPLASMA GONDII* IN URBAN RODENTS (*RATTUS RATTUS, RATTUS NORVEGICUS* AND *MUS MUSCULUS*) CAPTURED IN SÃO PAULO (SP), BRAZIL. PRELIMINARY RESULTS. **V. Muradian*, L.R. Ferreira,** and **S.M. Gennari**.

140 BIOLOGICAL CHARACTERIZATION OF *TOXOPLASMA GONDII* ISOLATES FROM FREE-RANGING CHICKENS FROM THE NORTHEAST REGION OF BRAZIL. **S.M. Gennari*, L.N. Oliveira, L.M. Costa Jr., C.B. Melo, J.C. Silva, C.M. Bevilaqua, S.S. Azevedo, E.M. Oliveira, A.C. Melo, D.A. Araújo,** and **V. Muradian**.

TAXONOMY, SYSTEMATICS, PHYLOGENY

141 SEPARATE GENITAL DUCTS IN THE SINUS SAC OF *DINURUS HIPPURI* (DIGENEA: HEMIURIDAE). **R.R. Yesudas*** and **J.M. Varghese**.

142 rRNA SEQUENCES FROM CESTODE LARVAE INHABITING THE INTESTINES OF COMMERCIAL SHRIMP OF THE GULF OF MEXICO. **J.T. Payne*** and **J. Gunderson**.

143 DIFFERENTIATION AMONG SPECIES OF *COSMOCERCELLA* STEINER, 1924 BASED ON MORPHOMETRICAL INFORMATION. **R. Mata-López*, S. Guillén-Hernández,** and **V. León-Règagnon**.

144 CONVERGENT STRUCTURAL CAUDAL FEATURES IN ASCARIDINAE AND RAPHIDASCARIDIDAE (NEMATODA, ASCARIDOIDEA). **H. Fagerholm*** and **S. Rassouli**.

145 DETECTING A COMPLEX OF CRYPTIC SPECIES OF *NEOECHINORHYNCHUS GOLVANI* SALGADO-MALDONADO, 1978 (ACANTHOCEPHALA: NEOECHINORHYNCHIDAE) INFERRED THROUGH NUCLEAR GENES. **A. Martínez-Aquino*, G. Pérez-Ponce De León,** and **M. García-Varela**.

MONDAY AFTERNOON, JUNE 3

1:00–1:50 H.B. WARD LECTURE, Statler + Waldorf

Presiding: L.A. Durden, Georgia Southern University, Statesboro GA

Time	Paper No.	
1:00		Introduction of Dr. DALE H. CLAYTON University of Utah, Salt Lake City UT
1:10	146	BALANCING THE TRIPOD: ACCEPTANCE OF THE 2008 HENRY BALDWIN WARD MEDAL. **D.H. Clayton**.

1:50–2:35 BUEDING VON BRAND LECTURE, Statler + Waldorf

Presiding: L.S. Roberts, Homestead FL

Time	Paper No.	
1:50		Introduction of Dr. AARON G. MAULE Queen's University Belfast, Belfast, Northern Ireland, United Kingdom
2:00	147	THE QUIRKS OF PARASITE NEUROBIOLOGY: PROVIDING OPPORTUNITIES FOR PARASITE CONTROL? **A.G. Maule*, N.J. Marks, A. Mousley, P. McVeigh, M.J. Kimber, C.C. Fleming, T.A. Day,** and **D.W. Halton**.

2:35–3:00 **COFFEE BREAK, Capitol Ballroom – Outer Foyer**

3:00–4:30 ASP AWARDS AND BUSINESS MEETING, Statler + Waldorf

ASP AWARDS

CLARK P. READ MENTOR AWARD LECTURE, Statler + Waldorf

Presiding: K. Sapp, High Point University, High Point NC
S.J. Upton, Kansas State University, Manhattan KS
J.K Moore, Colorado State University, Fort Collins CO

Time	Paper No.	
3:00		Introduction of Dr. DONALD W. DUSZYNSKI University of New Mexico, Albuquerque NM
3:10	148	STUDENTS, OPPORTUNITY, SERENDIPITY, AND W.B. YATES: "EDUCATION IS NOT THE FILLING OF A PAIL; IT IS THE LIGHTING OF A FIRE." **D.W. Duszynski**.

DISTINGUISHED SERVICE AWARD

Presiding: R. Overstreet, University of Southern Mississippi
Ocean Springs MS

The recipient of the 2008 Distinguished Service Award
is Dr. WILLIAM CAMPBELL
Drew University, Madison NJ

ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: J. Hawdon, George Washington Medical Center, Washington DC

The recipient of the 2008 New Investigator Award
is Dr. ASHTON BULLARD
University of Southern Mississippi, Ocean Springs MS

WILLIS A. REID, JR. STUDENT RESEARCH GRANT AWARDS

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

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: T. Cook, Sam Houston State University, Huntsville TX

ASP BUSINESS MEETING

Presiding: S. Nadler, University of California, Davis CA

Thank you for attending this year's ASP meeting
and have a safe trip home.

♦

See you August 14-17, 2009
at our next meeting in Knoxville TN

NOTES...

Abstracts for 2008 ASP

1

Schistosoma mansoni Isolated Muscle Fibers Inward Currents are Sensitive to Classical Voltage-Operated Ca^{2+} Channel Blockers and are Enhanced by Flatworm FMRFamide-like Peptides.

E.B. NOVOZHILOVA*, A.P. ROBERTSON, H. QIAN, and M.J. KIMBER, Department of Biomedical Sciences, Iowa State University, Ames, IA; P. MCVEIGH and A.G. MAULE, Biomolecular Processes: Parasitology, Queen's University Belfast, Northern Ireland, United Kingdom; and T.A. DAY, Department of Biomedical Sciences, Iowa State University, Ames, IA.

Pharmacological characterization of voltage-operated Ca^{2+} channels (VOCCs), in both free-living and parasitic flatworms, has been difficult since the currents carried by these channels are small in amplitude and run down quickly. While the presence of VOCCs in the parasite *Schistosoma mansoni* has been evident from molecular data, they have escaped pharmacological characterization. In this study, we have been able to consistently record inward currents carried by VOCCs in isolated *S. mansoni* muscle fibers, using whole cell configuration of the patch-clamp technique in voltage-clamp mode. Inward voltage-activated current was recorded, under conditions that suppressed outward K^+ conductance, by the replacement of internal K^+ with Cs^+ and enhanced with 15.0 mM Ba^{2+} as a charge carrier in addition to 2.0 mM Ca^{2+} ($I_{Ca/Ba}$). Whole cell $I_{Ca/Ba}$ was obtained from frayed muscle fibers by depolarizing them for 200 ms from a holding potential of –70 mV to +20 mV. A relatively small proportion of cells tested (less than 30%) had currents with amplitudes amenable to pharmacological characterization using common VOCCs blockers and neuropeptides. Currents showed little evidence of inactivation within the period of the 200 ms depolarizing pulse. Currents were sensitive to the phenylalkylamine VOCC blocker verapamil, which reduced their amplitude in concentration-dependent manner. The platyhelminth-derived FMRFamide-like peptide (FLP) YIRFamide significantly increased current amplitude at 1 μM. YIRFamide's ability to amplify the inward currents was reduced when verapamil was simultaneously present in the perfusion solution, indicating possible VOCCs involvement in carrying Ca^{2+} influx triggered by the flatworm FLP.

2

Ancylostoma caninum Daf-16 Binds to a Conserved Daf-16 Family Member-Binding Element.

X. GAO* and J. HAWDON, Microbiology, Immunology, and Tropical Medicine, George Washington University, Washington, DC.

The Forkhead/FOXO transcription factor DAF-16 plays an essential role in the regulation of development in the free-living nematode *Caenorhabditis elegans*. In response to adverse environmental changes, DAF-16 enters the nucleus and regulates genes involved in the formation of the developmentally arrested dauer larva. Insulin-like signaling, in response to improved conditions, negatively regulates DAF-16, resulting in resumption of reproductive growth. The infective third stage larva (L_3) of the parasitic hookworms is remarkably similar to the developmentally arrested dauer stage of *C. elegans*. DAF-16 orthologs have been identified and sequenced from *Ancylostoma caninum* and *A. ceylanicum*. We hypothesized that Ac-DAF-16 would bind to the *C. elegans*-conserved DAF-16 binding element (DBE) to regulate hookworm gene transcription. The entire coding sequence of Ac-DAF-16 was cloned into a mammalian expression vector to generate pCMV4-Daf16 and the FLAG-tagged recombinant DAF-16 (rDAF-16) expressed in HEK293T cells. Western blots of cell lysates, probed with anti-FLAG antibody and Ac-DAF-16 antiserum, confirmed DAF-16 expression. A streptavidin bead pull-down assay was performed to investigate the interaction between the recombinant Ac-DAF-16 and the biotin-labeled DBE. Recombinant DAF-16 strongly bound to the *C. elegans* DBE, and more weakly, to a DBE-like sequence located in the promoter of the Ac-dao-1 gene, which encodes an ortholog of a *C. elegans* FKBP-like protein. Recombinant DAF-16 failed to pull-down a labeled random primer, indicating that the interaction with DBE is sequence-specific. Luciferase reporter assays, conducted in NIH3T3 cells, indicated that rDAF-16 was able to drive expression *in vivo* from the DBE promoter sequence in starved cells, and expression was down-regulated by serum. Our data indicate that Ac-DAF-16 interacts with the conserved DBE and will allow us to identify DAF-16 regulated genes in hookworms.

3

Extracts of the Bitter Melon, *Momordica charantia*, Inhibit Activation of Hookworm Larvae.

K. BATICH* and J.M. HAWDON, Department of Microbiology, Immunology and Tropical Medicine, George Washington University Medical Center, Washington, DC.

Hookworms continue to present serious challenges to the health and economies of developing countries worldwide. Removal of adult parasites with anthelmintics will remain the only efficacious treatment for the foreseeable future, but increased use of anthelmintics will undoubtedly give rise to resistant hookworm populations. Resistance will require development of new anthelmintics to control hookworm and other nematode infections. A tea made from the tropical bitter melon plant, *Momordica charantia*, is used as a vermifuge in traditional Haitian medicine. Our lab has previously shown that an aqueous extract of *M. charantia* inhibits *in vitro* activation of *Ancylostoma caninum* L_3. Here, we report further investigations of the mechanism of inhibition. A water-soluble extract was made from dried *M. charantia* leaves and flash evaporated to 100% concentration. The dry weight of plant material in the extract was determined, and several concentrations of the extract were co-incubated with activation stimulus and L_3. After 24 hr, larvae were incubated with fluoresceinated albumin and examined under epi-fluorescent microscope to determine the percentage of feeding L_3. The *M. charantia*-soluble extract showed a dose-dependent inhibition of hookworm L_3 *in vitro* activation, with complete inhibition (no feeding L_3) at 24 mg/ml dry weight. Western blots were performed to determine if the extract inhibited secretion of the activation-associated secretory protein ASP-1. Excretory/secretory products from non-activated, activated, and *M. charantia*-inhibited L_3 were separated by SDS-PAGE, transferred to PVDF, and probed with ASP-1 antiserum. The extract inhibited feeding, but failed to inhibit secretion of ASP-1. Experiments to determine the mechanism of inhibition and the inhibitory components in the extract are underway. Supported by NIAID R21AI062857.

4

Effect of Post-Cyclic Transmission on Microhabitat Use of *Paulisentis missouriensis* (Acanthocephala) in Creek Chub.

H.A. ROBINSON* and M.A. BARGER, Department of Natural Science, Peru State College, Peru, NE.

Microhabitat specificity of helminths in the intestine of their vertebrate hosts is a well-documented phenomenon, but the mechanisms that produce preferential site selection are not fully understood. Previous work suggests that the microhabitat use of *Paulisentis missouriensis* (Acanthocephala), a common parasite of creek chub (*Semotilus atromaculatus*), is associated with the worm's sex and reproductive maturity. Gravid female worms occur around the first flexure of the intestine, whereas non-gravid females occupy the posterior part of the intestine; males coincide with gravid females. These results suggest that cystacanths of *P. missouriensis* establish in the posterior region of the intestine, migrate anteriorly, mate, and come to occupy positions centered around the first flexure. Creek chub acquire *P. missouriensis* through the consumption of a copepod intermediate host or post-cyclically by consuming other infected chub. This study documented the microhabitat use of *P. missouriensis* from experimentally infected fish to determine if post-cyclic transmission affects microhabitat use. Uninfected fish were exposed either by feeding worms directly to them or by allowing them to feed on infected chub. The exposed fish were dissected 1, 4, and 10 days post-ingestion. Worms fed directly to fish were located more anteriorly in the intestine of the recipient host than the intestine of the donor host. Worms transmitted from fish to fish, however, were located in the middle of the intestine. These results suggest that worms establish as soon as possible in the intestine of their new definitive host. Furthermore, the position of worms transmitted post-cyclically did not change over the course of the experiment, suggesting that worms do not engage in site-finding behavior immediately after establishment.

5

Core-Periphery Structure in Food Webs Drives Parasite Community Assembly in Naïve Fish Hosts.

T.K. ANDERSON*, Graduate Program in Ecology & Evolution, and M.V. SUKHDEO, Department of Ecology, Evolution & Natural Resources, Rutgers University, New Brunswick, NJ.

An enduring problem in parasite ecology is understanding the relationship between the structure of host communities and the establishment and subsequent diversity patterns of metazoan parasite communities. This study examined the colonization of naïve mummichog, *Fundulus heteroclitus*, by parasites within the New York–New Jersey Harbor Estuary complex. Caged naïve mummichog (n = 450 per site) were placed within four distinct salt marsh areas, reflecting a gradient in host species diversity (H = 0.29, 0.31, 0.33, 0.37) and time post-restoration (untouched, 0 year, 9 year, 19 year respectively). Mummichogs were held in cages for 10 weeks at each site to allow parasite infracommunities to establish: cages were sampled weekly (n = 30). The diversity of the parasite community was higher, and species accumulated more rapidly, in the untouched low-diversity salt marsh. Relative rate of parasite species accumulation and community diversity increased stepwise from low, to intermediate, to high in the 0-year, 9-year, and 19-year sites respectively. A *Swingelus* sp. monogenean and an *Ascocotyle* sp. trematode dominated the ecto- and endoparasite faunas. To explain the paradox of a low-diversity salt marsh having the highest parasite diversity and fastest rate of parasite colonization, we constructed a time series of food webs and synthesized trophic information to analyze how the host community assembled over time. During food web assembly, the relative proportion of specialist species increased and the generalists decreased. Strong asymmetry was observed in each stage of food web development (n* = 0.75, 0.75, 0.86, 0.81): asymmetry in the food web was driven by core-periphery structure (c = 0.82, 0.79, 0.83, 0.88). Host species' trophic breadths systematically influence parasite community assembly; core generalists within the food web represent stable trophic relationships allowing for complex parasite life cycle persistence.

6

Seasonal Occurrence and Population Structure of *Dactylogyrus* spp. (Platyhelminthes: Monogenea) on Nebraska Minnows.

A.K. KNIPES* and J. JANOVY JR., School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.

Key modes of speciation and dispersal of parasites can be determined from molecular phylogenetic techniques, but this work is most effective when it builds upon ecological field data. By combining a substantial field data set with the construction of a molecular phylogenetic hypothesis, we are seeking to elucidate the role of fish host movement and distribution in the evolution of highly host-specific symbiotic organisms, at both the local and global scales. *Dactylogyrus*, a highly diverse genus with more than 1,000 described species, is parasitic on the gills of cyprinids; the largest and widest continuously distributed fish family in the world's fresh waters. Thus far, research has focused on the characterization of a model system that includes 3 native North American minnow species and 9 *Dactylogyrus* species in a single drainage basin with 1st and 2nd order streams. The project has generated a massive ecological dataset that includes more than 32 collections, totaling approximately 9,300 *Dactylogyrus* spp. parasites from the gills of 742 cyprinids from three sites near Lincoln, Nebraska, U.S.A. Stable environmental differences between sites have been reflected in parasite population and community structures. These results suggest that greater environmental differences, for example between habitats on different continents, are likely to produce different evolutionary pressures on organisms, resulting in different modes of speciation. The current direction of this research is to expand the project to include 29 *Dactylogyrus* species and to use molecular phylogenetic techniques to determine the key modes of speciation and dispersal of parasites, in particular *Dactylogyrus* species; and to predict the role of host movement and distribution in the evolution of highly host-specific symbiotic organisms at both the local and global scales.

7

Teal (1957) and Odum (1957) Revisited: What is the Effect of Parasitism on Ecosystem Energy Flow?

S.E. LETTINI* and M.V. SUKHDEO, Department of Ecology, Evolution, and Natural Resources, Rutgers University, New Brunswick, NJ.

Ecologists measure energy flow through ecosystems using energy budgets to measure the amount of energy allocated to production, respiration, and decomposition by all organisms within the system. Parasites have never been included in these studies, and they were considered to be insignificant in these energetic processes. The goal of this study was to replicate these studies, using identical methods to study ecosystem energy flow, but with parasites included. Ecosystem energy budgets were developed for 2 New Jersey Pinelands streams, one with a high prevalence of parasitism and one with a low prevalence of parasitism. For all seasons, samples of leaf detritus, macroinvertebrates, fish, and parasites (dissected from fish and macroinvertebrates) were collected along 50-m transects, and bomb calorimetry (kj/m^2/yr) was used to measure the amount of energy allocated to production and decomposition at each trophic level. Respiration was estimated, in the field, for both fish and macroinvertebrates, by placing individuals in sealed containers and measuring changes in oxygen consumption with a dissolved oxygen probe. Our results indicate that predators within the system require only a small amount of the total systems energy budget (0.42%) and parasites require even less (0.06%) in order to persist within an ecosystem.

8

Efficacy of Fenbendazole, Formulated in a Commercial Primate Diet, for Treating Specific Pathogen-Free Baboons (*Papio cynocephalus anubis*) Naturally Infected with *Trichuris trichiura*.

L.C. CLINGENPEEL*, Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK; R.F. WOLF, S.K. DOAN, and A.N. JONES, Comparative Medicine, University of Oklahoma Health Sciences Center, Oklahoma City, OK; and K.M. GRAY and M.V. REICHARD, Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK.

Trichuris trichiura is a common intestinal nematode parasite of captive baboons (*Papio cynocephalus anubis*). We evaluated the efficacy of fenbendazole formulated in commercial primate diet (FBZ-PD) for treating specific pathogen-free baboons naturally infected with *T. trichiura*. Twenty-nine baboons, housed in 3 separate rooms, were fed FBZ-PD for 5 days, while 4 baboons housed in another isolated area served as untreated controls. Efficacy of FBZ-PD was measured as the reduction of *T. trichiura* eggs observed in host feces after treatment, as determined by quantitative fecal flotation examination. All (100%) baboons that received FBZ-PD stopped shedding *T. trichiura* eggs by 7 d post-treatment, and fecal examinations from all (100%) remained negative until at least 119 d post-treatment. However, eggs of *T. trichiura* were observed in the feces of 3 (10.3%) experimental baboons at 154 d post-treatment. Untreated control baboons shed *T. trichiura* eggs throughout the entire study. Our results indicate that FBZ-PD was efficacious for treating SPF baboons infected with *T. trichiura*.

9

Pre-Approved Drugs as a Source for Novel Schistosomicides.

D.S. RUELAS*, M. ABDULLA, and K. LIM, Department of Pathology and Sandler Center for Basic Research in Parasitic Diseases, UCSF, San Francisco, CA; B. WOLFF, J. WILLIAMS, and A.R. RENSLO, Department of Pharmaceutical Chemistry and the Bay Area Screening Center, UCSF, QB3, CA; and J.H. MCKERROW and C.R. CAFFREY, Department of Pathology and Sandler Center for Basic Research in Parasitic Diseases, UCSF, San Francisco, CA.

The bloodflukes, *Schistosoma* spp., cause schistosomiasis, or bilharzia, an infectious parasitic disease that afflicts 200 million people worldwide. Current control of schistosomiasis relies largely on one effective and inexpensive drug—praziquantel. Reliance on a single drug poses the obvious threat of parasite resistance, especially in endemic areas with high re-infection rates. Therefore, to identify novel anti-schistosomals, we developed a semi-automated (96-well plate formatted) phenotypic screen using schistosomula of *Schistosoma mansoni*. We screened

a library of 2,160 known drugs, bioactive compounds, and natural products to identify those that cause morphological and locomotive abnormalities in schistosomula. Our intent was to rapidly identify compounds for which pharmacokinetic and toxicological data are known, while minimizing the potential for downstream intellectual property conflicts and production costs. This resulted in the selection of 56 compounds that we tested against *in vitro* cultures of adult worms. We have made the results of these screen components available through a public database hosted by Collaborative Drug Discovery, Inc. [Supported by the Sandler Family Supporting Foundation].

10

Prevalence of Ectoparasites in Forest Birds on the Island of Oahu.

S.A. BADER*, K.L. KREND, and L.H. FREED, Department of Zoology, The University of Hawaii at Manoa, Honolulu, HI.

The origin of chewing lice (Phthiraptera) in Hawaiian forest birds is presently unknown. Lice may have arrived with the early colonizing birds of the Hawaiian Islands, but were largely undetected in diverse and intensive bird banding studies. Alternatively, lice are a recent arrival that accompanied some of the many species of birds introduced to Hawaii. A general pattern is that animals in small founder populations, or introductions, are unlikely to bring their ectoparasites with them to their new habitat. Lice were rarely detected in studies conducted during the 1990's on Oahu and on the Island of Hawaii. These studies involved detailed inspection of birds for molt. Chewing lice generally show high host specificity, but host switching is possible for birds of similar size. This study investigated the prevalence of avian lice in the Koolau and Waianae ranges on the Island of Oahu, at six study sites, from March-January 2008. Pole-based mist nets were used to capture 1,016 birds. The majority were introduced species (85.9%). All birds were visually examined for mites and lice. Mites were rarely observed. Native host species had significantly higher prevalence of ectoparasites than introduced species (0.95 *vs*. 0.65). There was no difference in prevalence of ectoparasites between the two mountain ranges, with similar host species (0.65 in both ranges). The prevalence of ectoparasites on the native amakihi (*Hemignathus flavus*) and apapane (*Himatione sanguinea*) on Oahu was significantly higher than the prevalence of ectoparasites on their related forms on the Island of Hawaii (0.96 *vs.* 0.38 for amakihi, 1.0 *vs.* 0.41 for apapane). Morphological and molecular studies are necessary for determining the origin and specificity of avian lice in Hawaiian birds.

11

PCR Assay for Detection of *Baylisascaris procyonis* Eggs and Larvae.

S. DANGOUDOUBIYAM, R. VEMULAPALLI, and K.R. KAZACOS, Department of Comparative Pathobiology, Purdue University, West Lafayette, IN.

Specific identification of *Baylisascaris procyonis* eggs in contaminated environments and larvae recovered from tissue samples is difficult since several other closely related species have morphologically similar developmental stages. In this study, we tested the hypothesis that *B. procyonis* eggs and larvae could be identified using conventional and/or real-time PCR applied to environmental and tissue samples. We designed a primer-pair for specific amplification of a 146 bp fragment from the parasite's mitochondrial cytochrome oxidase 2 gene. The PCR assay was optimized for both conventional (with agarose gel electrophoresis) and real-time (with SYBR Green dye) analyses of the amplified products. The lower limit of detection of the parasite genomic DNA was 100 pg in the conventional PCR and 100 fg in the real-time PCR. In both formats of the PCR assay, specific amplification was achieved with DNA extracted from a single *in vitro*-hatched *B. procyonis* larva and also from canine fecal samples spiked with as few as 20 unembryonated *B. procyonis* eggs per gram of feces. No DNA amplification was seen when the genomic DNA of *Toxocara canis, Toxocara cati, Ascaris suum, Toxascaris leonina,* or *Ancylostoma caninum* was used as template in the PCR. We also attempted to differentiate between *Baylisascaris* species using this PCR. No amplified product was obtained when genomic DNA from *B. transfuga* was used as template. However, the specific DNA fragment was amplified when the genomic DNA of *B. columnaris* was used, indicating the close relatedness of this species with *B. procyonis*. The real-time PCR assay was successfully used for detection of *B. procyonis* eggs in fecal samples from clinically patent dogs and naturally contaminated soil samples, and larvae from formalin fixed paraffin blocks and fresh tissues of infected animals. This PCR will be an efficient tool for detection and identification of *Baylisascaris* eggs and larvae, but should be used in conjunction with a history of exposure and related epidemiologic information.

12

Castrator or Cradle Robber? The Effects of a Parasitic Copepod on its Nudibranch Host.

M. WOLF* and C.M. YOUNG, Department of Biology, University of Oregon, Oregon Institute of Marine Biology, Charleston, OR.

A few marine parasites have major effects on the physiology, behavior, and population dynamics of their hosts. Parasitic castrators often comprise 1–10% of their host's body mass and reduce or eliminate the reproductive output of the host. Members of the genus *Ismaila* (Splanchnotrophidae) are endoparasitic copepods of opisthobranch molluscs, inhabiting a large area in the host's main body cavity and/or cerata. On the Oregon coast, *Ismaila belciki* can infect over 60% of their obligate hosts, the nudibranch *Janolus fuscus*, and comprise 3–6% of the host's mass. However, infected *J. fuscus* still produce viable larvae, suggesting that *I. belciki* is not a complete castrator. In this study, we examine the impact of *I. belciki* on the reproductive capabilities of its host to determine if *I. belciki* reduces the copulatory ability and/or female fecundity of the host. Juvenile *J. fuscus* were collected from Fossil Pt., Coos Bay, OR, and reared in isolation to reproductive maturity. Each unmated individual was then mated with an infected or uninfected individual. All egg masses produced over the following 13 days were collected, examined for viability, and weighed. There was no significant difference in the number or weight of viable egg masses produced by nudibranchs mated with infected or uninfected partners, suggesting that infected individuals are still able to produce and transfer viable sperm to their mate. To determine if *I. belciki* reduced the fecundity of the host, infected and uninfected *J. fuscus* were mated with one uninfected individual and then isolated. Egg masses were collected for 21 days, weighed, and the number of capsules and larvae counted in each mass from each individual. Uninfected individuals produced significantly larger egg masses with more egg capsules and viable larvae than infected individuals. Thus, although *I. belciki* is not a complete castrator, this parasite reduces the reproductive output of its host and may limit the natural population size of *J. fuscus*.

13

The Chosen Frozen: Cold-Tolerance and Survival of *Paragordius varius* (Nematomorpha: Gordiida) Larvae.

W.E. DOERFERT* and B. HANELT, Department of Biology, University of New Mexico, NM.

Cold-tolerance mechanisms among invertebrates have been studied for years. The ability to survive extreme cold is not only a survival mechanism, but is also an adaptation that protects entire populations of invertebrates from extinction. These studies have found that many nematodes survived the transition to their freezing points in air. However, for the majority of species tested, approximately 70% survived when frozen in water at –60° C. Therefore, the survival rate, of the majority of species treated, was greatest among the samples frozen in water at extremely low temperatures. Of these studies, however, few have discussed the idea of cold-tolerance of the larval stage. *Paragordius varius*, commonly known as horsehair worms, not only have free-living adult stages but also free-living larval stages. The viability of *P. varius* larvae was studied using a series of treatments that included: freezing at –30° C and –70°C, drying at room temperature, or a combination of both. The larvae that were non-dried were more viable than those that were dried pre-treatment. In fact, larvae frozen immediately at –70° C were most viable in comparison to the control group. Viability was judged on whether or not the larvae formed cysts in the paratenic host; *Physa* sp. snails. Of the samples frozen at –30°C and –70°C, viability was 24% and 84% respectively, when compared to cysts produced in the control group. This clearly indicates that viability increases when freezing temperatures decrease. The data suggest that viability is affected most by initial storage conditions. Once frozen at –70° C, larvae can then be stored for longer terms in temperatures of –30° C and still remain viable. When first stored at –30° C, however, viability is significantly decreased in comparison to the initial freezing of larvae in temperatures of –70° C. This study suggests that this evolutionary cold-tolerance mechanism that gordiids possess may have developed in response to extremely cold environments that once existed. This cold-tolerance mechanism will make the study of gordiids more tractable when focusing on mechanisms of preservation for future studies or projects.

14

An Integrated Control Strategy Against Coccidiosis in Broiler Chickens May Benefit from the Use of Probiotics.

J.L. MCPHERSON-KOMOROWSKI* and J.R. BARTA, Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada.

Coccidiosis is a major parasitic disease of poultry caused by protistan parasites that invade and inhabit the gut. Probiotics (defined or undefined commensal enteric bacteria, e.g. lactobacilli) could contribute to successful coccidiosis control because microflora are an important first line of defense against enteric infections. To assess this, groups of chickens were orally challenged with *E. tenella* and were either administered a probiotic or sham inoculated, and/or vaccinated or not vaccinated. Growth rate and food conversion efficacy of the birds was calculated over the challenge period, and lesions resulting from the parasite were scored blindly using a qualitative scale. Messenger RNA was isolated from cecal tonsils to detect differences in cytokine gene expression and to characterize the nature and intensity of any immune response. Lastly, chickens were bled, and ELISAs were performed to detect the level of antibodies against sporozoites to further characterize any immune response. These experiments examined the complex interactions among protistan pathogens, beneficial gut microflora, and the immune system of the chicken and may lead to more successful and widespread use of live coccidiosis vaccines in the broiler industry, thereby reducing the industry's reliance on in-feed prophylactic medications.

15

A Biogeographical Study of Gregarines (Apicomplexa: Eugregarinida) Parasitizing *Argia* spp. (Odonata: Zygoptera).

J.J. HAYES* and T.J. COOK, Department of Biological Sciences, Sam Houston State University, Huntsville, TX; and R.E. CLOPTON, Department of Natural Science, Peru State College, Peru, NE.

Gregarines (Apicomplexa: Eugregarinida) are ubiquitous parasites of invertebrates, especially insects. Over 20 gregarine species have been described from the insect order Odonata (dragonflies and damselflies) in the Old World, but only 6 species have been described from odonates in the Western Hemisphere. This survey focused on a single genus, *Argia*, with an exclusive New World distribution. Prior to this survey, only one species in this genus had been reported as a gregarine host. Our study examined gregarine infection in over 1,200 *Argia* individuals, representing 8 species from 15 localities in Nebraska, Kansas, Oklahoma, and Texas. At least two species of *Argia* were collected from each locality. Damselflies were dissected and examined for gregarine infection or curated for identification between June 2006 and September 2007. Sampling in 2006 recovered a previously undescribed gregarine from *Argia sedula* and *Argia translata*, which we subsequently described as *Nubenocephalus secundus*. In the 2007 survey, all eight *Argia* species were identified to be parasitized by a *Nubenocephalus* gregarine. *A. apicalis, A. immunda, A. sedula*, and *A. translata* were identified as being parasitized with a second gregarine species not in the genus *Nubenocephalus*. To date, there are only 3 described species of *Nubenocephalus*, 2 from species of *Argia*. Ongoing morphometric analyses will allow us to determine if the gregarines recovered in this study represent known taxa or new species.

16

The Geography of Host-Parasite Co-evolution.

N.K. WHITEMAN*, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA; A.J. DRUMMOND, Department of Computer Science, University of Auckland, Auckland, New Zealand; and P.G. PARKER, Department of Biology, University of Missouri–St. Louis, St. Louis, MO.

Host-parasite interactions occur across a spatial gradient, from host individuals to local populations, metapopulations and regional scales. Co-evolutionary trajectories are also shaped by history. This includes the phylogeographic histories of interacting host-parasite pairs, as well as the ecological and life-history traits that are canalized in particular parasite clades such as dispersal ability, transmission mode, life-cycle, and effective population size. Co-evolutionary interactions are shaped by microevolutionary forces acting across the spatio-temporal gradient, including genetic drift and natural selection within populations, and gene flow among populations. Understanding the processes underpinning community evolution depends on our ability to integrate population genetic structure, population history, and ecology (natural history) of interacting species

into realistic analytical frameworks. Phylogeographical tools and coalescent modeling can be used to jointly estimate population and lineage divergence times and gene flow among populations of hosts and parasites. Bayesian estimation of population size flux can be used to assess whether host and parasite populations are demographically linked over evolutionary time. We integrate these perspectives using the Galápagos Hawk, and its five ecologically and phylogenetically diverse ectoparasite species, as a case study in the geography of coevolution.

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Molecular Epidemiology and Landscape Genetics as Tools to Examine Foci of Parasite Transmission Within Host Populations.

C.D. CRISCIONE*, Department of Biology, Texas A&M University, College Station, TX; D. SUDIMACK, Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX; J.D. ANDERSON, Perry R. Bass Marine Fisheries, Research Station, Coastal Fisheries Division, Texas Parks and Wildlife Department, Palacios, TX; J. SUBEDI, Department of Sociology and Gerontology, Miami University, Oxford, OH; D.R. RAI and R.P. UPADHAYAY, Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX; J. BHARAT, Tribhuvan University Institute of Medicine, Majarajgung, Kathmandu, Nepal; and S. WILLIAMS-BLANGERO and T.J. ANDERSON, Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX.

We combine molecular epidemiological and landscape genetic approaches to examine the transmission dynamics of the human parasitic roundworm *Ascaris lumbricoides* in Jiri, Nepal. Our goal is to determine if there are focal points of transmission and if so, what are the factors that are correlated with these foci? We genotyped 1,094 adult nematodes using 23 microsatellite markers. The worms were collected from 165 households (320 individual human hosts) in an area less than 20 km^2. Genetic assignment methods make it possible to examine if there are distinct genetic clusters of parasites (i.e., focal points of transmission) within a host population. Landscape genetic analyses can then be used to test for correlations with ecological factors that may affect the distribution of genetic variation within and among these genetic clusters. Initial analyses indicate that there is significant genetic structuring of parasite genotypes within this small sampling area (i.e., small relative to host mobility). Several variables were examined for significant correlations with the observed genetic structure of the parasite. These variables included hosts nested within household, household, host age, host gender, host density, altitude, infection intensity, parasite gender, geographic distance, and time. One main result was the strong correlation of a household effect on the distribution of genetic variation among populations. This result highlights that a significant amount of parasite-to-host transmission is concentrated around households. Furthermore, these results illustrate how molecular analyses complement epidemiological information in providing a better understanding of parasite population biology.

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Inferring Transmission Patterns and Mating Dynamics of *Schistosoma mansoni* using Molecular Markers.

M.L. STEINAUER* and B. HANELT, Department of Biology, University of New Mexico, Albuquerque, NM; E.L. AGOLA, I.N. MWANGI, and G.M. MAINA, Centre for Biotechnology Research and Development, Kenya Medical Research Institute, Kenya; D.M. KARANJA, Vector Biology and Control Research Centre, Kenya Medical Research Institute, Kenya; G.M. MKOJI, Centre for Biotechnology Research and Development, Kenya Medical Research Institute, Kenya; and E.S. LOKER, Department of Biology, University of New Mexico, Albuquerque, NM.

Schistosomes infect 200 million people worldwide, and several million people suffer from severe morbidity as a consequence of these parasites. *Schistosoma mansoni* is the primary infectious agent of schistosomiasis in western Kenya, where drug treatment, HIV, and hybridization with other schistosomes possibly interact to exert selective pressures on this parasite. Our research program uses molecular and evolutionary techniques to address epidemiological issues related to this parasite in its environment. Because they live within the circulatory system, and cannot be easily removed from a living human, only indirect inferences can be made about adult worm populations. Our approach uses microsatellite data from the offspring of human infections, and parentage analysis, to infer the worm burden, genetic diversity, presence of clonal genotypes, mating systems, and fecundity

of these parasites. Using datasets generated from laboratory infections of mice and computer simulations, we show that these techniques are effective tools to make inferences about infrapopulations in humans from offspring data. Also, we show that, in the short term, worms are mainly monogamous but differ greatly in terms of the fitness of individuals and worm pairs, and that eggs passed in the feces and those retained in the liver are not random samples of the entire population. The data, collected from patients in the Lake Victoria Region of Kenya, indicate that worm populations in humans were generally very diverse and were not substructured among patients. Also, humans were infected with relatively few clones, indicating that they become infected with a diverse sample rather than obtaining several individuals derived from the same miracidium. Supported by NIH R01AI044913 and R01AI053695.

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Population Genetics of Selected Loci: Drug Resistance in Malaria.

T. ANDERSON*, Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX.

Resistance evolution is a re-occurring theme in the history of parasite control. Treatment programs inevitably impose strong selection on parasite populations and, as a consequence, drug resistance alleles spread. The rapid spread of resistance alleles within populations leaves distinctive scars within parasite genomes, as flanking alleles hitchhike with selected loci. We can use these characteristic patterns of variation to (a) identify genome regions that contain resistance alleles, and (b) learn about the numbers of origins of resistance alleles and the dynamics of resistance evolution. I illustrate this approach using work on resistance evolution in malaria parasites.

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***Histomonas meleagridis* (Trichomonadidae: Parabasala): Direct Transmission in the Turkey Host without the Aid of Vectors.**

L.R. MCDOUGALD*, A.L. FULLER, P.L. ARMSTRONG, and J. HU, Department of Poultry Science, University of Georgia, Athens, GA.

Histomoniasis is well known to be carried from bird to bird, encapsulated in the ova of the cecal worm (*Heterakis gallinarum*), and further protected in the environment when the ova are consumed by earthworms. However, this scenario does not explain the epidemic lateral transmision in a flock of turkeys, where an entire flock may be involved with 50–100% mortality. In a series of experiments in the absence of cecal worms or other vectors, we determined that histomoniasis could spread readily from infected to uninfected turkeys, when commingled in floor pens. Further tests showed similar results in battery cages if the wire floors were covered with paper or litter. Commingling of infected and uninfected poults, for as little as 48 hr, sometimes produced 90–100% infection transfer. Oral infection was not successful, but contact of the vent with liquid cultures or contaminated feces resulted in infection because of a phenomenon known as cloacal drinking. Stimulation of the dorsal vent lip stimulates rhythmic contractions, which result in any liquid being pulled inside. Such material is transferred immediately to the bursa of Fabricius and, within 15 min, to the ceca. Surprisingly, tests with chickens did not produce similar results. There was no evidence that uninoculated chickens could become infected from commingling with inoculated birds, suggesting that histomoniasis in chicken flocks results from residual contamination of facilities with ova of *H. gallinarum.*

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Molecular Insight into Host Specificity, Life Cycles, and Geographical Distribution of the Rhabdiasidae (Nematoda).

V.V. TKACH, Department of Biology, University of North Dakota, Grand Forks, ND; Y. KUZMIN, Institute of Zoology, Kyiv, Ukraine; and S.D. SNYDER, Department of Biology, University of Nebraska, Omaha, NE.

Nematodes of the family Rhabdiasidae are a relatively small, but globally distributed, group including parasites of amphibians and reptiles. They are generally found in host lungs, although several species parasitize the esophagus, mouth, and eyes of their hosts. Most rhabdiasids possess a unique life cycle that includes alteration of protandrous hermaphroditic parasitic generation (adult worms develop into females only) and bisexual free-living generation; some species show a mixture of both types of life cycles. Systematic and phylogenetic analyses of this group are impeded by high level of morphological uniformity among species, and there previously have been no

published phylogenetic analyses of the family. Number of known genera varies from 6 to 10, depending on the views of a particular author. We used nuclear ribosomal (ITS and LSU) DNA sequences to examine relationships among 20 rhabdiasids belonging to four nominal genera (*Rhabdias, Entomelas, Hexadonthophorus, Pneumonema*) and two putative new genera from five continents and 10 host families. Results of the analysis demonstrate that *Rhabdias* is paraphyletic, with parasites of snakes forming a distinct group distantly related to *Rhabdias* of amphibians. This is in agreement with available life cycle data. On the other hand, *Rhabdias* of lizards, at least in the New World, are most closely related to *Rhabdias* of amphibians based on both molecular and morphological analysis. In turn, *Rhabdias* of amphibians show no clear pattern of evolutionary host association or groupings based on geographical distribution. Remaining rhabdiasids from lizards form two clades, one comprised of members of *Entomelas* parasitizing limbless lizards in Europe and North America and the other comprised of nematodes from Australian skinks (*Pneumonema* and a new undescribed genus). Thus, Rhabdiasidae from reptilian hosts are divided into at least 4 separate groups, which suggests multiple independent evolutionary host switches. Among other results, molecular data support the synonymization of *Hexadontophorus* with *Entomelas*.

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Prevalence of Intestinal Parasites in Red Sokoto (Gudali) Goats Slaughtered in the Gwagwalada Area Council Abattoir, Gwagwalada, Abuja, Nigeria.

H.S. IDRIS* and H. UMAR, Department of Biological Sciences, University of Abuja, Abuja, Nigeria.

Rectal faecal samples from 600 slaughtered red Sokoto (Gudali) goats, between the age range of 1 and 50 months, collected within a period of 10 months, were analysed for parasites using the formal-ether sedimentation and culture techniques. Data collected were analysed using chi-square. Out of the 600 goats examined, 468 (78.00%) were infected with one or more genera of parasite. The prevalent intestinal parasites were *Bunostomum trigonocephalum* in 456 goats (76.00%), *Strongyloides papillosus* in 321 goats (53.50%),*Toxocara vitolorum* in 109 goats (18.17%), *Haemonchus contortus* in 88 goats (14.67%), *Trichuris globulosa* in 61 goats (10.17%), *Trichostrongylus* spp. in 29 goats (4.83%), *Fasciola gigantica* in 19 goats (3.17%), and *Eimeria* in 62 goats (10.33%). Of the 600 goats examined, 362 (60.33%) were females, while 238 (39.67%) were males. Cases of single (genus) and multiple (genera) infections of goats with intestinal parasites were also observed. More of the goats were observed with single infection, compared with those with multiple infections, wherein 46 of the 468 infected goats were cases of multiple genera infections.

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Expansion of *Leyogonimus polyoon* (Class: Trematoda) into the Mississippi River.

R.A. COLE*, USGS National Wildlife Health Center, Madison WI; J. SAUER, USGS, Upper Midwest Environmental Sciences Center, La Crosse, WI; J. NISSEN, USFWS, Region 3 Upper Mississippi River National Wildlife and Fish Refuge, Onalaska, WI; and M. STERNER III, USGS National Wildlife Health Center, Madison WI.

Beginning in 2002, recurring spring and fall water bird mortality events have occurred in Lake Onalaska (Navigation Pool 7 of the Upper Mississippi River). The intestinal trematodes *Cyathocotyle bushiensis* and *Sphaeridiotrema globulus* have been identified as the cause of the mortalities. The majority of water bird species affected have been American coot (*Fulica americana*) and lesser scaup (*Aythya affinis*), with a total mortality on the river from Pools 7–11 estimated at 48,000–60,000 birds since 2002. During the spring mortality event of 2007, we discovered a coot from Lake Onalaska infected with over 600 *Leyogonimus polyoon* in the small intestine. Larval stages of *L. polyoon* had not been found during snail surveys in 2004–2006 nor during examination of birds every spring and fall during mortality events. In the summer of 2007, up to 23% of snails examined at some sites in Lake Onalaska were found to be infected with larval stages of *L. polyoon*, indicating that the parasite has moved into the Mississippi River system and is established. Heretofore this parasite was limited to the Wolf River system in the north-central portion of Wisconsin. The introduced intermediate snail host *Bithynia tentaculata* has been found over 180 miles south of Lake Onalaska since its discovery there in 2004, and it will likely allow the spread of this parasite, as it has *C. bushiensis* and *S. globulus,* to other Pools along the Mississippi River.

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An Unusually Severe Infection of *Collyriclum faba* in an American Crow, *Corvus brachyrhynchos*.

M.C. STERNER III*, USGS National Wildlife Health Center, Madison, WI.

An adult female American crow (*Corvus brachyrhynchos*) from Maryland was presented to the National Wildlife Health Center in Madison, Wisconsin, with numerous crateriform nodules around the vent area. The nodules had coalesced, forming two large growths that completely surrounded the vent, making an exact count of nodules impossible but estimating well over 25 present. Each nodule contained two trematodes identified as *Collyriclum faba* and massive numbers of small brown eggs. This trematode is most commonly reported in passerines and galliformes, with an average infection consisting of 3 to 4 nodules, and only an occasional occurrence of this parasite is reported in corvids. Necropsy revealed at least 5 nodules within the body cavity. Internal granulomas in the messentery resulted in adhesions of the intestine to the messentery, surrounding body cavity, and other portions of the small and large intestine. Each internal nodule also contained two trematodes and large numbers of eggs. Histological sections taken of the external and internal nodules revealed thick-walled fibrosing, verminous, granulomas, indicating a severe reaction of the host to the presence of the parasites. Due to the large number of nodules around the vent, and internal damage resulting from nodules within the body cavity, it is believed that the infection of *Collyriclum faba* was a contributing factor in the death of this bird.

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The Role of Damselflies (Odonata) in the Transmission of *Halipegus eccentricus* to Anurans.

M.G. BOLEK*, Department of Biology, University of Nebraska at Kearney, Kearney, NE.

Haliegus eccentricus Thomas 1939 is a common hemiurid trematode in the eustachian tubes of frogs in North America. However the life cycle of this species has never been completely elucidated. Previous life-cycle studies on *H. eccentricus* suggest that it has a 3-host life cycle. Cystophorous cercariae are shed by *Physa gyrina* snail, first intermediate hosts, and are ingested by *Cyclops* and *Mesocyclops* copepod, second intermediate hosts, where metacercariae develop. Tadpoles ingest these microcrustaceans accidentally through respiratory currents, and it is assumed that worms survive tadpole metamorphosis and migrate to the eustachian tubes of frogs. Here I show, through field work and experimental infections, that the life cycle of *H. eccentricus* utilizes 4 hosts. Frogs become infected with *H. eccentricus* by feeding on infected damselflies; worms mature in the eustachian tubes of frogs releasing eggs within 50–60 days post infection. Cystophorous cercariae develop within 30–35 days post-exposure in *P. gyrina* snails and infect ostracod, *Cypridopsis* sp., second intermediate hosts where metacercariae develop. Exposure of damselfly larvae and bullfrog tadpoles to infected ostracods only resulted in the infection of damselfly larvae and not tadpoles. Because no morphological changes occurred, in the metacercaria stage of *H. eccentricus*, between the ostracod second intermediate host and damselfly larva host, this study suggests that odonates serve as paratenic hosts in the life cycle, which is exceptionally common among other hemiurids.

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Infection of *Babesia gibsoni* in Confiscated Pit Bull Terriers.

M.V. REICHARD*, T.J. YEAGLEY, J.E. HEMPSTEAD, K.E. ALLEN, L.M. PARSONS, S.E. LITTLE, M.A. WHITE, and J.H. MEINKOTH, Department of Veterinary Pathobiology, Oklahoma State University, Stillwater, OK.

Babesia gibsoni is a tick-transmitted protozoan parasite that infects dogs throughout the world. Even though *B. gibsoni* is transmitted by several species of ixodid ticks, a competent tick vector has not been confirmed in North America. In the United States, *B. gibsoni* is an emerging infectious agent most commonly reported in pit bull terriers or in dogs that have a history of fighting with a pit bull. It has been hypothesized that *B. gibsoni* is transmitted by the passage of infected blood from one pit bull to another, during a fight. Our objective was to determine the prevalence of *B. gibsoni* infection in pit bulls that were confiscated as part of dog fighting prosecutions from across the United States. Blood samples were collected by staff from the animal shelters or rescues where the confiscated pit bulls were being housed, and were mailed to the Center for Veterinary Health Sciences, Oklahoma State University, where they were tested for infection with *B. gibsoni*. Blood samples from random dogs not confiscated for fighting were collected from animal shelters and used as controls. DNA was

extracted from dog blood and tested for infection of *B. gibsoni*, using a nested PCR with primers that amplify the 18s rRNA gene for members of the order Piroplasmorida. Nested PCR products from positive samples were sequenced to confirm infection. Blood samples were collected from 158 pit bulls confiscated in Iowa, Michigan, Ohio, Pennsylvania, Virginia, Mississippi, and Washington—including 38 from a high-profile case of a now-incarcerated professional football player. Fifty-one (33.5%) of the pit bulls were infected with *B. gibsoni* and 1 (0.6%) dog was infected with *Theileria annae*. Pit bulls with scars on their face and head (70%), indicating they had been used for fighting, were 3 times more likely to be infected with *B. gibsoni* than dogs without scars. Blood was tested from 218 control dogs and 1 (0.5%) was infected with *B. gibsoni*. The 1 control dog that was infected with *B. gibsoni* was a pit bull. This is the first known report of *T. annae* in North America.

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Plant Parasitism — Evolution of New Utensils for Eating Vegan.

J.G. BALDWIN* and E. RAGSDALE, Department of Nematology, University of California, Riverside, CA, and D. BUMBARGER, Max-Planck-Institut für Entwicklungsbiologie, Tübingen, Germany.

Most soil nematodes in the Rhabditida De Ley and Blaxter, 2004 (=Secernentea) of Chromadorea are microbivores, including most Cephalobomorpha and Rhabditomorpha, with the stoma expressed as a passive cuticle-lined channel. By contrast, the stoma in plant parasites of Tylenchomorpha (Rhabditida) is a hollow cuticular hypodermic needle-like protrusible stylet. Classical light microscope-based hypotheses propose a widely accepted morphological transformation series that culminates in the protrusible stylet linked to plant parasitism. However, molecular-based phylogenetics contradict extant hypotheses of stylet evolution in Tylenchomorpha. These phylogenies instead point to a counter-intuitive morphological transformation to plant parasitism evolving within microbivorous Cephalobomorpha. Whereas superficially this extreme divergence appears unlikely, interpreting 3D computer reconstruction from serial TEM demonstrates new hypotheses of homology and a plausible hypothesis for stylet evolution that is congruent with molecular-based insight. This is accomplished by comparison of exemplar taxa from Tylenchomorpha (*Aphelenchus avenae*), Cephalobomorpha (*Acrobeles complexus*), and Rhabditomorpha (*Caenorhabitis elegans*). The cuticular lining of the open channel-like stoma, as well as the cuticular stylet, are both produced by a suite of distinctive hypodermal, arcade and pharyngeal cells. Whereas these cells and their relative positions are conserved, details of their expression effect highly divergent phenotypic expression of feeding structures. In Tylenchomorpha, hypodermal cells (cheilostom) are positioned to form the lining that guides the stylet. Arcade cells (gymnostom) are expressed between molts as reduced syncytia that form the cone and shaft of the stylet. The anteriormost pharyngeal radial muscle cells (stegostom) are homologs of stylet protractors and form stylet knobs. The stomatostylet, while phenotypically diverse and adaptive within Tylenchomorpha, is likely conserved with respect to underlying tissues and patterns of formation.

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Phylogeny of Acanthocephalans: Inferring the Evolution of Parasitism using Nuclear and Mitochondrial Gene Sequences.

M. GARCÍA-VARELA*, Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México (UNAM).

Acanthocephala (thorny-headed worms) is a phylum of endoparasites of vertebrates and arthropods. The phylum is divided into four classes: Archiacanthocephala, Palaeacanthocephala, Eoacanthocephala, and Polyacanthocephala. The phylum Acanthocephala has a near relationship with Rotifera, and currently both phyla form the clade Syndermata. In this study, I analyzed sequences of small-subunit (SSU) and large-subunit (LSU) ribosomal DNA and cytochrome c oxidase subunit 1 (cox 1) to species representing the 4 classes of the phylum and the 3 rotifer classes (Bdelloidea, Monogononta, and Seisonidea). Maximum parsimony (MP), maximum likelihood (ML), and Bayesian analyses of the combined dataset (SSU + LSU + cox 1 genes) support the monophyly of Acanthocephala. Archiacanthocephala is the sister group to the remaining acanthocephalans. The mammals were the ancestral hosts of the phylum, and the association with other aquatic vertebrates represents a subsequent episode of colonization. The phylogenetic analyses indicate that Bdelloidea is the free-living sister group to acanthocephalans.

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The Genetic Underpinning of Hidden Synapomorphies: Evolution and Development in Cestodes.

P.D. OLSON*, Department of Zoology, The Natural History Museum, London, United Kingdom.

Hidden synapomorphies are shared, derived features assumed to underpin observable synapomorphies. Thus, implicit in our estimation of morphological, behavioural, or other phenotypic synapomorphies is the assumption that such shared traits, in fact, also represent shared genetic programmes. Rarely, however, is convergence addressed at the level of the gene. With ever-increasing tools to interrogate genes and their products, we can now evaluate the correspondence between genotype and phenotype, and thus begin to really understand the processes underlying the phylogenetic patterns we observe. Among cestodes, phylogenetic analysis predicts their segmented bauplan to have evolved sequentially, involving the serial repetition of the reproductive organs and their somatic compartmentalization as separate processes. The genetics behind these processes are entirely unknown, making it impossible to compare their development outside of the group itself and also leaving open questions as to whether non-segmented and/or non-proglottized groups lack the genetic programme, or simply lack its expression. One approach being taken to address this ignorance is an examination of the roles of homeotic genes, which play primary roles in shaping animal bauplans throughout the Metazoa. Beginning by understanding their roles in a fully segmented tapeworm model (i.e., Hymenolepis), a number of Hox gene transcripts have been fully characterized and their spatial expression patterns examined by whole-mount *in situ* hybridization. Early results already implicate direct roles for some of these genes, in both the process of 'segmentation' (Post-2/AbdB) as well as in ovarian formation (Lox4/AbdA), and thus proglottization. Immediate aims of ongoing work are to examine expression patterns throughout their complex life cycle, resolve the anteroposterior polarity of adult cestodes, and examine the possible reversal of polarity during larval metamorphosis. Once accomplished, the roles of the genes may be further characterized via functional assays (e.g., RNAi) and their roles examined comparatively in non-model groups that show unusual forms of development such as spathebothriids and halpobpthriids, *et al*.

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Health Lessons from Analyses of Helminth-Rodent Model Systems.

D. MCKAY*, University of Calgary, Calgary, Alberta, Canada.

Parasitic helminths have been humans' constant companion and can cause considerable morbidity and mortality. Infection with parasitic helminths is a potent stimulus of the hosts immune system, that seeks to identify, destroy and eradiate the parasite. The parasites goal is to complete its life-cycle; this may require inhibiting, skewing, or delaying the immune response of its host. Thus, while parasitism is by definition a malevolent condition, one can ask, "would the immune response mobilized against infection with helminth infection confer any health benefit by blocking concomitant immunopathological reactions?" Adopting this view, we, and others, have been testing this paradigm. Work from my laboratory using murine models of colitis have shown that infection with the rat tapeworm, *Hymenolepis diminuta*, results in a significant amelioration of the colitis induced by the chemical dinitrobenzene (DNBS), but exaggerated the colitic response elicited by intra-rectal instillation of the hapten, oxazolone. The protective effect in the DNBS model was dependent on IL-10, and possibly regulatory immune cells also. Additional studies will be discussed to illustrate the lessons that helminth-rodent models have to teach us about immuno-regulation and how this can be exploited to develop new anti-inflammatory or immuno-regulatory treatments for a variety of diseases such as, inflammatory bowel disease, asthma and auto-immunity.

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The Evolution of Indiscrimination in Ectoparasitic Mites.

M.R. FORBES*, Department of Biology, Carleton University, Ottawa, Ontario, Canada.

Experimental and observational work on dragonfly–water mite associations has shown that these ectoparasitic mites often have negative fitness effects on their dragonfly hosts, but also that mites sometimes show low- or zero-fitness on host species that they attend. Why should such indiscrimination evolve, and why do some dragonflies appear to be winning the arms race? Our theoretical and experimental work shows that alternative host species abundance, and the cost of discrimination, influence whether discriminatory ability evolves among

mites and whether this behavior can invade a population of nondiscriminatory mites. We suspect that many cases favor host indiscrimination (e.g., moderate to high costs of discrimination coupled with near equal abundance of alternative host species). Our results further suggest that tracking of abundant host species might enable other host species to resist mites effectively.

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Regulation Mechanisms of Flea Numbers on their Rodent Hosts: Are Fleas Consumers or Prey?

H. HAWLENA*, Department of Biology, Indiana University, Bloomington, IN.

Mechanisms that regulate ectoparasite populations can influence the evolution and stability of host–parasite dynamics, but yet remain poorly understood. Through a series of experiments, we differentiated between "bottom up" (e.g., intra- and interspecific competition of parasites for limited resources either directly or via damaging the host), and "top down" (e.g., predation by the host) regulation mechanisms of fleas on rodent hosts. The "bottom-up" hypothesis was examined by (1) measuring blood engorgement rate of fleas at varying densities, (2) looking for negative correlations between fleas and competitor ticks in the field, and (3) testing the effect of flea addition and reduction on host body condition and survival. We investigated the "top-down" hypothesis by (1) measuring blood engorgement rate of fleas on grooming-restrained and grooming-allowed rodents, (2) manipulating the time devoted to host grooming and measuring subsequent flea survival, and (3) measuring flea killing rate by rodents as a function of initial flea densities. The results revealed that both mechanisms are effective in regulating flea numbers on their hosts, and thus fleas function simultaneously as consumers and prey. In support of the "bottom-up" hypothesis, (1) fleas at low densities consumed more blood than fleas at twice the density, (2) tick and flea densities were negatively correlated, and (3) increasing flea densities made juvenile rodent hosts less suitable resources for the fleas. The "top-down" hypothesis was also supported, as (1) flea engorgement rate on grooming-restrained rodents was greater than of those on grooming-allowed rodents, (2) flea survival was significantly reduced as rodents spent more time grooming, and (3) rodents, acting similarly to predators, killed fleas accordingly to the functional response types 1 or 3. These mechanisms may limit the parasite burden on an individual host, thereby preventing parasites from overexploiting the host population.

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Immunogenetics and Immune Defense Against an Avian Ectoparasite.

J.P. OWEN*, Department of Entomology, Washington State University, Pullman, WA.

Studies in the growing field of 'ecological immunology' include avian–ectoparasite systems, with a focus on ectoparasite effects on bird fitness and immunological defense. Data on specific immune responses to ectoparasites, and resultant effects on ectoparasite fitness, are sparse. Moreover, effects of immunogenetic variation on these interactions have not been tested directly. To fully understand co-adaptive processes in host–ectoparasite interactions, it is essential that we determine immunological mechanisms that impose a fitness cost on the parasite. Additionally, we need to know effects of host immunogenetic variations, which provide a substrate for ectoparasite selection on host defense. We characterized the immune response of the domestic chicken to a common blood-feeding ectoparasite of birds, and a pest of poultry, the northern fowl mite (*Ornithonyssus sylviarum*). These studies included longitudinal analyses of cellular and humoral responses in the host, histological measurements of local inflammatory responses to mite feeding, and comparisons of mite resistance between congenic and outbred birds with different immunogenetic backgrounds. Local skin inflammation at feeding sites blocked mite access to blood vessels, which initially prevented the first blood feeding stage (protonymph) from obtaining a blood meal and molting to the adult stage. Ultimately, adults were blocked from vessels, impairing egg production. These events forced mite populations to decline, demonstrating a mechanism for immunological resistance. Variation at the major histocompatibility complex (MHC)—a critical group of genes involved with immune function—influenced the level of resistance to northern fowl mite, when compared between congenic lines of hens or between outbred hens with different MHC haplotypes. These studies provide an immunological mechanism and associated immunogenetics for avian resistance to a blood-feeding ectoparasite. As such, they are valuable to future exploration of the reciprocal, coadaptive interactions between birds and ectoparasites.

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Parasite-Mediated Sexual Selection in the *Drosophila–Macrocheles* System.

M. POLAK*, Department of Biological Sciences, University of Cincinnati, Cincinnati, OH.

Research into parasite-mediated sexual selection (PMSS) historically has focused mainly on host mate choice favoring relatively unparasitized males. Further narrowing our understanding of the evolutionary potential of PMSS, is a lack of heritability estimates for parasite resistance and of the mechanisms maintaining genetic polymorphism in natural host–parasite systems. Through a comprehensive set of field and laboratory experiments, it is demonstrated that ectoparasitism by mites, *Macrocheles subbadius*, can drive both pre- and post-copulatory sexual selection in the host *Drosophila nigrospiracula*. Experiments involving the manipulation of mite loads reveal that the physical presence of the mites, *per se*, reduces male mating success in dose-dependent fashion by blocking male mounting and copulation attempts. The decline of mating success with mite load is significantly stronger among smaller males than larger males, because for any given mite load, small males have a larger surface area of their abdomens occupied by entrenched mites. Host body size is therefore acting as a tolerance-conferring trait. Experimental removal of the mites restores male mating success, eliminating, at least under the present laboratory conditions, the possibilities that the reduction in mating success results from host nutrient drain or costs accruing from the host's immunological response, which occurs as melanin deposition at the wound site. Sperm competition experiments reveal that parasitism reduces ejaculate quality, and competitive fertilization success, of male hosts. Replicate artificial selection experiments reveal that ectoparasite resistance is significantly heritable. Selection was performed on base populations recently derived from nature, and heritability estimates range from 11–15%. Comprehensive fitness assays of resistant and susceptible strains reveal significant costs of evolved resistance, suggesting that antagonistic pleiotropy is an important mechanism for the maintenance of genetic variation sustaining PMSS in the *Drosophila-Macrocheles* system.

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Host Defense Reinforces Host–Parasite Cospeciation.

S.E. BUSH*, Natural History Museum, University of Kansas, Lawrence, KS,
and D.H. CLAYTON, Department of Biology, University of Utah, Salt Lake City, UT.

Cospeciation occurs when interacting groups, such as hosts and parasites, speciate in tandem, generating congruent phylogenies. Cospeciation can be a neutral process in which parasites speciate merely because they are isolated on diverging host islands. Adaptive evolution may also play a role, but this has seldom been tested. We explored the adaptive basis of cospeciation using a model system consisting of feather lice (*Columbicola*) and their pigeon and dove hosts (Columbiformes). We reconstructed phylogenies for both groups using nuclear and mitochondrial DNA sequences. Both phylogenies were well resolved and well supported. Comparing these phylogenies revealed significant cospeciation, as well as correlated evolution of host and parasite body size. The match in body size suggested that adaptive constraints limit the range of hosts lice can use. We tested this hypothesis by transferring lice among hosts of different sizes to simulate host switches. The results of these experiments showed that lice cannot establish viable populations on novel hosts that differ in size from the native host. To determine why size matters, we measured three components of louse fitness: attachment, feeding, and escape from host defense (preening). Lice could remain attached to, and feed upon, hosts varying in size by an order of magnitude. However, they could not escape from preening on novel hosts that differed in size from the native host. Overall, our results suggest that host defense reinforces cospeciation in birds and feather lice by preventing lice from switching between hosts of different sizes.

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Parasite Infracommunities within Bluegill (*Lepomis macrochirus*) in the Raritan River, NJ.

C. MCCOY* and M.V. SUKHDEO, Department of Ecology, Evolution, and Natural Resources,
Rutgers University, New Brunswick, NJ.

Ecologists have become interested in the effects of urbanization on host community structure, but little is known about the effects of urbanization on parasite communities. Bluegills (*Lepomis macrochirus*) from the Raritan River, NJ are used as a model organism to study the effects of urbanization on parasite infracommunities. In the summer of 2007, bluegills were collected from 4 sites along the Raritan River, 1 in a rural area, 2 in a suburban

area, and 2 in an urban area. The degree of urbanization at each site was determined by GIS land-use data of the associated watershed. Fish were collected using baited minnow traps and seine net along a 50-m transect at each site. The bluegills were dissected and parasites were counted and identified to species. Eight random samples of macroinvertebrates were taken at each site to determine the invertebrate community. Diversity of the parasite and the macroinvertebrate communities was calculated using the Simpson's Diversity Index. No correlation was found between the level of urbanization and parasite diversity, intensity, or prevalence.

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Molecular Cloning and Characterization of Four Novel Schistosome α3 Fucosyltransferases.

N.A. PETERSON*, D.M. REINITZ, and T.P. YOSHINO, Pathobiological Sciences, University of Wisconsin–Madison, Madison, WI.

Heavily fucosylated carbohydrate epitopes (glycotopes), that are presented on the teguments of larval and adult schistosomes, are key determinants in the modulation of the host immune response and parasite evasion. Importantly, these glycotopes are differentially expressed amongst developmental stages and between sexes of the parasite. To better understand how and why differential glycotope expression occurs, this ongoing study seeks to identify and functionally characterize the enzymes responsible for glycotope synthesis, particularly members of the α3 fucosyltransferase (FucT) family. Sequences of known *Caenorhabditis elegans* and *Schistosoma mansoni* α3 FucTs were used to identify homologues in the *S. mansoni* EST and predicted protein databases. In total, four novel putative α3 FucT genes were identified. Gene transcription was confirmed, by reverse transcriptase (RT)-PCR, in larvae and adults of *S. mansoni*, with some genes exhibiting stage- and/or gender-specific expression. Furthermore, electrophoretic fractionation revealed the presence of additional, unexpected RT-PCR products that have been identified as splice variants. Interestingly, some variants are differentially expressed. Full coding sequences of all genes were obtained by 5' and 3' RACE. BLAST analyses, utilizing conserved domain and non-redundant protein databases, support that these genes participate in α1-3 fucosylation, and transmembrane prediction algorithms indicate that encoded proteins integrate in a type II topology that is characteristic for glycosyltransferases, in general. Current goals include the stable expression of the C-terminal catalytic domains in *Drosophila* S2 cells, which will enable determination of donor and acceptor specificities. Purified recombinant proteins will also be used to produce antibodies for immunohistological localization of these enzymes in the various developmental stages of the parasite.

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Assessing the Utility of Defined Probiotics during Live Vaccination against Coccidiosis in Broiler Chickens.

J.L. MCPHERSON KOMOROWSKI* and J.R. BARTA, Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada.

Coccidiosis is a major parasitic disease of poultry, caused by protistan parasites that invade and inhabit the gut. Probiotics (defined or undefined commensal enteric bacteria, e.g., lactobacilli) could contribute to successful coccidiosis control because microflora are an important first line of defence against enteric infections. To assess this, groups of chickens were orally challenged with *E. tenella*, following vaccination/sham vaccination with a commercial live oocyst vaccine, with or without concurrent administration of a defined probiotic culture. Growth rate and food conversion efficacy of the birds was calculated over the challenge period, and lesions resulting from the parasite challenge were scored blindly using a qualitative scale. Messenger RNA was isolated from cecal tonsils, to detect differences in local cytokine gene expression, to characterize the nature and intensity of any locally expressed immune response. Lastly, chickens were bled and ELISAs were performed to detect the level of antibodies against *E. tenella* sporozoites to characterize the humoral immune response. These experiments examined the complex interactions among protistan pathogens, beneficial gut microflora, and the immune system of the chicken, and may lead to more successful and widespread use of live coccidiosis vaccines in the broiler industry, thereby reducing the industry's reliance on in-feed prophylactic medications.

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Oral Transmission of *Trypanosoma cruzi* with Opposing Evidence for the Theory of Carnivory in the Sylvatic Cycle.

D.M. ROELLIG*, Department of Infectious Diseases and Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA; A.E. ELLIS, Athens Veterinary Diagnostic Laboratory, College of Veterinary Medicine, The University of Georgia, Athens, GA; and M.J. YABSLEY, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine and D.B. Warnell School of Forestry and Natural Resources, The University of GA, Athens, GA.

Trypanosoma cruzi, the causative agent of Chagas disease in humans, has become a parasite of increasing interest in the United States, following the diagnosis of two human autochthonous cases last year. Maintenance of *T. cruzi* in native U.S. wildlife populations increases the potential for zoonotic transmission in North America. While considerable research has been conducted on the molecular evolutionary ecology of *T. cruzi* in recent years, transmission studies pertaining to the sylvatic cycle are limited. In the southeastern U.S., only two vectors (*Triatoma* spp.) are present; however, the prevalence of *T. cruzi* in raccoons (*Procyon lotor*) and opossums (*Didelphis virginiana*) can be high. To investigate an alternative non-vector-based transmission method, we tested the hypothesis that raccoons scavenging infected hosts can result in infection. Macerated tissue from selected organs infected with the amastigote stage of *T. cruzi* was orally administered to experimental groups of raccoons (n = 2/group) at 2, 12, or 24 hr after collection of the tissue samples. Additionally, raccoons in control groups were inoculated intravenously (n = 2) or *per os* (n = 1) with trypomastigotes. To further elucidate transmission routes of *T. cruzi* to raccoons, infected *Rhodnius prolixus* were fed to raccoons (n = 2). Attempts to detect minicircle kDNA from blood and tissue, seroconversion and parasitemias revealed that no raccoons became infected after ingestion of amastigote-infected tissues collected from parasitemic animals. However, *per os* transmission can occur by ingestion of the infective trypomastigote stage or infected reduviid bugs. We can conclude from these findings that oral transmission of *T. cruzi* may be a route of infection for wildlife in sylvatic cycles, but the scavenging behavior of animals is not a factor.

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Fatal Infections of a Protistan Agent in Southeastern Ranid Frog Species.

J.O. COOK* and R.M. OVERSTREET, Gulf Coast Research Laboratory, The University of Southern Mississippi, Ocean Springs, MS.

Infections by the protistan agent *Dermomycoides* sp. caused mass mortality of tadpoles of the Mississippi gopher frog, *Rana sevosa*, in 2003 at the frog's primary breeding pond in coastal Mississippi, USA. The frog is one of the rarest in North America, with about 100 adult individuals known in the population. Fatal infections have also occurred in tadpoles of *R. sphenocephala* in other ponds in coastal Mississippi and in *R. capito*, *R. sphenocephala*, and *R. catesbeiana* in ponds in northwestern Florida. Adult frogs can be infected with *Dermomycoides* sp., but none have been shown to die from it. Tadpoles infected with *Dermomycoides* sp. rarely die, and individuals can undergo metamorphosis without losing the infection. We have documented infections in a wide range of anuran hosts throughout the continental United States, including the northern Gulf Coast states, Maine, and Oregon. The agent can occur in the intestinal cavity as well as intestinal, muscle, mesentery, kidney, liver, brain, and subdermal tissues. The agent is transmitted by the ingestion of spores, penetration of a motile aquatic stage, or ingestion of vectors. Funded in part by the U.S. Department of the Interior and the Mississippi Department of Wildlife, Fisheries, and Parks.

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Hirudinidae[3]: Towards a Revision of the World's Medicinal Leeches.

A.J. PHILLIPS*, The Graduate Center, The City University of New York, New York, NY and Division of Invertebrate Zoology, American Museum of Natural History, New York, NY; and M. SIDDALL, Division of Invertebrate Zoology, American Museum of Natural History, New York, NY.

Hirudindae contains the most notorious of the bloodfeeding leeches, the medicinal leeches. These worms gained in popularity with physicians practicing bloodletting, or phlebotomy, due to anticoagulants in the saliva that causes the bite to bleed freely, even after the leech has left. This treatment was performed worldwide, for centuries, with a member of the Hirudinidae native to the area. While a higher-level analysis of the Arhynchobdellidae, by Borda and Siddall (2003), found that the Hirudinidae is surprisingly comprised of two groups, this more intensely focused preliminary analysis shows that the Hirudinidae is actually split among three groups. A morphological analysis of twenty-two morphological characters, based on jaw dentition, sexual anatomy, and external morphology, failed to provide a resolution for most of the relationships in the family. DNA sequence data from nuclear 18S rDNA, nuclear 28S rDNA, mitochondrial 12S rDNA, and mitochondrial cytochrome c oxidase subunit I, were examined separately, and in combination, in a parsimony analysis. This analysis of representative species of the Hirudiniformes indicates that the world's medicinal leeches comprise multiple independent groups. Clade membership is only partially indicated by continental origin. The African Hirudinidae are split between two clades, with the unexpected results of the North African and Eastern European taxa being sister to select genera of Central and South America, one of which is a new genus with a unique morphology among leeches. These results suggest that, what was previously considered the family Hirudinidae, is actually 3 families: the Macrobdellidae Richardson, constituted by most New World taxa; the "true" Hirudinidae, with the type species (*Hirudo medicinalis*); and a new family, including the subset of African species grouped with *Limnatis nilotica* and associated New World taxa.

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Evolution of Feeding Preferences and Ecological Associations of Leech Species of *Placobdella, Haementeria,* and *Helobdella*.

A.F. OCEGUERA-FIGUEROA* and M.E. SIDDALL, Division of Invertebrate Zoology, American Museum of Natural History. New York, NY.

Of the 3 subfamilies of leeches of Glossiphoniidae proposed by Sawyer (1985), only the monogeneric Theromyzinae is monophyletic. The other 2, Haementeriinae and Glossiphoniidae, appear paraphyletic or polyphyletic in all phylogenetic analyses. Previous studies showed that the relatively common bloodfeeders *Placobdella* and *Haementeria* spp., as well as non-sanguivorous *Helobdella* (which includes world-wide distributed leeches that feed on haemolymph of oligochaetes and snails), form a group. This clade seems to be well supported, but the relationships between genera and among species are not resolved. Associated with feeding habits are a number of morphological (e.g.,. kind of salivary glands, mycetomes) and ecological (association with bacteria) characteristics. To develop a robust explanation of the evolution of these characteristics, we conducted a phylogenetic analysis of the clade formed by *Placobdella, Haementeria,* and *Helobdella*, using parsimony methods of phylogenetic inference and mitochondrial (12S, COI, ND1) and nuclear (18S rDNA) molecular data. Our results suggest that the common ancestor of the clade was haematophagous on vertebrates, and that this characteristic was lost in the clade of the species of *Helobdella*. Whole genome sequence data corroborate this view. Detailed examination of the internal anatomy of species of *Placobdella* and *Haementeria* reveals specialized bacteria-bearing mycetomes. Unexpectedly, though it is clear that mycetomes in *Placobdella* spp. and in *Haementeria* spp. are homologous in function, they are morphologically distinct, and each clade of leeches is associated with a completely different clade of bacteria.

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Amphibian Lungworms and Pesticides: A Balanced View of Host–Parasite Relationships and Ecotoxicology.

G.J. LANGFORD* and J. JANOVY JR., School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.

Agricultural lands are the most pervasive human landscape on Earth, forming a patchy network of natural and human-managed ecosystems. Agriculture has been cited as a factor in the decline of biodiversity worldwide. In particular, pesticides have been given much attention; most studies on pesticides have concentrated on strictly free-living organisms, and rarely consider parasites. Among the few studies that have incorporated parasites, a host-centric approach was taken, and thus little data are available on the effects of pesticides on the host–parasite relationship. To determine the effect pesticides have on a host–parasite relationship, the lungworm *Rhabdias joaquinensis*, and two species of amphibians, *Rana blairi* and *Acris crepitans*, were exposed to environmentally relevant amounts of pesticides. Mortality of juvenile lungworms and frog hosts was recorded throughout pesticide exposure. Following exposure, experimental infections were performed to assess the functionality of the host–parasite relationship. Results suggest that juvenile lungworms were significantly more sensitive to pesticide exposure than their amphibian hosts. In most experimental treatments, lungworms were killed during pesticide exposure, but few amphibians died during exposure. Surviving lungworms varied greatly in their ability to infect pesticide exposed hosts. However, it was clear that pesticide exposed host–parasite experiments resulted in lower parasite prevalence and intensity than seen in control experiments. Given the patchy network in most agricultural landscapes, it appears that environmental heterogeneity may allow parasites, and hosts exposed to various pesticide levels, to come into contact, which would influence host–parasite interactions.

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Infectious Parasites as Ambassadors for Biology in Books, Magazines, Newspapers, and Blogs.

C.W. ZIMMER*, Science writer, Guilford, CT.

Parasites have a powerful hold on the popular imagination. A string of science fiction novels over the past 50 years have exploited this fascination and terror, transforming real parasites into monsters. This attraction also makes parasites an excellent means by which to introduce people to important aspects of biology, from co-evolution to ecology to behavior. I will discuss my own experience writing about parasites in books, magazines, newspapers, and most recently on blogs. In addition, I will explore the work of other science writers and consider some of the pitfalls to be avoided in presenting parasites to the public.

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Public Awareness of Parasitology Through Art.

W.C. CAMPBELL*, Research Institute for Scientists Emeriti, Drew University, Madison, NJ.

The use of science as subject-matter in the arts is not new. Although still relatively uncommon, it does provide a small bridge between the two realms. This illustrated talk offers a personal view from that bridge. The paintings and poems here presented range from the grave to the frivolous. In the paintings, parasites are prominent but depicted in a manner far from precise. In the poems, parasites are usually the central characters, but sometimes they play a cameo role or even remain off-stage. With pictorial representation (especially if it is somewhat outlandish), it is fairly easy to catch the public eye; but paintings of parasites are seen by very few people. Poetry requires a degree of attention that few are willing to bestow (the public having discovered that the effort is not always rewarded); yet poems, if published, will reach more people. Art is personal, and the promotion of an underlying science is not its objective. Happily, however, enhanced public awareness is a probable outcome.

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Public Awareness of Parasitology Through Film.

D. DESPOMMIER, School of Public Health, Columbia University, New York, NY.

[No abstract received]

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Introduction to Symposium: Dogma in Parasite Ecology, Evolution, and Genetics.

G.W. ESCH*, Department of Biology, Wake Forest University, Winston-Salem, NC.

The many dogmas dealing with parasitology are both 'storied' and new. They produced great fame and a Nobel Prize for Ronald Ross, and great fame but ignominy for Fritz Schaudinn. The shadows cast by giants such as these, and others of the nineteenth and early twentieth centuries, are a significant part of our parasitological landscape. In recent years, however, we have seen a great spate of discoveries and advances in the ecology, evolution, and genetics of host–parasite interactions that hold great significance for the future of our discipline. Many of these ideas, concepts, and methodologies, both old and new, will be outlined and discussed by three presenters, i.e., Cam Goater, Mike Sukhdeo, and Dan Zarlenga. A brief question and answer session will follow.

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Parasite Behavior and Host Food Webs: The Worm's-Eye View.

M.V. SUKHDEO*, Department of Ecology, Evolution, and Natural Resources, Rutgers University, New Brunswick, NJ.

It would be easy to understand parasite transmission strategies if parasitologists could see the world from the parasites' perspectives. Parasite perceptions of their world can often be deduced from their behavior, but sometimes we can be quite wrong about the worm's-eye view. Consider the generally accepted idea that parasites recognize their specific hosts. This is an idea that reflects decades of work on host-finding behaviors by trematode miracidia. However, it is parasitological dogma. Even though parasitologists tend to believe this, very few parasites actually seem to recognize their own host. For example, the cercariae of trematodes can be completely oblivious to their host—even when they are only millimeters away from the host. In fact, the evidence now indicates that parasites are not selected for recognition of their hosts, but are selected for the space and time when contact with their host is maximized. This suggests that in the parasite's world, space and time provide predictable coordinates to identify host availability. Another way of saying this is that the interactions between the host and its parasite must consist of stable evolutionary associations. To explore this question, we would need to study the role of hosts and parasites in the ecosystem, as described by feeding relationships in food webs. Here we encounter one of the biggest dogmas from ecological thinking—that parasites are not significant actors in food web dynamics, and thus can be ignored. This is why most studies of food webs do not include parasites, and why it is difficult to integrate parasites into ecosystem processes. This dogma has to be changed. We propose an energetic perspective of food web dynamics that crosses all levels of natural organization, from the individual to the ecosystem, and which includes parasites. This would be the new dogma.

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Metacercariae, Minnows, and Myths: Experimental Ecology of a Host/Parasite Interaction.

C.P. GOATER*, Department of Biological Sciences, University of Lethbridge, Lethbridge, Alberta, Canada.

Trematode metacercariae traditionally are considered as immature adults encased by a cyst wall within tissues of an intermediate host. This stage of the trematode life-cycle is usually regarded as a resting stage, both ecologically and developmentally. Further, metacercariae typically are viewed as host- and tissue generalists. Because few metacercariae/host interactions are amenable to experimental manipulation, alternative scenarios have rarely been evaluated. Results from our experimental studies, involving two species of diplostomid trematode, challenge this dogma. Metacercariae of *Ornithodiplostomum ptychocheilus* and *Ornithodiplostomum* sp. are host specialists in fathead minnows. They are site specific, with the former confined to specific laminar regions of the optic lobes, the latter to the body cavity. Metacercariae of both species undergo a 24-hr period of migration within specific tissues, followed by an 8–10 wk period that includes sequential growth, consolidation, and encystment phases. The growth phase, in particular, involves extensive morphological modification to the tegument that is indicative of extensive metabolic interactions at the host/metacercariae interface. Most remarkably, both species undergo an obligate habitat shift, with development stages restricted to one site, encystment stages to another. Our revised view of metacercariae development has directed our experiments on metacercariae-induced affects on host fitness, host behaviour, and on metacercariae-mediated natural selection. Overall, the results of these experiments show that chronic reductions in host growth, survival, and behaviour are due to effects caused by the developing metacercariae. Because the developing stages are non-infective, parasite-induced alterations in host phenotype are best explained as side effects of persistent pathology.

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Genetic Diversity among Parasitic Nematodes and its Impact on Molecular Epidemiological Studies.

D.S. ZARLENGA JR.*, US Department of Agriculture, ARS, ANRI, Bovine Functional Genomics and Animal Parasitic Diseases Labs, Beltsville, MD.

Population studies on parasitic nematodes were once relegated to evaluating morphological characters in order to delineate parasite genera. With the advent and advancement of methods using isoenzymes, PCR, and DNA sequencing to generate biochemical markers, appraising species-level variation between populations, as well as among individual organisms within a single population, has been greatly enhanced. This capability has created both benefits and problems for epidemiological studies and population geneticists. In some instances, genetic markers have been successfully assigned to parasite phenotypes, but in others, high levels of within-population genetic variation have compromised comparative studies, as well as thwarted whole genome-sequencing efforts. Clearly, there is a need to develop tools to evaluate nematode genetics, but sequence heterogeneity within populations may, over the near term, require focus on polymorphism among exons rather than classic whole-genome shotgun sequencing. The level of genetic diversity within species raises several interesting questions: (1) Is abundant genetic heterogeneity attributable to large populations, diversifying natural selection, or elevated mutation rates? (2) Is recurrent and rapid genetic diversification a means to enhance population fitness in the presence of environmental or artificial stress? (3) Are we asymptotically reaching a limit in discriminating biologically relevant genotypes, and how can such studies advance our understanding of comparatively recent migrations and/or translocations? and (4) What roles do host genotype, species, and immune response play in diversifying or constraining worm populations? A recent review of literature may provide some insight into these, and other, issues related to genetic diversity and the role that human intervention plays in its expansion or contraction.

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Neuropeptide Identification in Phylum Platyhelminthes.

P. McVEIGH*, Biomolecular Processes: Parasitology, School of Biological Sciences, Queen's University Belfast, United Kingdom; G.R. MAIR, Leiden Malaria Research Group, Leiden University Medical Centre, Leiden, The Netherlands; M. ZAMANIAN and E. NOVOZHILOVA, Department of Biomedical Sciences, Iowa State University, Ames, IA; L. ATKINSON, Biomolecular Processes: Parasitology, School of Biologic Sciences, Queen's University Belfast, United Kingdom; M.J. KIMBER and T.A. DAY, Department of Biomedical Sciences, Iowa State University, Ames, IA; and A.G. MAULE, Biomolecular Processes: Parasitology, School of Biological Sciences, Queen's University Belfast, United Kingdom.

Parasitic flatworms include some of the most economically and medically important helminth parasites known to man, including *Schistosoma* spp. blood flukes—the causative agents of schistosomiasis. In addition to the *Schistosoma mansoni* genome sequence, appreciable numbers of expressed sequence tags (ESTs) are now available for many flatworms. Genomic data can aid essential research into helminth biology and thus have the potential to catalyse drug target identification and validation. With resistance to existing anthelmintics becoming a subject of increasing concern, the search for new therapeutic targets is essential. Although the helminth neuromuscular system is the site of action of most currently used anthelmintics, the neuropeptide signalling arm of the nervous system has not yet been exploited pharmacologically. Given the proven biological importance of helminth neuropeptides, neuropeptide signalling is an appealing focus for drug target discovery. However, essential receptor deorphanisation (ligand-receptor matching) studies are being hindered by an ignorance of endogenous flatworm neuropeptides. The current study was aimed to address this matter by identifying novel flatworm neuropeptides, through BLAST (Basic Local Alignment Search Tool) trawls of available genomic resources. Degenerate search strings were employed, and returned sequences were evaluated by manual identification of characteristic neuropeptide motifs. A total of 28 neuropeptide-like sequelogs were identified from 11 flatworm species. With the exception of neuropeptide F, and several novel FMRFamide-like peptides (FLPs), none of the putative neuropeptides display signature sequences common to neuropeptides known from other species. Several of the putative neuropeptides have been localised immunocytochemically within the nervous system of *S. mansoni*, revealing restricted expression patterns. Functional investigations employing physiology and gene silencing methods in *S. mansoni* are ongoing. This work was funded by The National Institutes of Health Grant ROI-AI49162.

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Ligand-Gated Ion-Channels in the Genome of *Haemonchus contortus*.

R.N. BEECH*, J. LIAN, and J. NABHAN, Institute of Parasitology, McGill University, Montreal, Quebec, Canada.

The nervous system of parasitic nematodes provides a primary target for anthelmintic drugs. A majority of the drugs available bind to, and activate, members of the ligand-gated ion-channel family. Many of the newly developed anthelmintics are also likely to exert their effects through these channels, highlighting their great importance for understanding parasite neurobiology as well as the mechanisms of action and resistance to many anthelmintic drugs. Bio-informatics analysis of the genome sequence data, available for the model sheep nematode *Haemonchus contortus*, has identified a large family of about 90 ligand-gated ion-channels. These include channels predicted to gate either anions or cations in response to ligands which include acetylcholine, GABA, glutamate, serotonin, histamine, and others. Targeted amplification of reverse transcribed mRNA, prepared from adult and larval *H. contortus* and using primers specific for predicted LGIC sequence and the sequence of either spliced leaders SL1 or SL2, has produced cDNA clones from 34 LGIC genes. Several of these show evidence of the alternative splicing typical of the similar channels found in the nematode *Caenorhabditis elegans*. With one exception, transcripts were trans-spliced to either SL1 or SL2. In one instance, different cDNA products from a single gene were identified that had been fused to either SL1 or SL2. Phylogenetic analysis, in comparison with the LGIC family from *C. elegans*, shows that a majority of the genes are directly homologous with those in the parasite. Some genes are present only within *C. elegans*, while others are unique to *H. contortus*. The great similarity in predicted protein sequence between several of the LGICs in *H. contortus* suggests that this gene family has undergone significant evolutionary change since the most recent common ancestor with *C. elegans*. Direct comparison between the LGIC families in a parasitic and non-parasitic nematode will help us to predict the utility of *C. elegans* as a model system for understanding the parasitic nematode nervous system.

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Sequence Variation in the Genome of *Haemonchus contortus*.

R.N. BEECH*, Institute of Parasitology, McGill University, Montreal, Quebec, Canada; E. REDMAN, Department of Infection and Immunity, Glasgow University, Glasgow, United Kingdom; K. MUNGALL and M. BERRIMAN, Sanger Genome Center, Cambridge, United Kingdom; and J.G. GILLEARD, Department of Infection and Immunity, Glasgow University, Glasgow, United Kingdom.

Populations of many parasitic nematodes are thought to contain extensive DNA sequence variation that has been used to explain the rapid development and spread of anthelmintic resistance. A detailed understanding of the characteristics of this variation would greatly increase our ability to understand the underlying genetic mechanisms. The genome sequence currently available for *Haemonchus contortus* has been derived from libraries containing DNA of many individual parasites, as well as one sequence prepared from the DNA of a single individual male. We have used this resource to investigate the nature and extent of sequence variability over the *H. contortus* genome. Overlapping, randomly chosen sequence reads suggest sequence divergence between alleles ranges from 0% to more than 30%, at which point it becomes impractical to identify overlapping sequence, based solely on similarity. Analysis of expressed sequence tags indicates that sequence divergence of coding regions is significantly less, from 0% to 5%. Comparison of overlapping BAC sequences, ranging from 50 kb up to 130 kb, finds that one continuous 47 kb segment includes a region of near identity extending up to 6 kb surrounded by sequence whose divergence ranges from 1% to more than 40%. Again, this variation is found predominantly within predicted non-coding sequence. The increased length of these sequences makes it possible to characterize insertions and deletions within the sequence much more reliably, and these range from single nucleotides up to almost 5 kb. Several of the insertions have similarity to reverse transcriptase, suggesting these may represent retrotransposons. Many regions within the overlapping BAC sequence are characteristic of transposons, including long inverted repeats, as well as being highly repeated within the genome. All of the longer insertion-deletion events lie outside of coding regions, either within introns or in intergenic regions. This work supports the conclusion that parasitic nematodes are highly variable, and provides a quantitative measure of both SNP and insertion-deletion variation.

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Amidating Enzymes — Functional Characterization and Gene Silencing in the Blood Fluke *Schistosoma mansoni*.

L. ATKINSON* and P. MCVEIGH, Parasitology, School of Biological Sciences, Queen's University, Belfast, Northern Ireland, United Kingdom; G.R. MAIR, Department of Parasitology, Leiden University Medical Centre, Netherlands; N. MARKS, Parasitology, School of Biological Sciences, Queen's University, Belfast, Northern Ireland, United Kingdom; M.J. KIMBER and T.A. DAY, Department of Biomedical Sciences, Iowa State University, IA; and A.G. MAULE, Parasitology, School of Biological Sciences, Queen's University, Belfast, Northern Ireland, United Kingdom.

The sequential action of two enzymes, PHM (peptidylglycine α-hydroxylating monooxygenase) and PAL (peptidyl-α-hydroxyglycine α-amidating lyase), is required by many bioactive neuropeptides for post-translational C-terminal amidation. In higher organisms, this reaction is catalysed by the bifunctional protein PAM (peptidylglycine α-amidating monooxygenase), which expresses PHM and PAL as two separate domains. However, in some invertebrates these enzymes are expressed independently on distinct genes, for example, in *Caenorhabditis elegans, Drosophila melanogaster* and *Lymnaea stagnalis*. Previous work has characterised schistosome PHM, suggesting that PHM and PAL are expressed as separate monofunctional proteins in *Schistosoma mansoni*. Here, we identify a cDNA encoding a novel schistosome PAL, reveal functional properties by transient expression of the protein, and examine expression patterns using immunocytochemistry. Expression analysis of schistosome PHM reveals widespread expression throughout the central and peripheral nervous system, and co-expresssion with selected amidated neuropeptides; particularly noteworthy were the high numbers of sensory structures innervated by SmPHM-expressing nerves, providing previously unseen detail of the schistosome peripheral nervous system. This study further investigates the role of schistosome PHM and PAL, using RNA interference (RNAi) in cultured schistosomula employing electroporation and soaking as modes of dsRNA delivery. Preliminary data indicate successful silencing of these genes, confirming that neurons in *S. mansoni* schistosomules possess a fully functional RNAi pathway. These data provide opportunity to interrogate neuronal targets in schistosomes using RNAi.

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A Potential Role for *Fasciola hepatica* Cathepsin L in Neuropeptide Signal Termination.

A. MOUSLEY*, L. MCGONIGLE, E. CAMERON, N.J. MARKS, and G.P. BRENNAN, School of Biological Sciences, Queen's University Belfast, Belfast, Northern Ireland; J.P. DALTON, Institute fot the Biotechnology of Infectious Diseases, University of Technology, Sydney, Australia; and A.G. MAULE, School of Biological Sciences, Queen's University Belfast, Belfast, Northern Ireland.

Fasciola hepatica is a flatworm parasite that causes fasciolosis in cattle and sheep. It is the most important flatworm parasite of livestock in Western Europe and is accountable for worldwide economic losses of ~$2 billion per year. The control of fasciolosis currently relies on the benzimidazole triclabendazole; however; resistance to this drug is spreading rapidly, such that the long-term control of liver fluke is dependent on the application of novel strategies. The neuromuscular system in helminths has been well established as a good drug target. Neuromuscular activity in the liver fluke *F. hepatica* is modulated by myoexcitatory neuropeptides with RFamide C-termini, including neuropeptide F (NPF) and members of the FMRFamide-like peptide (FLP) family. Although nothing is known about signal termination processes in flatworms, several lines of evidence implicate *F. hepatica* cathepsin L (FheCL) in the termination of neuropeptide-signalling: (1) FheCL has been observed in nerves and closely associated with muscle, (2) recombinant FheCL can efficiently cleave FLPs *in vitro*, and (3) FheCL inhibitors can enhance FLP-induced myoexcitation. Recently, RNA interference (RNAi) has been successfully used to silence cysteine proteases, including cathepsin L, in the newly excysted juvenile (NEJ) stage of *Fasciola*. This study uses the RNAi platform and immunocytochemistry/confocal microscopy to examine the effects of silencing cathepsin L on NPF- and FLP-expression, and behavioural assays to monitor resultant phenotypes in the NEJs. Results reveal an increase in RFamide/NPF expression following silencing of cathepsin L, in addition to aberrant phenotypes associated with NEJ movement that are comparable to FLP-induced changes in locomotion. These results further support a role for FheCL in neuropeptide signal termination and highlight the potential of signal termination proteases as novel drug targets.

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Identification and Characterization of Calcium-Interacting Proteins in Larval *Schistosoma mansoni*.

A.S. TAFT* and T.P. YOSHINO, University of Wisconsin-Madison, Madison, WI.

Using Serial Analysis of Gene Expression (SAGE), we recently documented that the transformation of the *Schistosoma mansoni* free-swimming miracidium to the molluscan sporocyst stage is associated with a multitude of gene expression changes. These changes are hypothesized to be either directly or indirectly related to stage-specific alterations in larval morphology or physiology. The goal is to determine which genes and processes may be involved in the penetration of the miracidium; and subsequent transformation to, and development of, the sporocyst stage. Previous studies have demonstrated that egg hatching and miracidial transformation can be interrupted by the use of calcium channel blockers and calmodulin inhibitors. The divalent cation, Ca++, is a cellular signal and/or cofactor involved in diverse processes including secretion, metabolism, muscle movement, and neuronal function. However, little is known about the role of calcium or calcium binding proteins in the miracidium and subsequent intramolluscan stages. A number of stage-specific calcium interacting genes were identified, using SAGE, that may be involved in calcium-dependent processes. SME16 (a 16kDa calcium binding protein), calcineurin B, and calponin were transcriptionally more abundant in miracidia, whereas calreticulin and two previously uncharacterized calmodulin homologues are upregulated in early developing sporocysts. We have previously demonstrated that SME16 is localized in the cilia and ciliary plates of the miracidia, suggesting its involvement in miracidial locomotion. Recombinant proteins have been expressed for several other calcium-interacting proteins for the purpose of immunolocalizing these proteins to specific larval tissues. This research will give us a better understanding of the proteins and enzymatic pathways required for miracidial transformation and subsequent sporocyst development.

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Application of RT-PCR to Study *in vitro* Development of *Cryptosporidium parvum* and its Viral Symbiont CPV.

M.C. JENKINS*, C.N. O'BRIEN, and B. ROSENTHAL, Animal Parasitic Diseases Laboratory, ARS, USDA, Beltsville, MD; and J. TROUT, J. KARNS And R. FAYER, Environmental Microbial Safety Laboratory, ARS, USDA, Beltsville, MD.

Cryptosporidium parvum and *C. hominis* contain a double-stranded RNA viral symbiont termed CPV (*Cryptosporidium parvum* virus). Recent studies in our laboratory have found a correlation between intracellular CPV levels and fecundity of *C. parvum* in dairy calves. One goal of our research is to more clearly understand the relationship between the viral symbiont and the parasite by altering *C. parvum* development and/or viral replication *in vitro*. Cell cultures were infected with *C. parvum* sporozoites, after which nucleic acids were extracted at various times post-infection. Viral and parasite targets were then amplified using standard and real-time RT-PCR assays. Semiquantitative PCR was conducted to relate intracellular levels of *C. parvum* to concentration of CPV. Preliminary analysis indicates that CPV replication changes during the course of *C. parvum* development *in vitro*. CPV is most abundant between 36–48 hours post-inoculation. Studies are underway to compare CPV development between gamma-irradiated and non-irradiated *C. parvum* sporozoites.

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Microsatellite Variation in the Salmonid Trematode *Crepidostomum farionis*.

W.D. WILSON* and T.F. TURNER, Department of Biology, University of New Mexico, Albuquerque, NM.

In order to examine the reciprocal interactions of the trematode *Crepidostomum farionis*, and the native, endemic Rio Grande cutthroat trout *Oncorhynchus clarki virginalis*, in several high-elevation streams in northern New Mexico, nine microsatellite markers have been developed in the trematode *C. farionis*. Three enriched libraries were created and subsequently cloned and screened for repeats. After screening 60 clones, 9 repeats were identified using the program msat Commander. Specifics of intra- and inter-population variation will be discussed.

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Isolation and Immuno-Chemical Localization of *Taenia solium* Gap Junctions.

K.L. WILLMS* and R. ZURABIAN, Department of Microbiology and Parasitology, Medical School, National Autonomous University of Mexico, Mexico City, Mexico; A. LANDA, Department of Microbiology and Parasitology, Medical School, National Autonomous University of Mexico, Mexico City, Mexico; and L. ROBERT, Department of Microbiology and Parasitology, Medical School, National Autonomous University of Mexico, Mexico City, Mexico.

Invertebrate gap junctions and their protein components, innexins, have been described in a number of species. Ultrastructural analyses have shown a large number of gap junctions in the neck and immature proglottid tissues of adult *Taenia solium* worms. In these helminths, cytoplasmic glycogen sacs are connected by numerous discrete gap junctions to other cells throughout the maturing strobilar tissue of these flatworms. Biochemical methods were used to purify membrane fractions containing GJs to relative homogeneity. Gap-junction-enriched pellets were obtained by ultracentrifugation in discontinuous sucrose gradients. Ultrastructural analysis of gap-junction enriched pellets revealed plasma membranes coupled by gap junctions. A transmembrane peptide sequence from a highly conserved innexin region was used to construct a 20 amino acid synthetic peptide coupled to keyhole limpet hemocyanin, and used to raise polyclonal antibodies in rabbits. The antiserum (Ab-Inx-pep) recognized both a 60- and 70-kDa protein in Western blot of the GJ-enriched pellet fraction. Immuno-histochemistry of larval and adult worm segments, treated with Ab-Inx-pep and a secondary anti-rabbit IgG coupled to fluorescein, revealed strong specific binding to the tegumentary surface of the worm, as well as patchy fluorescent areas in the parenchymal tissue. By electron microscopy, equivalent tissues, incubated with Ab-Inx-pep and secondary antibody to rabbit IgG coupled to colloidal gold, revealed strong specific binding to the microvesicular membranes of the tegumentary surface. The results indicate that both the tegument of cysticerci and adult *T. solium* contain innexin rich membranes, which may function as a tegumentary transport system of small molecules.

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Phylogenetic Relationships amongst Members of the Apicomplexa Inferred using a Multi-Gene and Multi-Genome Approach.

J.D. OGEDENGBE* and J.R. BARTA, Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada.

Parasites in the phylum Apicomplexa are important for understanding the evolution of parasitism and host adaptations from marine to terrestrial habitats. Important members of the group include the eimeriids, haemosporinids, cryptosporidida, adeleids, and piroplasms. The relationships among, and within, these recognizable groups of apicomplexan parasites have been poorly understood; the adeleids, in particular, have not benefited from molecular phylogenetic analysis, and phylogenetic hypotheses have been based primarily on morphological details. We used aligned sequences from the nuclear 18S and 23S rDNA, plastid polymerase, and mitochondrial COX I genes, individually and collectively, to infer the interrelationships among these various apicomplexan taxa. Maximum parsimony, maximum likelihood, and Bayesian methods were used for the various analyses, with appropriate taxonomic or functional outgroup taxa included. Taxa belonging to recognized groups within the Apicomplexa formed monophyletic clades. Analysis, using the individual genes, reasonably resolved the various apicomplexan groups with strong bootstrap support and high Bayesian posterior probabilities. The multi-gene, multi-genome (18S, 23S, rPo and COXI) analysis appeared to indicate that some members of the Apicomplexa, especially the eimeriids, occupied similar niches in different hosts, before their present adaptive hosts. New sequences generated in our lab, from marine and terrestrial gregarines and adeleids, were supplemented with additional sequences from GenBank, representing a range of other apicomplexan taxa to provide a phylogenetic reconstruction that suggests that gregarines form a monophyletic clade with the haemosporinids and cryptosporidia, and the adeleids form a monophyletic clade with the piroplasms. These well-supported clades differ from classical taxonomic groupings that were based solely on morphological features. These observations highlight the value of multi-gene, and multi-genome, molecular analyses for resolving evolutionary relationships among apicomplexan parasites.

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Snail Host Genetic Diversity across Space and Time.

E.A. THIELE*, Department of Biological Sciences, Purdue University, West Lafayette, IN;
G. CORRÊA-OLIVEIRA, Cellular and Molecular Parasitology, FIOCRUZ - Centro de Pesquisas René Rachou, Belo Horizonte, MG, Brazil; and D.J. MINCHELLA, Department of Biological Sciences, Purdue University, West Lafayette, IN.

The freshwater snail *Biomphalaria glabrata* is the principal intermediate host for the medically significant parasite *Schistosoma mansoni* within Brazil. Extensive studies have described the environmental factors likely to predict snail presence, or absence, within rural Brazilian villages; however, relatively little work has sought to assess the degree of genetic variation and subdivision among such municipal and regional microhabitats. Moreover, few of the genetic studies available have assessed variation on a temporal scale. In order to assess genetic variation of *B. glabrata* both spatially and temporally, we sampled snail populations located within 4 endemic villages in the state of Minas Gerais, Brazil, across several seasonal periods. Snails were genotyped at 8 microsatellite loci and genetic diversity was assessed by determining the number of alleles per locus (N_A) and the observed heterozygosity (H_O) of alleles at, and across, all loci. Population differentiation (F_{ST}) within, and among, villages was estimated in order to determine the degree of snail population structuring, and to investigate the influence of environmental variables on population subdivision. The results of these analyses and their epidemiological implications will be presented.

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For the Busy Parasite — So Many Choices, So Little Time: Host Utilization in the Field Corresponds with Laboratory 'Choice Experiments.'

J.T. DETWILER* and D.J. MINCHELLA, Biological Sciences, Purdue University, West Lafayette, IN.

A fundamental goal of parasite evolutionary ecology is to elucidate patterns of host use and determine the underlying mechanisms of parasite colonization. However, this task is often difficult because host specificity may be affected by many host and parasite-related factors. Comparing host use in both field and experimental settings may elucidate the ecological factors underlying the observed infection patterns. In our trematode-snail system, larval parasites develop in the snail species *Lymnaea elodes* (1st intermediate host). Upon reaching patency, larval parasites leave the 1st intermediate host, enter the abiotic environment, and then colonize one of several snail host species (2nd intermediate hosts). Larval parasites are short-lived in the abiotic environment, so host factors like species, size, abundance, and vagility are predicted to strongly influence parasite infection patterns. Two years of monthly sampling at a freshwater pond demonstrated that the snail *Helisoma trivolvis* was most frequently utilized as a 2nd intermediate host. Variation in host utilization corresponded to host abundance, suggesting that parasites colonized the most available hosts in any given month. A series of laboratory "choice experiments", where abundance was equalized, demonstrated that parasites actually preferred *H. trivolvis*. In the experiments, host size and vagility were not strong determinants of host preference by parasites. The results from both the field and experiments suggest that characteristics specific to a particular host species influence infection patterns. Preference for 2nd intermediate host species has evolutionary implications, because parasites within these hosts contribute to the component population within the final hosts in the life cycle.

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Heterogeneity among Parasites, Not Hosts, Controls Variation in Species Richness.

M.S. SOKOLOWSKI*, School of Marine and Atmospheric Sciences, Stony Brook, NY; T.H. CRIBB, School of Molecular & Microbial Sciences, University of Queensland, Brisbane QLD, Australia; A.D. DOVE, Veterinary Services and Conservation Medicine, Georgia Aquarium, Atlanta, GA; and S.B. MUNCH, School of Marine and Atmospheric Sciences, Stony Brook, NY.

The mechanisms that control species richness are a major theme in parasite ecology. Mechanisms controlling richness in intestinal helminthes include host size, age, sex, and feeding behavior, as well as interactions among parasites. This study aims to answer the broader question: which factor is more important in determining the distribution of the host population's parasite species richness, parasite heterogeneity (i.e., differences amongst parasites species), or host heterogeneity (i.e., differences amongst individual host of the same species).

We constructed models for each of these scenarios and compared them to a null model for richness in the absence of either source of heterogeneity. We applied these models to digenean species abundance distributions of seven fish host species from Heron and Lizard Islands, Australia. The parasite heterogeneity model fit the data best in 12 out of 14 host species. The host heterogeneity model never fit best. These results indicate that the primary driver of variation in species richness is heterogeneity among parasite species.

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The Role of Spatial Heterogeneity in Trematode Aggregation in the Mudsnail, *Ilyanassa obsoleta*.

W.D. ROSSITER*, Graduate Program in Ecology and Evolution, and M.V. SUKHDEO, Department of Ecology, Evolution and Natural Resources, Rutgers University, New Brunswick, NJ.

The aggregated nature of parasites in host populations is a universal property of the disease dynamics of macroparasites. In salt marsh systems, these dynamics are often strongly determined by abiotic mechanisms. We examined the patterns of trematode aggregation in populations of the mudsnail, *Ilyanassa obsoleta*. Surveys, collections, and dissections were conducted for snails across all habitat types (three replicates for each of four habitat types) in a New England-type salt marsh (Tuckerton, NJ) from April to October 2007 (n = 2,520 snails). *Himasthla quissetensis* and *Zoogonus rubellus* accounted for 54.9% (prevalence = 0.117) and 41.1% (prevalence = 0.088) of all infections respectively, with an average intensity of 1,847 larvae per host. In addition, infections by these species were strongly correlated with intertidal marsh surface habitats ($P = 0.0017$), suggesting that habitat determines the patterns of aggregation in these trematodes. Mark–recapture studies demonstrate that adult snails infrequently disperse across habitat types, suggesting that infection occurs in spatially explicit areas of the marsh surface. However, a 24-plot common garden manipulation, using 1,200 uninfected snails, reveals that snails from infected sites are more likely to be infected, irrespective of habitat location. These findings suggest that both spatial heterogeneity and variation in host susceptibility produce parasite aggregation in this system.

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Landscape and Parasite Distribution in Wood Frogs (*Rana sylvatica*).

E.E. PULIS*, Coastal Sciences, University of Southern Mississippi, Ocean Springs, MS, and R.A. NEWMAN and V. TKACH, Biology, University of North Dakota, Grand Forks, ND.

Frog populations are spatially structured, due to their dependence on water. Parasites using frogs as a resource may have similar spatial structure, to the extent that their dispersal and survival depend on the frog host versus factors that affect other hosts used in their life cycles. In this study, we sought to understand how landscape and habitat characteristics influence the spatial distribution of helminth parasites in wood frogs. We sampled up to 5 male frogs per pond each year, for a total of 444 frogs from 59 ponds, during the springs of 2004–2006. Using aerial photographs and GIS, we estimated landscape characteristics (wetlands, agriculture, grass, trees, roads, highways, and building sites) at several spatial scales (50, 100, 200, 300, 400 and 500 meters), with the wetland as the focal point. We used logistic regression and model selection to determine which variables provided the best prediction of parasite occurrence. We also considered the problem of understanding spatial distribution when limited sampling might fail to detect species presence. We identified 11 species of helminth parasites, including 1 new species of lung nematode (*Rhabdias bakeri*). The majority of the parasites were trematodes, which use the wood frog as an intermediate host. Nine of the parasites occurred at ≥10% of locations. Two parasites, including the directly-transmitted *Rh. bakeri*, were nearly ubiquitous, indicating that their distribution was not limited on this landscape. For other species, wetlands, proximity of trees, grass, and roads were the most common predictors of parasite occurrence on the landscape, although scale and direction of impact varied with the parasite. Analyses that simultaneously estimated occupancy and detectability resulted in different models than analyses not including detectability. Results suggest that multiple spatial scales are required to understand the relationship between parasite distribution and landscape features, and accounting for detectability is crucial.

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Parasite Assemblages of the Common Grass Shrimp along the Alabama Gulf Coast: Seasonal Distribution and use as an Environmental Indicator.

K.L. SHEEHAN*, Department of Marine Sciences, University of South Alabama, and Dauphin Island Sea Lab, Dauphin Island, AL; J. O'BRIEN, Department of Biological Science, University of South Alabama, Mobile, AL; and J. CEBRIAN, Department of Marine Sciences, University of South Alabama, and Dauphin Island Sea Lab, Dauphin Island, AL.

The common grass shrimp (*Palaemonetes pugio*) is a common prey species to economically and ecologically important fishes and crustaceans in estuarine habitats. *P. pugio* is host to a number of obligate, facultative, and transient symbionts. A survey including twenty-two sites was conducted around Mobile Bay, AL, during the winter (January), spring (May), and summer (September) of 2007, to determine the general prevalence and distribution of *P. pugio* parasites. Here we report on obligate parasites that are easily observed with the aid of dissecting microscope (mircophallid trematodes, haplosporidian hyperparasites, loricate ciliates, and bopyrid isopods) on, or within, live hosts. Overall abundance and frequency of all parasites was compared among seasons, and parasite assemblages were analyzed using multivariate techniques. Results indicate parasite frequency and abundance does not change seasonally; however, seasonal changes in parasite assemblages are common. The prevalence of the most common *P. pugio* parasite, the trematode *Microphallus turgidus*, was compared at two specific sites in Mobile Bay, with greater temporal resolution over a twenty-one month period. Trematode prevalence appears to be negatively correlated with nutrient concentrations, although manipulative lab experiments are needed to confirm this suggestion. The implications of this observational study are three-fold: (1) our results help develop a better understanding of the natural history of these organisms; (2) they provide a basis for further studies on the nature and ecological implications of the interactions between *P. pugio* and its parasites; and (3) the potential for the use of these parasites and hosts, as proxies for environmental stress in the form of nutrient enrichment, has emerged.

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Morphological Effects, Parasitological Outcomes, and Trade-Offs of Concurrent *Heligmosomoides bakeri* (Nematoda) Infection and Pregnancy in Cd-1 Mice.

M.R. ODIERE*, Institute of Parasitology, MacDonald Campus of McGill University, Montreal, Quebec, Canada; K.G. KOSKI, School of Dietetics and Human Nutrition, MacDonald Campus of McGill University, Montreal, Quebec, Canada; and M.E. SCOTT, Institute of Parasitology, MacDonald Campus of McGill University, Montreal, Quebec, Canada.

There is a growing interest in the link between individual immune system performance and fitness-related traits such as reproductive effort. This study provides an insight into how animals cope with simultaneous energy demands in the form of parasite infection and reproduction, and the costs and trade-offs of these interactions. A 2 × 3 factorial design, involving 2 levels of pregnancy (pregnant and non-pregnant) and 3 levels of infection dose (0 L_3= sham, 50 L_3= low and 100 L_3= high), were used. Mice were infected with parasite larvae at day 6, 11, and 16 of pregnancy. *H. bakeri* egg output was estimated from complete 24 hr stool collections at day 18 of pregnancy. At necropsy (day 19 of pregnancy), a c-section was performed; fetuses were removed and killed by exsanguination. Maternal organ masses and reproductive outcomes (fetal count, fetal weight, crown-rump length, placental weight, and tissue resorptions) were determined immediately thereafter. Small intestines were excised, and the gender and number of adult worms and number of 4th-stage larvae (L_4) were determined. Regardless of infection dose, pregnancy increased numbers of L_4, adult worms, and fecal egg count (FEC). In general, both infection dose and pregnancy increased organ masses (heart, lungs, spleen, liver, kidneys, pancreas, small intestines). Although infection dose caused no significant effect on fetal weight, there was a dose-dependent decrease in fetal crown-rump length. Only four fetal resorptions were observed and both occurred in low-dose pregnant mice. The increase in worm burden and FEC may indicate periparturient immunosuppression, whereby costly immune responses were suppressed and the released resources from this were then adaptively reallocated to the prioritized reproductive function (trade-off: reproduction prioritized over immunity). The reduced crown-rump length mimics the stunting that is seen in children with chronic helminth infections, making this model ideal to study such effects.

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Infections with Geographically and Genetically Different Strains of *Trypanosoma cruzi* in Two North American Reservoir Hosts Induce Dissimilar Infection Dynamics.

D.M. ROELLIG*, Department of Infectious Diseases and Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA; A.E. ELLIS, Athens Veterinary Diagnostic Laboratory, College of Veterinary Medicine, The University of Georgia, Athens, GA; and M.J. YABSLEY, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine and D.B. Warnell School of Forestry and Natural Resources, The University of GA, Athens, GA.

Trypanosoma cruzi, etiologic agent of Chagas disease, is capable of infecting a variety of mammalian hosts within a wide geographic range in the Americas. In addition, *T. cruzi* is genetically and biologically diverse, with molecular associations occurring between strain genotype and host origin. The objective of the present study was to determine dynamics of *T. cruzi* infection in *Didelphis virginiana* and *Procyon lotor*, and to provide experimental evidence for an observed host species–parasite strain dichotomy. Based on previous molecular typing and hemoculture evidence from wild-trapped animals, we hypothesized that raccoons would have a longer patent period than opossums, and that raccoons would be more competent reservoirs for all genotypes of *T. cruzi* compared with opossums. Individuals (n = 2 or 3) of each species were intraperitoneally or intravenously inoculated with 1×10^6 culture-derived *T. cruzi* trypomastigotes of Type IIa (North America-raccoon), Type I (NA-opossum), Type IIb (South America-human), or both Type I and IIa. One animal in each group was euthanized during acute (1 and/or 2 months) and chronic stages (4 months), and tissues collected for PCR and histopathology. Opossums had a more gradual increase in parasitemia, peaking around 35DPI, and a rapid decline by week six; raccoons quickly reached peak parasitemia at 18-21DPI and maintained relatively high parasitemia for 5 weeks. Additionally, raccoons became infected with all *T. cruzi* strains, while infection was not detected by PCR, serology, or hemoculture in opossums inoculated with Type IIa. Opossums inoculated with *T. cruzi* IIb had detectable infections by PCR analysis and cleared the infection at approximately 10DPI, as was evident by seroconversion and the absence of *T. cruzi* DNA after this day. Serology as determined by IFA demonstrated raccoons seroconverted sooner (3–7 DPI) than opossums (10 DPI). These results support our hypotheses and indicate that opossums and raccoons maintain different genotypes and the course of infection differs between species.

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Intestinal Helminths from 6 Species of Doves Residing in South Texas.

A.J. SMITH* and A.M. FEDYNICH, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, TX.

Three hundred forty-eight columbids representing 6 species (60 rock pigeons [*Columba livia*; RP], mourning doves [*Zenaida macroura*; MD], Eurasian collared doves [*Streptopelia decaocto*; ECD], white-winged doves [*Zenaida asiatica*; WWD], common ground doves [*Columbina passerina*; CGD], and 48 Inca Doves [*Columbina inca*; ID]), were collected in the summer of 2006 and examined for helminths. Twelve helminth species were recovered (9 nematodes and 3 cestodes), representing 486 individuals. Helminths occurred in 6 microhabitats, of which the jejunum was the most commonly occupied. Nematodes numerically dominated the component community in all host species. Overall, 37% of all columbids were infected with one or more helminth species (RP 48%, MD 37%, ECD 27%, WWD 37%, CGD 40%, and ID 4%). Mixed infections occurred in 22% of infected columbids (RP 10%, MD 9%, WWD 14%, and CGD 50%). Prevalence was similar among host sex within all dove species. However, prevalence was significantly different among host age, within species, for *Skrjabinia bonini* ($P = 0.01$) and *Hymenolepis* sp. ($P = 0.0002$) in RP adults. *Killigrewia delafondi* was higher ($P = 0.0001$) in adult WWD. Prevalence values were too low to test among columbid species. Based on percent similarity and coefficient of community indices, helminth component communities were dissimilar and number of shared helminth species varied among host species. New host records include CGD: *Ascaridia columbae*, *Splendidofilaria wehri*, *Ornithostrongylus quadriradiatus*, *Ornithostrongylus minutus*, *Oswaldostrongylus* sp., *Killigrewia delafondi*, and *Skrjabinia bonini*; for ID: *A. columbae*; for WWD: *Oswaldostrongylus* sp. and *Skrjabinia bonini*; and for MD: *Oswaldostrongylus* sp.

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Do Insecticides Alter Natural Host–Parasitoid Interactions in *Drosophila*?

N. MILAN* and T. SCHLENKE, Department of Biology, Emory University, Atlanta, GA.

Our previous work has shown that natural host plant toxins can have an effect on the interaction between fruitflies and their parasitoid wasps. Resistance to host plant toxins can help flies escape wasp parasitism in one of two general ways: volatile toxins can repel wasps from the toxic food (thus reducing the attack rate), and some toxins appear to limit growth of wasps inside the flies (thus increasing fly immune success). We now extend this work to two man-made toxins that many natural *Drosophila melanogaster* populations have evolved resistance against, the insecticides DDT and malathion. We are interested in whether *Drosophila's* natural parasites have evolved insecticide resistance capabilities similar to their hosts, or whether evolution of resistance against DDT and malathion by *D. melanogaster* has allowed resistant fly populations a temporary reprieve from normal parasitoid-induced mortality. This work should shed light on a potential drawback of insecticide use to control pests: that natural parasites may suffer worse than the hosts the toxins are meant to control.

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Identification of Host DNA and the Etiologic Agent for Epizootic Bovine Abortion in *Ornithodoros coriaceus*.

A.K. LONG*, M.B. TEGLAS, and V. KIRCHOFF, University of Nevada, Reno, Animal Biotechnology, Reno, NV.

Ornithodoros coriaceus is the only described vector for Epizootic Bovine Abortion (EBA), an economically important disease of cattle in the western United States. EBA is characterized by late-term abortion in cattle and diagnosed by postmortem examination of characteristic lesions and pathology in the fetus. Due to the difficulty of growing the etiological agent in tissue culture, alternative methods of disease management need to be explored. By determining the primary hosts of *O. coriaceus*, and identifying the etiologic agent within the same tick host, we can determine possible reservoir hosts of EBA. There is little evidence to support host preference for *O. coriaceus* due to the rapid feeding nature of soft ticks, making host identification by tick removal nearly impossible. DNA analysis of the tick gut contents, using vertebrate mitochondrial primers, provides a means to determine preferred host species of *O. coriaceus*. Species specific probes have been developed to detect degraded fragments of DNA remnants in old gut contents of the tick vector. Our objectives were to: (1) determine the length of time a bloodmeal can be accurately identified in *O. coriaceus*; (2) detect host DNA in field-caught *O. coriaceus*; and (3) detect the bacteria that causes EBA within the ticks that show positive results for host DNA. By utilizing polymerase chain reaction, in combination with reverse line blot technology, we can determine the source of the host bloodmeal in *O. coriaceus* and detect the bacterial agent of EBA. Preliminary results show DNA detection up to day 287 post feeding for ticks fed in the lab. Bloodmeal analysis shows rodents may play a larger role in the tick life cycle than originally believed, and that artiodactyls are preferred hosts of *O. coriaceus*.

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Multiple Species of *Phoreiobothrium* from the Blacktip Shark, *Carcharhinus limbatus*, from the Gulf of Mexico.

H.L. OWENS* and K. JENSEN, Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS.

During a survey of the adult tapeworm fauna of sharks from the Gulf of Mexico, the Blacktip shark, *Carcharhinus limbatus*, was found to host cestodes in the genus *Phoreiobothrium*. *C. limbatus* inhabits the world's tropical and warm temperate waters. As yet, 25 species of cestodes representing the orders Tetraphyllidea, Cathetocephalidea, and Trypanorhyncha have been reported to parasitize the species throughout its range. Little is known about tetraphyllidean diversity in *C. limbatus* in the Gulf of Mexico; no records exist for *Phoreiobothrium* from *C. limbatus* in this region. Between 2005 and 2007, 6 specimens of *C. limbatus* were collected off Ocean Springs, Mississippi, and 13 specimens were collected off Panama City, Florida, and their spiral intestines examined for cestodes. Whole mounts and histological sections of the cestode specimens were prepared for examination with light microscopy; scoleces were prepared for scanning electron microscopy. Overall, *C. limbatus* was found to host 3 species of Trypanorhyncha and 11 species of Tetraphyllidea. In addition

to 1–2 species each in the tetraphyllidean genera *Disculiceps*, *Anthobothrium*, and *Paraorygmatobothrium*, *C. limbatus* hosted 6 species of *Phoreiobothrium*. The diversity of *Phoreiobothrium* species is of special interest: all are new to science and collectively represent an unusually high number of congeners in a single host species. The new species of *Phoreiobothrium* from *C. limbatus* can be distinguished from the known species, and each other, based on characters such as scolex dimensions, number of subloculi, presence or absence of papillae, and distribution of vitellaria. Despite its cosmopolitan distribution, it has been suggested that several distinct populations of *C. limbatus* exist in the Gulf of Mexico. The complex species assemblage of *Phoreiobothrium* in *C. limbatus* from the Gulf of Mexico localities has the potential to inform us about its host's population structure.

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The Lecanicephalidean Fauna of Three Species of Eagle Rays of the Genus *Aetomylaeus* (Myliobatiformes: Myliobatidae).

K.R. KOCH* and K. JENSEN, Department of Ecology and Evolutionary Biology, The University of Kansas, Lawrence, KS.

The eagle ray genus *Aetomylaeus* comprises 4 species: *A. niehofii*, *A. maculatus*, *A. vespertilio*, and *A. milvus*. In general, members of this genus inhabit the waters of the Indo-West Pacific. Recent collecting efforts in this region resulted in specimens of 3 of the 4 *Aetomylaeus* species available for study, with the exception of *A. milvus*. While tapeworms have been reported from *A. niehofii* and *A. maculatus*, no tapeworm data exist from *A. vespertilio*. Moreover, no lecanicephalideans have been described from any of the 3 eagle ray species. As part of a survey of parasites of elasmobranchs from Borneo and Northern Australia, a total of 12 specimens of *A. niehofii* were collected (5 from Borneo and 7 from Northern Australia); 4 specimens of *A. maculatus* (all from Borneo); and 5 specimens of *A. vespertilio* (all from Northern Australia). In general, the 3 species of eagle rays hosted tapeworms representing 4 of the 5 orders of tapeworms known to parasitize elasmobranchs. The greatest diversity was seen among lecanicephalideans. The lecanicephalideans encountered were tentatively identified as belonging to the genera *Tylocephalum*, *Polypocephalus*, *Hornellobothrium*, and *Aberrapex*. In addition, specimens were recovered that appear to represent two genera new to science. In each host species, multiple congeners of both *Tylocephalum* and *Polypocephalus* were present. *Aetomylaeus niehofii*, *A. maculatus*, and *A. vespertilio* hosted at a minimum 9, 7, and 11 lecanicephalidean species, respectively. Preliminary data suggest that the 27 species of lecanicephalideans encountered are new to science. These data also suggest that each eagle ray species hosts a unique and similarly diverse assemblage of lecanicephalidean tapeworms.

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Coccidia from Mammals: Status of the Taxonomy and Methods for Collection, Preservation, and Sporulation of Fecal Stages.

R.S. SEVILLE*, Department of Zoology and Physiology, University of Wyoming/Casper, Casper, WY.

Coccidian species occurring in hosts in the Class Mammalia are likely one of the best studied and surveyed coccidian groups from a particular vertebrate host taxon. However, of the 5,416 named mammalian species in the 29 recognized mammalian orders, only 550–600 species, or 10–11%, have been examined for coccidia. From these hosts, 950+ coccidian species, in several genera, have been described and named, with the majority in the genera *Eimeria* (~800) and *Isospora* (~130). Recent analyses have noted that, since the origin of modern taxonomy in 1758, an average of 223 new mammal species have been described every decade. Today, the rate of species discovery is increasing, and it is now believed that 7,000+ living species of mammals will eventually be recognized. Thus, we know relatively little about the diversity of coccidian species in the Mammalia. In addition, the majority of mammal surveys and new species discoveries are occurring in areas of high conservation concern. Therefore, the opportunity for assessing coccidian diversity in these rich biotic regions is critical. Given the ease with which samples can be collected and processed, surveys for coccidia should be standard components of all biotic surveys and inventories of mammals. For these studies, it is essential that recovered oocysts be adequately described, following published guidelines, and representative photovouchers be archived in national collections. The taxonomy of coccidians from mammals, as for other host taxa, is somewhat confused by inadequate descriptions and the lack of studies of host specificity for many host–parasite groups. Incorporation of standard nucleic acid sequence characters may help resolve such issues in the future.

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Amphibian Coccidia: Taxonomy, Host Specificity, Ecology, and Phylogeny.

M.G. BOLEK*, Department of Biology, University of Nebraska at Kearney, Kearney, NE;
D.W. DUSZYNSKI, Department of Biology, University of New Mexico, Albuquerque, NM; and
S.J. UPTON, Division of Biological Sciences, Kansas State University, Manhattan, KS.

Here we review all published descriptions of amphibian coccidians: their host specificity, ecology, life history, and phylogenetic relationships. The class Amphibia has 3 orders, 56 families, 464 genera and 6,009 species. There are no coccidia known from 41 of the 56 (73%) families, 436 of the 464 (94%) genera, and 5,964 of the 6,009 (>99%) species. In the Anura (frogs), only 14 of the 44 (32%) families, 30 of the 388 (8.8%) genera, and 67 of the 5,283 (1.2%) species have been examined for coccidia, and 30 coccidia are known (18 *Eimeria*, 9 *Isospora*, 2 *Goussia*, and 1 *Hyaloklossia* species). In the Urodela (salamanders), 7 of the 9 (78%) families, 18 of the 64 (28%) genera, and 45 of the 553 (8%) species have been examined, and 21 coccidia are known (19 *Eimeria* and 2 *Isospora* species). In the Gymnophiona (caecilians), only 1 of 3 (33%) families, 1 of 12 (8%) genera, and only 1 of the 173 (0.6%) species have been examined, and 1 *Eimeria* species is known. From the data provided above, most species of amphibian coccidia appear to be host specific, whereas others can infect multiple species or genera. However, none are known to cross family boundaries. Recent ecological and transmission studies, among different genera of amphibian coccidia, indicate larval amphibian stadial host specificity among *Goussia* species, whereas *Eimeria*, *Isospora* and *Hyaloklossia* species can infect both larval and adult amphibians. Finally, to our knowledge, only a single amphibian coccidian has been sequenced, and currently their phylogenetic position is uncertain.

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Methods for Collection, Preservation, and Sporulation of Snake Fecal Stages to Help Resolve what We Still Don't Know about Snake Coccidia.

S.J. UPTON*, Division of Biological Sciences, Kansas State University, Manhattan, KS, and
D.W. DUSZYNSKI, Department of Biology, University of New Mexico, Albuquerque, NM.

Pough et al. (2004) presented a reasonable phylogeny of 17 families of snakes, being supported by molecular and morphological analyses; the primary dichotomy in this phylogeny is between the (suborder) Scolecophidia and all other snakes (Alethinophidia). Unfortunately, most of the nearly 3,000 snake species have never been surveyed for coccidia. To date, no coccidia have been reported from 12 of 17 (71%) of the families. These include Anomalepididae and Leptotyphlopidae (Glauconiidae), representing two (67%) of the 3 families within the order Scolecopjhidia and Acrochordidae, Aniliidae (Ilysiidae), Anomochilidae, Atractaspididae, Bolyeridae, Loxocemidae, Tropidophiidae, Uropeltidae, Xenopeltidae, and Xenophidiidae comprising 10 of 14 (71%) of the families in the order Alethinophidia. There are 457 genera of snakes, yet, snakes in only 71 (15.5%) of them, comprising only 140 (<5%) extant snake species, have been examined for, and reported to have, coccidia described from them. From these 140 snake species, about 134 coccidia species have been described, including 47 *Caryospora*, 2 *Cryptosporidium*, 2 *Cyclospora*, 54 *Eimeria*, 7 *Isospora*, 19 *Sarcocystis*, 1 *Wenyonella*, 2 *Tyzzeria*, and 1 *Toxoplasma* spp. It is likely that a number of these, especially *Eimeria* (oocysts of prey items passing through the snake gut) and *Isospora* (oocysts of *Sarcocystis* spp.) spp. are either spurious reports or misnamed, respectively. Because of this variety of oocysts found in snake feces, particular care must be taken to preserve and study them to get the most information possible.

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Collection, Preservation, and Sporulation of Fecal Stages from Birds: Concepts, Methods, and Challenges.

J.R. BARTA*, Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; and J.D. OGEDENGBE and J. COBEAN, Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada.

Monoxenous coccidia shedding fecal stages in birds are some of the most intensely studied apicomplexan parasites because of their importance in commercial poultry production and ease of relative ease of study. Parasites in the genera *Eimeria* and *Isospora* have been reported commonly. *Caryospora* and *Tyzzeria* species have

been reported less commonly. Fecal stages seem to sporulate well, if feces are collected as freshly as possible and immediately suspended in 2.5% w/v potassium dichromate in water, either prior to or after enrichment using flotation techniques. Sporulation is most successful if the oocysts are held at 20–26°C, with aeration via bubbling of compressed air in the sample or rotary agitation of the mixture in flasks or Petri dishes (note that stir bars do not usually work well for this purpose); moderate temperature and adequate oxygen are critical for good sporulation. Many species will sporulate poorly, or not at all, if refrigerated prior to sporulation; freezing temperatures will usually kill intact oocysts, even if suspended in cryoprotectants. Short-term storage of sporulated oocysts at 4°C is usually successful; oocysts remain infective for many months in this condition. Surface sterilization of many of these oocysts can be achieved by suspending oocysts in household bleach (5.25% sodium hypochlorite) for 10 minutes and then washing extensively with PBS. Isolated sporocysts must be obtained for cryopreservation. The oocyst walls must be removed using some grinding or shearing method, such as glass bead disruption. In our laboratory, we use filtration through Nitex monofilament print screening cloth to separate the resulting sporocysts from unbroken oocysts and oocyst wall debris, prior to further processing. Once free of the oocyst wall, sporozoites within sporocysts can be protected during cryopreservation by cryoprotectants. Ramp-cooling the samples from room temperature down to refrigerated temperatures, and then down to –80°C at a rate of 1°C/minute, produces the best survival rate. Samples are then transferred from –80°C to liquid nitrogen.

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The Emerging Role of Molecular Markers in Coccidian Speciation.

K.B. MISKA*, USDA-ARS, Animal Parasitic Diseases Laboratory, Beltsville, MD; and D. MOTRIUK-SMITH and R.S. SEVILLE, Department of Zoology and Physiology, University of Wyoming/ Casper, Casper, WY.

In recent years, molecular markers have been playing an increasingly important role in classification of coccidia. Sequences from the small (18S) and large (28S) subunits of ribosomal DNA have been used to reconstruct phylogenetic relationships. More recently, organellar sequences from the plastid genome, such as the 23S and ORF 470, have proven to be suitable phylogenetic markers. Internal transcribed spacer regions 1 (ITS1) and 2 (ITS2) have also been useful in distinguishing morphologically similar species; however, duplicate copies of this region can confound data analysis. Comparison of unpublished data of ITS1 and ITS2 sequences derived from *Eimeria*, rodent, and bird hosts will be discussed. Lastly, a portion of the gene encoding cytochrome c oxidase subunit I from mitochondrial DNA has also been used in reconstructing phylogenies of avian *Eimeria*. Methods describing *Eimeria* oocyst isolation, DNA extraction, and amplification will also be presented.

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Nothing Succeeds Like Excess.

S. NADLER*, University of California, Davis CA.

[No abstract submitted]

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Two New Cestode Species from the Dwarf Whipray, *Himantura walga* (Batoidea: Dasyatidae) from Borneo, with Comments on Site and Mode of Attachment.

M.E. TWOHIG*, J.N. CAIRA, and C.A. FYLER, Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT.

Spiral intestines of 12 specimens of the Dwarf whipray, *Himantura walga*, from Malaysian Borneo were examined for cestodes. These yielded new species of *Acanthobothrium* (Tetraphyllidea) and *Echinobothrium* (Diphyllidea). The new *Acanthobothrium* species differs from all but 4 of its Category 1 congeners in its possession of post-ovarian testes. It differs from the latter 4 species in its possession of fewer testes, shorter length, and fewer proglottids. The new *Echinobothrium* species is unique in its possession of trifid outer rostellar hooks; it is also the smallest member of its genus. The spiral intestine of *H. walga* consisted of 12 mucosal chambers. Most (89%) of the 35 specimens of the diphyllidean were found in chambers 2–4. In contrast, the 57 specimens of the new tetraphyllidean occurred throughout chambers 5–12, with 86% in chambers 6–10. Both species embedded their scolex within the lumen of mucosal crypts, with their hooks and/or spines penetrating the lamina propria. Both also eroded crypt epithelial lining and caused modest expansion of crypt diameter.

While the configuration of the mucosal surface may explain the preferred sites of attachment of both species, it does not explain their absence from other regions; histological sections and scanning electron microscopy showed the mucosal surface to be similar in configuration throughout the length of the spiral intestine. *Himantura walga* also hosted limited material of 1 rhinebothriine, 2 lecanicephalidean, and a trypanorhynch species, as well as 1–2 other new species of *Acanthobothrium*. In total, the cestode fauna of the Dwarf whipray consists of a suite of unusually small taxa. Although the cestode genera reported here are similar to those reported from other *Himantura* species, they are completely inconsistent with historical records from *H. walga* in Sri Lanka. This suggests that either the original host identifications are suspect, or that differences exist in the faunas of *H. walga* between these 2 localities.

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New Cestodes from Freshwater Stingrays of Indonesian Borneo.

J.N. CAIRA*, Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT;
K. JENSEN, Department of Ecology & Evolutionary Biology, University of Kansas, Lawrence, KS; and
F.B. REYDA, Biological Field Station, State University of New York College at Oneonta, Cooperstown, NY.

The rivers of Indonesian Borneo are fabled to be home to the poorly known "freshwater" stingrays *Himantura signifer* (White-edge freshwater whipray) and *Himantura oxyrhynchus* (Marbled freshwater stingray). Field work in 2007, conducted in the Kapuas River and in coastal areas in the vicinity of Pontianak in eastern Indonesian Borneo, yielded multiple specimens of both stingray species. The cestode faunas of both stingrays are described for the first time, based on samples of 14 individuals of *H. signifer* and 24 individuals of *H. oxyrhynchus*. *Himantura signifer* was found to host a minimum of 5 new species, consisting of 1 diphyllidean and 4 species of *Rhinebothrium*. *Himantura oxyrhynchus* hosted a minimum of 12 new species, consisting of 2 diphyllideans, 2 species of *Acanthobothrium*, 1 species of *Scalithrium*, at least 4 species of *Rhinebothrium*, 1 trypanorhynch, and at least 2 lecanicephalideans. The relatively greater diversity of cestodes seen in *H. oxyrhynchus* appears to be correlated with the fact that, while specimens of *H. signifer* were collected from uncontestably freshwater localities hundreds of kilometers up the Kapuas River, all specimens of *H. oxyrhynchus* were collected from coastal localities from essentially marine waters. Thus, these results are consistent with existing data on the potamotrygonid stingrays in the rivers of South America, which show that the cestode faunas of these truly freshwater rays are low, relative to those of their marine counterparts.

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Phylogeography of *Rhabdochona lichtenfelsi* (Nematoda) and the Recent History of Freshwater Basins in Central Mexico.

H.H. MEJÍA-MADRID*, Department of Zoology, Instituto de Biología, UNAM, Mexico City, Mexico;
E. VÁZQUEZ-DOMÍNGUEZ, Laboratoy of Macroecology, Instituto de Ecología, UNAM, Mexico City, Mexico;
and G. PÉREZ-PONCE DE LEÓN, Department of Zoology, Instituto de Biología, UNAM, Mexico City, Mexico.

Geological history of the west-central region of Mexico suggests that extant freshwater basins are the result of different vicariant events that fragmented ancient watercourses and lakes within the Mesa Central. The phylogeography of *Rhabdochona lichtenfelsi*, a nematode parasite specific to endemic goodeids in Mexico, is used to infer the biogeographical history of fragmentation, and recent evolution, of the Mesa Central drainages. Sampling sites included the major freshwater river basins of the Mesa Central, Mexico. Haplotype diversity and phylogeographic structure of 10 populations of *R. lichtenfelsi*, sampled from the complete range of this species, were analysed with partial sequences of cytochrome *c* oxidase subunit I (456 bp). Analyses performed included phylogenetic tree estimation methods (NJ, MP, and ML), genetic diversity, distance and structure estimates, and nested clade analysis. High overall haplotype diversity (range 0.40–1.00; mean = 0.67; total = 0.96), unique haplotypes, and strongly structured populations (gene flow estimates Gst = 0.317 and Nm = 1.07, 0.36) were found in the basins sampled. Three phylogenetically and demographically identifiable clades were recovered. These clades fit an isolation by distance model (permutational χ^2 statistic at $P < 0.005$ and $P < 0.001$). Significant population expansion was observed for two clades and for the entire population. Time of divergence was estimated in 1.0 and 0.84 Ma for the different clades. The distribution of *R. lichtenfelsi* haplotypes does not correspond to the present distribution of the basins of Mesa Central, but instead reflects the distribution of those

basins during a recent geological period (Pleistocene). While our current knowledge of the evolution and geographical relationships of the Mesa Central basins comes from studies of freshwater fish encompassing a more ancient history, our results suggest that during the last million years, old basins and connections existed where today stand isolated freshwater bodies, thus unravelling a novel biogeographical history for the Mesa Central of Mexico.

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Taxonomic Status, Geographic Distributions, and Origins of Human Head and Body Lice.

J.E. LIGHT*, M.A. TOUPS, J.M. ALLEN, and D.L. REED, Florida Museum of Natural History, University of Florida, Gainesville, FL.

Human head lice (Anoplura: *Pediculus*) are pandemic, parasitizing countless school children worldwide due to the evolution of insecticide resistance, and human body lice are responsible for the deaths of millions as a result of vectoring several deadly bacterial pathogens. Despite the obvious impact these lice have had on their human hosts, it is unclear whether head and body lice represent two morphological forms of a single species, or are two distinct species. To assess the taxonomic status of head and body lice, we compare phylogenetic and population genetic methods using the most diverse geographic and molecular sampling presently available. Our analyses find reticulated networks, gene flow, and a lack of reciprocal monophyly, all of which indicate that head and body lice do not represent genetically distinct evolutionary units. Because there also are inconsistencies of morphological, behavioral, and ecological variability between head and body lice, we therefore contend that no known species concept would recognize these louse morphotypes as separate species. We recommend recognizing head and body lice as morphotypes of a single species, *P. humanus*, until compelling new data and analyses indicate otherwise. Interestingly, head lice are subdivided into three deeply divergent mitochondrial clades (Clades A, B, and C), each having unique geographical distributions. Previous data suggest that head lice belonging to mitochondrial Clade B may have originated in North America, however, geographic sampling and sample sizes have been limited. With newly collected lice, we calculate the relative frequency, geographic distribution, and genetic diversity of louse mitochondrial clades to determine louse geographic origins. In agreement with previous studies, genetic diversity data support a North American origin of Clade B lice. It is likely that head lice belonging to this mitochondrial clade migrated to other geographic localities (e.g., Europe and Australia) recently, and, if not already present, may disperse further to occupy all geographic regions.

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Phylogeny and Evolution of Bat Flies (Streblidae, Nycteribiidae).

K. DITTMAR*, Department of Biological Sciences, University at Buffalo, Buffalo NY;
C. DICK and B. PATTERSON, Department of Zoology, Field Museum of Natural History, Chicago, IL; and
M. GRUWELL, Department of Biological Sciences, University at Buffalo, Buffalo NY.

Bat flies are poorly studied, highly derived, ectoparasitic, blood sucking flies. Like many ectoparasites, they show patterns of progressive eye and wing reduction. Little is known about their basic ecological parameters. We here present a comprehensive worldwide sampling from a variety of bat hosts (Mega- and Microchiroptera), and elucidate their evolutionary history using genetic and morphological data. Consistent with previous studies, we show that Streblidae are not monophyletic. Furthermore, we trace host associations and geographical distribution in a phylogenetic context, and present preliminary data on their eye evolution.

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Bloodsuckers and their Bacteria: A Systematic Symbiont Survey.

S.C. WATSON* and M.E. SIDDALL, Sackler Institute of Comparative Genomics, American Museum of Natural History, New York, NY.

Symbiotic bacteria are often found in association with invertebrates (e.g., aphids) that have nutritionally restricted diets. Although blood is a rich source of protein, it tends to be deficient in a variety of essential nutrients such as folic acid, pyridoxine, and other vitamins. Parasitic bugs, lice, and sanguivorous flies (tsetses, hippoposcids, streblids) each host obligate symbiotic bacteria that are believed to provide additional nutrients necessary for survival and reproduction. Predictably, blood-feeding leeches also harbor symbiotic microorganisms. The nature of the association varies from obligate intracellular *Reichenowia* species in

specialized organs of leeches in the genus *Placobdella*, to the presence of normally free-living *Aeromonas* species in the crop of hirudinids. The leech family Hirudinidae has been found to be polyphyletic with leeches in the New World clade harboring a symbiont that differs from their European counterpart. The latter is now understood to be a complex of at least three distinct species of *Hirudo*. The crop-associated microbial flora has only been determined for one species of European medicinal leech. We have profiled the symbiotic microflora of a wide range of leeches from a global distribution, characterizing both the culturable species of *Aeromonas* and non-culturable *Rikinella*-like bacteroidetes.

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Comparative EST Libraries from Medicinal Leeches.

M.E. SIDDALL*, Sackler Institute of Comparative Genomics, American Museum of Natural History, New York, NY; G. MIN, Department of Biological Sciences, Inha University, Incheon, Republic of Korea; S.C. WATSON, Sackler Institute of Comparative Genomics, American Museum of Natural History, New York, NY; and I.N. SARKAR, Marine Biological Laboratory, Woods Hole, MA.

The transcriptional profile of 2 species of medicinal leech were examined through the development of expressed sequence tag (EST) libraries. The salivary complexes of wild *Macrobdella decora* and of commercially available *Hirudo verbana* were used for the generation of general cDNA profiles, as well as libraries subtracted against gonadal and muscle tissues so as to enrich salivary-specific ESTs. High-throughput sequencing allowed for the rapid characterization of thousands of transcripts, all of which were subject to annotation and comparison versus core sequences in public databases, against a pre-existing library from *Haementeria depressa*, and through cross referencing to the recently published complete genome of *Helobdella robusta*. In addition to revealing key information regarding the relative contributions of structural, translational, and other cellular functions, the EST library approach holds promise for examining the evolution of anticoagulation in leeches and for discovering single-copy nuclear loci useful for tree-of-life scale phylogeny reconstruction.

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Evolution of Life Cycles and Host Associations among the Hymenolepididae: How Many Switches?

V.V. TKACH*, Department of Biology, University of North Dakota, Grand Forks, ND; B.B. GEORGIEV, Central Laboratory of General Ecology, Sofia, Bulgaria; and D.J. LITTLEWOOD, The Natural History Museum, London, United Kingdom.

Hymenolepididae is the largest family of the Cyclophyllidea and the Cestoda as a whole. Its members are parasitic in birds and mammals as adults and in various aquatic and terrestrial arthropods as larvae; life cycles of the Hymenolepididae are the best studied among all cestodes (Beveridge, 2001). Combined with taxonomic diversity and global distribution, it makes them an outstanding model for evolutionary research. However, interrelationships among hymenolepidids have never been analyzed using molecular phylogenetic tools. We studied phylogenetic interrelationships among representatives of more than 50 hymenolepidid genera collected from various vertebrate and invertebrate hosts around the world, using partial sequences of the nuclear lsrDNA gene. The obtained phylogeny allowed us to trace the evolutionary associations of hymenolepidids with their intermediate and definitive hosts and to understand the interrelationships among hymenolepidids possessing aquatic and terrestrial life cycles. The phylogenetic tree shows that several basal hymenolepidid clades consist entirely of parasites of aquatic birds using aquatic crustaceans as intermediate hosts, while two large clusters of more-derived taxa show a number of secondary switches of hosts and environment. One of these clusters includes bird parasites possessing aquatic life cycles and crustacean intermediate hosts, with secondary transition to aquatic and terrestrial annelids among Aploparaksinae. The other cluster includes parasites of mammals using mainly insects and collemboles as intermediate hosts. However, this group features secondary switch to aquatic environment and crustacean intermediate hosts among parasites of water shrews (*Neomys*), as well as switches to miriapod intermediate hosts on at least two different occasions. Hymenolepidids of birds with terrestrial life cycles (other than Aploparaksinae) also belong to this group and are more closely related to mammalian hymenolepidids than to other bird hymenolepidids. This study was supported by grants from the Royal Society and NERC (UK) for DTJL and VVT.

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Manipulation of Host Food Availability and Number of Exposures to Assess the Crowding Effect on *Hymenolepis diminuta* in *Tribolium confusum*.

A.W. SHOSTAK* and J.G. WALSH, Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada.

The "crowding effect" is characterized by decreased size or fecundity of individual parasites as the number of parasites per host increases, often in strict inverse relation to parasite numbers. A crowding effect has been reported on larvae of the cestode *Hymenolepis diminuta* in their intermediate hosts, tenebrionid beetles; and exploitation competition, as parasites encounter limited critical resources such as nutrients or space, has been hypothesized as the cause. However, these studies were not well quantified. We use a recently developed set of geometric approximations for *H. diminuta* in *Tribolium confusum* to estimate parasite volume and study the crowding effect on this parasite in its intermediate host, with greater resolution than previous studies.
We manipulated number of parasites, host diet, and number of exposures. Parasites in hosts on reduced food availability were smaller, but regardless of host diet, parasite size was unaffected until an intensity of at least 5–10 parasites per host. Crowding did not follow a strict inverse relationship. Daily gain in parasite volume peaked partway through the developmental period and preceded the first evidence of crowding. Parasites that established during a second exposure had a transient developmental delay, but eventually grew as large or larger than parasites from a single exposure with the same total intensity. Parasites responded to crowding by differential allocation of resources. Cercomer volume decreased even with slight crowding; the capsule surrounding the scolex was not reduced until crowding became more severe, and scolex width was reduced only in the most extreme conditions. The results support the hypothesis that the crowding effect in this system is driven by nutrient, and not space, limitations, but also suggest that the nutritional relationship of parasite to host is more complex than usually assumed in models of the crowding effect.

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Discrimination in Hawaiian Streams: Not All Hosts Treat *Camallanus cotti* Equally.

W.F. FONT*, Department of Biological Sciences, Southeastern Louisiana University, Hammond, LA.

Each of the five species of native Hawaiian gobioid stream fishes has a different host-parasite relationship with the nematode *Camallanus cotti*. This alien roundworm has been introduced into Hawaiian streams with the introduction of exotic fish hosts, mainly livebearers (Poeciliidae) such as mosquitofish, guppies, green swordtails, and short fin mollies, species which have been deliberately placed into streams throughout the archipelago for mosquito control and as aquarium releases. Four of the 5 native gobioids are capable of hosting this exotic parasite. Only *Sicyopterus stimsoni* remains uninfected because of its trophic ecology; this species of goby scrapes diatoms from rocks and does not eat copepods, which are intermediate hosts for *C. cotti*. Female roundworms can produced viable juvenile offspring in *Stenogobius hawaiiensis*, but data suggest that most specimens do not survive beyond third stage juveniles in this host. The roundworm reaches its greatest abundance in the sleeper, *Eleotris sandwicensis*, but because it is incapable of complete maturation in this host, this fish may be regarded as an ecological sink for the parasite. Furthermore, because large sleepers are more heavily infected than juvenile sleepers, following a dietary switch from microcrustacea to fishes and macrocrustacea, paratenic hosts may be involved in transmission. Both postlarval *Awaous guamensis* and *Lentipes concolor* occur syntopically near stream mouths, but only *A. guamensis* becomes infected at that location. Only after migrating to stream headwaters does *L. concolor* become infected, even in the absence of poeciliid reservoir hosts.

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Seasonality and the Long-Term Variation of the Prevalence of Tropical Aquatic Helminth Parasites.

D. PECH, M.L. AGUIRRE-MACEDO, and V.M. VIDAL-MARTÍNEZ*, Departmento de Recursos del Mar, CINVESTAV-IPN Unidad Mérida, México.

Seasonality, related to rainfall, appears as a powerful driver of the percentage of infected hosts (PIH) with helminth parasites in tropical aquatic ecosystems from Yucatan Peninsula. Using a scale-dependent approach, we investigated the temporal scales of maximum variability of helminth PIH, host abundance, and rainfall for

the snails *Pyrgophorus coronatus* (4 years on a monthly basis, 6 helminth species), and *Cerithidea pliculosa* (7 years, 3 species), and for the native cichlid fish *Cichlasoma urophthalmus* (4 years, 7 species). Results show that seasonal rainfall plays an important role on PIH by causing an immediate or lagged favorable condition, increasing this infection's parameter values in a year scale, supporting the hypothesis of seasonal distribution patterns of parasites in tropical aquatic environments. The presence of stochastic natural events, such as hurricanes, cause depletion effect in the dynamic of parasites infecting their host, and the magnitude of their effects seems to depend upon the previous historical fluctuation of the host-parasite abundance patterns. Finally, in spite of this heterogeneity and the hurricanes affecting the study sites, the temporal distribution of PIH shows frequency cycles. Most of these cycles are in a year scale, suggesting that the environmental changes are within the range of variability naturally affecting the study sites.

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Stress, Immunity, and Blood Parasites (*Leucocytozoon*, *Haemoproteus*, and *Plasmodium* spp.) in a Free-living Population of White-crowned Sparrows, (*Zonotrichia leucophrys oriantha*) in Colorado.

C. MURDOCK* and M. DIETZ, University of Michigan, School of Natural Resources & Environment, Ann Arbor, MI; M. ROMERO, Tufts University, Biology Department, Medford, MA; and J. FOUFOPOULOS, University of Michigan, School of Natural Resources & Environment, Ann Arbor, MI.

Life history theory assumes that reproduction is expensive and competes for resources with other costly activities such as immune defense. Anthropogenic environmental variability may exacerbate this trade-off when resources become limiting. Evidence from lab and field studies show that habitat degradation increases stress levels, parasite loads, and malnutrition of animals. This study, conducted during the summers of 2003 and 2004, examined mechanisms through which food availability, stress, and blood parasitaemias impact individuals within a breeding population of White-crowned Sparrows. We experimentally reduced parasitaemias, and manipulated food availability, to study the effects on circulating corticosterone and immune function. A standard stressor was applied to each bird to measure baseline, post-stressor, and change in corticosterone, to assess an individual's sensitivity to a stressor. Birds were injected with phytohemagglutinin in the wing web, and swelling was measured to assess immune responsiveness. We collected blood samples to quantify blood parasitaemias. Males were more sensitive to the stressor during the early breeding season than late breeding season, and immune responsiveness increased throughout the season for all birds. Infection with blood parasites increased baseline corticosterone and decreased wing web swelling. Drug treatment lowered baseline corticosterone in males and increased swelling in both sexes. Males were more sensitive than females to the applied stressor, and there was no difference in wing web swelling between the sexes. Birds receiving both drug and food treatments had higher swellings than birds who did not receive either treatment. Thus, environmental variability throughout the breeding season could affect immune responsiveness, which in turn influences susceptibility to blood parasite infection. Once infected, birds experience higher baseline stress levels than uninfected birds. Furthermore, males and females are modulating their stress responses differently, due to the distinct reproductive costs the sexes experience while breeding.

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Trematode Communities of *Pyrgophorus coronatus* in 4 Waterbodies of Yucatán.

M.L. AGUIRRE-MACEDO* and A.T. SABASFLORES-DÍAZ DE LEÓN, Departamento de Recursos del Mar, CINVESTAV-IPN Unidad Mérida, Mexico.

Pyrgophorus coronatus is a hydrobiid snail widely distributed in open cenotes (=sinkholes) and non-permanent waterbodies (=aguadas) of Yucatan. At least 12 species of trematodes have been found infecting this snail species in Yucatán. To determine the local species richness and temporal dynamics of the trematode community of *P. coronatus* in 4 waterbodies from Yucatán, we conducted monthly sampling for one year cycle in the open cenotes of Chaamac and Noc-choncunchey; a flooded quarry called Mitza, and a waterspring known as Baldiosera, localized in the coastal lagoon of Celestún. Between 200 and 250 snails per month were collected from each locality. Snails were measured and examined at the laboratory by compression between two slide glasses. A total of 13 species of trematode cercariae and 3 metacercariae were identified. The maximum (12) number of species was found in Baldiocera waterspring and the minimum (6) in the Mitza quarry and Chaamac

cenote. The maximum number of species found in a single month, in any of the locations, was 6. Only 2 species were shared between localities. The most frequent species found was *Crassicutis cichlasomae*, present in 100% of the sampled months at Chaamac, in 91% at Noc-Choncunchey, and in 66% of months sampled at Mitza. *Oligogonotylis manteri*, *Phagicola nana*, and *Genarchela astyanactis* were present in 66% of the months, at one location each. Prevalence values for all species in cercarial stage never exceeded 11% at any locality through the year. The highest values of prevalence of the metacercariae of *C. cichlasomae* reached 30 % in Chaamac. The highest similarity (>75%) between localities was found between the two cenotes, whereas the lowest similarity (<30%) occurred between Celestún and the cenotes. Species richness and the temporal dynamics of each trematode species was characteristic for each location, suggesting that local factors are the major forces structuring these parasite communities in *P. coronatus*.

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Ancient Egyptian Medicine.

O.M. AMIN*, Institute of Parasitic Diseases, Tempe, AZ.

This presentation addresses the roots of Ancient Egyptian Medicine and its celestial origins, with special reference to the training of physicians in the Mystical School of Life, medical papyri (including case descriptions and treatments), practitioners and their specializations, and remedies and their signatures vs. the signatures of the patients and their different maladies. The special relationship between medicine, magic, and priesthood is emphasized as well as between medicine, the Milky Way Galaxy, and the Orion Constellation.

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Arabic Medicine.

O.M. AMIN*, Institute of Parasitic Diseases, Tempe, AZ.

This presentation deals with the origins of Arabic Medicine in the early centuries, schools of study, major original contributions, and translations from Latin and Greek sources. The most famous of the roughly 500 known practitioners through the 18th Century, whose work helped save Europe from the dark ages during the medieval centuries, are presented. A special reference is made to original works in surgery, ophthalmology, herbology, epidemiology, pathology, toxicology, pharmacology, hospitals, and environmental, chemical, and veterinary sciences.

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Intestinal Parasitic Infections among School Children in Kota Kinabalu, Sabah, Malaysia.

H. MAHSOL*, Institute for Tropical Biology & Conservation, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia; and A. SAPAAT, School of Science & Technology, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia.

A study was conducted to determine the infection of intestinal parasites among school children from three schools located in Kota Kinabalu, Sabah, Malaysia. Stool samples were collected from 400 students, age range from seven to nine years old, and examined for intestinal parasites by using direct smear, Modified Kato-Katz, and formalin-ethyl acetate concentration technique. Among these school children, 260 (65%) were infected with one or more of 17 intestinal parasitic species. On the other hand, 164 (63%) were determined as single infections, whereas 96 (36%) were mixed infections. The most frequent parasite was *Giardia lamblia* (18.6%). Other parasites were *Ascaris lumbricoides* (15.26%), *Entamoeba histolytica* (14.2%), *Iodamoeba butschlii* and *Trichuris trichiura* (10.79%), *Endolimax nana* (8.42%), *Entamoeba coli* (7.36%), *Hymenolepis nana* (4.47%), *Entamoeba hartmanni* (3.16%), *Strongyloides stercoralis* and *Taenia saginata* (1.5%), and *Chilomastix mesnili*, *Isospora bellii* and fish helminth *Dyphyllobothrium latum* (1.05%). Lastly, three species of helminths consisting of *Dypillidium caninum*, *Trichuris vulpis*, and the rat tapeworms *Hymenolepis diminuta* (0.5%), had also been revealed. The results suggests that prevention and control programs for intestinal parasites should be discussed in the design of long term use in this area.

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Metronidazole-Induced Programmed Cell Death in *Giardia duodenalis*.

A.E. ONIKU*, S. BAGCHI, and T.A. PAGET, School of Pharmacy, The Universities of Kent and Greenwich, Chatham, Kent, UK.

The death of cells by apoptosis is a vital mechanism for maintaining developmental and homeostatic processes within multicellular eukaryotes. Over the past ten years, research has unearthed evidence of PCD mechanisms within increasingly "simple" unicellular organisms, and recently, PCD has been observed in *Giardia duodenalis*, an amitochondrial protozoan parasite, in response to curcumin. In this study, we have investigated the response of *Giardia* to oxidative stress and metronidazole, a drug commonly used for the treatment of *Giardia* infections in humans. Biochemical, flow cytometry, light, and fluorescent microscopy methods were used to investigate the effects of hydrogen peroxide (H_2O_2) and metronidazole on the organism. Both H_2O_2 and metronidazole were able to induce a form of cell death which exhibited key biochemical and morphological indicators of apoptosis. The externalisation of phosphatidylserine and DNA fragmentation were observed within the cells and were shown to be dose responsive. Additionally, this process was insensitive to inhibitors of caspases (key proteases involved in PCD). Our data, along with that from previous studies, indicates that PCD is a ubiquitous mechanism used to remove 'damaged' cells. Such a mechanism is important for unicellular parasites, where evasion of the host immune system is vital for the maintenance of infection.

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Endoparasitic Helminths and Host Distribution in Selected Populations of Malagasy Lemuroids.

C.T. FAULKNER* and A. CHAPMAN, University of Tennessee, College of Veterinary Medicine, Knoxville, TN; R. JUNGE, St. Louis Zoo, St Louis, MO, G. CRAWFORD, San Francisco Zoo, San Francisco, CA; and C. WELCH, The Madagascar Faunal Group, Betampona Reserve, Tamatave, Madagascar.

Fecal samples (n = 229), representing 7 genera of wild-caught and captive Malagasy lemuroids, were examined for diagnostic products of endoparasitic helminths as part of the Madagascar Fauna Group's health monitoring program (http://www.savethelemur.org). Individuals in the host genus *Eulemur* accounted for most of the infections and 55/229 specimens were positive for at least 1 endoparasite species. Eggs of *Callistoura* sp. were predominate in 29/55 infected *Eulemur* spp., and in 5/17 infected *Varecia* spp. Strongylate-type eggs, probably from *Lemurostrongylus* sp. (62 × 38 µm) and *Pararhabdonema* sp. (75 × 40 µm), had a broader host-distribution in *Eulemur* spp., *Varecia* spp., *Indiri indiri*, *Hapalemur* spp., and *Propithecus* spp. Pinworm eggs from the genus *Lemuricola* were found in *Eulemur* spp., *Varecia* spp., *Lepilemur* spp., and *Propithecus* spp. Spiruroidea eggs (50 × 30 µm, thick-shelled with larva), presumably *Mastophorus muris*, were found only in 2 samples from *Daubentonia madagascariensis*, and likely reflect the insectivorous dietary habits of the host. *Trichuris* spp. eggs (90 × 45 µm) occurred in feces of 15/55 infected *Eulemur* spp. The dimensions of these eggs are much larger than other *Trichuris* spp. from primate hosts, and may represent an undescribed species unique to *Eulemur* spp.

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Malaria Sporozoite Migration through the Mosquito Hemocoel.

J.F. HILLYER*, J.G. KING, and J.D. GLENN, Department of Biological Sciences and Institute for Global Health, Vanderbilt University, Nashville, TN.

Mosquitoes are obligate vectors of *Plasmodium* parasites. One step required for malaria transmission involves the migration of sporozoites from the mosquito midgut to the salivary glands. During this process parasites must travel from one end of the insect to the other, while bathed in a soup of cellular and humoral immune molecules. The objective of this work was to study the migration of parasites within the mosquito hemocoel (body cavity) by assessing both the efficiency of this process and the mechanical routes used by parasites to reach their destination. Using a molecular assay that detects parasite ribosomal RNA, we found that the process of sporozoite migration through the hemocoel is highly inefficient: in a pulse-chase experiment that quantified sporozoites in the salivary glands, versus the rest of the hemocoel, only 19% of sporozoites invaded the salivary glands, and sporozoites that failed to invade within 8 hr died and were degraded. Then, using intravital imaging that tracked the movement of transgenic fluorescent parasites from the midgut to the salivary glands, we found

that the mosquito circulatory system plays an integral role during this process: parasites are released from oocysts and slowly move toward the posterior of the insect, until they enter the heart portion of the dorsal vessel through ostia located in the anterior portion of each abdominal segment. Once in the heart, sporozoites are rapidly shuttled to the head, by the peristaltic contraction of the dorsal vessel, where they exit into the hemocoel and slowly begin their migration toward the posterior of the insect. Taken altogether, these data show that, while salivary gland invasion is inefficient, the location where sporozoites exit the dorsal vessel likely increases *Plasmodium*'s chance of invasion because they are released near the salivary glands. In addition, results from ongoing experiments, assessing the role of the mosquito immune system in sporozoite killing and the molecular basis of salivary gland invasion, will be discussed.

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Ticks and Tick-Borne Pathogens and Symbionts of Black Bears in Florida and Georgia.

L.A. DURDEN*, Department of Biology, Georgia Southern University, Statesboro, GA; T.N. NIMS, Georgia Wildlife Resources Division, Social Circle, GA, M. SAVAGE, Southeastern Cooperative Wildlife Disease Study, Athens, GA; and M.J. YABSLEY, D.B. Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA.

Ticks were collected from 37 black bears, *Ursus americanus floridanus*, in northern Florida (17 bears) and southern Georgia (20 bears) in order to ascertain the tick and tick-borne pathogen and symbiont fauna associated with this host. Five species of ticks were recorded: the lone star tick, *Amblyomma americanum* (n = 22), Gulf Coast tick, *Amblyomma maculatum* (n = 11), American dog tick, *Dermacentor variabilis* (n = 29), blacklegged tick, *Ixodes scapularis* (n = 66), and the first record of *Ixodes affinis*(n = 1) from this host. Seven species of rickettsiae were detected and sequence-confirmed from these ticks: *Ehrlichia chaffeensis* and *Rickettsia amblyommii* in *A. americanum*; *R. amblyommii* in *A. maculatum*; *Rickettsia bellii* and *Rickettsia montanensis* in *D. variabilis*; and *Rickettsia cooleyi*, *Rickettsia* TR39-like, and *Rickettsia* sp. Is-1 in *I. scapularis*. Of these, *E. chaffeensis*, and possibly *R. amblyommii*, are zoonotic pathogens.

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A Role for Endogenous Nitric Oxide Production in *Giardia duodenalis*.

S. BAGCHI*, Medway School of Pharmacy, Universities of Kent and Greenwich at Medway, Central Avenue, Chatham Maritime, Chatham, United Kingdom; R. STEUART and R. THOMPSON, WHO Collaborating Centre for the Molecular Epidemiology of Parasitic Infection, School of Veterinary and Biomedical Sciences, Murdoch University, Murdoch, Western Australia; and T.A. PAGET, Medway School of Pharmacy, The Universities of Kent and Greenwich at Medway, United Kingdom.

Nitric oxide (NO) is a ubiquitous signalling molecule that acts in a variety of physiological and pathological roles, including the regulation of apoptosis. It is produced enzymatically, from arginine, through the action of NO synthase (NOS). Recent studies have shown that the protozoan parasite *Giradia* produces NO via an inducible type NOS and also exhibits a form of programmed cell death. The significance of NO production by *Giradia* is not clear; however, it may play a role in regulating host immune response, or it is possible that this molecule controls parasite population density by inducing apoptosis in a concentration/population size-dependent manner. In this study, we have focused on the potential of NO for regulating population size. To do this, we studied NO production in a number of *Giardia* isolates, as well as the effects of exogenously supplied NO on cell viability, necrotic, and apoptotic death. We have shown that NO is produced at relatively constant levels of all 9 isolates of *Giardia* in the presence of arginine (range 6–20 μM NO $h^{-1}10^6 cells^{-1}$). The effects of the NO donor S-nitrosoglutathione (GSNO) show that increasing concentrations of NO induce cell death. When trophozoites of *Giardia* were exposed to increasing concentration of GSNO, we observed a decrease in viability. We were able to identify apoptotic and necrotic activity occurring in response to GSNO, and we discuss the significance of this data with reference to our hypothesis.

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Partial Purification and Characterization of Excretory/Secretory (e/s) Antigens of the Rumen Amphistome *Gastrothylax crumenifer*.

M.K. SAIFULLAH*, Section of Parasitology, Department of Zoology, Aligarh Muslim University, Aligarh, India; G. AHMAD, Department of Microbiology & Immunolgy, TTUHSC, Lubbock, TX; and W.A. NIZAMI and S.M. ABIDI, Section of Parasitology, Department of Zoology, Aligarh Muslim University, Aligarh, India.

Amphistomiasis is one of the most common diseases of buffalo in tropical countries. In some localities, the prevalence of infection in individual hosts can reach tens of thousands of flukes. Adult amphistomes, especially those inhabiting the rumen, have low pathogenecity. However, migrating immature stages cause severe pathological disturbances, including hemorrhagic inflammation in the alimentary tract, edema, and anemia. Considering the importance of immunological diagnosis of amphistomes, particularly during the pre-monsoon period when the rumen parasites stop shedding eggs, the present investigation was carried out to identify *Gastrothylax crumenifer* excretory/secretory antigens that may be useful for the immunodiagnosis of rumen amphistomiasis. For the present study, excretory/secretory (E/S) proteins, obtained after the *in vitro* incubations of *G. crumenifer*, were purified through gel filtration using Sephadex G-200 and then characterized by Enzyme Linked Immunosorbent Assay (ELISA), sodium-dodecyl-sulphate poly acrylamide gel electrophoresis (SDS-PAGE), and Western blot analysis. The gel filtration indicated three fractions, F1, F2, and F3, of the E/S proteins. Fractions F1 and F3 were resolved as two distinct peaks, fraction F2 being dispersed. ELISA using hyperimmune sera raised in rabbit against the E/S proteins collected *in vitro* and analyzed the antibody titer against the individual purified fractions F1, F2, and F3 of the E/S proteins. ELISA revealed that the F1 fraction of the *G. crumenifer* offer a better sensitivity by detecting the IgG titer up to a dilution of 1:12800 of the hyperimmune sera. Fractions F2 and F3 seem to be weak antigens detecting IgG titer up to a dilution of 1:50 of the hyperimmune sera. SDS-PAGE and western blotting identified antigenic polypeptides in the individual E/S fractions. Western blot detected few antigenic polypeptides, a 33-kDa polypeptide being immunodominant in all the three E/S fractions. It is concluded that this preliminary study could be helpful for the diagnosis of amphistomiasis.

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Minimally Destructive Utilization of Mummies in Archaeohelminthological Studies.

D.J. RICHARDSON*, Bioanthropology Research Institute, Quinnipiac University, Hamden, CT; K. REINHARD, Forensic Sciences, School of Natural Resources, University of Nebraska, Lincoln, NE; and R. BECKETT and G. CONLOGUE, Bioanthropology Research Institute, Quinnipiac University, Hamden, CT.

Although important pathoecological data may be derived from the study of intestinal helminths of mummies, this important source of archaeological information has been sorely under-utilized. This underutilization is due largely to the fact that curators view the acquisition of material for archaeoparasitological studies as being a highly destructive process, and that the potential data do not justify the means of acquisition. Developments in recent techniques in the observation and extraction of intestinal contents from mummies, primarily endoscopy, provide minimally destructive means to obtain material with which to conduct archaeoparasitological studies. Colonic contents that may be easily extracted from both human mummies and mummies of non-human animals are particularly well suited to helminthological examination. Examination of statistically substantial numbers of mummies using these techniques will provide valuable prevalence and intensity data that may not be easily gleaned from the study of coprolites, which have been the focus of the majority of archaeohelminthological studies. Further, examination of fecal material from mummies circumvents any doubt that the material is of human origin, and that the material is associated with a specific host, so that findings may be placed into a larger pathecological context. Of primary interest to our immediate research program is examination of endosopcially-collected feces from mummies of non-human animals. There is tremendous paucity of archaeohelminthological data from non-human animals. Data gathered from this material may provide valuable insight into the evolution of human zoonoses within a cultural context.

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Theory and Application of Molecular Biology to Coprolites with Specific Parasite Targets.

K. DITTMAR*, Department of Biological Sciences, University at Buffalo, Buffalo NY.

Coprolites are mainly known as fossilized remnants of dinosaur dung. However, many archaeological sites contain coprolites of younger age, originating from wild or domesticated animals and humans. Past research has shown that these dietary waste products may reveal important information about food preferences, as well as about prevalent parasitic diseases. Molecular approaches, such as PCR-based high-throughput screens, and pyrosequencing, might be used to discover DNA evidence of parasitic infections. Large scale geographical or cultural screening of coprolites will thus add to our knowledge of parasite dispersal and evolution.

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Problems of Interpreting Prehistoric Oddities from Arid Archaeological Sites: Taeniids, Hymenolepidids, and Flukes.

K.J. REINHARD*, School of Natural Resources, University of Nebraska at Lincoln, Lincoln, NE; A. ARAÚJO, Escola Nacional da Saúde Pública, Fundação Oswaldo Cruz, Rio de Janeiro, RJ, Brazil; M.H. FUGASSA, Departamento de Biología, Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Mar del Plata, Mar del Plata, Argentina; and A. JIMÉNEZ-RUIZ, Harold W. Manter Laboratory of Parasitology, University of Nebraska at Lincoln, Lincoln, NE.

The identification and interpretation of 'ordinary' parasites from archaeological sites has become standard in archaeoparasitology. However, there have been unusual discoveries in arid North America of flukes, teaniid tapeworms, and hymenolepidid tapeworms that are difficult to diagnose, based on isolated eggs in coprolites and mummies. Focusing on sites in northeastern Mexico, and then northward into Arizona and Nevada, the evidence of parasitism and false parasitism with these species is presented. We conclude that it is impossible to completely discount all of these oddities as false parasites. Therefore, they may provide us with clues to the biodiversity of human parasites in ancient populations.

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Eared Grebes: Where have all their Helminths Gone?

A.S. DIDYK*, Department of Biology, The University of New Brunswick, Moncton, New Brunswick, Canada, and J.R. JEHL JR., National Museum of Natural History, The Smithsonian Institute, Washington, DC.

Forty-eight eared grebes, *Podiceps nigricollis* Brehm 1831, collected over 3 years from Wyoming at the end of July 2006 (n = 10); from staging areas on Mono Lake in California (n = 6) and Great Salt Lake in Utah (n = 22) from September to December, 2004–06; and from spring staging grounds on the Salton Sea in southern California in March and April of 2007 (n = 10), were examined for intestinal parasites. All 48 grebes were infected: the numbers of helminths per grebe ranged from 2 to 451 individuals (mean: 120.6); the number of helminth species ranged from 2 to 8 (mean: 4.2). Cestodes dominated the helminth communities of their hosts at all 4 collection sites, accounting for 97% of all individuals. Grebes, as a group, are among the most heavily parasitized of all bird species. Although the composition of species was similar to that of grebes reported from fresh water lakes on breeding grounds in Canada, both parasite abundance and diversity were much reduced away from the breeding grounds. It appears most of the parasite burden is lost during the short migration from breeding to staging areas. Small populations of parasites are sustained throughout the extended staging and wintering periods, during which time the grebes undergo several episodes of extreme physiological and morphological changes. The combination of these changes, together with the grebes' restricted diets in hypersaline, hyperalkaline habitats, and their unique feather-eating habits, are discussed as possible factors in the dramatic reduction in parasite loads.

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Impact of Eutrophication on Wood Frog, *Rana sylvatica* Tadpoles Infected with *Echinostoma trivolvis* Cercariae.

L.K. BELDEN*, Department of Biological Sciences, Virginia Tech, Blacksburg, VA.

Environmental context can influence the outcome of host–parasite interactions. One important change that is occurring in some freshwater system is eutrophication from increased inputs of nitrogen and phosphorous. Utilizing tadpole infection with trematode cercariae as a host-parasite system, this study examined (1) growth, development and the maintenance of trematode *Echinostoma trivolvis*, infection levels in second intermediate host larval wood frogs, *Rana sylvatica*, reared outdoors in mixed infection groups, and (2) post-infection impacts of eutrophication on *R. sylvatica* tadpoles infected to varying degrees with *E. trivolvis* cercariae and reared under eutrophic or control conditions in mixed infection groups in outdoor mesocosms. Results from the growth and development experiment suggest no impact of infection with 50 cercariae on *R. sylvatica* growth and development, as compared with uninfected controls. Results from the second experiment, investigating the impact of eutrophication on infected tadpoles, found that survival to metamorphosis of the individuals in the highest infection treatment (80 cercariae) was reduced regardless of eutrophication treatment. However, for individuals surviving infection with 80 cercariae, and for individuals infected with only 20 cercariae, no impact on mass at metamorphosis was documented, although individuals were larger at metamorphosis in the eutrophic tanks. These data demonstrate that infection with *E. trivolvis* can impact *R. sylvatica* survivorship, at least above some threshold infection level, and that once infection has occurred, eutrophication may have minimal impacts on tadpole hosts. Future studies will address whether host susceptibility to infection is altered by eutrophication.

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Species Richness in Trematode Communities of Snail Hosts from Yucatán, México.

R. RODRÍGUEZ-OLAYO*, N.A. HERRERA-CASTILLO, and M. AGUIRRE-MACEDO, Recursos del Mar, CINVESTAV-IPN Unit Mérida, Yucatán, México.

Studies in communities of larval trematodes, in first intermediate hosts, have contributed to a better undertanding of the ecological relationships among organisms in the aquatic environment and in human and animal diseases. In México, there is a shortage in the knowledge of communities of larval trematodes in snail hosts. In this study, our aim is to describe the species richness of trematodes in snail hosts, as a first step to get information regarding larval trematode communities. Five snail species, *Melampus coffeus*, *Batillaria* sp., *Cerithidea pliculosa*, *Biomphalaria obstructa*, and *Pyrgophorus coronatus*, were collected, at different times, from 12 different localities in Yucatán including ponds, sinkholes, watersprings, and coastal lagoons. With the exception of *P. coronatus*, where 15 trematodes were recorded, in all other snail hosts species richness was poor (3–5). The great heterogeneity in the habitat, the lifespan, and the spatial and temporal sampling effort of the snails can explain differences in species richness.

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Moderate *Echinostoma trivolvis* Infection has no Effects on Physiology and Fitness-Related Traits of Larval Pickerel Frogs (*Rana palustris*).

S.A. ORLOFSKE*, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA;
L.K. BELDEN, Department of Biological Sciences, Virginia Tech, Blacksburg, VA; and
W.A. HOPKINS, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA.

High infection levels of the trematode *Echinostoma trivolvis* decrease survival and growth of young amphibian larvae. However, in nature parasites are highly aggregated, which results in a large proportion of the amphibian population being only moderately infected. Responses at these more common low infection levels remain poorly studied. Thus, we investigated the sub-lethal effects of moderate (10, 30, and 90 cercariae) *E. trivolvis* metacercariae infection on growth and development of *Rana palustris* tadpoles. We also examined changes in metabolism as a potential underlying physiological mechanism of reduced growth. Furthermore, we quantified tadpole intestine size, which can exhibit plasticity in response to changing metabolic demands, and characterized metacercariae distribution in the tadpole kidneys. There were no changes in survival, development, intestine size, or growth related to metacercariae infection, at any of the three levels, at 1 month post-infection. Similarly,

metacercariae did not significantly increase metabolic rates during encystment or at 1 month post-infection. Metacercariae encysted in the pronephros significantly more than in the mesonephros, but tended to occur equally in right and left kidneys. Modest, ecologically relevant infections consistently showed a lack of effect on fitness-related traits of tadpoles.

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A Test of the Microsatellite Analysis of Pooled *Schistosoma mansoni* Miracidia Derived from Naturally-Infected Patients.

B. HANELT* and M.L. STEINAUER, Department of Biology, University of New Mexico, Albuquerque, NM; I.N. NDUNGU, G.M. MAINA, E.L. AGOLA, J.M. KINUTHIA, and G.M. MKOJI, Centre for Biotechnology Research and Development, Kenya Medical Research Institute, Nairobi, Kenya; D.M. KARANJA, Kenya Medical Research Institute, Centre for Vector Biology and Control Research, Kisumu, Kenya; and E.S. LOKER, Department of Biology, University of New Mexico, Albuquerque, NM.

Advances in molecular tools have resulted in rapid expansion in the power and use of molecular markers to address ecological questions. Recently, a robust and high-throughput method has been pioneered to study the molecular epidemiology of *Schistosoma mansoni* using 21 microsatellite alleles, which provides an opportunity to characterize the adult worm diversity within and between human hosts. One difficulty in applying this technique to adult worm populations is their inaccessible location within the human host. Short of resorting to autopsy or surgery, sampling must be done indirectly by examining progeny (miracidia). However, since a person with a moderate level of infection passes 30,000 eggs/day, adequate and representative sampling of adult allele frequency becomes problematic. Larger studies, involving hundreds of patients and the processing of thousands of single miracidia, will quickly become cost and effort prohibitive. An alternative technique is to use pools of miracidia, reducing the amount of genotyping and expanding the number of analyzed progeny. In this study, we tested whether genotyping pooled samples are as sensitive as sampling individuals and whether pooled data could be used as a test of patient's worm burden. Miracidia were collected from the feces of several patients from the Lake Victoria region of Kenya. For each patient, genotypes for 13 loci were generated for varying sizes of pools of miracidia (10, 50, and 100). The data suggests that the pools of 100 most closely represent the average of 100 individually genotyped miracidia. Genotype scores for pools were converted to allele frequency and total number of loci per patient. These measures were correlated with patient factors such as Kato count, HIV status, previous praziquantel treatment and geographic location. These data suggest that pooling can be a cost-effective method to characterize diversity, allowing the study of large subject populations (support by NIH grants R01AI044913 and R01AI053695).

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The Vegetarian and the Blood Feeder: Alternative Life Cycle Strategies of *Megalodiscus temperatus* in Tadpoles and Metamorphosed Anurans.

M.G. BOLEK*, Department of Biology, University of Nebraska at Kearney, Kearney, NE, and J. JANOVY JR., School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.

Megalodiscus temperatus (Stafford, 1905) is a common paramphistome trematode of North American amphibians, with a 2-host life cycle, that has been reported to infect frogs, and rarely, tadpoles. In this study, we document the alternative life-cycle strategy of *M. temperatus* in tadpoles and metamorphosed anurans. We show through field work and experimental infections that *M. temperatus* can establish in both anuran life stages, and worms become gravid and release eggs in both tadpoles and metamorphosed frogs. However, worms exhibit differences in route of infection, development, egg production, and diet in tadpoles and metamorphosed anurans. These alternative life history strategies of *M. temperatus* suggest different selective pressures on the development and reproductive success of these worms in tadpoles and metamorphosed anurans, and we discuss the evolutionary avenues for, and constraints on, amphibian trematode life cycles presented by these two different anuran life stages.

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Local Adaptation: Geographic Variation in Trematode Release by Gastropod Hosts in Response to Temperature.

J. KOPRIVNIKAR*, Department of Biological Sciences, University of the Pacific, Stockton, CA, and R. POULIN, Department of Zoology, University of Otago, Dunedin, New Zealand.

The host–parasite interaction is subject to co-evolutionary dynamics. Parasites with greater dispersal ability than their hosts are particularly likely to show local adaptations. Trematode parasites are known to show local adaptations to host populations, but can also exhibit adaptations to local environmental conditions. Given the importance of temperature for the emergence of trematode infective stages (cercariae) from gastropod first intermediate hosts, we investigated whether trematodes of the intertidal snails *Zeacumantus subcarinatus* and *Z. lutulentus*, from different latitudes (differing in mean annual temperatures) on the South Island of New Zealand, responded differently to temperature increases. The emergence of one trematode species, *Maritrema novaezealandensis* (Microphallidae), was not impacted by increased temperature and did not differ among locations. In contrast, the emergence of a second species *Acanthoparyphium* sp. (Echinostomatidae), increased at warmer temperatures. In particular, *Acanthoparyphium*-infected snails from the location with the coolest annual temperature showed the greatest increase in cercarial output. Our results demonstrate that various trematode species may be impacted differently by temperature changes resulting from global warming. In addition, intraspecific variation, likely resulting from trematode adaptation to local climatic conditions, may result in different impacts on ecosystems at different locales.

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Toxicity of Metam Sodium to *Ascaris suum* Eggs in Biosolids from Five Locations.

G.D. CAIN, Department of Comparative Medicine, University of Tennessee College of Veterinary Medicine, Knoxville, TN.

Of the many pathogens present in biosolids (sewage sludge), *Ascaris* sp. eggs are probably the most resistant to current sewage treatment methods. Our earlier studies (Cain, 1995, 2006) demonstrated that metam sodium (MAS; N-methyl dithiocarbamate, sodium salt), a widely-used agricultural fumigant, was a powerful biocide for *A. suum* eggs in biosolids. In these studies, we optimized treatment methods for laboratory-scale studies of MAS toxicity, and determined the minimum effective dose of MAS over a wide range of conditions including solids concentrations, pH, and temperature. Because sewage sludges from different regions vary widely in composition, we conducted laboratory studies on toxicity of MAS to *A. suum* eggs in sludge samples from treatment plants in Knoxville, TN; Lockport, NY; San Marcos, TX; Cedar Rapids, IA; and Turlock, CA. We also carried out full-scale studies on 800-gallon batches from a treatment plant in Maryville, TN. Laboratory results demonstrated a two-log reduction in viable eggs, in samples from all test sites, over a range of 2%–30% dry solids. MAS was similarly effective in the full-scale test for sludge at 2% solids. In the course of these studies, we determined that when *A. suum* eggs were agitated with a magnetic stirring bar during treatment, egg recoveries were greatly reduced, presumably because of breakage. It was further observed that treatment with KOH (pH 12 – a condition for meeting EPA vector attraction reduction standards) also reduced egg recovery.

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Toxicity of Amphotericin B on *Leishmania major* Promastigotes.

D.R. BIENEK*, P.C. THOMAS, M.L. COEN And P.K. FU, Naval Institute for Dental and Biomedical Research, Great Lakes, IL.

In recent years, a growing number of deployed military personnel in the Middle East have been infected, at an alarming rate, with cutaneous leishmaniasis. Currently, no reliable topical treatment for use in field operations has been cleared by the Food and Drug Administration. As such, infected personnel must be evacuated, at great expense, for treatment. Our goal is to identify potential compounds that could be used to develop a nontoxic, effective topical treatment for cutaneous leishmaniasis. Initial experiments determined the *in vitro* parasiticidal effect of amphotericin B (Fungizone) on *Leishmania major* promastigotes. The LD_{50} of a single application of Fungizone was estimated to be 0.065 and 0.038 µg/ml on day 1 and 2 post-treatment, respectively. When a second dose of Fungizone was administered after 18 hours, the LD_{50} was 0.0316 µg/ml. The efficacy of

Fungizone as a parasiticidal agent was also influenced by parasite density. At a seeding density of 2×10^6 or 1×10^6 parasites ml^{-1}, the number of parasites in flasks containing 0.3 µg/ml of Fungizone, was significantly lower ($P < 0.02$) than those containing 0.15 µg/ml. To ensure that the test compounds are not toxic to host cells, human skin fibroblasts were tested with ≤1,000-fold greater concentrations. Inasmuch as some strains of *L. major* may develop drug-resistance, our investigations include the assessment of encapsulated forms of amphotericin B, and combination therapy of amphotericin B with other anti-microbial compounds such as salts of fluoride. From these collective results, we believe that there is merit in proceeding to test the efficacy of these compounds on *L. major* amastigotes and cutaneous lesions.

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An ABCG Homologue Gene in Multi-Drug Resistant *Plasmodium yoelii*.

I. FERRER- RODRIGUEZ*, Inter-American University of Puerto Rico, Bayamon Campus, Department of Natural Science and Mathematics, Puerto Rico; G. GONZALEZ RUIZ, Inter-American University of Puerto Rico, Bayamon Campus, Department of Natural Science and Mathematics, Puerto Rico; B. GONZALEZ VAZQUEZ, Inter-American University of Puerto Rico, Bayamon Campus, Department of Natural Science and Mathematics, Puerto Rico; and A.E. SERRANO BRIZUELA, University of Puerto Rico, Medical Sciences Campus, San Juan, Puerto Rico.

Malaria drug resistance poses a formidable challenge to public health systems worldwide. Multi-drug resistance is often mediated by membrane proteins belonging to the ATP-Binding Cassette (ABC) superfamily of transporter, which translocates substrates across cell membranes. One of such groups of transporters belongs to the ABCG subfamily, which plays a critical role in drug resistance in neoplastic cancer cells. We identified the *Plasmodium yoelii* ABCG homologue gene (pybcrp) in PlasmoDB 5X coverage (Contig 56). Computed topology predictions revealed a structure typical of half transporters, consisting of an ABC and a transmembrane domain composed of six transmembrane helices (TM). The ABCG homologue gene shares 85% and 57% identity at the amino acid level with the homologue genes in *P. berghei* and *P. falciparum*, respectively. To ascertain if point mutations were present in the drug resistance lines of *P. yoelii*, the open reading frame of the gene was PCR amplified and sequenced in *P. yoelii* NS (chloroquine selected), NS/1100 (mefloquine selected), and ART (artemisinin selected) lines. Preliminary results revealed four amino acid substitutions in NS/1100 and two in ART, as compared to the NS parental line. In addition, expression on the gene was confirmed in intraerythrocytic stages of the parasite by RT-PCR. Currently, we are performing additional experiments to measure gene copy number and expression levels of the *P. yoelii* ABCG homologue.

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The Occurrence of Species of *Toxocara* in Wild Mammal Populations from Egypt.

N.A. RADWAN, A.I. KHALIL* and R.A. EL MAHI, Department of Zoology, Faculty of Science, University of Tanta, Tanta, Egypt.

Toxocara canis is a zoonotic helminth of significant medical importance. Domestic and wild mammals act as reservoirs. Adult *T. canis* was found in 31 (53.4%) domestic dogs, 20 (48.6%) red foxes, 27 (52.7%) grey wolves, and 25 (59.5%) Egyptian mongooses. *Toxocara cati* was found in 27 (58.6%) wild cats. The grey wolf and the Egyptian mongoose represent new host records in Egypt. The mean intensity and abundance of *T. canis* were highest in grey wolves and lowest in red foxes. The prevalence, intensity, and abundance varied with host species, sex, and season. These findings are discussed in relation to previous reports elsewhere in the world. Adults recovered from different hosts were compared morphometrically, and the surface features were described using SEM. Adult *T. canis* recovered from different hosts were similar morphologically, except for those recovered from grey wolves, which had inflated lips, and the cuticular ornamentation was variable. Attention is drawn to the role of these wild hosts in the transmission of infection to humans.

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Influence of Diet on Helminth Species Richness in South Texas Doves.

A.J. SMITH*, Caesar Kleberg Wildlife Research Institute, Texas A&M Kingsville, TX, and
A.M. FEDYNICH, Caesar Kleberg Wildlife Research Institute Texas A&M Kingsville, TX.

Four species of native columbids, the Inca Dove (*Columbina inca*; INDO), Common Ground-Dove (*Columbina passerina*; COGD), Mourning Dove (*Zenaida macroura*; MODO), and White-winged Dove (*Zenaida asiatica*; WWDO), and two introduced species, the Eurasian Collared-Dove (*Streptopelia decaocto*; ECDO) and Rock Pigeon (*Columba livia*; ROPI), reside in South Texas. Though dietary habits of all but the INDO and CGDO are well known, little information is available linking basic food habits of the doves with helminth infections. Crop contents and helminths of 258 doves collected from 10 June–6 October, 2007 were examined. The crop contents of INDO, ECDO, and ROPI consisted primarily of commercial cultivated seeds (millet 55%; sorghum, 44%; and sorghum, 87%, respectively). INDO primarily foraged at residential birdfeeders, whereas ECDO and ROPI fed at cattle feedyards. These doves also had low (1–3 helminth species) parasite species richness. Doves that foraged in rural areas (WWDO, MODO, and GCDO) had a diet that consisted mainly of doveweed (*Croton* spp.) and grass (*Panicum* spp.) seeds, but no one plant species dominated numerically in their diet. Helminth species richness in these doves tended to by higher (6–10 helminth species). Seed species richness varied among dove species and was lowest in the ROPI (4 seed species) and highest in the CGDO (18 seed species). In addition, direct lifecycle nematodes tended to be absent in urban-feeding doves, while those doves feeding in rural areas had more species of nematodes. Data indicate a correlation between feeding habits and parasite infection. Diversity of diet breadth, and differences in foraging behavior (urban versus rural), plays an important role in shaping helminth communities.

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Day Length, Rather than Temperature, Predicts Transmission of a Trematode Cercaria to an Estuarine Snail.

B.L. FREDENSBORG*, Department of Biology, University of Texas-Pan American, Edinburg, TX.

Temperature is considered an important factor in parasite transmission. Among larval trematodes, there is a strong positive relationship between temperature and the production of cercariae, the infective stage to the next host in the life cycle. However, there are few field studies demonstrating a correlation between temperature and the transmission of cercariae, and other factors related to host activity or nutritional status are rarely considered. In this study, I investigated the effect of temperature and day length on the recruitment of metacercariae of the trematode *Acanthoparyphium spinulosum* to the marine snail *Cerithidea californica* in a tidal channel in Carpinteria Salt Marsh (CSM), Southern California. Day length was used as an indicator of the abundance of benthic diatoms grazed upon by *C. californica*. This snail serves as both first- and second- intermediate host, and cercariae penetrate and encyst as metacercariae in the buccal mass of conspecifics. From September 2006 to May 2007, mark-recapture studies were conducted on snails from a channel site within CSM. After approximately 30 days, marked snails were recovered, dissected, and examined to quantify *A. spinulosum* metacercariae in the buccal mass of snails. Water temperature was monitored continuously 1 cm above the substratum and 2 meters from the channel bank. A partial correlation analysis showed that mean day length for each 30-day period was strongly and positively correlated to the mean daily number of *A. spinulosum* metacercariae recruited to *C. californica* ($r = 0.976$, $P = 0.024$, $n = 5$). Mean daily temperature was not significantly related to either mean daily recruitment rate of metacercariae or mean day length ($P = 0.558$ and $P = 0.279$, respectively). These results suggest that factors related to day length (i.e., food abundance) may be more important than temperature in the transmission of cercariae. Future studies on the transmission of infectious diseases should therefore also consider factors that influence host nutritional status.

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Macroparasite Community Analyses of Pacific Sardine (*Sardinops sagax*) Populations in the California Current System.

R.E. BALDWIN*, CIMRS Oregon State University, Hatfield Marine Science Center, Newport, OR, and K.C. JACOBSON, NMFS, NOAA Fisheries, Hatfield Marine Science Center, Newport, OR.

The Pacific sardine (*Sardinops sagax*) fishery crashed in the 1950s off the coasts of Oregon and Washington (USA). The sardine fishery resumed in 1999, and there is an interest by the fishing industry in reassessing the management of sardines in the California Current off of western North America. Identifying Pacific sardine populations using macroparasites is a new approach to an ongoing multidisciplinary study between fisheries scientists from Canada, the United States, and Mexico. Macroparasites, naturally acquired parasites as biological tags, have successfully differentiated populations of various fish species, but have had limited use in fish stock assessments in the United States. Parasite community analysis (e.g., prevalence and intensity) suggests that there are at least four sardine populations between Vancouver Island (British Columbia, Canada) and San Diego (California, USA). Four parasite species have emerged as potential biological tags in my study area. The trematode *Lecithaster gibbosus* is common only off of Vancouver Island, British Columbia, Canada. The trematodes *Myosaccium ecaude* and *Parahemiurus* sp. were found throughout the study area, but were most prevalent off of southern California. Although not as common as *M. ecaude*, the nematode *Anisakis* sp. was present and has been used previously to assess fish population structure. These initial data suggest that macroparasites can be another tool (identify population structure and movement) for the management of Pacific sardine populations in the California current. Future work will include developing microsatellites for two of the more widely distributed parasite species, (*Anisakis.* sp. and *M. ecaude*), to assess the applicability of using parasite population genetic structure to identify sardine population structure.

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Genetic Variation in Ribosomal Internal Transcribed Spacer (ITS-1) Region of *Leishmania donovani* Promastigotes of Indian Isolates.

S. THAKUR*, S.T. PASHA, V.R. MITTAL, and A. RAI, Division of Biochemistry and Biotechnology, National Institute of Communicable Diseases (NICD), 22-Shamnath Marg, New Delhi, India.

High levels of inter- and intra-species variation have been observed in rapidly evolving Internal Transcribed Spacer (ITS) of the ribosomal operons of *Leishmania* spp. from both Old and New World. To analyze this target, we attempted 95 visceral Leishmaniasis-positive clinical samples (Spleenic/Bone Marrow aspirates) from Bihar, India for *L. donovani* isolation, out of which 48 transformed into promastigotes in Tobie's Biphasic/M199 medium after incubation at 22–25°C for 5 days. DNA was extracted from all cultured promastigotes, along with eight primary isolates (before serial passages). All these isolates were confirmed to be *L. donovani* by species-specific PCR for kinetoplast DNA (kDNA). Thus, we had the DNA of cultured promastigotes, varying from primary isolation stage to the 30-passages stage. ITS-1 region (between SSU RNA & 5.8S RNA) for all 48 isolates were PCR amplified. Agarose gel electrophoresis of amplified product revealed an amplicon of 418 bp (new pattern) in case of all 48 isolates, which have undergone multiple passages, against 316 bp amplicon for all eight primary isolates, as earlier reported. Further analysis by direct sequencing confirmed that the ITS-1 sequence pattern of all 48 isolates (new pattern) was 100% homologous to each other and showed 33% homology to sequence of eight primary isolates and to NCBI-submitted sequence. Nucleotide position from 21–332, in new pattern sequence, was totally a novel sequence and replaced nucleotides from 21–230 in earlier reported sequence pattern (316 bp). These observations inferred that, prior to passages, there was no size and sequence variation of ITS-1 region, while single to multiple passages of promastigotes introduced size variation. Effect of passaging on virulent genes has been reported in *L. donovani*, but not yet on the non-coding region. The molecular basis of this needs to be established, but this finding can give a new dimension to species identification, strain differentiation, and population genetics.

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The WySTEP Program: Training Pre-Service Educators to Practice Science in the Secondary Science Classroom.

S. JENSEN*, D. MOTRIUK-SMITH, and R.S. SEVILLE, Department of Zoology and Physiology, University of Wyoming/Casper, Casper, WY.

The Wyoming NSF-EPSCoR Science Teacher Education Program (WySTEP) provides University of Wyoming secondary science education students with the opportunity to gain hands-on research experience and develop lesson plans based on their research for use in their student teaching residency. During 2007–2008, one STEP Fellow worked with a mentor researcher in the parasitology laboratory at the University of Wyoming/Casper Center assisting with collection, identification, and genetic analysis of *Eimeria* species from squirrel hosts. From this experience, the student increased her understanding of the scientific process and learned new techniques, data analysis, and interpretation. The student also developed several prospective teaching units involving ecology, parasitology, and genetics. A teaching unit involving genetic engineering was selected for further development, after discussion with a mentor high school teacher from the local school district. The high school mentor is the teacher the Fellow is working with during her spring 2008 student teaching residency. The unit was implemented in a high school biology course and included the theoretical background (transcription, translation, and recombinant DNA) and hands-on activities for 50+ students. For the hands-on activity, *Escherichia coli* cells were transformed with the pGLO plasmid containing green fluorescence protein gene (GFP). GFP expression was detected by exposure to UV light. The depth of topics covered and hands-on activities were adjusted depending on grade level of students (freshmen to seniors).

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Functional Genomic Screen of Early Larval *Schistosoma mansoni* Development using RNA Interference.

M.M. MOURAO*, Department of Biochemistry and Immunology, Univerdade Federal de Minas Gerais, Belo Horizonte, MG, Brazil; N. DINGUIRARD, Department of Pathobiological Sciences, University of Wisconsin, Madison, WI; G.R. FRANCO, Department of Biochemistry and Immunology, Univerdade Federal de Minas Gerais, Belo Horizonte, MG, Brazil; and T.P. YOSHINO, Department of Pathobiological Sciences, University of Wisconsin, Madison, WI.

To date, RNA interference (RNAi) represents the only method currently available for modulating gene-specific expression in *Schistosoma* spp., although large-scale (i.e., multigene) application of this technology to functional genomic investigations of early larval stage development has not been done. In the present study, 35 genes were selected, based on abundant expression in *in vitro*-cultured *S. mansoni* miracidia and/or primary sporocysts, to determine if gene silencing or knockdown by RNAi was associated with definable phenotypic changes in larval development. Double-stranded RNAs (dsRNA) of approximately 500 bp were synthesized and used to treat freshly-hatched and isolated miracidia at a concentration of 50 nM dsRNA in CBSS plus glucose. Controls included larvae cultured in CBSS alone or CBSS containing green fluorescent protein (GFP) dsRNA. Miracidia were allowed to transform to sporocysts in the presence of dsRNAs and further cultivated for 7 days, after which time sporocysts were photographed with a digital camera, attached to a fluorescent inverted microscope, and observed for various phenotypes including failure/delay in transformation, loss of movement, tegumental lysis/death, and size changes. For the latter phenotype, sporocyst lengths were measured from captured images using Metamoph software and statistically analyzed using the Mann-Whitney test. Of the phenotypes being evaluated, only larval size was affected by dsRNA treatment, and this was observed in 12 of 35 transcripts tested, including GST26, elongation factor alpha, zinc finger 1, amd members of the SMAD signaling molecules family, among others. Moreover, transcript abundance for 5 of the 12 genes exhibiting the "size" phenotype showed a significant knockdown by real-time qPCR, while 1 was upregulated by dsRNA treatment. Results demonstrate that the efficacy of dsRNA treatment is gene-dependent and may result in either up- or down-regulation of transcript levels. Data suggest that the "size" phenotype may represent a disruption of developmental signals, nutrient processing, or metabolic imbalance.

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Differentiation of Gene Expression Between Tachyzoites and Bradyzoites of *In Vitro*-Cultured *Neospora caninum*.

K. SEUNG-WON, K. CHANG-HEE, L. EUN-HANG, C. SE-EUN*, J. SUK-CHAN, and Q. DONG-VAN, Department of Bacteria and Parasitology, National Veterinary Research and Quarantine Service, Anyang, South Korea.

Interconversion between tachyzoites and bradyzoites of *Neospora caninum* plays a pivotal role in transmission of the parasite. Although significant efforts have been made toward understanding the mechanisms that trigger and control stage conversion of the parasite, little is known about this process. We used annealing control primer (ACP)-based PCR technique to characterize the differences in gene expression between tachyzoites and bradyzoites of *N. caninum*. The *in vitro* stage conversion of *N.caninum*-infected Vero cells was induced by treatment of infected cultures with 70 μM sodium nitroprusside (SNP). Subsequently, the gene expression profiles of the tachyzoites and bradyzoites were analyzed through comparison of the level of expression. ACP-based PCR revealed 85 genes that were consistently differentially expressed between tachyzoite and bradyzoite stages. Of the 85 differentially expressed genes (DEGs) identified, 10 were cloned into Topo TA cloning vector, sequenced, and further analyzed by BLAST. These differentially expressed genes include a combination of known genes and as yet unidentified genes. The present work provides candidate genes for further investigation on the molecular basis of stage conversion from tachyzoites to bradyzoites of *N.caninum.*

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SmZF1, A *Schistosoma mansoni* Zinc Finger Protein, has a Nuclear Localization and is Able to Activate Gene Transcription.

M.G. DRUMMOND, Department of Biochemistry and Immunology, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil; C. CALZAVARA-SILVA, Aggeu Magalhães Research Center, FIOCRUZ, Recife, Pernambuco, Brazil; D.S. D'ASOLFO, Department of Clinical Biochemistry, Facultad de Ciencias Químicas, Universidad Nacional de Córdoba, Córdoba, Argentina; M.M. MOURÃO*, F.C. CARDOSO, and M.A. RAJÃO, Department of Biochemistry and Immunology, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil; E. GAVA, Department of Morphology, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil; N.P. KORITSCHONER, Department of Clinical Biochemistry, Facultad de Ciencias Químicas, Universidad Nacional de Córdoba, Córdoba, Argentina; and G.R. FRANCO, Department of Biochemistry and Immunology, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.

During its life cycle, the parasite *Schistosoma mansoni* is exposed to diverse environmental conditions and presents different morphologies and patterns of gene expression. Thus, understanding the parasite gene transcription regulation is of particular importance. We have previously showed that SmZF1, a putative transcription factor in *S. mansoni*, is able to specifically bind DNA oligonucleotides *in vitro*. In this work, we demonstrated the sub-cellular localization of SmZF1 fusion proteins expressed in mammalian cells, as well as the native protein precise localization in distinct parasite stages. We also verified the SmZF1 ability to activate gene transcription in mammalian cells. Our results show that the fusion proteins YFP-SmZF1 and SmZF1-myc were detected in transfected COS-7 cells, mainly at nuclear sites, when monitored by fluorescence microscopy and western blotting. Additionally, total cellular extracts of transfected cells could bind *in vitro* to a specific oligo containing the SmZF1 binding site. Furthermore, the native SmZF1 was localized in *S. mansoni* adult worm nuclear extracts by western blotting, using a polyclonal anti-SmZF1 antibody. The nuclear localization of SmZF1 in male adult worms, schistosomulum, and cercariae, was demonstrated by immunohistochemistry experiments as well. Notably, YFP-SmZF1 increased transcription in COS-7 cells using a heterologous luciferase reporter system. Taken together, these results strongly support that SmZF1 may act as a *S. mansoni* transcription factor.

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Recombinant Expression of *Toxoplasma gondii* Surface Antigen SAG2 in the Methylotrophic Yeast *Pichia pastoris*.

Y. L. LAU*, School of Arts and Sciences, Monash University Sunway Campus, Selangor, Malaysia, and M. Y. FONG, Department of Parasitology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia.

Toxoplasmosis, caused by the obligate intracellular parasite *Toxoplasma gondii*, is widespread throughout the world (Bhopale, 2003). It may provoke severe problems in immunodeficient individuals, such as AIDS patients. In pregnant women, toxoplasmosis infection is a very severe problem, because transplacental transmission can occur and caused neonatal malformations, neurological damage, blindness, or fetal death. Routine diagnosis of toxoplasmosis is based on serological detection of antibody in the patient. Antigens used in these serological assays are usually proteins derived from *T. gondii* cells that are propagated in mouse or *in vitro* culture. Growing and maintaining this parasite poses a biological hazard to laboratory personnel handling the culture. Attempts to produce antigens through safer means, such as recombinant DNA technology, have been made. Progress has been focused on the surface antigens, such as SAG1 and SAG2, which are the major surface antigens of tachyzoites (Couvreur et al., 1988). Surface antigen 2 (SAG2) of *T. gondii* is a major surface protein, known as an attachment ligand (Grimwood and Smith, 1996), that has good antigenicity and immunogenicity (Aubert et al., 2000). However, recombinant SAG2 expressed in *Escherichia coli* (E-rSAG2) showed only partial protection against a lethal infection of *T. gondii*, which might be due to the incorrect folding of protein expressed (Mishima et al., 2001). To express SAG2 in a conformation that is closer to that of the native molecule, the *Pichia pastoris* cell expression system was used in the present study. To this end, the *P. pastoris* expression system leads to very high levels of secretion into an almost protein-free medium, is genetically stable, and can be scaled-up without loss of yield (Cregg et al., 1993). Thus, in our present study, we postulated that recombinant SAG2 produced in *P. pastoris* would also possess sufficient antigenicity for serorecognition. We characterised this antigen in western blot assays and *in vivo* experiments. The capability of the recombinant protein to induce protective immunity in BALB/c mice was examined.

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Hydatidosis in South India.

J.M. VARGHESE*, G.P. VARGHESE, and R.R. YESUDAS, Department of Zoology, Mar Ivanios College, University of Kerala, India.

Hydatidosis is caused by the larval stages of *Echinococcus granulosus*. *E. granulosus*, a tape worm of cosmopolitan distribution, inhabits the small intestine of dogs, and in larval form it infects many mammals, including man. The natural intermediate hosts are cattle, sheep, and goat. Beyond the economic loses in these agricultural animals, it is also dangereous to human health. No report is available on the prevalence of hydatidosis in South India, hence the present study. Of the 612 hosts examined, 82 were infected. In 66 cases, the infection was restricted to the liver, 12 had infection in lungs alone, and 4 had infection in both liver and lungs. The number of cysts in lungs as well as liver varied from 1 to 10. The colorless fluid drawn from the cyst contained granular deposits, the “hydatid sand”. Feeding the dogs with infective slaughter offals plays a significant part in the infection cycle, and the infection thus tends to be epidemic. The senior author reported that 9.7% of the stray dogs in South India were infected with *E. granulosus*. Human infection usually results from intimate association with infected dogs and can also be through food, water, or raw vegetables contaminated with the eggs of the tapeworm. Although human hydatidosis has been reported from several parts of North India, there is no documented case from South India. However, it is still it a potential threat to human health.

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Infiltration and Acquisition of Helminths within the Invasive Cuban Treefrog, *Osteopilus septentrionalis*, in West Central Florida.

N. ORTEGA*, W. PRICE, K. OLIVER And T. CAMPBELL, Department of Biology, University of Tampa, Tampa, FL.

The Cuban treefrog, *Osteopilus septentrionalis*, was introduced to North America in the 1920s and has since spread throughout the southeastern U.S. It is known to consume native amphibians and reptiles and is considered a superior competitor at the adult and tadpole stage. In the summer/fall of 2005–2007, 107 Cuban treefrogs were collected from a rural residential area and from natural wetlands in northeast Hillsborough County, Fl, and examined for helminths. The purpose of this study was to investigate the exchange of parasites between this invader and native herpetofauna, while also examining the roles of host length and sex on parasite prevalence and mean intensity. At least 8 species of helminths were isolated, 6 of which are new host records for the Cuban treefrog; 82 (76%) hosts harbored at least 1 species of helminth. Four nematode species, *Cosmocercoides variablilis*, *Oswaldocruzia lenteixeirai*, *Physaloptera* sp., and *Rhabdias* sp.; an unidentified larval acuariid nematode; one cestode, *Cylindrotaenia americana*; an acanthocephalan cystacanth, *Centrorhynchus* sp.; and an unidentified trematode metacercaria were found. The three most-prevalent parasites were *C. variabilis* (42%), metacercaria (35%), and acuariid larvae (24%). *Cosmocercoides variablilis* and *C. americana* were most likely acquired from native sympatric host species in Florida. *Oswaldocruzia lenteixeirai* has not been previously reported from North America and was probably introduced with the Cuban treefrog. A significant correlation was found between helminth intensity and host length. Excluding *C. americana* and *Rhabdias* sp., host sex was linked to significant differences in prevalence; there was no significant difference between mean intensity and sex for any parasite species. These parasite exchanges suggest the potential for parasite-mediated competition. In Florida, helminth acquisition for this semi-arboreal host is associated with diet and direct contact with skin-penetrating nematodes.

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Exposure to Snail Host Chemical Cues does not Induce Early Hatching of *Echinostoma trivolvis* Miracidia.

L.K. BELDEN*, P.D. WIDDER, L. FISCHER, and A. CARTER, Department of Biological Sciences, Virginia Tech, Blacksburg, VA; and J.M. WOJDAK, Department of Biology, Radford University, Radford, VA.

Many aquatic organisms use chemical cues to mediate behaviors, or to time life history transitions. While it is well known that various environmental cues, including temperature, light, and pH, can influence trematode egg hatching, little is known about whether chemical cues from potential hosts can stimulate development and hatching. In this study, we hypothesized that *Echinostoma trivolvis* miracidia would hatch sooner when exposed to cues from their first intermediate host, *Planorbella trivolvis*, as compared to when they were exposed to cues of a non-host snail or to untreated water. To test this hypothesis, we set up 25 plastic cups (5 replicates/treatment) in the laboratory at room temperature, each containing 6,600 *E. trivolvis* eggs in 30 ml of dechlorinated tapwater. Eggs were collected from the feces of infected hamsters and rinsed multiple times in dechlorinated tapwater before being placed in the cups. Each day, we added 100 µl of the appropriate cue to each cup. The treatments were: (1) dechlorinated water; (2) high dose of *P. trivolvis* cue (received cue everyday); (3) low dose of *P. trivolvis* cue (received cue once/week and water on other days); (4) non-host snail cue, *Goniobasis proxima*; and (5) non-snail invertebrate cue, earthworms. Chemical cues were taken from containers containing approximately 6.3 g of the appropriate organisms in 800 ml of water. We did not find support for our hypothesis. In each treatment, miracidia emerged for the first time on day 13. Using data from day 13 onward, linear regressions of the proportion of eggs hatching each day, versus time, were not significant for any treatment. There were also no apparent differences among cue treatments in timing of egg hatching or total egg hatching success by day 40. A roughly equal proportion of miracidia emerged each day for 4 weeks during our study, with a total hatching success at the end of that time of ~53%. In this system, it appears unlikely that chemical cues of hosts stimulate development or hatching of trematode eggs.

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Effects of a Parasitic Larval Nematode on Mating Behavior in the Western Mosquitofish, *Gambusia affinis*.

R. DEATON* and S. NOBLE, Department of Biological Sciences, Sam Houston State University, Huntsville TX.

We examined the effects of the parasitic larval nematode, *Eustrongylides ignotus*, on male mate choice in the western mosquitofish, *Gambusia affinis*. We hypothesized that parasite presence influences male mate choice either directly (via reduction in male mating behavior due to presence of parasite in females) or indirectly (via reduction in male mating behavior due to reduced condition of infected females). Specifically, we tested the predictions that (1) males would mate preferentially with uninfected over infected females (scoring both mating attempts and association time with females); and (2) parasitized females would be in poorer condition than non-parasitized females (measured as soluble fat stores). Males preferred to mate with non-parasitized over parasitized females but showed no differences in association time between females. The nematode did not decrease female body condition, but did decrease female mass and appeared to decrease female fecundity via reduction in broods (# embryos). Results support that parasites affect male mate choice in mosquitofish; however, the mechanisms used by males to differentiate between parasitized and non-parasitized females remain untested. This study suggests that parasites may play a role in sexual selection via male mate choice in a fish exhibiting a coercive mating system.

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Immunodiagnosis of Human *Wuchereria bancrofti* Infection using a Pair of Monoclonal Antibodies against Worm Antigen.

M.A. HENDAWY*, Theodor Bilharz Research Institute, Parasitology Department, Imbaba, Giza, Egypt; W.A. MANSOUR and F.M. SALAH, Theodor Bilharz Research Institute, Immunology Department, Imbaba, Giza, Egypt; I.S. RABIA, Theodor Bilharz Research Institute, Parasitology Department, Imbaba, Giza, Egypt; N.A. EL-GAMAL, Zagazig University-Faculty of Medicine, Tropical Medicine Department, Zagazig, Egypt; and A.A. EL-BASSIOUNY and Z.A. DEMERDASH, Theodor Bilharz Research Institute, Immunology Department, Imbaba, Giza, Egypt.

This study was designed to prepare monoclonal antibodies (MAbs) against filarial worm antigen (FWA), with immunodiagnostic potential for human filariasis. These MAbs were initially screened and then tested for their specificities against different parasite antigens (*S.mansoni* SEA, *Echinococus granulosus*, and *Fasciola hepatica*) by ELISA. From a panel of anti-filarial antigen Mabs, a pair of MAbs (9F/10B & 5F/ 6H) highly reactive with filarial antigen, and showing no cross reactivity against other parasites antigens, were selected and characterized. The pair was found to be of IgG1 subclass. Identification of target antigens recognized by MAbs was performed using immunoelectrophoresis, SDS-polyacrylamid gel electrophoresis, and enzyme-linked immunoelectrotransfer blot techniques. Both MAbs recognized one band with 88 kDa molecular weight by western blots. Chemical nature of MAbs target antigens was identified by periodate treatment method and proved to be glycoprotein in nature. The pair of MAbs was employed in sandwich ELISA for the detection of circulating filarial antigen (CFA); one MAb (9F/10B) was used as antigen-capturing antibody and the other (5F/6H) as peroxidase conjugated antigen-detecting antibody. The assay reached a lower detection limit of 125 ng/ml of filarial antigen. CFA levels were measured in serum samples from 71 filariasis patients (47 with microfilaraemia and 24 with elephantiasis), 45 patients with other parasites including schistosomiasis, fascioliasis, and echinococcosis and 39 healthy individuals as negative control. CFA levels were detected in sera of 68 out of 71 filariasis patients, showing an overall sensitivity of 95.8% (91.7% sensitivity for microfilaraemia group and 100% sensitivity for elephantiasis group). All negative control sera were negative for CFA, while 3 patients out of the other parasite group were positive for CFA, giving an overall specificity of 96.4%. These findings suggest that (9F/10B) MAb and (5F/6H) MAb could be used as a reliable diagnostic indicator for the activity of human filariasis and as a cure monitor, particularly in control programs for endemic areas.

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Detection of *Leishmania* (*l.*) *chagasi* in Canine Skin.

W.A. STARKE-BUZETTI*, N.G. QUEIROZ, M.F. NEVES, and R.D. VIVEIROS, Departamento de Biologia e Zootecnia, UNESP, Ilha Solteira, SP, Brazil; A.C. NORONHA JR., Centro de Controle de Zoonoses, Ilha Solteira, SP, Brazil; and R.Z. MACHADO and T.F. OLIVEIRA, Departamento de Patologia Veterinária, UNESP, 14879-000, SP, Brazil.

Canine visceral leishmaniasis (CVL) is caused by a protozoan parasite of the species *Leishmania* (*L.*) *chagasi*, endemic for humans and dogs in many regions of Brazil. The purpose of the present study was to evaluate the methods for demonstration of *Leishmania* in the skin of dogs from three different groups of clinical signs: asymptomatic, oligosymptomatic, and symptomatic *Leishmania*-infected dogs. Lesional or non-lesional skin tissues from the dogs were obtained and processed for histochemical (HE) and immunohistochemical (IMHC) methods, and the results were also compared with current serological tests such as the indirect fluorescence antibody test (IFAT), ELISA, and a polymerase chain reaction PCR method. This study demonstrated a good agreement between IMHC and HE methods for demonstration of intact *Leishmania* amastigotes in the skins. These methods detected high numbers of the parasites in skin, irrespective of the presence of lesions, particularly in asymptomatic and oligosymptomatic dogs. In the asymptomatic group, 87.5% of dogs were negative by serological tests, but 50% of them had parasites in their skins, although with mild inflammatory reaction or without any macroscopic dermatological alterations. In the oligosymptomatic group, 88.2% and 41.2% of dogs were positive by serological and parasitic direct observation (IMHC or HC tests), respectively. On the other hand, 100% of symptomatic dogs showed several forms of clinical dermatological lesions, and 88.9% were serum positive and had intact amastigotes, with parasite load ranging from mild to intense. By PCR, DNA of *Leishmania* sp. was detected in skins of all animals, regardless of their clinical status or the results of serological, IMHC, or HC tests, indicating more sensitivity with PCR method. PCR on skin was a sensitive procedure for diagnosing canine visceral leishmaniasis, but direct observation of the intact parasite in skin biopsies, particularly by immunohistochemistry, must be a valuable and conclusive method to support the diagnosis of this disease.

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School-Based Comprehensive Intervention to Prevent Re-Infection by *Giardia lamblia* and *Ascaris lumbricoides* among Tarahumara Indigenous Children of Northern Mexico.

J. MONÁRREZ-ESPINO*, C. ROCÍO PÉREZ ESPEJO, M. ITZEL LOYA MONTIEL, and S. PIZARRO CHÁVEZ, Unidad de Investigación en Epidemiología Clínica. Instituto Mexicano del Seguro Social. Chihuahua, Chih., México; R. ALVARADO ROJAS, E. PÉREZ GARCÍA, and A. BALLEZA CARREÓN, Hospital Rural Oportunidades No. 26. Instituto Mexicano del Seguro Social, Calle Atlante y Zacatepec S/N. Colonia Deportiva, Guachochi, Chih., México; R. CABALLERO HOYOS, Unidad de Investigación Epidemiológica y en Servicios de Salud del Adolescente. Instituto Mexicano del Seguro Social. Tonalá, Jal., México; and G. VÁZQUEZ MENDOZA, Centro Coordinador de Desarrollo Indígena. Comisión Nacional para el Desarrollo de los Pueblos Indígenas de México. Guachochi, Chih., México.

The objective was to assess the effectiveness of an intervention to prevent reinfestation by *G. lamblia* (GL) and *A. lumbricoides* (AL) in Mexican indigenous schoolchildren after 20 weeks. A school-based prospective comparative ecological study; two boarding schools hosting 100–120 children, aged 4–15 years, were selected based on physical infrastructure: intervention (IS), modern; control (CS), poor. After initial diagnosis, children with positive stool samples received supervised treatment with oral nitazoxanide. Diagnoses were made with at least one positive microscopic result in two serial samples using the Faust technique, as reported by independent observations of two trained lab technicians. Post-treatment samples were taken, and only children with negative results were followed-up. The intervention included school infrastructure improvements and maintenance and an educational preventive program for children, parents and school personnel; no activities were undertaken in the CS. Results showed baseline prevalence for GL in the IS and CS was 51.7% *vs.* 37.8% ($p<0.01$), and 37.5% *vs.* 16.6% ($P < 0.01$) for AL, respectively. In the IS, 35.7% did not speak Spanish compared to 6.7% in the CS ($P < 0.01$). Cure rates were similar in the IS and CS for GL (79% *vs.* 81%) and AL (97% *vs.* 100%). Final prevalence and reinfestation rates for GL was 10.4% *vs.* 10.8%, and 17.2% *vs.* 21% in the IS and CS, respectively. No children were infested/reinfested with AL in either school. Follow-up rates were 80–83% in the CS and 90–95% in the IS. It is concluded that supervised antiparasitic treatment, every semester, could be a cost-effective strategy to control GL/AL infestations, as children appear to get infected outside the school.

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Neurocysticercosis in Slovenia from 2001–2007.

J. LOGAR* and B. SOBA, Institute of Microbiology and Immunology, Medical Faculty, University of Ljubljana, Ljubljana, Slovenia; and J. TOMAZIC, Department of Infectious Diseases and Febrile Illnesses, University Medical Centre Ljubljana, Ljubljana, Slovenia.

Cysticercosis is caused by the larvae of the pork tapeworm, *Taenia solium*. Human cysticercosis is acquired by the ingestion of food or water contaminated with the eggs excreted by human carriers in their feces, or can result from autoinfestation. By digestion process in the host, the larvae released from eggs migrate with the blood into tissue, most often to the central nervous system, where they can cause neurocysticercosis-NCC. This disease is rare in most developed countries, but is endemic in Latin America, Asia, and Africa. The aim of this study was to examine serologically whether the patients with neurological disorders in Slovenia had been infected by the larvae of *T. solium*. From January 2001 to the end of December 2007, 243 patients of both sexes and from different parts of Slovenia were serologically screened by enzyme-immunoassay (*T. solium*, cysticercosis IgG ELISA, Novum Diagnostica GMBH). Twelve ELISA-positive sera were then retested by western blot test (WB IgG LDBIO Diagnostics Lyon, France), and five of them were proved (by antibodies with minimum of two well-defined bands among six bands on the strip; 6–8 kDa, 12 kDa, 23–26 kDa, 39 kDa, 45 kDa, 50–55 kDa) to be positive for NCC. The mean age of the five (3 women, 2 men) NCC patients was 43.8 years. NCC serological results of five patients corresponded to the imaging findings concerning the cysts in their brain. All NCC-positive patients were detected in the capital of Ljubljana. It was ascertained that they were all foreign born and that they immigrated to Slovenia from countries of the former Yugoslavia. In spite of the low NCC prevalence, 0.25 per $l0^5$ inhabitants, and the mean annual incidence of 0.04 per 10^5 inhabitants, it is suggested that the clinicians and public health authorities in Slovenia should pay more attention to this disease in the future, especially among the immigrants and tourists from endemic areas.

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Shedding of Oocysts by Dogs Fed Different Tissues from Naturally *Neospora caninum*-infected Bovines.

G.T. CAVALCANTE*, Department of Parasitology, Institute of Biomedical Science, University of São Paulo, São Paulo, Brazil; and R.M. MONTEIRO, R.M. SOARES, S.M. NISHI, F.A. NETO, and S.M. GENNARI, FMVZ-USP, São Paulo, SP, Brazil.

Neospora caninum is a protozoan parasite of domestic and wild animals. Coyotes and dogs are the definitive hosts of the parasite. Many epidemiological studies support the association of the presence of dogs with high rates of *N. caninum* abortion or infection in cattle. In order to evaluate the whole of different bovine tissues as modes of *N. caninum* transmission, pups were fed different tissue samples of 4 bovines naturally infected with *N. caninum* (indirect immunofluorescent antibody test, IFAT ≥ 400). A total of 20 mixed breed pups, 2–3 months old, negative to *N. caninum* (IFAT < 50) were divided into groups according to the tissue given: 5 were fed a mixture of muscles (diaphragm and masseter); 5 with heart, 3 with liver, 4 with brain; and 3 pups were used as non-infected control. All were vaccinated and dewormed. Daily, the total fecal volume (24 ht collection) was homogenized and examined for *N. caninum* oocysts (sucrose flotation technique). Fecal examinations were carried out until 10 days after the last shedding day, and the dogs that presented no oocysts shedding had fecal examination carried out until 30 days after tissue ingestion. The oocysts were sequenced with ITS-1 rDNA gene. The PCR ITS-1 products were directly sequenced and submitted to the BLAST search in order to identify the coccidian species. Compatible sequences of *N. caninum* (100% similarity) were found in dogs that ingested masseter/diaphragm (2 dogs, 40%), heart (2 dogs, 40%), liver (1 dog, 33%), and brain (3 dogs, 75%). The total mean oocysts elimination was 2,304, 5,409, 317, and 2,878 for dogs that ingested masseter/diaphragm, heart, liver, and brain, respectively. Sera from pups, collected at day 15 and 30 after tissue ingestion, resulted negative to *N. caninum* (IFAT < 50). This is the first report showing that other bovine tissues, apart from brain, can infect dogs with *N. caninum*.

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One Case of Feline Leishmaniosis in Brazil.

K.D. BRESCIANI*, Departamento de Apoio, Producao e Saude Animal, UNESP – Universidade Estadual Paulista, Faculdade de Odontologia, Aracatuba, Sao Paulo, Brazil; A.C. SERRANO, DAPSA (FOA) – UNESP , Araçatuba, São Paulo, Brasil; V.M. LIMA, Departamento de Clínica, Cirurgia e Reprodução Animal (DCCRA) Faculdade de Odontologia de Araçatuba (FOA), São Paulo, Brasil; F.L. BONELLO and R.O. VASCONCELOS, DCCRA (FOA) – UNESP, Araçatuba, São Paulo, Brasil; E.S. SAVANI and S.R. D'AURIA, Laboratório de Zoonoses e Doenças transmitidas por Vetores do Município de São Paulo, CCZ, São Paulo, SP, Brasil; and C.M. NUNES, DAPSA (FOA) – UNESP , Araçatuba, São Paulo, Brasil.

A male feline, indoor, mixed breed, four years old, was sent to the Zoonosis Control Center (CCZ) in Araçatuba, São Paulo, to be euthanized. This animal presented diarrhea, dehydration, apathy, and cutaneous lesions. After obit, fecal samples were taken for coproparasitological exams and made the poplíteo left lymph node imprints to observe the presence of *Leishmania* spp. amastigota forms. The serum was tested to leishmaniosis diagnostic with imunofluorescence indirect reaction test (RIFI) and indirect imunoenzimatic test (ELISA) to detect antibodies against *Leishmania* spp. and both results were negative; however, in polymerase chain reaction (PCR) to observe the parasite, the result was positive. It is the first case of visceral feline leishmaniosis in Araçatuba and serologic and citologic investigations must be performed in this endemic area.

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Frequency and Intensity of Gastrointestinal Helminths in Domestic Cats From Brazil.

K.D. BRESCIANI*, Departamento de Apoio, Produção e Saúde Animal, Faculdade de Odontologia de Araçatuba (FOA) – Universidade Estadual Paulista Julio de Mesquita Filho – UNESP , Campus de Araçatuba, Araçatuba, São Paulo, Brasil; M.N. ISHIZAKI and C.N. KANETOUKY, DAPSA (FOA) – UNESP, Araçatuba, São Paulo, Brasil; T.R. MONTANO, Departamento de Clínica, Cirurgia e Reprodução Animal (DCCRA) Faculdade de Odontologia de Araçatuba (FOA) – Universidade Estadual Paulista Julio de Mesquita Filho (UNESP), Araçatuba, São Paulo, Brasil; S.H. PERRI, DAPSA (FOA) – UNESP, Araçatuba, São Paulo, Brasil; R.O. VASCONCELOS, DCCRA (FOA) – UNESP, Araçatuba, São Paulo, Brasil; and O.A. NASCIMENTO, DMVPRA (FCVA)-UNESP, Jaboticabal, São Paulo, Brasil.

Gastrointestinal parasites are etiologic agents of many diseases that can be transmitted by pets. This study was aimed at verifying the frequency and intensity of helminths in domestic cats living in the urban area of Aracatuba, Sao Paulo State. Sixty mixed-breed domestic cats, aging 3 months to 10 years, were studied. Parasitological necropsy was made, and the collection of parasites present in the contents of the gastroenteric compartiments were identified and counted. A total of 52 (86.67%) animals were found infected by one or more species of helminths. In the stomach, the presence of *Physaloptera praeputialis* was observed in 12 animals (20%). Helminths were found in the small intestine from 50 cats (83.33%), of which 46 cats (76.67%) were co-infected with *Ancylostoma* spp.; 15 (25%) with *Dipylidium caninum*, and 1 (1.67%) with *Hydatigera taeniformes*. In the liver, 17 (28.33%) cats were infected with *Platynosomum fastosum*. *Ancylostoma* spp. were found in 789 male and 860 female cats, of which 40 (86.96%) had *A. braziliense* and 11 (23.91%) had *A. tubaeforme*. Fisher's Exact Test depicted a significant association between the presence (or not) of helminths in the liver and the age group of the cats ($P = 0.0293$). The high frequency of infected cats, especially with *Ancylostoma* spp., indicated the zoonotic potential of these helminths in the urban area of Aracatuba.

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Parasitic Frequency and Intensity of Gastroenteric Helminths in Domestic Dogs in Brazil.

K.D. BRESCIANI*, M.N. ISHIZAKI, C.N. KANETO, T.P. MONTANO, S.H. PERRI, and R.O. VASCONCELOS, Departamento de Apoio, Producao e Saude Animal, UNESP – Universidade Estadual Paulista, Faculdade de Odontologia, Aracatuba, Sao Paulo, Brazil; and A.A. NASCIMENTO, Departamento de Medicina Veterinaria Preventiva e Reproducao Animal, UNESP – Universidade Estadual Paulista, Faculdade de Ciencias Agrarias e Veterinarias, Jaboticabal, Sao Paulo, Brazil.

This study had, as its objective, the determination of the helminthic fauna in domestic dogs living in the urban zone of the city of Araçatuba in the state of Sao Paulo, Brazil. Parasitological necropsies were done on 65 dogs,

36 males and 29 females, with ages from 3 months to 8 years, in order to identify and count the helminthes. Three (4, 62%) had *Physaloptera praeputialis* in a density of 1 or 2 specimens. Thirteen (20%) were the hosts to 1 to 29 specimens of *Trichuris vulpis*. In the small intestine, we counted from 1 to 967 specimens of *Dipylidium caninum* in 39 of the dogs (60%), of 1 to 49 examples of *Toxocara canis* in 16 of the dogs (24, 62%), and from 1 to 984 *Ancylostoma* spp. in 49 dogs (75, 38%). There was no correlation ($P > 0.05$) between the helminthoses and the sex or age of the dogs. *D. caninum* was responsible for the most intense infections, while parasites of the genus *Ancylostoma* were the most prevalent. Parasitic infections due to *A. braziliense* occurred in 22 dogs, with varying intensity (1 to 112). Association of *A. braziliense* with *A.caninum* was seen in 12 animals. The elevated frequency and intensity of helminthic infections, especially due to *Ancylostoma* spp. and *Toxocara*, emphasize the risk of these zoonoses.

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Natural Infection with *Cryptosporidium galli* in Canaries (*Serinus canaria*), in a Cockatiel (*Nymphicus hollandicus*), and in Lesser Seed-Finches (*Oryzoborus angolensis*) from Brazil.

M.V. MEIRELES*, D.C. SIMÕES, A.A. NAKAMURA, and R.G. ANTUNES, Curso de Medicina Veterinária, Universidade Estadual Paulista, Araçatuba, São Paulo, Brazil.

Proventricular infection by *Cryptosporidium* spp. or *Cryptosporidium galli* has been associated to mortality, weight loss, diarrhea, and pasty feces. The purpose of this study is to report the occurrence of natural *C. galli* infection in canaries (*Serinus canaria*), lesser seed-finches (*Oryzoborus angolensis*), and in a cockatiel (*Nimphycus hollandicus*) in Brazil. The birds examined in this report were 4 adult female canaries, 8 adult female lesser seed-finches, and 1 adult cockatiel, all with clinical complaints of apathy and sporadic mortality. Fecal samples were collected and screened for *Cryptosporidium* spp. by negative malachite green method. After necropsy, proventricular smears were stained by Kinyoun modified acid-fast stain, mucosal smears were stained by Giemsa, and tissue sections were processed for histopathology. Amplification of *Cryptosporidium* spp. fragments of actin gene and 18S rRNA gene were accomplished by nested PCR, following sequencing and aligning of amplified fragments with published *Cryptosporidium* spp. sequences. Oocysts and other developmental stages of *Cryptosporidium* were observed in fecal samples, in proventricular stained smears, and in sections of proventriculum. There were also infections with concurrent pathogens, such as budding yeast cells, probably *Candida* spp., coccoid bacteria, and *Isospora* spp. Amplification of *C. galli* fragments were obtained, for actin gene and 18S rRNA gene, from fecal samples and proventricular smears. Chronic fecal shedding of *C. galli* was found in fecal samples from 1 cockatiel and from 1 lesser seed-finch.

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Comparison Between Four Coproparasitological Techniques for Efficiency in the Diagnosis of Helminths Eggs or Protozoa Oocysts in Cats.

É.D. RIBEIRO, Departamento de Apoio, Producao e Saude Animal, UNESP – Universidade Estadual Paulista, Faculdade de Odontologia, Araçatuba, Sao Paulo, Brazil; A.F. AMARANTE, Departamento de Parasitologia, Instituto de Biociencias, Universidade Estadual Paulista – UNESP, Botucatu, Sao Paulo, Brazil; and A.C. SERRANO, C.V. TAPARO, R.F. NUNES, M.N. ISHIZAKI, and K.D. BRESCIANI*, Departamento de Apoio, Producao e Saude Animal, UNESP – Universidade Estadual Paulista, Faculdade de Odontologia, Araçatuba, Sao Paulo, Brazil.

This study aimed at evaluating the occurrence of endoparasitoses in domestic felines, and at analyzing the effectiveness of Willis-Mollay's, Faust's, Sedimentation, and Direct Test methods in diagnosing these diseases. Fecal samples of 198 cats, sent by their owners to Araçatuba City's Animal Disease Control Center, were examined. Influence of age, sex, and breed of the animals, in the occurrence of helminths and gastrointestinal protozoa, was evaluated. The comparison between the techniques mentioned above were carried out by the chi-quare test (χ^2)and Cochran's Q-test by evaluating positivity as regards the occurrence of gastrointestinal parasitoses. No infection was detected in 47 (23.7%) out of the 198 examined cats. Monoparasitism was found in 85 (42.9%) of the felines. Mixed infections with 2, 3, and 4 parasites occurred in 57 (28.8%), 5 (2.5%), and 4 (2.0%) animals, respectively. *Ancylostoma* spp. were the predominant parasite, occurring in 129 cats (65.2%), followed by *Cystoisospora* spp. in 61 (30.8%), *Dipylidium caninum* in 18 (9.1%), *Toxocara cati* in 9 (4.5%), *Taenia* spp. in 9 (4.5%), *Sarcocystis* spp. in 2 (1.0%), and *Giardia* in 2 (1.0%). No association was noticed

between the diagnosed parasites and the variables of breed, sex, and age ($P < 0.05$). In this work, *Ancylostoma* spp. proved to be the major parasite in cats. Willis' technique showed higher effectiveness in diagnosing *Ancylostoma* spp. eggs (76 = 45.5%), whilst the Direct Test had the least effectiveness rate (49 = 29.3%). Willis' and Faust's techniques were superior in detecting *Cystoisospora* spp. and showed the same positivity (30 = 18.0%). Most of *Dipylidium caninum* cases were diagnosed by the Sedimentation technique (14 = 8.4%). In the face of the results, the association of Willis' and Sedimentation techniques is recommended in laboratorial routine for diagnosis of gastrointestinal parasites.

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Occurence of *Toxoplasma gondii* in Urban Rodents (*Rattus rattus*, *Rattus norvegicus*, and *Mus musculus*) Captured in São Paulo (SP), Brazil: Preliminary Results.

V. MURADIAN*, L.R. FERREIRA, and S.M. GENNARI, Department of Veterinary Preventive Medicine and Animal Health, University of Sao Paulo, Sao Paulo, Brasil.

Toxoplasmosis is a parasitic zoonosis, caused by *Toxoplasma gondii*, that can infect humans and warm-blooded animals. Cats are infected mainly by ingestion of tissue cysts in raw meat, or by predation. Mice, rats, and small birds seem to be the most important prey to domestic cats due to living close to homes, making it easy to establish the prey-predator relationship, and can become *T. gondii* reservoirs to domestic felines. In order to determine the occurence of *T. gondii* in urban rodents, and their role as toxoplasmosis reservoirs to cats, rodents were captured with cages in different parts of the city of São Paulo from April 2005 to February 2008. All rodents were bioassayed in mice, in an attempt to isolate *T. gondii* from their tissues. 210 rodents were examined (190 *Rattus rattus*, 16 *Rattus norvegicus*, and 4 *Mus musculus*). All bioassayed mice were seronegative. All mice had their brains fresh-examined under a microscope, and no tissue cysts were found. Brain and heart tissues from 126 rodents were kept frozen to have their DNA extracted, in order to run PCR in an attempt to check for possible presence of *T. gondii* DNA. At this moment, only brain samples are being analyzed and, depending on the amount of the tissue collected, more than one aliquot from each sample is being examined. So far, 62 brain samples (one from each rodent) were analyzed and none of them were positive.

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Biological Characterization of *Toxoplasma gondii* Isolates from Free-Ranging Chickens from the Northeast Region of Brazil.

S.M. GENNARI*, Department of Veterinary Preventive Medicine and Animal Health, University of São Paulo, São Paulo, Brazil; L.N. OLIVEIRA, Department of Veterinary Preventive Medicine and Animal Health, University of São Paulo, São Paulo, Brazil; L.M. COSTA JR., Centro de Ciências Agrárias e Ambientais, Universidade Federal do Maranhão, Chapadinha, Maranhão, Brasil; C.B. MELO, Faculdade de Agronomia e Medicina Veterinária, Universidade de Brasília, Brasília, DF, Brasil; J.C. SILVA, Departamento de Medicina Veterinária, Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brasil; C.M. BEVILAQUA, Faculdade de Veterinária, Universidade Estadual do Ceará, Fortaleza, Ceará, Brasil; S.S. AZEVEDO, Unidade Acadêmica de Medicina Veterinária, Centro de Saúde e Tecnologia Rural, Universidade Federal de Campina Grande, Patos, Paraíba, Brasil; E.M. OLIVEIRA, Escola de Medicina Veterinária, Salvador, Bahia, Brasil; A.C. MELO, Universidade Federal do Piauí, Parnaíba, Piauí, Brasil; D.A. ARAÚJO, Department of Veterinary Preventive Medicine and Animal Health, University of São Paulo, São Paulo, Brazil; and V. MURADIAN, Department of Veterinary Preventive Medicine and Animal Health, University of São Paulo, São Paulo, Brasil.

Toxoplasmosis is a parasitic zoonosis caused by *Toxoplasma gondii*, which can infect humans and warm-blooded animals. Cats are infected mainly by ingestion of tissue cysts in raw meat or by predation, and they can shed *T. gondii* oocysts to the environment. The prevalence of *T. gondii* in free-ranging chickens is a good indicator of the soil contamination with *T. gondii* oocysts because these chickens usually feed from the ground. Prevalence of *T. gondii* was evaluated in 152 chickens from 22 cities in states of Pernambuco, Rio Grande do Norte, Maranhão, Bahia, Ceará, Sergipe and Alagoas, all in the northeast region of Brazil. Antibodies were determined by Modified Agglutination Test (MAT $\geq$ 5) with 81 (53.3%) positive birds, with titres varying from 5 to 5,120. Brains and hearts from the positive chickens were bioassayed in mice. Pools of these tissues, previously digested with acid pepsin, were inoculated in a group of three mice per chicken. *T. gondii* was isolated in mice that were inoculated

with tissues of 23 (28.4%) chickens, and these isolates were found in all states: two (20%) in Pernambuco, four (23.5%) in Rio Grande do Norte, two (14.3%) in Maranhão, four (40%) in Bahia, six (35.3%) in Ceará, one (20%) in Sergipe, and four (50%) in Alagoas. Out of the 243 inoculated mice, 56 (23%) were infected and, out of these, 15 (26.8%) died of toxoplasmosis. Six out of the 23 groups with *T. gondii* isolation had mice mortality, up to 100% in five of these groups. Association between anti-*T. gondii* antibodies and isolation of the agent was found ($P < 0.001$), with more isolates obtained from chickens with the highest antibodies titre. However, it was not observed association between the occurrence of mortality in mice and the titre of antibodies in the chickens ($P = 0.087$).

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Separate Genital Ducts in the Sinus Sac of *Dinurus hippuri* (Digenea: Hemiuridae).

R.R. YESUDAS* and J.M. VARGHESE, Department of Zoology, Mar Ivanios College, University of Kerala, India.

The existence of separate genital ducts in the Family Dinurinae (Digenea: Hemiuridae) is first reported by this present study. *Dinurus*, the single genus under Dinurinae, includes flukes parasitic in the stomach of dolphin fishes, *Coryphaena hippurus* and *C. equiselis*. A complete description of *Dinurus* is not available, so most of the organ structure is uncertain. This study, using light and scanning electron microscopy (SEM), revealed the existence of independent genital ducts within the sinus sac of *D. hippuri*. *Dinurus* is hermaphroditic, and the reproductive system is limited to the anterior body division, the prosoma. The distal part of the male and female reproductive system is protected within the sinus sac of anterior prosoma. Previous reports revealed the presence of a common hermaphroditic duct in *Dinurus* opening out by a common genital aperture (GA). In the present study, separate male and female genital apertures were observed in adult worms under SEM. The male reproductive system ends with a GA on cirrus located posterior to the oral sucker ventrally. Female GA formed a genital atrium which opens out just below the male GA. Different from the previous reports, histology revealed the presence of separate genital ducts inside the sinus sac. In *D. hippuri*, the pars prostatica and metraterm did not forming a hermaphroditic duct.

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rRNA Sequences from Cestode Larvae Inhabiting the Intestines of Commercial Shrimp of the Gulf of Mexico.

J.T. PAYNE* and J. GUNDERSON, Biology Department, Tennessee Technological University, Cookeville, TN.

Bait shrimp from the Gulf of Mexico, belonging to the genera *Penaeus, Farfantepenaeus,* and *Litopenaeus*, often harbor small cestode larvae in their intestinal tract. There may be hundreds attached to the intestinal lining by their single sucker, with the largest numbers found just posterior to the hepatopancreas. Viewed from the attached side, they are nearly spherical in outline, with a diameter of 60–70 micrometers. Nothing in their simple morphology serves to indicate even an approximate identity; however the identity of larval cestodes can, in theory, be determined by using gene sequences. DNA was extracted from individual larvae frozen in two-microliter aliquots of clean seawater. Full-length small subunit rRNA gene sequences were amplified from the DNA of individual larvae by using PCR primers complementary to the conserved ends of metazoan sequences. DNA sequencing was carried out on a LI-COR 4200 automated sequencer using primers complementary to conserved regions of metazoan rRNA genes. The sequences obtained did not match any in GenBank. PAUP (v. 4, beta 10) was used to construct trees from our new sequences and from cestode sequences downloaded from GenBank. The trees indicate that our sequences belong to tetraphyllideans, and probably to either oncobothriids or phyllobothriids. Our sequences do not fall unambiguously into either of these two families. More sequence information, including at least large subunit rRNA sequence information, will be required for a more definite taxonomic placement of these larvae.

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Differentiation among Species of *Cosmocercella* Steiner, 1924 Based on Morphometrical Information.

R. MATA-LÓPEZ*, Department of Ecology and Evolutionary Biology, University of Toronto, Ontario, Canada; S. GUILLÉN-HERNÁNDEZ, Escuela de Biología, Departamento de Ecología, Facultad de Medicina Veterinaria y Zootécnia, Mérida, Yucatán, Mexico; and V. LEÓN-RÈGAGNON, Laboratorio de Helmintologia, Departamento de Zoología, Instituto de Biología, UNAM, Mexico.

At the present, *Cosmocercella* Steiner, 1924 comprises a small group of nematodes parasitic in amphibians and reptiles from North and South America and Asia; only eight species being recognized as valid. Differentiation among these species has been based on characters such as the number and position of the sexual papillae in males and the size of eggs in females; however, new information has not been added in recent descriptions of new species and, in a recent revision of the genus, we found that some morphological characters have been misunderstood in species descriptions. Specimens of five species of *Cosmocercella* from the USNPC were included in a comparative study: *C. anothecae, C. haberi, C. iwatsukii, C. minor, C. phyllomedusae,* and *Cosmocercella* sp. specimens recently collected from two states in Mexico. Specimens examined were mounted on temporary slides with glycerol for microscopical observation. Measurements in millimeters were obtained, and a morphometrical matrix with 18 taxa and 36 characters was constructed in Excel; information such as range, average, and standard deviation were calculated to general comparison. Images of taxonomic characters were obtained with a digital camera. Information was analyzed by Principal Components Analysis (PCA), a correlation matrix between characters was established, and morphometric traits were considered in the analysis. Eigen values were obtained from the covariance matrix, and the first two components were plotted. Analyses results provided new information to recognize each species and provided additional elements for their diagnosis. A qualitative comparison, based on morphology of plectanes among these five species, was made, resulting in a differentiation in the structure and size of these kind of papillae and in the distance among each pair. We found morphological correlation between specimens of *C. haberi* from different localities in North America; however, analyses distinguished the recently collected material from Mexico as a different taxon.

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Convergent Structural Caudal Features in Ascaridinae and Raphidascarididae (Nematoda, Ascaridoidea).

H. FAGERHOLM*, Department of Biology, Laboratory of Aquatic Pathobiology,Åbo Akademi University, Åbo/Turku, Finland, and S. RASSOULI, Department of Biology, Åbo Akademi University, Åbo/Turku, Finland.

Reproductive structures are often found to be conservative features isolating animal species. This is also true for species and groups of the Ascaridoidea, with some 50 genera. A notion was made previously on the anteriormost pairs of the four distal papillae on each subventral side of the tail of the male of the Ascaridinae, regularly to be joined. This feature is of interest, considering the systematic position of the parasite genera included (*Ascaris, Parascaris, Baylisascaris*), thus excluding *Toxocara*. In an analysis of the species *Hysterothylacium auctum* (Rudolphi, 1802), a similar but convergent distribution of the distal papillae is here suggested for the Raphidascarididae. Some 30 male specimens of *H. auctum*, from the intestine of Zoarces viviparus from the northern Baltic Sea, were fixed in glacial acetic acid, stored in 80% ethanol, and cleared in lactophenol. Worms were cut just anterior to the cloacal opening, and tails were mounted individually under a supported cover-glass and turned dorsal-side down. The distribution of the delicate caudal sensors was studied using a Nomarski interference phase contrast microscope. Although the distribution of the caudal papillae was less stable than previously observed in the ascaridine *Ascaris suum*, a distinct distribution pattern emerges where the anteriormost distal papillae are joined to form double papillae. It was also found that in *H. auctum*, the two pairs of the paracloacal group were separate on each subventral side of the tail. The distribution of the numerous subventral proximal papillae were not analysed. The results call for further studies of genera within the Raphidascarididae to establish any systematic pattern to imply their evolutionary history.

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Detecting a Complex of Cryptic Species of *Neoechinorhynchus* Golvani Salgado-Maldonado, 1978 (Acanthocephala: Neoechinorhynchidae) Inferred Through Nuclear Genes.

A. MARTÍNEZ-AQUINO*, G. PÉREZ-PONCE DE LEÓN, and M. GARCÍA-VARELA, Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad Universitaria, Mexico.

Neoechynorhynchus golvani is an intestinal parasite of freshwater and marine fishes, distributed in neotropical regions. In this study, the genetic variability of 15 populations from north, south, and central Mexico was estimated through two nuclear genes (ITSs and D2-D3 from 28S rDNA). The length of both genes ranged from 700 to 779 bp and 813 to 821 bp, by ITSs and 28S rDNA, respectively. The genetic divergence among the populations was 15% by ITSs and 10% by 28S rDNA. The phylogenetic analyses of both data sets, plus genetic divergence, suggest that some populations of *N. golvani* represent a complex of cryptic species composed by 4 lineages: (1) Gulf Central of Mexico, (2) lowland waters of south, (3) Occidental Central, and (4) a linage that has a wide distribution from Northwest and Southeast of Mexico and Central American. The allopatric speciation of the 4 linages could be due to microvicariant events of the region, and to ecological and phylogenetics associations of the interaction host–parasite.

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Balancing the Tripod: Acceptance of the 2008 Henry Baldwin Ward Medal.

D. CLAYTON*, University of Utah, Salt Lake City UT.

[No abstract submitted]

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The Quirks of Parasite Neurobiology: Providing Opportunities for Parasite Control?

A.G. MAULE*, N.J. MARKS, A. MOUSLEY, and P. MCVEIGH, School of Biological Sciences, Queen's University Belfast, United Kingdom; M.J. KIMBER, Biomedical Sciences, Iowa State University, Ames, IA; C.C. FLEMING, Pest Molecular Biology Group, Agri-Food Biosciences Institute, Belfast, United Kingdom; T.A. DAY, Biomedical Sciences, Iowa State University, Ames, IA; and D.W. HALTON, School of Biological Sciences, Queen's University Belfast, United Kingdom.,

Helminth parasite nervous system function is augmented by a broad variety of neuronally derived, intercellular signalling molecules. Our interest in this system stems from the remarkable success of the empirically discovered anthelmintics that negatively impact nerve/muscle function in parasitic worms. For decades, these drugs have formed our primary defence against diverse parasites and, although they continue to display commendable efficacy, we are witness to the pervasive erosion of their utility by the scourge of drug resistance. We have failed to capitalise on the successes of the empirical screening era, such that we are now largely bereft of alternative control options or next-generation anthelmintics. Accumulated evidence reveals highly developed neuropeptidergic networks in helminths, networks which play crucial roles in worm biology—yet neuropeptide signalling remains an untapped resource for parasite control. We have focused on helminth FMRFamide-like peptide (FLP) signalling systems which impact, amongst other things, diverse motor activities such as locomotion, reproduction, and alimentation. Key to the discovery and validation of novel drug targets from neuropeptide/FLP signalling networks in parasites is improving our scant understanding of them. Many of our efforts in this regard have uncovered quirks in parasite neurobiology that could provide foci for parasite control. For example, in nematodes, we have used RNA interference (RNAi) to probe FLP function and have discovered atypical responses to RNAi triggers in plant parasites. Also, in flatworm parasites, we have identified multiple, novel neuropeptides using in silico approaches and have applied RNAi to probe unusual neuropeptide signal termination processes. This lecture aims to highlight the appeal of neuropeptide-based neuronal processes to a variety of helminth parasite control strategies.

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Students, Opportunity, Serendipity, and W.B. Yates: "Education is Not the Filling of a Pail; it is the Lighting of a Fire."

D.W. DUSZYNSKI*, Department of Biology, University of New Mexico, Albuquerque, NM.

I grew up in Chicago, the only child of 1st generation Polish Americans. My father labored at two 8-hr jobs, and my mother sewed in a sweat shop, doing piece-work. I was the first person in my family to finish high school and college, and earn advanced degrees. The inspiration from my parents was: "work hard, go to college, and something good will come of your life." In college I met a parasitologist, Bob Calentine, who changed the intellectual direction of my life. In graduate school I met three people, each of whom helped focus that direction. Bill Marquardt introduced me to, and stimulated my fascination of, the coccidia. John Ubelaker taught me that at a university, the lights are on at night. And Gerald Schmidt shared his insatiable humor with me and taught me to do what you love, even if it's something as lowly as taxonomy. At UNM, I started slowly in 1970, tried to learn (not always successfully) from my many mistakes in teaching, and tried to learn how not to make (egregious) mistakes in science by watching what others were doing right. I did this by attending at least 4–6 parasitology meetings each year, at which I listened. I met and spoke to many of the leaders in all aspects of parasitology, including Clark P. Read, not just to those doing coccidian biology. I tried to learn something from each of them. In 1972, in my parasitology class at UNM, two young men entered my life who were to become my first two graduate students: Al Marchiondo and George Conder. They changed my life forever. They were followed by Bob Jost, John Davis, Steve Upton, Gary Eastham, Janice Moore, Dave Reduker, Brent Parker, Lynn Hertel, Todd Hill, Scott Gardner, Connie Wash, Angela Welford, Mike Patrick, Patty Wilber, Brent Pickering, Wade Wilson, Damien Scott, John Hnida, Kim Decker, Xiaomin Zhao, Meg (Ryan) Friggens, Ingrid Asmundsson, and Andrew Lynch. Each of these students taught me more about life and science than I ever taught them, but most had to have at least one fire lit during their tenure—and there are different kinds of fires. I am grateful for having known every one of them and, mostly, for the dynamics they created in my lab by their overlapping personas over 32 yrs.

Author Index for 2008 ASP

ASP Meeting History

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1970 Washington DC ¶
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2007 Merida, Yucatan, Mexico §§¶ ¶
2008 Arlington TX
2009 Knoxville TN
2010 Colorado Springs CO (*tentative*)

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