

W/DA 2008



57th Annual International Conference of the Wildlife Disease Association



• • •
Wildlife Diseases: Northern and Western Frontiers
Official Program and Abstracts
Edmonton, Alberta Canada
August 3-8, 2008

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WDA 2008



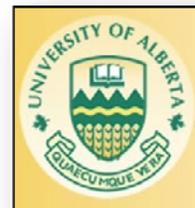
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57th Annual International Conference of the
Wildlife Disease Association
August 3-8, 2008
Edmonton, Alberta

Program & Abstracts

Conference Co-hosts



Regional Partner Hosts



Held in Conjunction with



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Federation of Alberta Naturalists
WDA Student Chapter presentation
WDA Sections presentation
US Geological Services
AAWV

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Special thanks to the American College of Zoological Medicine for sponsoring continuing education

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WDA 2008 Program

SUNDAY, AUGUST 3

8:30 – 12:00 Journal of Wildlife Diseases Editorial Board Meeting

Aurora

12:00 – 1:00 Lunch

1:00 – 5:00 WDA Council Meeting

Aurora

4:30 – 5:45 Student Career Workshop

Wild Rose

6:00 – 7:00 Student Mentor Kick-off

Wild Rose

7:00 – 10:00 Alberta Welcome: Opening reception

Wild Rose

MONDAY MORNING, AUGUST 4

8:00 – 8:30 Opening Ceremonies & Conference Welcome

Maple Leaf

Fish and Wildlife Honour Guard with RCMP Representatives

Lorne Babiuk, Vice President Research, University of Alberta

Ken Crutchfield, Fisheries Management Director, Fish and Wildlife Division

Charles van Riper III, President, Wildlife Disease Association

8:30 – 11:45 Feature Symposium: Wildlife Health in a Changing North

Maple Leaf

Presiding: Brett Elkin and Susan Kutz

8:30 1 International Polar Year and it's Legacy

***David S. Hik**

9:00 2 Landscape Change: Drivers for Ecosystem and Wildlife Health

***John Nishi and *Brad Stelfox**

9:30 – 10:00 **BREAK**

10:00 3 Grizzly Bears: Coupling Landscape Change and Population Performance

***Marc Cattet**

10:30 4 Climate Change and Disease in Norwegian Wildlife: Case Studies

***Bjornar Ytrehus**

- 11:00 5 Wildlife Health in a Changing North: A Model for Global Change
*Brett Elkin and *Susan Kutz

MONDAY AFTERNOON, AUGUST 4

1:00 – 4:00 Contributed Papers: Socio-political Challenges of Disease Management

Maple Leaf

Presiding: Scott Wright

- 1:00 6 The Cured Approach for the Management of Animal Disease in Nunavut, Canada
*Carla R. Baker
- 1:15 7 Facilitating the ‘Talking and Walking Together’ of Indigenous and Mainstream Sciences
*Cheryl M. Bartlett, Albert Marshall and Murdena Marshall
- 1:30 8 Engaging Indigenous and Rural People in Detecting Emerging Infectious Diseases
*Ryan K. Brook and Susan J. Kutz
- 1:45 9 Sociopolitical Challenges to Disease Prevention and Biosecurity in Live Bird Marketing Systems in Central America
*Patrice N. Klein, Fidelis N. Hegngi, Jose J. Bruzual, Cesar A. Sandoval and Mara E. Gonzalez Ortiz
- 2:00 10 Veterinary Students and Wildlife Conflicts in Uganda
*Jerry Haigh, Claire Card, John-Bosco Nizeyi, Ludwig Siefert, Nigel Caulkett and Gil Basuta
- 2:15 11 The Influence of Human Visitor Activity on Spatial Patterns of Parasite Infection
Chris O’Brien and *Charles van Riper III
- 2:30 12 Surveillance and Training Activities of Highly Pathogenic Avian Influenza H5N1 in Migratory Birds in Mexico
*A. Alonso Aguirre, Hector M. Zepeda-Lopez, Ana Lilia Sandoval, Eduardo Carrera, Alberto Lafon-Terrazas, Luis Lecuona and Antonio Gomez-Mendieta
- 2:45 13 Lead Toxicity in Wisconsin Wildlife
*Julia A. Langenberg, Sean M. Strom and Nancy K. Businga

3:00– 3:30 BREAK

- 3:30 14 Wildlife and Zoonotic Diseases: Potential Impact of Climate Change
*James N. Mills
- 3:45 15 Improving Guidance for Safe Handling of Wildlife: Insights from a Wildlife Biologist’s Death
*M. A. Wild, D. Wong, C. Higgins, J. G. Powers, T. R. Spraker, E. Perez, P. Mead and A. Chanlongbutra

4:00 – 4:30 American Association of Wildlife Veterinarians Cutting Edge Speaker
Maple Leaf

4:00 Introduction: Jonathan Sleeman

4:05 16 Climate Change: Trends, Future Scenarios, and Impacts on Wildlife Populations and Disease Dynamics
*** Susan Haseltine**

4:30 WDA 2009: Semiahmoo Resort and Spa, Blaine Washington USA
Joe Gaydos

MONDAY EVENING, AUGUST 4

5:00 – 6:45 Student Speed Dating
Tuckey Gym

7:00 – 10:00 WDA Poster Session
Tuckey Gym

7:00 **Student Snappies.** A fun session for all conference registrants. Students in the WDA poster competition will provide short snappy summaries of their posters.

7:30 **General Poster Viewing.** The only scheduled session for viewing all posters. Judging of the Student Poster Competition also occurs. All posters remain in place for opportunistic viewing until Tuesday afternoon.

Posters in WDA Student Poster Competition

P1 Retrospective Identification of Canine Papillomaviruses in Captive African Wild Dogs
Susan K. SchommerWm. Kirk Suedmeyer, Dae-Young Kim and *Jennifer R. Ballard

P2 Evaluation of Hematological Values in Free-Ranging African Buffalo
***B. R. Beechler, A. E. Jolles and V. O. Ezenwa**

P3 Health Assessment of American Oystercatchers (*Haematopus palliatus palliatus*) in Georgia and South Carolina
***Daphne Carlson Bremer, Terry Norton, Kirsten Gilardi and Christine Kreuder Johnson**

P4 Diseases in Dogs Parapatric to Wolves in Coastal British Columbia
***Heather M. Bryan, Paul. C. Paquet, Chris T. Darimont and Judit E. Smits**

P5 Qualitative Analysis of Farmed and Wild Cervid CWD Data in Alberta
***Paul E. Clyburn, Sylvia Checkley, Robert Hudson and John Berezowski**

P6 Endoparasites of Greater Sage-Grouse in Oregon
***Brian S. Dugovich, Robert J. Bildfell, Colin M. Gillin, Christian A. Hagen and Michael L. Kent**

- P7 Survey for Infectious Agents in Mule Deer in Southern Saskatchewan
***Champika Fernando, Janet Hill and Trent Bollinger**
- P8 Three Years of Surveillance for Avian Influenza in Hunter-Harvested Waterfowl on the Texas Gulf Coast, What Have We Learned?
***Pamela J. Ferro, Todd Merendino, Dayna Cox, Markus J. Peterson, Matt Nelson, David Hailey, Kevin Kreigel, David Butler and Blanca Lupiani**
- P9 A Pantropic Study of Rabies Virus in Arctic Fox
***Lori A. Gildehaus and Erich H. Follmann**
- P10 Influence of Mercury Toxicity on Hemoparasite Prevalence in *Tachycineta bicolor*
***M. Camille Harris, Daniel A. Cristol and Dana M. Hawley**
- P11 Population Dynamic Consequences of Impaired Survivorship and Reproductive Success in Deer Mice following Sin Nombre Virus Infection
***Sean M. Lavery and Frederick R. Adler**
- P12 Hair Cortisol Concentration: A Potential Non-Invasive Biomarker of Long-Term Stress in Free-Ranging Grizzly Bears
***Bryan J. Macbeth, Marc R.L. Cattet, Gordon B. Stenhouse and David M. Janz**
- P13 Evaluation of the Elk Brucellosis Test-and-Slaughter Program and Continued Studies on the Epidemiology of Brucellosis in Feedground Elk
***Laura L. Meadows, William Edwards, Terry Kreeger, Cynthia Tate and Todd Cornish**
- P14 Seroprevalence of West Nile Virus and Other Arboviruses in Crested Caracaras (*Caracara cheriway*) in Florida
***Nicole Nemeth, James Dwyer, Joan Morrison, Richard Bowen and James Fraser**
- P15 Experimental Exposure of Swallow Bugs to West Nile Virus
***Paul Oesterle, Nicole Nemeth, Paul Doherty, Richard Bowen, Jeffrey Hall, Robert McLean and Larry Clark**
- P16 Frequency of Rabies Antibodies in Tropical Bat Communities in Fragmented Landscapes in Puebla, Mexico
***Oscar Rico, Elizabeth Loza-Rubio, Edith Rojas, Rodrigo Medellín and Gerardo Suzán**
- P17 Effects of Hunting Pressure for Chronic Wasting Disease Control on Movement Patterns of Mule Deer in Southern Saskatchewan
***Erin Silbernagel, Nicole Skelton and Trent Bollinger**
- P38 “Project Tripwire” – Monitoring Wildlife Health through Wildlife Rehabilitation Centers
***Dave L. McRuer, Edward E. Clark, Jr**

General Posters

- P18 Longitudinal Studies of Population Cycles and Hantavirus in Montana Voles (*Microtus* spp).
***Arlene Alvarado, Amy Kuenzi and Richard J. Douglass**

- P19 Canine Distemper Virus Discovered in Feces of North American Bobcats (*Lynx rufus*)
***Anne Ballmann, James Guy, Roger Powell and Michael Stoskopf**
- P20 Health Assessment of Steller Sea Lions in Alaska, USA
Camilla Lieske, *Kimberlee Beckmen and Kathy Burek
- P21 DNA Extraction Method for *Histoplasma capsulatum* in Soil and Feces
***Kevin T. Bentler and Jenny Carlson**
- P22 Influence of Previous LPAI Virus Infection on Susceptibility of Wood Ducks to H5N1 HPAI Virus
***Taiana P. Costa, David E. Stallknecht, Justin D. Brown, Elizabeth W. Howerth and David E. Swayne**
- P23 Detection of Volatiles in the Uropygial Gland Secretions of Gray Catbirds (*Dumetella carolinensis*)
Rebecca Whelan, Tera Levin and *Mary Garvin
- P24 Avian Pathology Atlas on the Web
***Romona Haebler, Mark Pokras and Lou Sileo**
- P25 Thirty Years of Mortality Assessment in Whooping Crane Reintroductions: Patterns and Implications
***Barry K. Hartup, Marilyn G. Spalding, Nancy J. Thomas, Gretchen A. Cole and Young Jun Kim**
- P26 Use of Genetic Analysis to Evaluate the Alabama River as a Barrier to the Movement of Raccoons and the Raccoon Rabies Virus Variant
***Shylo R Johnson, Antoinette J. Piaggio, Melissa Neubaum and Mike Dunbar**
- P27 Population Size, Aggression, and Infection with Sin Nombre Virus (SNV) in Adult Female Deer Mice (*Peromyscus maniculatus*) in Montana
***Amy Kuenzi, Arlene Alvarado and Richard Douglass**
- P28 Alopecia in Moose infested with Deer Keds (*Lipoptena cervi*)
***Knut Madslie, Jonas Malmsten, Ketil Isaksen, Erling J. Solberg and Bjørnar Ytrehus**
- P29 Epizootic Hemorrhagic Disease Virus in Captive Bison, Elk, White-Tailed Deer, Cattle, and Goats from Colorado
***Pauline Nol, Will K. Reeves and Jack C. Rhyan**
- P30 Role of Gray Catbirds (*Dumetella carolinensis*) in the Overwintering of Eastern Equine Encephalitis Virus
***Jennifer C. Owen, Mary Garvin, Amanda Jo Williams and Frank R. Moore**
- P31 Described Diversity of Influenza Subtypes is Dependent on Amplified Length and Specificity of PCR Primer Sets for Sediment Samples from Alaskan Migratory Bird Ponds
***Jonathan A. Runstadler, Danielle Mondlach and Lori Gildehaus**
- P32 Blood Lead, Cadmium and Mercury Concentrations in Endangered Marine Species Inhabiting Andaman Sea and the Gulf of Thailand
***S. Siripattawan, P. Yatmark, N. Trakranrungsie, S. Munanunsup, P Jull, K. Adulyanukoson, K. Kittiwatanawong, P. Ratanakorn and U. Siripattawan**

- P33 Johnes's Disease in a Free-Ranging White-Tailed Deer from Virginia and Subsequent Surveillance for *Mycobacterium avium* subspecies *paratuberculosis*
*Jonathan M. Sleeman, Elizabeth J. B. Manning, John H. Rohm, Jerry P. Sims¹, Susan Sanchez, Richard W. Gerhold and M. Kevin Keel
- P34 Low-Pathogenic Avian Influenza Detection in Mallards (*Anas platyrhynchos*)
Kaci VanDalen, *Heather Sullivan, Susan Shriner, Nicole Mooers, Kevin Bentler and Alan Franklin
- P35 Molecular Ecology of Rabies in the Arctic
*Sara M. Turner and Jonathan A. Runstadler
- P36 Wildlife and Foodborne Zoonoses at the Agriculture/Wildlife Interface
*Joaquín Vicente and Christian Gortazar
- P37 Degenerative Cardiomyopathy in Vancouver Island Marmots (*Marmota vancouverensis*)
*Douglas P. Whiteside, Sandra R. Black, Stephen R. Raverty and Malcolm McAdie

TUESDAY MORNING, AUGUST 5

7:15 – 8:15 Prayer Breakfast
Evergreen

8:15 – 8:45 WDA Graduate Research Recognition Award Presentation
Maple Leaf

8:15 Introduction: Kevin Keel

8:20 17 Enzootic and Epizootic Vertebrate Hosts of Buggy Creek Virus (Togaviridae)
*Valerie A. O'Brien and Charles R. Brown

8:45 – 12:00 Terry Amundsen Student Oral Competition
Maple Leaf
Presiding: Kevin Keel

8:45 18 Detection of an Exotic Orbivirus, Epizootic Hemorrhagic Disease Virus Serotype 6 (EHDV-6) in the United States
*Andrew B. Allison, Virginia H. Goekjian, and David E. Stallknecht

9:00 19 Manipulative Experiments Monitoring SNV Transmission and Viral RNA Shedding in Deer Mouse Populations in Outdoor Enclosures
*Karoun H. Bagamian, James N. Mills and Richard J. Douglass

9:15 20 The Ecology of Aspergillosis in Seabirds: Evaluation of Available Diagnostic Tests
*Julia D. Burco, Lisa A. Tell, J. Gregory Massey, Judy St. Leger and Michael H. Ziccardi

9:30 21 Serodiagnosis of Dengue Virus in Black Howlers (*Alouatta pigra*) in Southeastern Mexico
*Salomé Cabrera, Gerardo Suzán, Rosa María del Angel, Juan Ludert, Domingo Canales Espinosa, Enrique Yarto and Pedro Américo D. Dias

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9:45 22 Evidence of Persistent Viral Infections in Semi-Domesticated Reindeer (*Rangifer tarandus tarandus*) in Northern Norway: Impact on Animal Health, Husbandry, and the Ecosystem
***Carlos das Neves and Morten Tryland**

10:00 – 10:15 **BREAK**

10:30 23 Host/Parasite Adaptation seen during the course of a *Sarcoptes scabiei* Epidemic in Red Foxes (*Vulpes vulpes*) in Norway
***Rebecca K. Davidson, Set Bornstein and Kjell Handeland**

10:45 24 Application of a Molecular Tool to Describe the Diversity and Distribution of GI Parasites in Northern Cervids
***Nathan P. deBruyn, Eric P. Hoberg, Neil Chilton, Kathreen Ruckstuhl and Susan Kutz**

11:00 25 White-Tailed Deer Habitat Use in New York: Implications for Disease Management
***Amy C. Dechen, David M. Williams and William F. Porter**

11:15 26 The Effects of Biodiversity on Zoonotic Disease
***Laurie Dizney, Philip D. Jones and Luis A. Ruedas**

11:30 27 Validation of Diagnostic Tests and Development of Molecular Epidemiological Tools for Brucellosis
***Amanda M. Fluegel, Todd Cornish, William Edwards and Ken Mills**

11:45 28 Coccidiosis Epornitic in Lesser Scaup on a North Dakota Lake
***Richard Gerhold, Michael Yabsley, Krysten Schuler, David Green, Mauritz Sterner and Erika Butler**

TUESDAY AFTERNOON, AUGUST 5

1:00 – 4:45 **Terry Amundsen Student Oral Competition, continued**
Maple Leaf
 Presiding: Holly Ernest

1:00 29 Forest Fragmentation affects Vector Abundance and Infection with *Trypanosoma cruzi* and *Trypanosoma rangeli* in a Panamanian Landscape
***N. L. Gottdenker, A.M. Santamaría, H. Membache, J. Calzada, A. Saldaña, V. Pineda and C.R. Carroll**

1:15 30 First Report of *Trypanosoma cruzi* Infection in Raccoons and Opossums from Kentucky
***Chad Groce and Cheryl D. Davis**

1:30	31	Incorporating Heterogeneous Deer Distribution into Chronic Wasting Disease Management in the Aspen Parkland of East-Central Alberta *Thomas J. Habib and Evelyn H. Merrill
1:45	32	Suitability of a Synthetic Semen Extender for the Cryopreservation of Epididymal Sperm from Plains Bison (<i>Bison bison bison</i>) *S. Krishnakumar, D. Whiteside, R. Jaiswal, B. Elkin and J. Thundathil
2:00	33	Use of the North American Animal Disease Model for the Study of Avian Influenza *Nicole L. Lewis, Javier Sanchez, John Vanleeuwen and Caroline Dube
2:15	34	Local Movement and Habitat Use of Avian Influenza Shorebird Hosts at Delaware Bay, USA *Angela M. Maxted, M. Page Luttrell, Ginger Goekjian and David E. Stallknecht
2:30	35	The Interacting Effects of Social Aggregation and Sex on the Ectoparasite Burden of Free-Ranging Raccoons *Ryan J. Monello and Matthew E. Gompper
2:45	36	Japanese Encephalitis Virus Reservoir Competency in North American Birds *Nicole Nemeth, Angela Bosco-Lauth and Richard Bowen
3:00 – 3:30 BREAK		
3:30	37	Cliff Swallows, Swallow Bugs, and West Nile Virus: A Mechanism for Overwintering? *Paul Oesterle, Nicole Nemeth, Ginger Young, Nicole Mooers, Stacey Elmore, Richard Bowen, Paul Doherty, Jeffrey Hall, Robert McLean and Larry Clark
3:45	38	First Detection of <i>Borrelia</i> spp. in Mongolian Reindeer (<i>Rangifer tarandus</i>) *Sophia Papageorgiou, Tsetseg Battsetseg and Janet E. Foley
4:00	39	Prevalence of Antibodies against Rift Valley Fever Virus in Kenyan Wildlife *Melinda K. Rostall, Alina Evans, F. Gakuya, J. T. Paweska, L. Akoolo, P. J. Van Vuren, T. Manyibe, J. M. Macharia, T. G. Ksiazek, D. R. Feikin, R. F. Breiman and M. Kariuki Njenga
4:15	40	Zoonotic Disease Surveillance at the Human-Wildlife Interface *Jennifer Siembieda, Woutrina Miller, Carol Cardona, Christian Sandrock, Walter Boyce, Nancy Anderson, Michael Ziccardi and Christine Johnson
4:30	41	Experimental Infection of Black-Tailed Deer (<i>Odocoileus hemionus</i>) with Deerpox Virus *Kimberly A. Thompson, Rob Bildfell, Ling Jin, Peregrine L. Wolff and Colin M. Gillin
5:00 – 6:00 American Association of Wildlife Veterinarians Business Meeting <i>Maple Leaf</i>		
6:00 – 7:00 Canadian Association of Zoo and Wildlife Veterinarians Business Meeting <i>Maple Leaf</i>		

TUESDAY EVENING, AUGUST 5**7:00 – 10:00 WDA Auction***Wild Rose***WEDNESDAY, AUGUST 6****8:00 – 9:30 Contributed Papers, concurrent session: Rabies and Hendra Viruses***Maple Leaf*

Presiding: Rick Gerhold (AAWV)

8:00 42 Management of an Outbreak of Rabies (West Texas Gray Fox Strain) in Coyotes in West Texas
***Ken Waldrup, Ernest Oertli, Tom Sidwa, Katherine Parker and Erika Quinones**

8:15 43 Lack of Field Performance of Raboral V-RG® in Producing Antibody Responses in Free-Ranging Striped Skunks (*Mephitis mephitis*) in Flagstaff, Arizona
***Krista Wenning, David Bergman, Dennis Slate, Charles Rupprecht, Barbara Worgess, Elisabeth Lawaczeck and Chad Heuser**

8:30 44 National Wildlife Health Center Update on Bat White-Nose Syndrome
***A. Ballmann, D. Blehert, D. Green, H. Ip, C. Meteyer, K. Miller, V. Stearns-Bocshler, M. Sterner and N. Thomas**

8:45 45 Bats, Rabies, and African Lyssaviruses
Ivan V. Kuzmin, Wanda Markoteer, Louis Nel and *Charles E. Rupprecht

9:00 46 Reproduction and Nutritional Stress are Risk Factors for Hendra Virus Infection in Little Red Flying Foxes (*Pteropus scapulatus*)
***Raina K. Plowright, Hume E. Field, Craig Smith, Anja Divljan, Carol Palmer, Gary Tabor, Peter Daszak and Janet E. Foley**

9:15 47 Modeling the Effects of Flying Fox Urbanization on Hendra Virus Dynamics
***Raina K. Plowright, Patrick Foley, Peggy Eby, Andy Dobson, Janet Foley, Hume Field and Peter Daszak**

8:30 – 9:15 Contributed Papers, concurrent session: Herptiles*Aurora*

Presiding: Valerie O'Brien

8:30 48 Mortality Summary (2000-2007) in Endangered Captive Kihansi Spray Toads (*Nectophrynoides asperginis*)
***Denise McAloose, Jennifer Pramuk, Bonnie Raphael, Paul Calle, Wynona Shellabarger, Andrew Odum, Michael Garner and Ann Duncan**

8:45 49 Parasites in Cold-Stunned Green Turtles (*Chelonia mydas*) in Florida
***E.C. Greiner, B.A. Stacy, T McIntosh, A.M. Foley, B.F. Sears and J.L. Miller**

9:00 50 Investigating Factors Influencing Ranavirus Infection and Disease
***Debra L. Miller, Matthew J. Gray and Jason T. Hoverman**

9:30 – 9:50 **Primer on Elk Island National Park (EINP): M. J. Pybus**
Maple Leaf

10:15 – 10:30 Buses leave for EINP

11:45 – 5:00 **Lunch, tours, hikes**

5:00 - 10:00 WDA Picnic at Oster Lake, EINP

8:00 – 10:00 **Buses return to Edmonton periodically**

THURSDAY MORNING, AUGUST 7

8:15 – 9:45 Contributed Papers, concurrent session: Disease Ecology- Avian I
Maple Leaf
 Presiding: Joe Gaydos

8:15 51 Ecological Models for the Community Dynamics of Avian Influenza in Waterfowl
 Communities
***Andy Dobson, Leslie Reperant and Thijs Kuiken**

8:30 52 Laboratory Evaluation of Abiotic Environmental Factors affecting Avian Influenza Virus
 Persistence in Aquatic Habitats
***Justin D. Brown and David E. Stallknecht**

8:45 53 The Wild Bird Global Avian Influenza Network for Surveillance (GAINS) Project
***Damien O. Joly, Kristine Smith, Marcela Uhart, Martin Gilbert and William Karesh**

9:00 54 Ecological Divergence of Two Sympatric Lineages of Buggy Creek Virus, an Arbovirus
 associated with Birds
***Charles R. Brown, Abinash Padhi, Amy T. Moore, Mary Bomberger Brown, Jerome E.
 Foster, Stephanie A. Strickler, Martin Pfeffer, Valerie A. O'Brien and Nicholas Komar**

9:15 55 Aspergillosis associated with Presumed Infectious Bursal Disease in Captive Whooping
 Cranes (*Grus americana*)
***Marie E. Pinkerton and Barry K. Hartup**

9:30 56 Bald Eagle Reintroduction to the Channel Islands - DDTs And PCBs
**A.E. Little, D.K. Garcelon, P.B. Sharpe, J.E. Haas, *S.K. Taylor, L. S. Cesh and C.S.
 Gorbic**

8:15 – 9:45 Contributed Papers, concurrent session: Wildlife-Domestic Interface
Aurora
 Presiding: Terry Kreeger

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8:15	57	Transmission of <i>Pasteurella haemolytica</i> between Free-Ranging Bighorn and Domestic Sheep *David L. Hunter, Lisa M. Cowan, Karen M. Rudolph and Alton C. S. Ward
8:30	59	<i>Mycoplasma</i> in a Desert Bighorn Sheep Population in Northwestern Arizona *Lisa A. Shender
8:45	59	Long Term Monitoring of Bighorn Sheep (<i>Ovis canadensis</i>) that have been in Contact with Domestic Livestock *Mark L. Drew
9:00	60	Distribution and Habitat Selection of Parturient Elk on Cattle Summer Pasture around Riding Mountain National Park: Potential Implications for Bovine Tuberculosis Transmission *Ryan K. Brook
9:15	61	Ecological Complexity and the Management of TB in a Wildlife Reservoir *Richard J. Delahay
9:30	62	Progress in the Control of Tuberculosis in Spanish Wild Boar *J. Vicente, J. de La Fuente, C. Ballesteros, V. Naranjo, I. G. Fernandez de Mera, J. Francisco Ruiz Fons, M. P. Martín-Hernando, J. M. Pérez-de-la-Lastra, R. Juste, A. Aranaz and C. Gortazar

9:45 – 10:15 BREAK**10:15 – 11:30 Contributed Papers, concurrent session: Tools & Techniques***Maple Leaf*

Presiding: Justin Brown (AAWV)

10:15	63	Surgical Placement of Abdominal Transmitters in Two Mule Deer (<i>Odocoileus hemionus</i>) *Mark L. Drew
10:30	64	Physiological and Pathological Effects of Surgical Implantation of Radiotransmitters in Massasauga Rattlesnakes (<i>Sistrurus catenatus catenatus</i>) Andrew M. Lentini, *Graham Crawshaw and David McLelland
10:45	65	<i>In Vivo</i> Imaging reveals the Pathogenesis of Monkeypox Viruses in Prairie Dogs *Tonie E Rocke, Nicola Pussini, Angela Londono-Navas, Elizabeth Falendyz, and Jorge E Osorio
11:00	66	Effectiveness of FTA® Cards for Avian Influenza Virus Field Surveillance *Shamus P. Keeler, Rebecca Poulson, Ginger Goekjian and David E. Stallknecht
11:15	67	Impact of Trapping Method on Detection of Avian Influenza Viruses *Jane Parmley, Catherine Soos, Keith McAloney, Bruce Pollard, Fred Kibenge, Emily Jenkins and F.A. Leighton

10:15 – 11:30 Contributed Papers, concurrent session: Genes, Vaccines & Immobilization*Aurora*

Presiding: Elena Garde (CAZWV)

10:15	68	Integrating Genetic Tools in Disease Ecology: Value-Added Wildlife Sampling Strategy *Holly B. Ernest
10:30	69	Humoral Immune Responses of White-Tailed Deer (<i>Odocoileus virginianus</i>) to <i>Mycobacterium bovis</i> BCG Vaccination and Experimental Challenge with <i>M. bovis</i> *P. Nol, K. P. Lyashchenko, W. R. Waters, J. C. Rhyan and M. D. Salman
10:45	70	Oral Vaccination of Wildlife against TB using a Lipid Bait Matrix *Matthew R. Lambeth, Frank M. L. Cross, Bryce M. Buddle and Frank E. Aldwell
11:00	71	Capture Mortalities in Moose, Brown Bears, Wolverines, Eurasian Lynx, and Gray Wolves: A Review of 5,959 Captures *Jon M. Arnemo
11:15	72	Butorphanol, Azaperone and Medetomidine (BAM) for Field Immobilization of Plains Bison *Todd K. Shury, William R. Lance and David L. Hunter

11:30 – 12:30 WDA Business Meeting (open to all registrants)*Maple Leaf***12:30 – 1:40 LUNCH****THURSDAY AFTERNOON, AUGUST 7****1:45 – 3:45 Contributed Papers, concurrent session: Disease Ecology- Avian II***Maple Leaf*

Presiding: Jane Parmley

1:45	73	Avian Filarioid Nematodes of the World: A Synopsis with Emphasis on Pathogenic Species *Cheryl M. Bartlett
2:00	74	Pox Virus Outbreak in Magellanic Penguins from Argentine Patagonia *Marcela Uhart, Virginia Rago, Ariel Pereda and Pablo Beldomenico
2:15	75	West Nile Virus Surveillance in Wild Birds and Mammals from the state of Chiapas, Mexico *Gerardo Suzán, José Estrada, Andres Gómez, Héctor Zepeda and A. Alonso Aguirre

2:30	76	Lead in Free-Ranging Ducks from Argentina Wetlands Hebe Ferreyra, Marcelo Romano, *Marcela Uhart and Pablo Beldomónico
2:45	77	Exposure of Black Vulture (<i>Coragyps atratus</i>) to Various Viruses in Mississippi *Richard B. Minnis, Sherman Jack, Danny L. Magee, Amanda Deese and Kyle VanWhy
3:00	78	Natural Highly Pathogenic Avian Influenza H5N1 Infection of Wild Birds: Species-Related Variations in Severity of the Encephalitic Disease *D. Gavier-Widén, C. Bröjer, E. Ågren, H. Uhlhorn, K. Bernodt and T. Mörner
3:15	79	Molecular Analysis of Temporally-Sampled Avian Influenza *Sara M. Turner and Jonathan A. Runstadler
3:30	80	Spatial Epidemiology of Avian Influenzas in Wild Migratory Waterfowl across the Conterminous United States 2006-2007 *Matthew L. Farnsworth, Alan B. Franklin, Thomas J. DeLiberto, Susan A. Shriner, Seth Swafford, Kaci VanDalen, Brandon B. Schmit, Heather Sullivan and Kerri Pedersen

1:45 – 3:45 Contributed Papers, concurrent session: Surveys & New Reports

Aurora

Presiding: Ryan K. Brook

1:45	81	Seroprevalence against Sin Nombre Virus in Resident and Dispersing Deer Mice Brent N. Lonner, Dean Waltee, *Richard J. Douglass, Amy J. Kuenzi and Kevin Hughes
2:00	82	Cowpox Virus Infection in Eurasian Lynx (<i>Lynx lynx</i>) in Sweden *Morten Tryland, Marie-Pierre Ryser-Degiorgis, Malachy I. Okeke, Carl Hård af Segerstad, and Torsten Mörner
2:15	83	Disease Surveillance in Wisconsin Free-Ranging Fisher <i>Martes pennanti</i> *Matt Watrud, Julia Langenberg, Nancy Businga
2:30	84	Necropsy Findings in Grey Squirrels (<i>Sciurus carolinensis</i>) in Ontario, Canada, 1993-2008 G. D. Campbell, *K.M. Welch and I.K. Barker
2:45	85	A Previously Unidentified <i>Chorioptes</i> Species infesting Outer Ear Canals of Moose (<i>Alces alces</i>): Characterization of the Mite and Pathology of Infestation *Gete Hestvik, Monika Zahler-Rinder, Dolores Gavier-Widén, Ronny Lindberg, Roland Mattsson, David Morrison and Set Bornstein
3:00	86	First Report of Phocine Distemper Viral Infection in Northern Sea Otters (<i>Enhydra lutris kenyoni</i>) from Alaska *Tracey Goldstein, John A. Hammond, Jonna A. K. Mazet, Verena A. Gill, Angela M. Doroff and Kathy A. Burek
3:15	87	Amyloid-Producing Disseminated Carcinosarcoma in a California Sea Lion (<i>Zalophus californianus</i>) *Howard Steinberg, Roberta Wallace and Vickie Clyde
3:30	88	Prevalence of Intestinal Helminth Parasites in Rhesus Monkey of Nepal *D. D. Joshi and V. Malla

3:45 – 4:15 BREAK

4:15 – 5:00 Carleton Herman Lecture
Maple Leaf

4:15 Introduction: Ed Addison

4:20 89 Disease, Wildlife Research, and the Public's Perception of Risk
***Mark S. Hafner**

THURSDAY EVENING, AUGUST 7

6:00 – 12:00 WDA Banquet and Awards
University of Alberta Faculty Club, Second Floor

FRIDAY MORNING, AUGUST 8

8:30 – 10:00 Contributed Papers: Disease Ecology - Ungulates
Wild Rose
Presiding: Damien Joly

8:30 90 Incidence of Hemorrhagic Disease in Virginia is Associated with Winter and Summer Climatic Conditions
***Jonathan M. Sleeman, Jay E. Howell, W. Matthew Knox and Philip J. Stenger**

8:45 91 Factors Affecting Epizootics of Winter Ticks
***Bill Samuel**

9:00 92 Evidence of Embryonal Death in Scandinavian Moose (*Alces alces*)
***Jonas Malmsten and Anne-Marie Dahlin**

9:15 93 Pathological Investigations of the Decline of North Slope Muskoxen
***Kimberlee Beckmen, Stephen Arthur, Josephine Afema, Jonna Mazet, Kathy Burek and Elizabeth Lenart**

9:30 94 Is Paratuberculosis an Emerging Disease in Spanish Wildlife?
***Christian Gortazar, Maria Paz Martín-Hernando, Jose Manuel Pérez-de-la-Lastra, Rafael Reyes-García and Joaquín Vicente**

9:45 95 Transmission through the Wildlife-Livestock Interface: Foot and Mouth Disease in Mongolia
***Damien O. Joly, Enkhtuvshin Shiilegdamba, Amanda Fine, Angela Yang, Wendy Weisman and Bolortsetseg Sanjaa**

10:00 – 10:30 BREAK

10:30 – 12:00 Contributed Papers: Chronic Wasting Disease
Wild Rose
Presiding: Matt Farnsworth

10:30	96	Ecology of Chronic Wasting Disease-Positive and Negative White-Tailed Deer in Wyoming *David R. Edmunds, Frederick G. Lindzey, Ronald G. Grogan, Walter E. Cook, Terry J. Kreeger and Todd E. Cornish
10:45	97	Selective Predation and the Control of an Emerging Wildlife Disease: Can Wisconsin Hunters Limit CWD? *Erik E. Osnas
11:00	98	Deer, Corridors, and Disease: Using Corridor Theory to Project Routes of CWD Spread *Chris Garrett, Evelyn Merrill, Margo Pybus, David Coltman and Fangliang He
11:15	99	Genetic Analysis of CWD-Infected Deer in Western Canada *David Coltman, Trent Bollinger, Evelyn Merrill, Stephanie Nakada, Margo Pybus and Greg Wilson
11:30	100	Infectivity of Prions following Ingestion and Excretion by American Crows (<i>Corvus brachyrhynchos</i>) Kurt C. VerCauteren, John L. Pilon, Paul B. Nash, *Gregory E. Phillips and Justin W. Fischer
11:45	101	Evaluation of Rectal Biopsy for Preclinical Diagnosis of Chronic Wasting Disease in Free-Ranging Rocky Mountain Elk *Jenny G. Powers, Terry R. Spraker, Mark S. Graham, Katherine O'Rourke, Michael W. Miller and Margaret A. Wild

ABSTRACTS: ALL ORAL SESSIONS

1

International Polar Year and its Legacy

***David S. Hik**

Canadian International Polar Year Secretariat & Department of Biological Sciences, University of Alberta, Edmonton, AB, Canada

I will present a concise overview of efforts to address wildlife health during the International Polar Year (IPY) 2007-2008, and the development of plans to coordinate and sustain Arctic and Antarctic research and monitoring activities in the longer-term. IPY is an interdisciplinary program of science, research, training and education involving some 50,000 researchers from more than 60 nations. Research undertaken during IPY has the potential to greatly improve our understanding of physical, biological and social change in the polar regions, and to provide a comprehensive snapshot of the state of the polar environment. Three aspects of IPY activities have particular relevance to Arctic ecology. First is the emphasis placed on the effects of global warming on Arctic wildlife populations (including caribou and reindeer, birds, and marine mammals, among others), and the cascading impacts on northern peoples. In many regions, northern communities have been actively participating in the monitoring of zoonoses, country food safety and wildlife health. Second is an emphasis on data access and management. The overarching objective of IPY data management is to ensure the security, accessibility and free exchange of relevant data that both support current research and leave a lasting legacy. This requires a comprehensive view of data management and in some cases new data management structures and approaches. Finally, IPY has provided an unprecedented opportunity to demonstrate the scientific process by engaging the public with exciting, diverse, and interdisciplinary research projects, and to engage scientists, northerners, and policy-makers in a concerted effort to better understand and address polar and global issues.

2

Anthropogenic Landscape Change and Its Implications for Wildlife Disease Ecology

***John S. Nishi^{1,3}, and J. Brad Stelfox^{2,3}**

¹EcoBorealis Consulting Inc., Millarville, AB. ²Forem Technologies Ltd., Bragg Creek, AB. ³ALCES® Landscape Ecology Group

In Alberta, the provincial landscape has undergone dramatic transformation over the past century owing to human activities in a natural resource-based economy. The combined footprint of human settlements, infrastructure, agricultural production, forestry, and hydrocarbon extraction has and will continue to transform the provincial landscape into the future. These human-caused landscape-level dynamics present a broad suite of ecological, economic, and social issues that challenge our collective understanding and ability to extract resources and manage landscapes in a sustainable manner. We suggest that these anthropogenic landscape changes also have profound implications for wildlife and ecosystem health, because landscape change is likely an important causal driver of interactions between host, pathogen, and environment. In this presentation, we examine various socio-economic and environmental patterns that have helped shaped Alberta landscapes to the present. We also explore scenarios for land use and attempt to describe plausible emerging patterns that may influence and challenge wildlife disease ecologists in the future.

3

Grizzly Bears: Coupling Landscape Change and Population Performance

***Marc Cattet**

Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada

Grizzly bears in Alberta are threatened by factors related to industrial and recreational development of wilderness areas, including habitat loss and high rates of human-induced mortality. This threat is intensified by results of DNA-based surveys conducted over the past 4 years that suggest the number of bears inhabiting provincial lands (excluding national parks) could be fewer than 500. The Alberta Grizzly Bear Recovery Plan identified a need to understand effects of human activity on grizzly bears and their habitats as a key recovery action to ensure persistence of provincial grizzly bear populations. The Foothills Research Institute Grizzly Bear Research Program is addressing this need by providing knowledge and developing tools to investigate causal relationships between human-caused landscape change and grizzly bear population performance. The basic premise of this research is that environmental conditions influence wildlife health and that human activity indirectly alters this relationship through modification of landscape conditions or directly through long-term stress in individual bears. We hypothesize that long-term stress negatively affects growth, immunity and reproduction ultimately leading to changes or limitations in populations. We have prepared extensive data sets that describe the spatial configuration of landscape structure and change coupled with wildlife health information of grizzly bears across the effective range of the species in Alberta, and our analyses of these data provide strong evidence linking landscape condition, long-term stress, and wildlife health. Advances in knowledge and development of novel techniques from this research provide a foundation for management and conservation for other species at risk, not just grizzly bears.

4

Climate Change and Disease in Norwegian Wildlife: Case Studies

***Bjornar Ytrehus**

National Veterinary Institute, Oslo, Norway

Norway, stretching from 58 to 81° N, includes dramatically varying landscapes from temperate deciduous forests to polar tundra, and is in many respects a European counterpart of the northern areas of America. The environment of this part of Europe is however, to a greater extent, shaped by human encroachments. Throughout history, the human inhabitants of Norway, struggling for survival in harsh environments, utilized all parts of their natural environment, leaving virtually no true wilderness. The continuation of these traditions, together with strong cultural and political currents of self-government, does on the one hand pose a risk of local over-exploitation and inappropriate wildlife management, while the transition from a society dependent on local natural resources to a modern industrial nation on the other, creates dramatic ecological changes resulting from reforestation and the abandonment of hayfields. Global warming, together with these large-scale changes, can have a large impact on the ecology and health of wildlife. In recent years, several disease problems seem to have emerged, or be on the increase, in vulnerable wildlife populations: a major die-off in an introduced musk ox population; widespread alopecia due to intense deer ked infestation on moose; incidents of elaphostrongylosis in reindeer; and ergotism in moose may all be associated with atypical weather conditions. But - are these precursors for the coming disease problems associated with climate change, or are they just coincidental to changing ecological conditions?

5

Wildlife Health in a Changing North: A Model for Global Change

Brett Elkin¹ and Susan Kutz²

¹NWT Wildlife Division, Yellowknife, NT, Canada; ² University of Calgary, Calgary, AB, Canada

The north has unique attributes that make it an ideal model system for the study of wildlife disease ecology. Northern fauna - including hosts, pathogens and vectors - exist in a relatively simple system, providing a unique opportunity to study and tease out theoretical intricacies of disease ecology. While the north still remains relatively pristine and undisturbed, rapid change is starting to occur. This provides a unique opportunity to understand the effects of these changes, and serve as a model for what these same changes may look like in more complex systems around the world.

6

The Cured Approach for the Management of Animal Disease in Nunavut, Canada

***Carla R. Baker**

Fisheries & Oceans Canada, Central and Arctic Region, Iqaluit, NU, Canada

The prevalence of animal disease in Nunavut, Canada's newest and most northern territory is largely unknown. Although there are reported cases of enzootic diseases, it is presumed that many cases are not reported. It is also suspected that the prevalence of some diseases may be increasing and/or exist in animal population(s) at a higher level than previously believed. Recently, it has been discovered that brucellosis in marine mammals may be more prevalent than previously reported (Nielsen, personal communication). Discovery of potentially harmful zoonotic agents in Nunavut wildlife used for food requires the establishment of a comprehensive system to manage and mediate threats to human and animal health. This system requires a multi-level and cooperative approach that must be acceptable to the governing bodies with roles in animal disease management in Nunavut. The CURED approach is proposed as a means to establish a solid foundation of the necessary elements of animal disease management which will provide the groundwork for national and territorial strategies. The CURED approach is symbolized as five interlinked units in a chain: communication, unity, roles and responsibilities, efficiency, and documentation. The strength of the CURED chain is dependent on Nunavummiut (people of Nunavut) engagement at the community level through to government agencies having open communication and a coordinated response to observations and information collected on potentially diseased animals. The approach requires that concerns are addressed quickly and that information and observations are properly documented for future research and for the comparison of trends in disease occurrences.

7

Facilitating the “Talking And Walking Together” of Indigenous and Mainstream Sciences

***Cheryl M. Bartlett¹, Albert Marshall² and Murdena Marshall²**¹Cape Breton University, Sydney, NS, Canada; ²Eskasoni Mi'kmaq First Nation, NS, Canada

Mainstream-trained research scientists and others in government, universities, consulting agencies, and elsewhere increasingly find themselves as participants in ecosystem or wildlife health initiatives wherein there is a desire to include Aboriginal communities and traditional knowledge. An inherent challenge (which may or may not be acknowledged, recognized, or faced) within this desire is: how do mainstream and Indigenous knowledges talk to, and walk with, each other? Insights that can help address this challenge can be drawn from the “Integrative Science” (IS) initiative in Cape Breton, Nova Scotia. The initiative, now in its 12th year, involves university scientists and Mi'kmaq First Nations' Elders, plus a few other key individuals and community organizations (community-based, participatory action research methodologies are used). The IS vision from the outset was to bring together Indigenous and mainstream scientific knowledges and ways of knowing. The initial arena was post-secondary science education but IS rapidly expanded into the arenas of science research, applications, and outreach to Aboriginal youth and community. Insights from IS that can help facilitate the “talking and walking together” of Indigenous and mainstream sciences include various lessons learned, a broadened view of science, and a few “big picture” science knowledge visuals. Significance of the latter reside with the intent that participants in IS efforts be able to weave back and forth between Indigenous and mainstream sciences (as circumstances may dictate) rather than attempting to merge the two, and also try to avoid knowledge domination, assimilation, or marginalization.

8

Engaging Indigenous and Rural People in Detecting Emerging Infectious Diseases

***Ryan K. Brook^{1,2} and Susan J. Kutz¹**¹Faculty of Veterinary Medicine and ²Faculty of Medicine, University of Calgary, Calgary, AB, Canada

Disease surveillance and detection of emerging diseases first requires that a baseline of existing pathogens is established. Contemporary disease monitoring programs are largely focused on areas with relatively high human population densities and in comparatively close proximity to university trained disease experts. These programs are generally effective in and around cities and towns, but are constrained in more rural and remote regions that are logistically challenging to monitor due to their overall size, difficulties in access, and relatively lower priority given the few people present. Despite these challenges, it is imperative that wildlife diseases be detected early as they can have important ecological and human health implications. Given the limited understanding of pathogens, combined with the poorly understood impacts of human development and climate change, surveillance approaches are needed to detect diseases that are predicted and those that are not. We discuss challenges and opportunities associated with developing a disease monitoring strategy that incorporates the local ecological knowledge of rural and indigenous people with conventional science-based diagnostics. Our approach emphasizes generating a common understanding of the needs of the communities and the researchers, using lay people as ‘eyes on the land’ through their frequent observation and consumption of wildlife.

9

Sociopolitical Challenges to Disease Prevention and Biosecurity in Live Bird Market Systems in Central America

*P. N. Klein¹, F. N. Hegngi¹, J. J. Bruzual², C. A. Sandoval² and M. E. Gonzalez Ortiz³¹USDA APHIS/Vs, Riverdale, MD, USA; ²USDA APHIS/IS, Washington DC and Panama; ³OIRSA, El Salvador

USDA/APHIS VS and IS, in collaboration with OIRSA, conducted training workshops on Biosecurity in the Live Bird Marketing System (LBMS) to address prevention and control of HPAI in 6 Central American countries and the Dominican Republic (DR) during 2007. This program was tailored to the needs of these countries in which the LBMS is not included in routine surveillance. Participants included representatives from the Ministries of Agriculture, Health, Environment, Education, and Labor, local veterinarians and biologists, international organizations (FAO, USAID, IICA, OIRSA), officials from local municipalities, aviculture associations, and LBM owners. Objectives of the training workshop program were to provide a platform for education, exchange of ideas and expertise, open discussion of issues common and unique to each country relative to avian disease prevention and control in the LBMS, and opportunities for inter-governmental regulatory agency coordination and collaboration in the control of the LBMS in regards to avian health and public health. The 3-day program included scientific and technical presentations on avian influenza, each country's National AI Response Plan, the social and economic impacts of their aviculture industry, the dynamics of their LBMS including sales of domestic and wild birds, public health concerns, and regulatory challenges. Participants visited a local typical LBM to evaluate the market infrastructure and conditions that impact biosecurity, and to identify which regulatory agencies control the LBMS in regards to avian health and public health. Participants presented and discussed their findings and recommendations on the final day. Results of the workshops and future action plans will be presented.

10

Veterinary Students and Wildlife Conflicts in Uganda

*Jerry Haigh¹, Claire Card¹, John-Bosco Nizeyi³, Ludwig Siefert³, Nigel Caulkett² and Gil Basuta³¹Western College of Veterinary Medicine, Saskatoon, SK, Canada; ²University of Calgary, Calgary, AB, Canada; ³Makerere University, Kampala, Uganda

Since 2002 sixty-nine Canadian veterinary students from the Western College of Veterinary Medicine in Saskatoon have joined 26 African students from Makerere University, Department of Wildlife and Animal Resource Management (WARM) on a one-month rotation that focuses on the wildlife-livestock- human interface. We have spent time in three national parks, Kibale, Queen Elizabeth (QENP), and Lake Mburo (LMNP). The main issues examined in Kibale have to do with primates, with particular reference to zoonoses, crop raiding by baboons and chimpanzees, and the emerging problem of elephant population growth in a small forested park. We discussed chimpanzee politics and chimpanzee attacks on human infants. In QEP we carried out research on brucellosis in cattle and Uganda kob, studied new immobilizing drug cocktails in kob and cape buffalo, and assisted with lion research and medical cases. We were involved in medical emergencies in baboons, buffalo, and warthogs. Growing numbers of cattle in the park also are of grave concern and were particularly severe in 2007 when an estimated 40,000 head appeared with the Basongora pastoralists who returned from the Democratic Republic of Congo. We have also witnessed a decline in predator and raptor (especially vulture) numbers due to poisoning. In LMNP and the nearby government cattle breeding centre we focused on diseases transmissible between wildlife and livestock, and saw the effects of the disappearance of browsing species and the prolonged use of the park by large numbers of cattle. The response by WCVM students to the overall experience has been uniformly positive.

11

The Influence of Human Visitor Activity on Spatial Patterns of Parasite Infection

Chris O'Brien and *Charles van Riper III

US Geological Survey SBSC, University of Arizona, Tucson, AZ, USA

Human recreation can directly influence wildlife species distributions, but little is known about indirect cascading effects on parasites. Parasites with complex life cycles, that span multiple trophic levels and move from vertebrates to invertebrates and back in a single generation, have the potential to be greatly influenced by human recreation patterns. High human use levels can artificially concentrate parasite hosts, thus potentially influencing transmission of wildlife diseases. In this study we link human recreation at a National Park in Arizona to wildlife disease patterns. We test the hypotheses that human recreation affects spatial patterns of waterfowl habitat use, and that this in turn affects the prevalence of a trematode parasite in an endangered intermediate (amphipod) invertebrate host. An observational study and a randomized experiment supported our hypothesis that human recreation directly affects the foraging location of waterfowl. We found that waterfowl chose to forage in areas more distant from visitor use paths at a desert spring pond, and that these areas supported greater rates of amphipod parasite infection in the initial year of our study. In the second year, when visitor use was reduced, waterfowl did not show as strong a pattern of differential space use and amphipod parasite prevalence was reduced. Our findings clearly demonstrate that human recreation can indirectly affect spatial patterns of parasite abundance and wildlife disease. These results have important implications for the management of areas that are maintained for human leisure activities and wildlife, especially in systems where disease is ecologically important.

12

Surveillance and Training Activities of Highly Pathogenic Avian Influenza H5N1 in Migratory Birds in Mexico

***A. Alonso Aguirre¹, H. M. Zepeda-Lopez², A. L. Sandoval², E. Carrera³, A. Lafon-Terrazas⁴, L. Lecuona⁵ and A. Gomez-Mendieta⁶**

¹Wildlife Trust, Columbia University, New York, NY, USA; ²Laboratorio Medicina de Conservacion, Instituto Politecnico Nacional, Mexico, D.F., Mexico; ³Ducks Unlimited de Mexico, Monterrey, Mexico; ⁴Universidad Autonoma de Chihuahua, Chihuahua, Mexico; ⁵USDA APHIS Wildlife Services, Mexico Field Office, Mexico D.F., Mexico; ⁶SEMARNAT Direccion General de Vida Silvestre, Mexico, D.F., Mexico

In 2006 we began surveillance and training activities for highly pathogenic avian influenza (HPAI) H5N1 supported by Canada/Mexico/U.S. Trilateral Committee for Wildlife and Ecosystem Conservation and Management. Primary objectives of this truly continental and trans-disciplinary project were to 1) develop a continental avian influenza monitoring plan to be shared by the three countries; 2) develop a series of regional training workshops in Mexico; and 3) train Mexican diagnosticians in testing for H5N1 at the BSL-4 facility in Winnipeg, Canada and have specialized technicians in Mexico standardize techniques. To date, a total of 13 training workshops have been conducted for federal and state personnel, NGOs, and universities in field techniques, sample collection/preservation, monitoring, diagnostics, surveillance, and personnel safety to evaluate the potential impacts of HPAI H5N1 in migratory birds in the event of a contingency. We trained 650 individuals. These workshops were coupled with active sampling at 28 priority wetlands throughout the country. At least 200 specimens per wetland were collected with a total of almost 10,000 specimens collected to date. Currently we are testing these samples at the certified Conservation Medicine Laboratory. Avian influenza matrix positive specimens will be sent to USDA NVSL-Ames. All collaborators are attempting to integrate an intercontinental wildlife disease database to be shared by the three countries. In this manner, we used resources already in place to build this diagnostic capacity for wildlife in Mexico.

13

Lead Toxicity in Wisconsin Wildlife

***Julia A. Langenberg, Sean M. Strom and Nancy K. Businga**

Wisconsin Department of Natural Resources, Madison, WI, USA

As part of the state's assessment of ongoing lead (Pb) risks to wildlife, Wisconsin has monitored Pb exposure in selected species including bald eagles, trumpeter swans, common loons, American woodcock, and grey wolves. A review of 14 years of trumpeter swan mortality data indicates that approximately 30% of trumpeter swan mortalities were attributed to Pb toxicity. Similarly, approximately 13% of 845 live-sampled trumpeter swans had blood Pb levels above background concentrations (0.2 µg/ml). Eight years of necropsy data for bald eagles shows approximately 15% of 580 bald eagle deaths in WI can be attributed to Pb toxicity. There is a noticeable seasonal increase in the eagle Pb toxicity cases between October and December contiguous with deer hunting seasons in WI, suggesting Pb ammunition could be a major source of Pb exposure in eagles. Since 2006, Pb toxicity has been identified as the cause of death for 36% of examined common loons; pieces of lead fishing tackle were recovered from the GI tracts of loons in all cases of Pb toxicity. In a study of lead exposure in apparently healthy American woodcock, bone lead concentrations considered to be toxic in waterfowl were regularly observed in all age classes of woodcock. Stable isotope analysis on young of year woodcock did not rule out anthropogenic sources of lead. It is clear numerous species of WI wildlife are being exposed, either directly or indirectly, to potentially harmful levels of Pb and Pb poisoning remains a significant mortality factor for several species. Wisconsin is developing public education programs and assessing the need for further hunting and fishing regulations to reduce the ongoing impacts of lead on the state's wildlife.

14

Wildlife and Zoonotic Diseases: Potential Impact of Climate Change

***James N. Mills**

Division of Viral and Rickettsial Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Assessments of the potential effects of climate change on zoonotic disease are largely speculative, and most treatments to date have dealt with vector-borne diseases. The directly-transmitted (non-vector-borne) zoonotic diseases (e.g., Ebola and Marburg hemorrhagic fevers, hantaviral diseases, the South American hemorrhagic fevers, SARS, Nipah virus encephalitis) are associated with wildlife hosts whose distribution, population dynamics, and resistance to disease may be strongly affected by climate. Yet these diseases have received scant treatment in the context of climate change. A large proportion of recognized zoonotic disease agents, hosts and vectors are tropical in origin, and the large majority of those likely remain undescribed. The rodents and bats in particular constitute 63% of all mammal species, are frequent hosts of zoonotic agents, and many species are predicted to shift their ranges poleward in coming decades. Climate change may affect incidence of zoonotic diseases through its effect on 4 principal characteristics of host and vector populations that relate to transmission to humans: geographic distribution, population density, prevalence of infection by zoonotic pathogens, and pathogen load. These individual mechanisms may interact with each other and with other factors such as anthropogenic disturbance to produce varying effects on pathogen transmission within host populations and to humans. Because climate change effects on most zoonotic diseases act through wildlife hosts and vectors, understanding and mitigating these effects will require multidisciplinary studies involving the collaboration of ecologists, wildlife biologists, and public health scientists.

15

Improving Guidance for Safe Handling of Wildlife: Insights from a Wildlife Biologist's Death

***M. A. Wild¹, D. Wong², C. Higgins², J. G. Powers¹, T. R. Spraker³, E. Perez⁴, P. Mead⁵ and A. Chanlongbutra²**

¹National Park Service, Biological Resource Management Division, Fort Collins, CO, USA; ²National Park Service, Office of Public Health, Washington, DC, USA; ³Colorado State Veterinary Diagnostic Laboratory, Fort Collins, CO, USA; ⁴National Park Service, Risk Management Division, Washington, DC, USA; ⁵Centers for Disease Control and Prevention, Fort Collins, CO, USA

Wildlife health professionals can assist biologists in investigating wildlife mortality events by providing disease and diagnostic information and by ensuring that human health risks are considered. The plague-associated death of a wildlife biologist at Grand Canyon National Park, Arizona, in November 2007 underscores the need for this approach. A biologist necropsied a mountain lion (*Felis concolor*) and one week later he was found deceased. His death was confirmed as due to pneumonic plague. *Yersinia pestis* of the identical sub-type was subsequently isolated from the mountain lion carcass. The biologist's death highlighted a National Park Service need to examine and improve existing guidance on safe handling of wildlife—a need that likely exists in other federal, state, and university programs. A team including wildlife health, risk management, and public health representatives collaborated to develop comprehensive guidance that uses job hazard analysis as a foundation to identify and mitigate risks. Collection of mortality information is an important tool in wildlife management and proper sampling and/or disposal of animal carcasses can help protect human, as well as animal health. Interdisciplinary consultation and collaborative development of safe work practices that mitigate and put human health risks in perspective are critical to helping ensure that this crucial work can continue.

16

Climate Change: Trends, Future Scenarios, and Impacts on Wildlife Populations and Disease Dynamics

*** Susan Haseltine**

Associate Director for Biology, U.S. Geological Survey

The ecological consequences of climate change have the potential to directly and indirectly affect wildlife populations and disease dynamics including the seasonality of wildlife disease events. This presentation will provide an overview of observed and predicted changes affecting both individual species and ecosystems. It will also explore the critical knowledge gaps in understanding climate change and wildlife disease, and suggest some recommendations for addressing these issues.

17

Enzootic and Epizootic Vertebrate Hosts of Buggy Creek Virus (Togaviridae)

***Valerie A. O'Brien and Charles R. Brown**

University of Tulsa, Tulsa, OK, USA

Arboviruses occur in primarily enzootic cycles with periodic epizootics. Invasive species can play important roles in virus epizootics because they often have not been exposed historically to the viruses they encounter. We studied the role of the cliff swallow (*Petrochelidon pyrrhonota*) and the introduced house sparrow (*Passer domesticus*) in the transmission dynamics of an ecologically unique arbovirus, Buggy Creek virus (BCRV; Togaviridae, *Alphavirus*). BCRV is vectored primarily by the cimicid swallow bug (*Oeciacus vicarius*), a nest-based ectoparasite of the cliff swallow and house sparrow. In 2006 and 2007, we blood-sampled adult and nestling cliff swallows and house sparrows living in cliff swallow colonies for BCRV. Cliff swallows, compared to house sparrows, showed lower incidence of BCRV by RT-PCR (2.4% vs. 26.1%), lower cytopathic effect of virus on Vero cells (27.8% vs. 75.0%), and lower mean virus titers (3.25 vs. 4.52 log₁₀ PFU/mL serum). While cliff swallow nestlings appeared to suffer no ill effects of virus infection, house sparrows had increased mortality when infected: fledging success was 37.8% in virus-positive sparrow nestlings and 78.9% in virus-negative ones. BCRV apparently exists in an enzootic cycle among swallow bugs and cliff swallows, and may occur as epizootics when house sparrows invade swallow colonies and come into contact with infected bug vectors. The greater amplification of Buggy Creek virus in the introduced house sparrow increases the likelihood that mosquitoes could transfer this virus out of its enzootic niche and into contact with humans, domestic animals, and other wildlife.

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Detection of an Exotic Orbivirus, Epizootic Hemorrhagic Disease Virus Serotype 6 (EHDV-6), in the United States

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Epizootic hemorrhagic disease virus (EHDV) is a *Culicoides*-transmitted orbivirus that infects domestic and free-ranging ruminants and is provisionally distributed throughout Africa, North America, Australia, and East Asia. Currently, of the ten recognized serotypes of EHDV, only EHDV-1 and EHDV-2 have been reported from North America. During the autumn months of 2006, EHDV isolates were recovered from moribund or dead white-tailed deer (*Odocoileus virginianus*) in the midwestern United States that could not be identified as either EHDV-1 or EHDV-2 by virus neutralization tests or by serotype-specific RT-PCR. Additional comprehensive testing using antisera and VP2-specific primers directed against EHDV serotypes non-indigenous to the United States identified the isolates as EHDV-6, a serotype previously only described from Australia. In 2007, EHDV-6 was recovered again from white-tailed deer in the midwestern United States, demonstrating the virus is capable of overwintering in northern temperate regions and suggesting that it may become, or already is, endemic in the United States. Interestingly, preliminary genetic characterization of the virus indicates it is a reassortant apparently derived from exotic EHDV-6 and indigenous EHDV-2 (Alberta). The epidemiological significance of the introduction of exotic EHDV into the United States and its potential impacts on domestic and free-ranging ruminant populations will be discussed.

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Manipulative Experiments Monitoring SNV Transmission and Viral RNA Shedding in Deer Mouse Populations in Outdoor Enclosures***Karoun H. Bagamian¹, James N. Mills² and Richard J. Douglass³**¹Emory University, Atlanta, GA, USA; ²National Center for Zoonotic, Vector-borne, and Enteric Diseases, Centers for Disease Control and Prevention, GA, USA; ³Department of Biology, Montana Tech, Butte, MT, USA

Sin Nombre hantavirus (SNV), hosted by the widespread deer mouse (*Peromyscus maniculatus*), is responsible for the majority of human hantavirus pulmonary syndrome cases in the United States. Since 1993, several long-term ecological surveys of SNV infection dynamics in deer mouse populations have answered multiple questions about SNV transmission. However, these results have led to new inquiries that can only be answered using controlled experiments. Subsequent laboratory studies were unsuccessful at demonstrating SNV transmission in experimentally infected, caged deer mice. Therefore, the next step in SNV research is to explore transmission patterns of naturally infected deer mice in a controlled field setting. In May - October 2007, we completed three manipulative experiments investigating SNV transmission in enclosed wild deer mouse populations. We are the first group to observe multiple SNV transmission events within a deer mouse population in a controlled, semi-natural setting. During the field season, we collected data and biweekly saliva samples from the experimental mice. Using a quantitative PCR assay, the saliva samples of all SNV infected mice in the experiment will be examined to determine whether there is a correlation between shedding of viral RNA in the saliva and a) levels of viral RNA in the blood and/or b) transmission events. These results, as well as additional observational data, will be presented.

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The Ecology of Aspergillosis in Seabirds: Evaluation of Available Diagnostic Tests***Julia D. Burco¹, Lisa A. Tell², J. Gregory Massey¹, Judy St. Leger³ and Michael H. Ziccardi¹**¹Wildlife Health Center, School of Veterinary Medicine, University of California, Davis, CA, USA; ²Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, CA, USA; ³SeaWorld of California, San Diego, CA, USA

Aspergillosis is a fungal infection caused by ubiquitous saprophytic fungi, *Aspergillus* spp. Seabirds undergoing rehabilitation are extremely susceptible to aspergillosis. Due to the high prevalence of *Aspergillus* spp. infections, the poor prognosis of infected individuals, and the difficulty in detecting sub-clinical infection, it is critical to identify a test, or a series of diagnostic tests, to detect this disease in seabirds that are prone to infection. In order to identify clinically promising diagnostic options, serology, hematology, radiology, and tracheal washes were used to detect aspergillosis at sequential time periods during rehabilitation of susceptible seabird families. Evaluation occurred at an aquatic bird rehabilitation facility in Fairfield, CA from February of 2006 through August of 2007. A total of 55 individuals (14 positive, 41 negative) were included in this prospective study. Histopathology and culture on animals that died during rehabilitation were the gold standard for diagnosis. Diagnostic test sensitivities and specificities were calculated, and a multiple logistic regression model was created to help dictate which diagnostics were most useful in detecting disease. Preliminary results indicate that tracheal wash and plasma galactomannan levels, as well as changes in CBCs and plasma electrophoresis, show promise as early indicators of disease. Tracheal wash culture and radiographs prove useful in detecting the more severe cases that often have overt clinical signs.

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Serodiagnosis of Dengue Virus in Black Howlers (*Alouatta pigra*) in Southeastern Mexico

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As humans are progressively entering areas occupied by wild populations of nonhuman primates, the risk of shared infections between humans and nonhuman primates increases. Because dengue virus is reported in human populations living near forest fragments occupied by black howlers in southern Mexico, we surveyed several populations of this endangered primate species for the presence of this infection. To test this, we sampled a total of 50 individuals belonging to 14 groups of black howler monkeys (*Alouatta pigra*) in Tabasco and 34 individuals belonging to 8 groups in Campeche during the wet season (May - November). All groups lived in fragmented landscapes in which distances from the fragments to the nearest human settlements ranged from 0.5 to 2km. We used Platelia™ Dengue NS1 AG, ELISA kits, and Panbio™ Duo Cassette to identify IgG and IgM Dengue antibodies. All samples were negative; however, this information is valuable to infer the ecology of this infectious disease in wild howler monkeys. Continued serologic monitoring of black howler monkeys populations is needed, particularly in highly fragmented areas where the probability sharing vectors and infections with humans is higher, and where contact rates between humans and these primates are increasing.

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Evidence of Persistent Viral Infections in Semi-Domesticated Reindeer (*Rangifer tarandus tarandus*) in Northern Norway: Impact on Animal Health, Husbandry, and the Ecosystem

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Semi-domesticated reindeer constitute one of the most important animal species in the Norwegian arctic region with an estimated population of over 230 000 animals with high ecological and economical value. Mortality estimations reach 55% in calves in some areas. Diseases can account for some of these deaths and preliminary studies in the 1990s identified the presence of antibodies against alphaherpesvirus and pestivirus, both known to have an abortion potential and to cause severe diseases in cattle and other wild ruminants. In this study, a large serosurvey was conducted to evaluate the presence of these viruses and to identify biological and ecological risk factors. Results showed an overall alphaherpesvirus seroprevalence of 49% and an overall pestivirus seroprevalence of 13%. Biometric and ecological parameters such as animal density, age and body weight were positively correlated to seroprevalence while others such as geographical area of season of sampling were also found to be relevant. PCR amplicons of the expected size (260bp) were amplified from DNA extracted from trigeminal ganglions from reindeer, using primers from the UL27 gene of alphaherpesvirus. Sequencing and comparison with other published alphaherpesvirus sequences showed a homology of 100% with CvHV-2. This represents the first proof of a specific reindeer alphaherpesvirus (CvHV-2) in Norwegian semi-domesticated reindeer. For CvHV-2, routes of infection and clinical symptoms have been addressed in an experimental infection study, and a reactivation study has been started in an attempt to isolate and characterize the virus. The close genetic similarity within the Alphaherpesvirinae subfamily brings a question to be addressed in the future whether cross-infections are possible and whether semi-domesticated reindeer (or wild ruminants) may serve as reservoirs for husbandry animals, since both alphaherpesvirus and pestivirus have been the targets of successful eradication campaigns in domestic animals in Norway

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Host/Parasite Adaptation seen during the course of a *Sarcoptes scabiei* Epidemic in Red Foxes (*Vulpes vulpes*) in Norway

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The Norwegian red fox (*Vulpes vulpes*) population was naive to *Sarcoptes scabiei* prior to the late 1970s when this mite was recorded for the first time and a still ongoing epidemic started. In this study the prevalence of sarcoptic mange and serologically identified *S. scabiei* exposure was investigated in 363 Norwegian red foxes, shot by hunters during two different study periods (1994-1995 and 2002-2005). The sarcoptic mange diagnosis was based upon the presence of clearly visible lesions in the skin of the cadaver with confirmatory demonstration of *S. scabiei*. Serodiagnosis was based upon an indirect-ELISA. There was a significant decrease in the prevalence of both mange cases and seropositive animals from the first to the second study period, despite increasing red fox population levels during the same period. Mange prevalence fell more than threefold, from 30% to 7%, whilst seroprevalence showed a less dramatic decrease, from 53% to 19%. The smaller decrease in seroprevalence compared to mange cases reflected a significantly higher ratio of seropositive-mange negative versus seropositive-mange positive foxes during the second study period, 40:18, compared to the first, 14:18. These results strongly indicate that some adaptation between the fox and the parasite has occurred during the course of this long lasting epidemic and that low-grade or sub-clinical, and even recoveries, occur amongst exposed foxes.

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Application of a Molecular Tool to Describe the Diversity and Distribution of GI Parasites in Northern Cervids

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Climate change is driving a northward shift in the distribution of wildlife, including cervids. Temperate white-tailed deer (*Odocoileus virginianus*) and mule deer (*O. hemionus*) are host to a diversity of gastrointestinal (GI) nematode species (Trichostrongylidae), many of which can induce considerable morbidity and population-level impacts. Expansion of *Odocoileus* species northwards may lead to parasite spill-over into naïve caribou (*Rangifer tarandus*) hosts. Paramount to detecting and managing for parasite expansion and emerging disease is the establishment of baselines for species diversity and distribution. Currently, little is known of trichostrongyles in Canadian cervids. In fact, our recent trichostrongyle survey of 20 wild cervids in central Alberta and Saskatchewan revealed four new host and five new geographic records. A challenge to determining diversity is that many trichostrongylid eggs are morphologically indistinguishable and post-mortem recovery and examination of adult nematodes is necessary to establish species identification. To better describe the diversity of parasite fauna in northern cervids, we have developed a rapid, non-invasive molecular tool, Single Stranded Conformation Polymorphism (SSCP), for broad-scale screening of cervid fecal pellets for trichostrongyles. SSCP is a simple PCR-based technique that allows for species-specific electrophoretic discrimination using ITS-2 rDNA from parasite eggs. Trichostrongyle eggs in fecal pellets from caribou, white-tailed deer, and mule deer are being screened using SSCP to determine parasite diversity and range in northwestern Canada. Results outlining trichostrongyle diversity and distribution and implications for threatened caribou populations will be reported.

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White-Tailed Deer Habitat Use in New York: Implications for Disease Management

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Patterns of habitat use in wildlife populations inform our understanding of the biological requirements and behavioral decisions made by individuals, and ultimately assist ecologists in managing and conserving wildlife populations. This information is especially useful in understanding the dynamics of a contagious disease like chronic wasting disease (CWD) in white-tailed deer (*Odocoileus virginianus*), where landscapes that are attractive to animals based upon optimization of forage and predator avoidance, as well as social behaviors that increase aggregations between infected and susceptible animals may significantly influence disease spread within and between populations. We are developing a Risk Assessment Mapping Program (RAMP) defined by behavioral, spatial, and climatic factors to identify the probability of disease spread from a point of first occurrence. We deployed 92 GPS collars on white-tailed deer in central New York to evaluate parameters associated with patterns of habitat utilization. We used utilization distributions to characterize multiple core areas across sex/age classes and conditional modeling to illustrate habitat use vs. availability among study animals. Our results revealed significant sex-/site-specific differences in home range sizes based on habitat composition/configuration and a distinct seasonal influence on land cover choice. These data provide preliminary estimates of factors likely to contribute to spatial overlap of animals, and to our understanding of disease spread.

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The Effects of Biodiversity on Zoonotic Disease

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A growing body of work demonstrates that loss of biodiversity negatively impacts ecosystem functions. One function, or service, that biodiverse ecosystems provide is suppression of zoonotic diseases, which are defined as diseases carried by wildlife hosts that can spill over into human populations. Ebola, SARS, West Nile Virus, hantavirus, avian influenza and Lyme disease are just a few of the recently emerged zoonotic diseases. Disease suppression has been shown for Lyme disease by the dilution effect, whereby increasing species diversity decreases disease prevalence in the host populations. But does a dilution effect apply to other disease systems? Over three years, small mammals were trapped in 5 forested urban parks using a web sampling grid, covering 3.14 Hectares and including 352 live-traps. Blood samples from captured animals were tested for hantaviral antibodies using ELISA. Population density was calculated using the program. This research reveals that increased levels of mammal species diversity decrease the amount of hantavirus, a zoonotic disease hosted by deer mice, *Peromyscus maniculatus*, in forested ecosystems. No other ecological or environmental variable that was considered in this study, alone or in combination, predicted the amount of Hantavirus in an ecosystem. By suppressing zoonotic disease, biodiversity provides a service that directly affects human health and well-being, a phenomenon that will hopefully help strengthen conservation efforts.

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Validation of Diagnostic Tests and Development of Molecular Epidemiological Tools for Brucellosis

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Brucellosis, caused by the bacterium *Brucella abortus*, is endemic in bison (*Bison bison*) and Rocky Mountain elk (*Cervus elaphus nelsoni*) in the Greater Yellowstone Area of Wyoming, Montana, and Idaho. Current diagnostic methods used to identify infection in elk include serological testing and bacterial culture, but the correlation between serology and culture results is poor, bacterial culture is slow and likely to be positive only later in gestation or following abortion or parturition, and isolates cannot be sufficiently characterized to trace outbreaks. There is a need for more informative, sensitive, and rapid diagnostic tests to detect brucellosis. As part of the Wyoming Game and Fish Department's brucellosis surveillance program, elk were trapped using corral traps and serologically tested for brucellosis on two elk feed grounds in the winters of 2005 and 2006. Twenty-six seropositive cow elk aged ≥ 1.5 years were killed and necropsied. Paired tissue samples were collected and processed for bacterial culture, PCR, and immunohistochemistry (IHC). Tissue sections were stained with an anti-*B. abortus* polyclonal antibody for IHC. *Brucella abortus* was isolated from 40.9% (9/22) of the seropositive cow elk. Tissue homogenates were evaluated by PCR to identify the presence of *B. abortus* in fresh tissue, *B. abortus* was not detected in any sample by PCR or IHC. Molecular diagnostic methods did not surpass culture for the detection of infected elk in the winter. Fifty-two isolates of *B. abortus* from WY were genotyped using a multiple locus variable number tandem repeats analysis (MLVA) and cluster analysis was performed for epidemiological purposes.

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Coccidiosis Epornitic in Lesser Scaup on a North Dakota Lake

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A mortality event involving approximately 1,150 lesser scaup (*Aythya affinis*) occurred during a ten-day period in April 2007 on Pheasant Lake in Dickey County, North Dakota. Five refrigerated scaup carcasses collected at the lake were submitted to the USGS's National Wildlife Health Center for postmortem examination. Gross examination disclosed generalized emaciation in all birds and mild to moderate dilative enteritis in four birds. Histological examination of the intestines revealed numerous expansive areas of necrosis that surrounded thousands of oval, 10-15 μm diameter oocysts and many degenerate inflammatory cells. Parasitological findings included very large numbers of *Eimeria aythiae* oocysts and mixed cestode and trematode infections from all five birds. Two frozen carcasses were submitted to the Southeastern Cooperative Wildlife Disease Study at the University of Georgia for molecular characterization of the coccidia. An approximately 400 bp section of the 18S rRNA region was amplified by PCR from extracted coccidia DNA from both birds. Sequence analysis of the amplicons revealed a 97% identity to *E. reichenowi* and *E. gruis* isolated from three crane species and a 96% identity to *E. phalacrocoraxae* isolated from double-crested cormorants. Prior coccidiosis outbreaks have occurred at Pheasant Lake in 1989, 1990, 1991, and 2006. An aeration system operating at the lake likely contributed to the coccidiosis outbreaks. Following the 2007 outbreak, the aeration system was removed.

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Forest Fragmentation affects Vector Abundance and Infection with *Trypanosoma cruzi* and *Trypanosoma rangeli* in a Panamanian Landscape

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Anthropogenic land use change is associated with infectious disease emergence in wildlife, domestic animals, and humans. This project investigates relationships between forest fragmentation and transmission of the vector-borne parasites *Trypanosoma cruzi* and *Trypanosoma rangeli* in a rural landscape of Panama. *T. cruzi*, agent of Chagas disease in humans, and *T. rangeli*, believed to be non-pathogenic to humans, can infect a wide range of wild mammal hosts. *Rhodnius pallescens*, the principal reduviid bug vector of Chagas disease in Panama, was collected from its primary habitat, the palm *Attalea butyracea*, in continuous forests and forest fragments. Collected bugs (n=641) were tested for infection with *T. cruzi* and *T. rangeli* by a duplex PCR assay. The percentage of palms infested with *R. pallescens* was higher in fragmented forests and deforested sites (range: 77.1% to 91.4%) than in continuous, protected forests (57.1%). The mean number of bugs captured in mid-secondary and early secondary forest fragments was significantly higher than the number of bugs captured in continuous forests (Tukey's HSD, early-secondary fragments p=0.016, mid-secondary fragments p= .023). The proportion of *T. cruzi* infected vectors was significantly higher in forest fragments (76.9%) as compared to continuous forests (58.4%)($X^2 = 11.84$, p= 0.0006). An opposite trend was seen for *T. rangeli* infection, with a significantly higher proportion of *T. rangeli* infection in continuous forests (56.4%) as compared to forest fragments (31.3%) ($X^2 = 19.17$, p=0.000001). These results suggest that forest fragments are important sources for *R. pallescens* and *T. cruzi* transmission.

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First Report of *Trypanosoma cruzi* Infection in Raccoons and Opossums from Kentucky

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Only six autochthonous cases of human Chagas' disease have been documented in the U.S. However, as many as 50/1000 immigrants may be infected with the etiologic agent, *Trypanosoma cruzi*, a parasite also common in mammals indigenous to the southern U.S. The goal of our study was to determine if the sylvatic cycle of *T. cruzi* infection occurs in Kentucky, and if present, to assess the prevalence of infection in Warren and Barren counties. Raccoons and opossums were live-trapped between June and December, 2007. Animals were anesthetized with isoflurane, and blood samples were collected using a Vacutainer system. Sera were frozen at -80°C for subsequent analysis, and whole blood samples were inoculated, in duplicate, into liver infusion tryptose (LIT) medium and cultured at 27°C. To date, eighteen *T. cruzi* isolates from raccoons have been positively identified by hemoculture. A total of 18/46 raccoon samples and 15/49 opossum sera were judged to be seropositive by immunofluorescence antibody test (IFAT). We are currently determining the antibody titers of positive samples using ELISA. To our knowledge, this is the first report of *T. cruzi* from the state of Kentucky. NIH Grant 2 P20 RR-16481 from the National Center for Research Resources is gratefully acknowledged.

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Incorporating Heterogeneous Deer Distribution into Chronic Wasting Disease Management in the Aspen Parkland of East-Central Alberta

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Alberta's management plan for chronic wasting disease (CWD) in mule (*Odocoileus hermionus*) and white-tailed (*O. virginianus*) deer uses targeted culls to reduce deer density; the goal is to decrease contact rates, a primary driver of disease spread, which are assumed to increase with density. However, due to the social grouping behavior of deer and the high level of heterogeneity in the landscape, density alone may be insufficient to assess relative contact rates. I hypothesize that the distribution of "high quality" habitat, defined as areas with a high resource selection function (RSF) value, will influence deer proximity across the landscape. Distribution of deer groups was obtained from a complete aerial census of the study area, and the RSF was developed from telemetry data from ~130 radio-collared deer. Proximity of deer groups will be modeled as a function of the density of deer groups and an index of quality-habitat aggregation. Analyses will be conducted at various spatial scales, ranging from the individual home-range size of 9 km², to 300 km², the scale at which density estimates and culls are currently conducted. If including the habitat index improves model fit at one or more spatial scales, then contact rates likely depend on more than the simple density estimates which currently form the basis for CWD management.

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Suitability of a Synthetic Semen Extender for the Cryopreservation of Epididymal Sperm from Plains Bison (*Bison bison bison*)*S. Krishnakumar^{1,5}, D. Whiteside^{2,3,5}, R. Jaiswal¹, B. Elkin^{2,4,5} and J. Thundathil^{1,5}

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Wood bison (*Bison bison athabascae*) are threatened in Canada due to the prevalence of brucellosis and tuberculosis. The overall goal of our research program is to develop methods for salvaging the genetics of wood bison. We previously reported a method for the successful cryopreservation of epididymal sperm using plains bison as a model. The objective of this study was to evaluate the suitability of a synthetic (Andromed®; animal protein-free) semen extender for the cryopreservation of epididymal sperm from plains bison. The cauda epididymides (n = 19) recovered from slaughtered plains bison were minced and incubated in TALPH buffer for 3 h at 36 °C. The resulting sperm pellet from each of the bulls was diluted in either Triladyl® or Andromed® semen extender and cryopreserved. Frozen-thawed sperm were evaluated for motility, viability, and acrosome integrity (n = 6), tyrosine phosphorylation in sperm proteins (n = 3) and in vitro fertilization (n = 3) using a heterologous IVF system. There was no significant difference in motility (60% each), viability (46% and 39.5%), acrosome integrity (91 and 87.5%), respectively for sperm cryopreserved in Triladyl® or Andromed®. Sperm proteins at 35 kDa were found to be more intensely tyrosine phosphorylated in the Triladyl® group. However, there was no significant difference in the fertilization rate (60% and 53%, respectively) for sperm cryopreserved in these extenders. In conclusion, there was no significant difference between extenders for most sperm characteristics suggesting that Andromed® (animal protein-free) is a suitable alternative to Triladyl® for the cryopreservation of epididymal sperm from wood bison.

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Use of the North American Animal Disease Model for the study of Avian Influenza

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It is of interest to the scientific community as well as the Canadian Food Inspection Agency (CFIA) to evaluate the risks that affect the spread of highly pathogenic avian influenza (HPAI). Because wild birds are a natural host of AI, but generally do not show severe clinical signs, the potential of this natural disease reservoir to spread HPAI to farms is a very real problem. Several animal disease models have been implemented to evaluate how diseases spread in populations and measure the consequences of disease outbreaks. Recently the North American Animal Disease Spread Model (NAADSM) has been used to study Foot and Mouth Disease and it is of interest to apply this model to the study of HPAI. In our research, a disease simulation model was created using the NAADSM simulation program on a potential HPAI outbreak in Ontario, Canada. Using various scenarios, from several predictors, such as farm type and detection rate, the model generated the total mean number of farms that would be infected with HPAI. NAADSM will provide CFIA with a better understanding of the characteristics of the disease and its potential effect on domestic and wild birds. This particular model is being used in different countries and has become an important decision-making tool. It will allow CFIA to create more effective policies and therefore more appropriate regulations can be developed. A description of this application with a discussion of the main findings will be presented.

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Local Movement and Habitat Use of Avian Influenza Shorebird Hosts at Delaware Bay, USA

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A high prevalence of infection with avian influenza viruses (AIV) occurs in migrating shorebirds, particularly ruddy turnstones (*Arenaria interpres*), as they pass through the Delaware Bay en route to their breeding grounds in the Arctic. To better understand the transmission dynamics of these viruses at this site and determine if species related differences in AIV prevalence are related to habitat use, we conducted a radio-telemetry study of ruddy turnstones during May 2006. Thirty birds were tracked for up to 22 days and nights; a mean of 39.7 (range 13-127) locations were determined per bird. All birds showed a strong preference to roost at night in expansive salt marsh, usually near herring or laughing gull breeding colonies. Ruddy turnstones exhibited more limited and predictable local movements than sympatric shorebirds such as red knots, but shifted their feeding and roosting areas a mean of 2.4 (range 0-7) times, and crossed the bay 1.1 (range 0-4) times. Dispersal movements coincided with peak shorebird numbers and avian influenza prevalence, suggesting clonal AIV strains could be moved into new sites. Further characterization of host and virus ecology is needed at this locale to identify the source and transmission mechanisms of AIV at Delaware Bay.

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The Interacting Effects of Social Aggregation and Sex on the Ectoparasite Burden of Free-Ranging Raccoons

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Parasites are predicted to increase asymptotically with host contact, but a variety of outcomes are plausible due to host-parasite interactions at the individual (e.g., physiological or behavioral effects) and population level (e.g., dilution effects). We investigated how increases in social aggregation affected ectoparasite prevalence and intensity of free-ranging raccoons (*Procyon lotor*). Raccoon populations were subjected to differential resource provisions for two years; a clumped food distribution to aggregate hosts (n=5), a dispersed distribution to control for the effects of food but not aggregate hosts (n=3), and a no food treatment (n=3). The intensity of non-replete and replete (fully engorged with blood) adult American dog ticks (*Dermacentor variabilis*) were greater in aggregated populations, primarily due to greater infestations of male raccoons. Conversely, the intensity of lice (*Trichodectes octomaculatus*) on male raccoons declined in aggregated populations due to a greater number of hosts harboring fewer parasites. Intensity of lice on female raccoons was threefold lower than on male raccoons and did not differ due to treatment. The intensity of fleas (*Orchopeas howardii*) did not differ among treatments and displayed no correlation with host characteristics. Results from this study suggest that parasite life history characteristics and host ecology are critical in predicting how parasite populations will respond to alterations in host social aggregation and rates of contact.

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Japanese Encephalitis Virus Reservoir Competency in North American Birds

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Japanese encephalitis virus (JEV) is a mosquito-borne virus, with ardeid birds and pigs believed to be major amplifying hosts. The current distribution includes portions of Asia, India, and Russia, with recent emergence in Indonesia, Papua New Guinea, Australia, and Pakistan. Because of the history of intercontinental spread of JEV, we assessed the ability of several species of North American birds to amplify three strains of JEV upon experimental inoculation and examined protection afforded by pre-existing West Nile virus (WNV) antibodies against JEV in red-winged blackbirds. Viremia and shedding differed by JEV strain and bird species. Crows inoculated with a Japanese strain had no detectable viremia ($<10^{1.7}$ PFU/ml) or shedding ($<10^{0.7}$ PFU/ml). Crows, pheasants, grackles, blackbirds, finches, starlings, and chickens inoculated with an Indian strain had minimal ($10^{1.7-3.5}$ PFU/ml) to no viremia or shedding, while great egrets had moderate viremia ($10^{3.5-6.0}$ PFU/ml) and low oral shedding ($10^{0.7-3.1}$ PFU/ml). Pigeons, grackles, blackbirds, finches, and starlings inoculated with a Vietnamese strain had low to moderate viremia and low oral shedding. Many birds inoculated with Japanese and Indian strains failed to seroconvert by 14 days post-inoculation (DPI), while those with the Vietnamese strain did. Antibodies to WNV in blackbirds protected against JEV viremia, with evidence of cross reaction of antibodies to JEV and WNV on 14 DPI. No birds had JEV-associated morbidity. These results suggest that JEV infection would likely circulate differentially among North American bird species, similarly to what has been seen with WNV. Birds immune to WNV would likely fail to transmit JEV.

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Cliff Swallows, Swallow Bugs, and West Nile Virus: A Mechanism for Overwintering?

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Cliff swallows (*Petrochelidon pyrrhonata*) may be an important reservoir host for West Nile virus (WNV) because of their breeding ecology, reservoir competency status, and potentially high exposure rates. Swallow bugs (*Oeciacus vicarius*) are a hematophagous ectoparasite, and are highly dependent on cliff swallows; these parasites reside in the mud nests of cliff swallows, and feed primarily on these birds. Swallow bugs are likely exposed to WNV because they feed on nesting cliff swallows, which are concurrently exposed to an abundance of mosquitoes. Since swallow bugs remain within cliff swallow colonies throughout the year, they may provide an overwintering mechanism for WNV if they are able to transmit the virus. To test the hypothesis that swallow bugs are capable of transmitting WNV, we experimentally infected cliff swallow nestlings, allowed swallow bugs to feed on these birds during the acute infection period, and then let the exposed swallow bugs feed on naïve cliff swallow nestlings. Although swallow bugs ingested blood with high levels of infectious WNV (up to 10^{6.8} PFU/ml serum), there was no transmission from infected birds to naïve nestlings via these parasites as evidenced by lack of seroconversion at 23 days post-exposure to bugs. Therefore, swallow bugs do not appear to be a competent vector for WNV, and likely do not serve as an overwintering mechanism for the virus.

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First Detection of *Borrelia* spp. in Mongolian Reindeer (*Rangifer tarandus*)

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Reindeer occur in fragmented populations within two areas of the Mongolian taiga. These populations have low body condition scores, are subject to poor nutrition, and have tested *Brucella* positive in the past. During Mongolian reindeer health assessments in 2007 we observed an encouraging 70% birth rate, but identified a number of unthrifty animals with musculo-skeletal problems. Currently, Mongolian herders from grassland steppes, adjacent to the taiga, are moving cattle and goats to the taiga for grazing. Introduction of cattle and goats into the taiga creates opportunities for disease transmission to reindeer and alterations of the taiga ecosystem. In 2007 forty-nine serum samples were collected from seven reindeer herds and analyzed for *Borrelia* spp. using a standard protocol for indirect fluorescent antibody (IFA) testing. Western blot testing is currently being performed and collection of skin tissue for *Borrelia* spp. PCR testing has just been completed. Of the forty-nine reindeer sampled 39.1% were IFA positive for *Borrelia* spirochetes. This is the first known report of *Borreliosis* in reindeer. The increase in musculo-skeletal problems and presence of exposure to infectious organisms in the reindeer, coupled with the generalized poor body condition of the herds, is cause for concern regarding the overall health of this species. Though *Brucella suis* has been considered the inciting infection responsible for these problems, *Borrelia* spp. may also be a contributing factor to adverse health in these animals and further investigation is warranted to ascertain the etiology of Mongolian reindeer health problems.

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Prevalence of Antibodies against Rift Valley Fever Virus in Kenyan Wildlife

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Rift Valley fever virus (RVFV) is an arbovirus associated with periodic outbreaks, mostly on the African continent, of febrile disease accompanied by abortion in livestock, and a severe, fatal haemorrhagic syndrome in humans. However, the maintenance of the virus during the inter-epidemic period (IEP) when there is low or no disease activity detected in livestock or humans has not been determined. This study reports prevalence of RVFV-neutralizing antibodies in sera (n=896) collected from 16 Kenyan wildlife species including at least 35% that were born during the 1999-2006 IEP. Specimens from seven species had detectable neutralizing antibodies against RVFV, including African buffalo, black rhino, lesser kudu, impala, African elephant, kongoni, and waterbuck. High RVFV antibody prevalence (>15%) was observed in black rhinos and ruminants (kudu, impala, buffalo, and waterbuck) with the highest titres (up to 1:1280) observed mostly in buffalo, including animals born during the IEP. All lions, giraffes, plains zebras, and warthogs tested were either negative or less than two animals in each species had low (1:16) titres of RVFV antibodies. Of 249 sera collected from five wildlife species during the 2006-2007 outbreak, 16 out of 19 (84%) of the ruminant (gerenuk, waterbuck, and eland) specimens had RVFV-neutralizing titres 1:80. These data provide evidence that wild ruminants are infected by RVFV but further studies are required to determine whether these animals play a role in the virus maintenance between outbreaks and virus amplification prior to a noticeable outbreak.

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Zoonotic Disease Surveillance at the Human-Wildlife Interface

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Wild animals are an important source of recently emerging zoonotic diseases. Increasingly widespread distribution of zoonotic pathogens from wild animals may reflect increased recognition or increased human-wildlife interactions. Our objective was to identify zoonotic pathogens in wildlife and evaluate risk factors associated with pathogen shedding at three San Francisco area wildlife hospitals. We screened 343 birds and terrestrial mammals for bacteril and protozoa, and 8,826 birds and 282 marine mammals for influenza A virus from 2007-08. Fecal samples and swabs (oropharyngeal/cloacal or nasal/rectal) were collected from wild birds and marine mammals. Standard culture and biochemical methods were used to detect *Escherichia coli* (O157:H7), *Salmonella* spp., *Campylobacter jejuni*, *Vibrio* spp., and *Yersinia* spp. To detect influenza A viruses, real-time RT-PCR and virus isolation were used. Protozoa (*Giardia* spp. and *Cryptosporidium* spp.) were detected by direct immunofluorescence assay and specific identification by molecular DNA methods. Among all species screened, we detected *Campylobacter* spp. in 12% (*Campylobacter jejuni* susp. *jejuni* in 2.4%), *Salmonella* spp. in 4% (*Salmonella* B, C-1, D and E in 0.6%, 0.9%, 0.3% and 0.3%, respectively), *Vibrio cholerae* in 9%, influenza A viruses in 1%, *Cryptosporidium* in 1%, and *Giardia* spp. in 4%. Wild animals are shedding zoonotic pathogens while hospitalized at wildlife rehabilitation centers. Further work is needed to assess the public health risks associated with close contact with wildlife in this and similar occupational settings.

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Experimental Infection of Black-Tailed Deer (*Odocoileus Hemionus*) with Deerpox Virus

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The pathogenic potential of deerpox virus (DPV) was investigated via experimental infection of black-tailed deer fawns (*Odocoileus hemionus*). Fawns were inoculated intracutaneously (n=2) or intravenously (n=1). Two control fawns were similarly inoculated with saline. Horizontal transmission also was studied (n=2). One fawn was commingled with infected fawns and another was exposed by commingling plus scarification with a scab from an inoculated fawn. All exposure routes resulted in gross and histological cutaneous lesions typical of a poxviral infection. Successful transmission of DPV was confirmed in 4 out of 5 fawns via one or more of PCR, virus isolation, and serum neutralization tests. Four of the treatment fawns failed to develop systemic clinical signs other than a mild elevation in temperature. The commingled fawn developed the most severe lesions and became depressed and reluctant to eat by day (d)14 post-exposure. CBC parameters were unremarkable. Gross lesions started as papules and erythematous areas of skin (d6 post-infection[PI]), progressed to pustules (d9 PI), and then to crusting lesions (d13 PI). At necropsy (d27 PI), lesions were visible as areas of alopecia and scarring. Hydropic changes were seen in skin biopsies at d3 PI and microscopic changes progressed in a pattern typical of poxviruses. Intracytoplasmic poxviral inclusions were visible in oral mucosal epithelial cells of the commingled fawn, the only animal to develop oral lesions. These results demonstrate that DPV can cause cutaneous, mucocutaneous, and oral lesions in black-tailed deer fawns and should be considered as a differential diagnosis for poxviral diseases such as sheeppox and contagious ecthyma.

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Management of an Outbreak of Rabies (West Texas Gray Fox Strain) in Coyotes in West Texas

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In March 2007, an increasing number of rabid coyotes were noted in an area along and west of the Pecos River. The infection was typed as West Texas Gray Fox variant, a variant unique to Texas. Over the next two months, more cases were noted farther west and south of the original cases. There was also an increase in the number of other species infected with this variant in that area. In April 2007, additional vaccine/baits were distributed in a designated area to control the spread of this outbreak. In cooperation with USDA Wildlife Services, follow-up surveillance showed an average of 40% of coyotes within the distribution area had consumed vaccine/baits. No further rabid coyotes were noted within the vaccine/bait distribution area through December, 2007, although three cases appeared south of the baited area. Additional cases noted in January 2008, resulted in revision of the rabies vaccine/bait distribution area in West Texas.

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Lack of Field Performance of Raboral V-RG® in Producing Antibody Responses in Free-Ranging Striped Skunks (*Mephitis mephitis*) in Flagstaff, Arizona

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Skunk rabies occupies a broad geographical range in the U.S.; however, there currently is no licensed oral rabies vaccine (ORV) available. To determine if Raboral V-RG® is effective in producing a rabies virus neutralizing antibody (RVNA) response in striped skunks under field conditions, a multi-agency coalition initiated a field study in Flagstaff, Arizona. In April 2005, 1,875 coated sachet baits (CS) were distributed at a density of 75 baits/km² in the vaccine study area. Twelve striped skunks were captured during the post-ORV treatment; all had RVNA titers ≤ 0.05 international units (IU) by the rapid fluorescent focus inhibition test. In 2006, 3,000 baits were distributed throughout an expanded study area. Tetracycline biomarker was added to the bait coating to aid in determining whether skunks encountered the baits. Fifty-four striped skunks were trapped during post-ORV treatment: 46 had RVNA titers ≤ 0.05 IU, 6 had RVNA titers between 0.06 IU and 0.5 IU, and 2 had RVNA titers above 0.51 IU. However, of the 8 skunks with a positive RVNA response, 7 of them had a record of recent parenteral immunization with Rabdomun®. In addition, tetracycline biomarker results showed no correlation between the presence of RVNA and the presence of biomarker. There were multiple skunks with several tetracycline marks without any evidence of RVNA. All skunks were confirmed negative for rabies virus using the Direct Fluorescent Antibody test. Given these results, we conclude that the current formulation of the Raboral V-RG® is ineffective in producing a RVNA response in striped skunks under field conditions.

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National Wildlife Health Center Update on Bat White-Nose Syndrome

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Morbidity and mortality among hibernating bats in the northeastern United States recurred during winter 2008 after first being reported in New York in 2007. Bat species involved include little brown bats (*Myotis lucifugus*), big brown bats (*Eptesicus fuscus*), Northern long-eared bats (*Myotis septentrionalis*), eastern pipistrelles (*Pipistrellus subflavus*), and endangered Indiana bats (*Myotis sodalis*). A white substance, suspected to be a fungus, on the muzzle of affected bats is a common finding for which the condition was named, although other parts of the body are sometimes involved as well. The most consistent finding among affected individuals has been emaciation. In addition, pulmonary congestion has been observed in some animals. Affected hibernacula are characterized by large numbers of bats hibernating near cave or mine entrances with weak or dead bats found on the ground or roosting at nearby houses. Diagnostic evaluation by multiple institutions, thus far, has failed to identify a single cause for the mortalities. Microbiological cultures yielded numerous fungal and bacterial isolates while viral cultures failed to find a consistent underlying etiology. Several species of intestinal trematodes identified were previously linked to transmission of *Neorickettsia risticii* in horses and bats. On-going, collaborative laboratory and field research continues. In certain caves, as many as 90% of the bat populations are estimated to have died or disappeared. The effects of these bat mortalities on plant pollination and insect control are a concern for the agricultural industry and public health.

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Bats, Rabies, and African Lyssaviruses

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Rabies is an acute, progressive encephalitis of mammals caused by agents in the Genus Lyssavirus. In the Americas, only a single species of lyssavirus persists, while in Africa, at least 4 distinct viral species have been documented. Two of these, Lagos bat virus and Duvenhage virus, have bats as primary reservoirs, and recent surveillance activities in sub-Saharan Africa support the existence of other lyssavirus species. Representative bat species in both the Megachiroptera and Microchiroptera have been identified as suggested keystone reservoirs based upon virus isolation and serological studies from animals collected in a diversity of urban and rural habitats. Unfortunately, routine laboratory-based surveillance for rabies, and subsequent lyssavirus characterization, is lacking over most of the continent. Moreover, although current modern commercial human and veterinary vaccines and biologicals are pure, potent, safe, and efficacious against all traditional rabies viruses, cross reactivity against select bat lyssaviruses is much less than ideal. Given their obvious public health and agricultural significance, and the high potential virility of pathogens associated with bats, a greater focus upon combined ecological and epidemiological studies of lyssaviruses, and their presumed reservoirs, is needed throughout Africa.

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Reproduction and Nutritional Stress are Risk Factors for Hendra Virus Infection in Little Red Flying Foxes (*Pteropus scapulatus*)

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Hendra virus (HeV) is a lethal paramyxovirus which emerged in humans in 1994. Poor understanding of HeV dynamics in *Pteropus* spp. (flying fox or fruit bat) reservoir hosts has limited our ability to determine factors driving its emergence. We initiated a longitudinal field study of HeV in little red flying foxes (LRFF; *Pteropus scapulatus*) and examined individual and population risk factors for infection, to determine probable modes of intraspecific transmission. We also investigated whether seasonal changes in host behaviour, physiology and demography affect host–pathogen dynamics. Data showed that pregnant and lactating females had significantly higher risk of infection, which may explain previously observed temporal associations between HeV outbreaks and flying fox birthing periods. Age-specific seroprevalence curves generated from field data imply that HeV is transmitted horizontally via faeces, urine or saliva. The highest seroprevalence was observed when animals showed evidence of nutritional stress, suggesting that environmental processes that alter flying fox food sources, such as habitat loss and climate change, may increase HeV infection and transmission. These insights into the ecology of HeV in flying fox populations suggest causal links between anthropogenic environmental change and HeV emergence.

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Modeling the Effects of Flying Fox Urbanization on Hendra Virus Dynamics

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Hendra virus is one of several zoonotic pathogens that recently emerged from *Pteropus* spp. bats (fruit bats or flying foxes) in Australasia. Despite a high case fatality rate in people, and lack of effective therapy or vaccines, there is little known about the underlying causes of its emergence. Hendra virus outbreaks have occurred sporadically, in a pattern that coincides with dramatic changes in flying fox ecology, including urbanization and decreased migratory behaviour. We used computational models to evaluate how these anthropogenically induced changes to flying fox biology may have changed Hendra virus dynamics, and ultimately led to emergence. Our models predict that aggregation in urban areas, in combination with decreased migratory behaviour, lead to endemic dynamics within urban clusters and seed travelling waves of infection to peri-urban and rural populations. Decreased migration leads to declining herd immunity, and thus to more intense outbreaks after local reintroduction of virus. These processes could increase the likelihood of viral transmission from flying foxes to spill-over hosts such as humans and horses.

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Mortality Summary (2000-2007) in Endangered Captive Kihansi Spray Toads (*Nectophrynoides asperginis*)***D. McAloose¹, J. Pramuk¹, B. Raphael¹, P. Calle¹, W. Shellabarger², A. Odum², M. Garner³ and A. Duncan⁴**¹Wildlife Conservation Society, Bronx, NY, USA; ²Toledo Zoological Society, Toledo, OH, USA; ³Northwest ZooPath, Monroe, WA, USA; ⁴Detroit Zoological Society, Royal Oak, MI, USA

Native to the southern Udzungwa Mountains in eastern Tanzania and first discovered in 1996, Kihansi spray toads (*Nectophrynoides asperginis*; KSTs) were only known to exist in a unique 4 ha spray wetland created by the falls of the Kihansi River in the Kihansi Gorge. Habitat modification associated with the Lower Kihansi Hydropower Project and initiation of power production in 1999 caused a significant decline in KSTs in the gorge. Infectious disease was subsequently postulated as a contributing factor but its role remains unproven. Presently, KSTs are thought to be extinct in the wild. Captive populations are maintained at the Wildlife Conservation Society's Bronx Zoo and the Toledo Zoological Society. To assess disease presence in the captive populations, necropsy records from November 2000 through December 2007 were reviewed and summarized. Significant infectious diseases included nematodiasis (*Rhabdias* sp., *Strongyloides* sp.), *Batrachochytrium dendrobatidis*, bacterial sepsis, and intravascular ciliated protozoa. Also identified but of undetermined significance were a novel rickettsia-like organism and ranavirus. Significant non-infectious diseases included metabolic bone disease and (glossal and intestinal) squamous metaplasia. Identification of disease processes that can impact animal health is critical in captive management and propagation of endangered species. In captive KSTs it affected husbandry practices, medical interventions, and development of a reintroduction strategy.

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Parasites in Cold-Stunned Green Turtles (*Chelonia mydas*) in Florida***E.C. Greiner¹, B.A. Stacy¹, T McIntosh¹, A.M. Foley², B.F. Sears¹ and J.L. Miller¹**¹College of Veterinary Medicine, University of Florida, Gainesville, FL, USA; ²Florida Fish and Wildlife Conservation Commission, Jacksonville Field Laboratory, Jacksonville, FL, USA

A cold weather front rapidly lowered the surface water from 12C to 3C in January 2008 along the shore of St. Joseph Bay, FL. A total of 96 cold-stunned green turtles were recovered from a stretch of about 15 km and 33 of these died. Thirty of the dead turtles were frozen and necropsied 3 months later. Fourteen species of digenetic flukes, one species of coccidian (*Caryospora cheloniae*) and one ciliate (*Balantidium* sp.) were recovered by standard helminth technics as well as fecal flotation and sedimentation. Twenty nine of 30 turtles were infected. They ranged in straight carapace length from 21.7 to 33.9 cm and weighed 1.3 to 5.2 kg. Prevalence ranged from 3% in *Angiodictyum parallellum* and *Deuterobaris proteus* to 83% for *Schizamphistomoides spinulosum*. The flukes represented 7 digenetic fluke families. Intensities ranged from 1 to 450 per individual fluke species. Total intensities for all flukes recovered from a turtle ranged from 2 to 501 (mean = 63.9) flukes/host. The number of parasites per infected turtle ranged from 1 to 7.

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Investigating Factors Influencing Ranavirus Infection and Disease

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Ranavirus, an amphibian pathogen, was identified over a half century ago, yet its potential significance to amphibian population declines has only recently been recognized. This pathogen has been identified as the primary etiology in mass die-offs of amphibian populations in the United States and has been documented to co-occur with other significant amphibian pathogens, specifically *Aeromonas hydrophila* and *Batrachochytrium dendrobatidis*. PCR has revealed that *Ranavirus* is prevalent in wild populations and may be found with no clinical disease or histopathological lesions. The importance of subclinical infection remains unclear; however, we have shown experimentally that water quality may influence the onset of clinical ranaviral disease, suggesting that various environmental or anthropogenic stressors may negatively impact populations infected with *Ranavirus* by suppressing host immunity. Further, a captive colony of mixed anuran species concurrently infected with *Ranavirus*, *A. hydrophila*, and *B. dendrobatidis*, exhibited a wide range of lesion severity for any one pathogen. Concurrent infection suggests invasion by one pathogen may increase the likelihood that another pathogen can invade the host. Moreover, disparity in lesion severity likely reflects species-specific sensitivity to a particular pathogen. Whether these pathogens interact synergistically in wild amphibian populations remains to be explored.

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Ecological Models for the Community Dynamics of Avian Influenza in Waterfowl Communities

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Understanding the dynamics of avian influenza requires the development of mathematical models that provide insight into the mechanism that lead to outbreaks of the pathogen in wild waterfowl populations. We have developed relatively simple mathematical models for avian influenza that can be customized to examine the potential for outbreaks in specific waterfowl communities. Here we use the model to examine the role that climate might play in driving outbreaks; this provides important insight into how monitoring efforts might be focused. We then illustrate how the intrinsic dynamic property of the multi-host models may be important in creating opportunities for recombination events that lead to the ‘unexpected’ emergence of recombined strains of avian influenza virus.

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Laboratory Evaluation of Abiotic Environmental Factors affecting Avian Influenza Virus Persistence in Aquatic Habitats

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Wild birds in the orders Anseriformes and Charadriiformes are the reservoir for avian influenza (AI) viruses. Within these aquatic bird populations, AI is transmitted through an indirect fecal-oral route involving contaminated water on shared aquatic habitats. Species of birds within these two avian orders are diverse and occupy very different aquatic habitat types, ranging from fresh water marshes to marine habitats. Spatial and temporal trends for AI transmission in wild birds are well-documented. While the biology of the avian hosts is known to be an important determinant in AI epidemiology, preliminary laboratory-based data on AI persistence in water suggests that the conditions within aquatic habitats may also be influential factors. The objective of this research was to determine the variation in environmental stability of twelve wild bird-origin AI viruses in water under natural ranges of pH (5.8 to 8.6), salinity (0 to 30 parts per thousand), and temperature (4C to 37C) that occur in aquatic bird habitats. Individual viruses differed in their overall ability to persist in water and in their response to the three water variables examined. Consistent trends in viral persistence response to changing pH, temperature, and salinity, however, were evident among the AI viruses and are summarized in the response functions. The results of this research suggest that the variable pH, temperature, and salinity of water habitats that are present in nature can significantly impact the ability of AI viruses to remain infective in these environments.

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The Wild Bird Global Avian Influenza Network for Surveillance (GAINS) Project

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The Global Avian Influenza Network for Surveillance (GAINS) is a consortium-based program that conducts surveillance for highly pathogenic avian influenza, monitors wild bird populations, and trains individuals in wild bird sampling and census techniques around the world. GAINS currently supports activities in over 30 countries on six continents, has trained over 1000 people, and has collected samples from almost 40,000 birds. Gains surveillance includes systematic monitoring of wild birds along major global flyways, with georeferenced observations of over 100,000,000 birds now entered into the publicly available mapping and database systems. One of the primary purposes is to share international disease information through an interactive, open access web-based database, available online at www.gains.org. We discuss findings from this project and their impact on our understanding of the role of wild birds in the epidemiology of highly pathogenic avian influenza H5N1.

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Ecological Divergence of Two Sympatric Lineages of Buggy Creek Virus, an Arbovirus associated with Birds

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Most arboviruses show distinct serological subtypes or evolutionary lineages. The evolution of different strains is assumed to reflect differences in ecological selection pressures, but few studies have examined the extent of ecological differences between sympatric lineages. Buggy Creek virus (BCRV) is an unusual RNA virus (*Alphavirus*, *Togaviridae*) vectored by a cimicid swallow bug (*Oeciacus vicarius*) and amplified in cliff swallow (*Petrochelidon pyrrhonota*) and house sparrow (*Passer domesticus*). There are two lineages of BCRV (A and B) that differ from each other by > 6% at the nucleotide level. Using over 400 BCRV isolates collected from bug vectors in southwestern Nebraska, we found that lineage A peaked in occurrence about two weeks earlier than lineage B within a summer. Lineage A was more commonly found at bird colony sites in culverts, whereas lineage B was more common at bridge sites. The proportion of lineage A isolates at a site increased both with cliff swallow colony size and with the likelihood of immigrant cliff swallows passing through a site, while that of lineage B declined both with colony size and with the likelihood of bird immigration. Lineage A was more likely to be found at sites with house sparrows and lineage B at sites with only cliff swallows. Bugs on the outsides of nests were more likely to have virus of lineage A, whereas lineage B was more likely to be found in bugs inside the nests. Lineage A was more cytopathic on Vero cells than lineage B. The two lineages may have diverged in their transmission dynamics, with lineage A more dependent on birds and lineage B more a bug-only virus.

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Aspergillosis associated with Presumed Infectious Bursal Disease in Captive Whooping Cranes (*Grus americana*)*Marie E. Pinkerton¹ and Barry K. Hartup^{2,3}¹Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin, Madison, WI, USA; ²International Crane Foundation, Baraboo, WI, USA; ³Department of Surgical Sciences, School of Veterinary Medicine, University of Wisconsin, Madison, WI, USA

Between April 2003 and September 2007, 6 juvenile captive whooping cranes (*Grus americana*) from the International Crane Foundation in Baraboo, Wisconsin that were submitted to the University of Wisconsin-Madison Veterinary Medical Teaching Hospital Pathology Service for necropsy had histologic evidence of infectious bursal disease. Of these, 5 also had unilateral obstruction of the distal airways with intraluminal granulomas with intralesional fungi morphologically consistent with *Aspergillus* sp. Fungal cultures yielded *Aspergillus fumigatus* or *Aspergillus* sp. All 6 cranes had lymphoid necrosis in the bursa of Fabricius, spleen, and other lymphoid tissues. In 4 cranes, electron microscopy of bursa or spleen demonstrated birnavirus-like particles in the cytoplasm of lymphocytes and macrophages. Limited virus isolation attempts were unsuccessful. PCR for infectious bursal disease virus (IBDV) was attempted in one case and was weakly positive. Further testing is underway. The role of IBDV is uncertain in these cases, but it may have served as a co-factor with other stressors, leading to immunosuppression and opportunistic fungal infection. Serologic evidence of exposure to IBDV serotype 2 has been previously demonstrated in captive whooping cranes, and has been associated with a wasting syndrome in released cranes in Florida.

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Bald Eagle Reintroduction to the Channel Islands - DDTs And PCBs

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By the early 1960s, bald eagles (*Haliaeetus leucocephalus*) disappeared from all of the California Channel Islands, primarily due to the eggshell thinning effects of DDE. Today, bald eagle populations throughout much of the U.S. have largely recovered such that the U.S. Fish and Wildlife Service no longer considers the species endangered. However, bald eagles on the California Channel Islands continue to be impacted by DDTs and PCBs in the southern California Bight due to historic manufacturing and dumping practices in the adjacent mainland areas. In 2002, an effort to restore bald eagles to the northern Channel Islands was initiated by the Montrose Settlements Restoration Program with the goal of establishing a self-sustaining population on the Channel Islands. We evaluated the first 5 years of this restoration effort considering: 1) nestling survival, 2) first-year post-fledging survival, 3) DDE and total PCB blood concentrations at fledging, and 4) change in DDE and total PCB blood concentrations between release and targeted or opportunistic recapture of individual eagles. We concluded that blood concentrations of DDE and PCB of the translocated population at the time of fledging had no adverse effects on nestling or first year survival. However, DDE and total PCB blood concentrations increased with age and the effects on future survival and reproduction are unknown. Continued monitoring of the translocated individuals and their reproductive success will be necessary to determine if ongoing exposure to DDT and PCBs throughout their lives eventually causes detrimental effects.

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Transmission of *Pasteurella haemolytica* between Free-Ranging Bighorn and Domestic Sheep*David L. Hunter¹, Lisa M. Cowan², Karen M. Rudolph³ and Alton C. S. Ward²¹Turner Endangered Species Fund, Bozeman, MT, USA, ²Caine Veterinary Teaching and Research Center, University of Idaho, Caldwell, ID, USA; ³Wildlife Health Laboratory, Idaho Department of Fish and Game, Caldwell, ID, USA

Two studies involving transmission of *Pasteurella/Mannheimia haemolytica* between a free-ranging bighorn sheep (*Ovis canadensis*) and a flock of domestic sheep (*Ovis aries*) are presented. In each instance, bighorn sheep captured subsequently died of pneumonia. *Pasteurella* spp. were isolated from nasal and pharyngeal swab samples obtained from the bighorn and domestic sheep shortly after the two species had contact. All *P. haemolytica* isolates were serotyped and evaluated biochemically. Restriction enzyme analysis (REA) was performed on *Pasteurella* isolates having identical biochemical profiles that were cultured from both species. Recovery of identical isolates of *P. haemolytica* after contact between bighorn and domestic sheep indicated that transmission of *Pasteurella* species likely occurred between the species on the range. Due to the potential for transmission of pathogenic *Pasteurella* between the two species on shared habitat, we support the management strategy of maintaining physical separation of bighorn and domestic sheep. In the case where either a bighorn or domestic sheep is suspected as having had contact with the other species, we recommend the animal be immediately removed.

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Mycoplasma in a Desert Bighorn Sheep Population in Northwestern Arizona

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In recent years, *Mycoplasma* infections have been implicated in the decline of several bighorn sheep (BHS) populations throughout the western United States. In the Kanab Creek population of desert BHS in northwestern Arizona, observations of coughing sheep in conjunction with a sharp decrease in lamb recruitment prompted an investigation into the population's herd health. In May 2006, 11 adult BHS were captured via net-gun; one animal died due to capture-related trauma. Samples collected included blood, feces, oropharyngeal (OP) swabs, and lung tissue from the mortality. Serology titers were positive for parainfluenza-3 (n=7) and bovine respiratory syncytial viruses (n=10) and negative for infectious bovine rhinotracheitis and *Chlamydia*. Fecal samples were processed via the Baermann technique; no lungworm larvae were detected. Cultures of OP swabs yielded β -hemolytic *Pasteurella* (*Mannheimia*) *haemolytica* in two animals. More importantly, 8 of 11 samples were culture positive for *Mycoplasma*, which were later identified as *M. ovipneumonia*. In January 2008, banked sera from these 11 animals were submitted for *Mycoplasma* serology. Results indicated that 9 samples had positive titers, ranging from 1:320 to 1:2560. Despite the extremely high prevalence of *M. ovipneumonia* in sampled animals, the Kanab Creek population has not experienced drastic declines as have some western state BHS herds carrying this pathogen. In fact, an aerial survey conducted in March 2008 documented an increase in the lamb:ewe ratio as compared to September 2006 survey data; however, due to the discrepancy in survey months, this increase should be interpreted cautiously.

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Long Term Monitoring of Bighorn Sheep (*Ovis canadensis*) that have been in Contact with Domestic Livestock

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Pneumonia in bighorn sheep (*Ovis canadensis*) (BHS) is commonly associated with *Pasteurella* spp. although the epidemiology of disease outbreaks is often unclear. Contact between BHS and domestic sheep or goats often is considered a potential source of disease agents that can lead to die-offs of BHS. The Idaho Department of Fish and Game Wildlife Health Laboratory has examined, sampled, and/or housed 15 BHS that had contact with domestic livestock. Five of these animals were maintained in captivity for up to three years for repeated sampling and clinical observation. Sampling included collection of blood for serology, feces for parasitology, and oropharyngeal swabs for bacteriology. Samples were collected when animals were initially captured, and at various times from a few days to 30 days after capture. The animals maintained long term were sampled at about 3-4 mo intervals for up to 3 yr. No clear primary pathogen or clinical result was common to all animals, but a variety of *Pasteurella* spp. were isolated from these BHS and some animals shifted to isolates that are associated with domestic livestock. However, none of the BHS housed long-term developed clinical illness and none died of respiratory disease. A clear definition of contact between domestic livestock and BHS is needed to better define the risk factors associated with contact for disease management purposes. In addition, further definition of normal respiratory flora in BHS is needed to help wildlife managers make appropriate decisions on animal translocations using the parameters commonly used for health evaluation of BHS.

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Distribution and Habitat Selection of Parturient elk on cattle summer pasture around Riding Mountain National Park: Potential Implications for Bovine Tuberculosis Transmission

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Bovine tuberculosis (TB) may be transmitted between wild elk and cattle via shared feed, direct contact, or through urine and feces. TB continues to be an important concern for farmers around Riding Mountain National Park in southwestern Manitoba, as the same strain has been repeatedly identified in both wild elk and cattle that are in close proximity. Elk calving on farmland outside the protected areas was first identified in a regional mail survey of 786 farmers. One hundred and forty-six VHF- and GPS-collared adult cow elk were then monitored from 2002-2005. The spatial and temporal knowledge of 102 farmers was obtained using on-farm participatory mapping interviews. During the annual calving period (19 May to 18 June), the home ranges of 27% of the parturient elk were outside protected areas. Farmers identified 67 natality sites on lands outside protected areas and they indicated that calving on agricultural lands has increased substantially in the last two decades from being non-existent. Identification of high risk pastures allows mitigation of these sites using fencing, livestock guardian dogs, and carefully timed movements of grazing cattle. Identifying ways of facilitating wolf survival on agricultural landscapes may also discourage elk from calving on farmland.

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Ecological Complexity and the Management of TB in a Wildlife Reservoir

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Bovine tuberculosis is a serious disease of cattle in the UK where the Eurasian badger (*Meles meles*) is implicated as a source of infection. Options for management of transmission to cattle include culling or vaccinating badgers, and changes to cattle husbandry practices to minimize interactions. The results of intensive field studies suggest that the disturbance of badger population structure and behavior caused by culling may have counter-productive epidemiological consequences. Eradication of *M. bovis* in badgers seems very unlikely given that the infection is endemic and is also found in many other wild mammals. But the sustainability of an open-ended culling policy is questionable. Field studies suggest that it may be possible to deliver vaccine to a large proportion of a target badger population in an oral bait. However, the efficacy of the only candidate vaccine (BCG) is unknown, and there are technical challenges associated with bait and vaccine formulation. Manipulating farm husbandry techniques may be an important means of managing infection in cattle on farms where specific risks can be identified, but the potential benefits of such measures are as yet unquantified. Badger vaccination and changes to farm husbandry practices require considerable further research before their impact on cattle herd breakdown rates can be quantified.

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Progress in the Control of Tuberculosis in Spanish Wild Boar

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Recent epidemiological, pathological, and microbiological evidence strongly suggests that European wild boar (*Sus scrofa*) are able to maintain mycobacterial infection in the wild and are probably able to transmit the disease to other species, thus acting as a true wildlife reservoir at least in Spanish Mediterranean ecosystems. Southern Spain has high densities of wild ungulate species due to intensive management that includes artificial feeding and watering, containment of populations behind high wire fences, and translocations. In this research, controlled experimental infections were conducted for a better understanding of the pathobiology and immune response of wild boar to mycobacterial infection. Advances in the characterization of the mechanisms involved in host–pathogen interactions and host cell responses to *M. tuberculosis* complex in wild boar revealed new mechanisms of protective immunity which are useful for vaccine development and as a model to improve TB immunoprophylaxis and treatment. New tests were developed for the diagnosis of TB in live wild boar that improve epidemiological studies and could be incorporated into control programs. Finally, the development of effective oral vaccines and appropriate field delivery systems, which include behavioral studies, also are ongoing. However, vaccination strategies should be combined with other control measures to reduce risk factors of disease transmission identified in epidemiological studies.

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Surgical Placement of Abdominal Transmitters in Two Mule Deer (*Odocoileus hemionus*)

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Abdominal transmitters were surgically implanted in two adult female mule deer (*Odocoileus hemionus*) for evaluation of transmitter performance and the surgical technique. The transmitters were sterilized in ethylene oxide and allowed to aerate for 72 hours at room temperature. Deer were captured in a linear drive net after pursuit with a helicopter. After initial physical restraint, each deer was given a combination of telazol (4.5 mg/kg) and xylazine (2.5 mg/kg) IM for anesthesia. Deer were transported by snow machine or ATV to the surgery site and placed in dorsal recumbency on ensolite pads. The ventral midline was shaved and scrubbed. An L=block of lidocaine was placed cranial and lateral to the incision site. Standard midline ventral surgical approach allowed access to the rumen and reticulum. The radio-transmitters were placed into an absorbable mesh bag and the bag sutured to the wall of the rumen. The abdomen was flushed with warm saline and the abdominal wall closed using standard techniques. The deer were given long acting tetracycline (2.5 mg/kg) IM and the xylazine portion of the anesthetic combination was antagonized with tolazoline (3 mg/kg) IV. Both animals recovered from the procedure with no known complications. The transmitters are functioning normally to date, which is approaching 6 months post-surgery. The techniques used may provide a method for abdominal implantation of radio-transmitters in ruminants that avoid some of the complications of subcutaneous or muscle shelf techniques.

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Physiological and Pathological Effects of Surgical Implantation of Radiotransmitters in Massasauga Rattlesnakes (*Sistrurus catenatus catenatus*)

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The study of secretive snakes, such as rattlesnakes, has benefited from the use of radiotelemetry. However, the principal assumption is that the transmitter has no effect on the study animal. To test the validity of this assumption, behavioral and physiological parameters that could be affected by implanted transmitters were examined using control, sham-operated, and transmitter snakes in a laboratory setting. Examination of thermal preference provided evidence that behavior was affected by implanted transmitters. Transmitter snakes selected higher temperatures up to 6 wk following surgical implantation, likely due to a febrile response to infection or inflammation associated with the presence of the transmitter. Feeding behaviour also was affected by surgically implanted transmitters. Post-operative anorexia was seen in all snakes immediately following the initial treatment and persisted only in the transmitter group. This resulted in an overall reduction in food consumption by transmitter snakes, which was reflected in lower cumulative weight gain and lower linear growth. Inflammation and infection were evaluated using gross examination, histopathology, bacteriology, hematology and plasma protein electrophoresis. Inflammation and infection occurred despite careful surgical procedures and advanced veterinary care. Radiotelemetry remains a useful tool in field studies of secretive species such as the massasauga. However, the detrimental effects associated with surgically-implanted transmitters need to be considered, and should guide the further development of refined implantation equipment and techniques.

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In Vivo Imaging reveals the Pathogenesis of Monkeypox Viruses in Prairie Dogs*T. E. Roche¹, N. Pussini¹, A. Londono-Navas², E. Falendyz², and J. E. Osorio²¹ National Wildlife Health Center, USGS, Madison, WI, USA; ²School of Veterinary Medicine, University of Wisconsin, Madison, WI, USA

Monkeypox viruses (MPXV) cause human monkeypox, a zoonotic smallpox-like disease with significant public health importance. The virus circulates enzootically in rodents in Central and Western African rainforests. In 2003, monkeypox emerged for the first time in the Western Hemisphere when the disease occurred in 37 people exposed to ill prairie dogs (*Cynomys* spp.) infected at pet stores upon contact with exotic rodents from Ghana. To study various aspects of MPXV pathogenesis, including the potential impact on indigenous rodents in the U.S., we constructed recombinant viruses expressing the luciferase gene (MPXV-luc+) that can be used to monitor viral infection *in vivo* using biophotonic imaging. Groups of 3 black-tailed prairie dogs (*C. ludovicianus*) were infected via the intranasal (IN) route with either the Congo or USA MPXV-luc+ strain. A fourth sentinel animal was added to each group to monitor the dynamics of natural transmission. Two other animals served as uninfected controls. The animals were anesthetized and imaged on day 1 post-infection (PI) and every other day thereafter in order to track the course of infection. Blood samples and fecal, oral, nasal, and ocular swabs also were collected to measure viremia and viral shedding. Luminescence indicative of viral replication was visualized in the nares as early as day 1 PI in IN infected animals, travelled to lymph nodes a few days later, and then progressed to the skin where pox lesions ultimately developed. Sentinel animals showed evidence of infection by day 9 PI. These studies provide a better understanding of the virulence of MPXV strains, their pathogenesis in prairie dogs, and shedding from infected animals, an index of their transmission potential to humans and other animals.

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Effectiveness of FTA® Cards for Avian Influenza Virus Field Surveillance

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Current diagnostic methods for detection of avian influenza viruses (AIV) primarily rely on virus isolation in embryonating chicken eggs and/or PCR. In most cases, tracheal or cloacal swabs are collected in transport media with samples either refrigerated (4°C) or frozen (<-70°C) prior to testing. Maintaining such a cold chain is not always possible under field conditions and sample quality can be adversely affected during processing if the cold chain is interrupted. Finders Technology Associates (FTA®) cards (Whatman, Newton, MA) is filter paper containing ingredients that lyse cells, inactivate virus and bacteria, and bind and stabilize nucleic acid for further analysis by molecular techniques. With the proper permit, the card can be shipped or mailed to a laboratory from anywhere in the world. This study evaluated the FTA® cards for use as an AIV surveillance tool. Three specific criteria were evaluated: diagnostic sensitivity, storage, and field validation. The average sensitivity for AIV isolates was $1 \times 10^{4.68}$ EID₅₀/ml. FTA® cards were stored at room temperature for 120 days and sampled at days 0, 1, 10, 20, 30, 60, 90, and 120. Viral RNA was consistently detected on the cards up to 20 days after which detection efficiency declined. By 120 days, viral RNA was undetectable for 4 of the 6 viral isolates. Twenty positive and 5 negative cloacal swabs from ducks and migratory shorebirds were applied to FTA® cards. RNA for AIV was detected for 65% (13/20) of the duck samples and 70% (14/20) of the shorebird samples with no false positives. Overall, the FTA® cards were determined to be an effective surveillance tool, particularly for areas where cold storage is not possible.

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Impact of Trapping Method on Detection of Avian Influenza Viruses

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Since Canada's Interagency Wild Bird Avian Influenza Survey was initiated in 2005, two methods have been used to capture birds for banding and avian influenza testing: 1) bait trapping and 2) netting from airboats. During the 2007 surveillance season, a pilot study was conducted in Atlantic Canada to assess whether method of trapping affected the proportion of ducks that tested positive for avian influenza virus by RRT-PCR. Between July 30 and August 28 2007, combination fecal and oropharyngeal samples were collected from 523 ducks captured by one of the two trapping methods within a 700 km² area on the border of New Brunswick and Nova Scotia. Multilevel modeling showed that, overall, samples collected from ducks caught in bait traps were 2.7 (95% C.I.: 1.2, 6.1) times more likely to test positive for avian influenza by matrix RRT-PCR than were those caught by airboat. Focal areas of unusually high bird densities may occur in association with bait traps given that their main function is to attract and contain ducks that feed around and within them. Our results suggest that ducks are more likely to spread or become exposed to avian influenza viruses while concentrated around or within traps. Further research is required to confirm if the ducks caught within a single bait trap share the same virus strains and to determine whether the difference in virus detection between trapping methods is observed in other regions.

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Integrating Genetic Tools in Disease Ecology: Value-Added Wildlife Sampling Strategy

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Advanced studies in disease ecology and epidemiology depend on complete and accurate knowledge of individuals sampled. As opposed to investigations in domestic animals and humans, studies of wildlife involve population-level collection of disease data with little or no accompanying information on kinship relationships among those sampled (parent off-spring, sibships, and detailed family tree). Individual identity, sex, or species may be unknown in trace samples (e.g., feces, guano, blood spots, hair, pelts, feathers) collected from the wild to assess disease exposure in cryptic, dangerous, and endangered animals. Furthermore, replicate samples may unintentionally be collected from the same individual. In the case of trace sample "mark-recapture" studies, identification of replicates is essential. Increasingly, the high costs (financial, effort, risks to endangered species and humans) associated with securing wildlife samples oblige researchers to obtain as much useful information as possible from each specimen (value-added strategy). Discoveries (particularly PCR) in recent decades provided the laboratory tools for genomic analysis on a practical scale. Presently, computational tools to analyze the reams of PCR-generated data are being developed at a break-neck pace. DNA methodologies are available to supply much individual-identifying information needed to assess gender-specific afflictions and familial susceptibilities in wildlife. However, keeping abreast of state-of-the art analytic methods in population and kinship genetics can be mind-boggling for researchers focused on wildlife health and diseases. In this brief plain-language review, I provide practical tips and thoughts on future directions for successful integration of genetic analysis into wildlife epidemiology and disease ecology research. Case studies are employed to illustrate applications in sea otters with encephalitic diseases, mountain lions poisoned by rodenticides, West Nile virus in raptor and corvid populations, and deer with chronic wasting disease.

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Humoral Immune Responses of White-Tailed Deer (*Odocoileus virginianus*) to *Mycobacterium bovis* BCG Vaccination and Experimental Challenge with *M. bovis*

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Monitoring serum antibody production kinetics to multiple mycobacterial antigens can be useful as a diagnostic tool for the detection of *Mycobacterium bovis* infection as well as for the characterization of disease progression and efficacy of intervention strategies in several species. Humoral immune responses to multiple *M. bovis* antigens by white-tailed deer vaccinated with BCG via oral (n=10) and parenteral routes (n=6) were evaluated over time after vaccination and after experimental challenge with virulent *M. bovis*, and compared to those of unvaccinated deer (n=6). Antibody responses were evaluated using rapid test (RT), multiantigen print immunoassay (MAPIA), and immunoblot. The MAPIA and RT detected minimal to no antibody responses over baseline to multiple *M. bovis* antigens in vaccinated white-tailed deer after challenge. This was in contrast to the presence of more readily detectible antibody responses in non-vaccinated deer with more advanced disease. Immunoblot data were inconsistent, possibly due to confounding responses elicited by exposure to environmental non-tuberculous mycobacteria, but did suggest the occurrence of unique antibody responses by certain vaccine groups to Ag85 and HSP70. These findings support further investigation into the potential use of antibody-based assays, such as MAPIA and RT, as ante-mortem tools to assess disease progression in white-tailed deer in both controlled and field vaccine trials.

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Oral Vaccination of Wildlife against TB using a Lipid Bait Matrix

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Bovine tuberculosis (bTB) is responsible for adding considerable costs to the agricultural sector in several countries. A factor complicating test and slaughter programs undertaken to control bTB in domestic herds is the presence of a reservoir of disease in wild animal populations. In New Zealand the brushtail possum (*Trichosurus vulpecula*) is responsible for infecting cattle and deer while in the United Kingdom and Ireland the badger (*Meles meles*) has a role in the spread of bTB. Bovine tuberculosis also has an impact on wild animal populations such as white-tailed deer (*Odocoileus virginianus*) in the USA as well as buffalo and lion in South Africa. We formulated the human vaccine for tuberculosis (*M. bovis* BCG) into an edible lipid matrix for oral-vaccination of wildlife. This lipid matrix can be blended with a variety of flavoring and attractant agents for uptake by various target species. The lipid-based oral BCG vaccine provided protection against bTB challenge equivalent to the standard subcutaneous injection of BCG in captive possums, cattle, badgers, and white-tailed deer. Furthermore in a controlled field trial, oral vaccination of free-living possums with lipid encapsulated BCG significantly reduced the occurrence of new cases of bTB. Our aim is to produce an oral bait-based vaccine to be used as part of bTB control programs to reduce the spread of *M. bovis* from wildlife vectors to domestic animals. Further application of such a vaccine could be in the control of bTB in wildlife populations with high conservation or recreational value.

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Capture Mortalities in Moose, Brown Bears, Wolverines, Eurasian Lynx, and Gray Wolves: A Review of 5,959 Captures

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From 1984 through 2007 a total of 5,955 chemical immobilizations were carried out on moose (n = 3,449 captures), brown bears (1,317), wolverines (562), Eurasian lynx (503), and gray wolves (128). Moose, bears, and wolves were darted from a helicopter. Adult and subadult wolverines were darted from a helicopter, in the den, or after physical restraint, whereas cubs were injected after physical restraint. Adult and subadult lynx were darted from a helicopter, in snares or traps, or in a tree, whereas kittens were injected after physical restraint. Immobilizing drugs included etorphine or etorphine-xylazine (moose), etorphine-acepromazine (bears), medetomidine-tiletamine-zolazepam (bears, wolves), xylazine-ketamine (wolverines, lynx), medetomidine-ketamine (bears, wolverines, lynx, wolves) and tiletamine-zolazepam (wolves). Capture mortalities included immediate deaths due to anesthesia, stress, trauma (animals euthanized), and drowning, and mortalities within 30 days post-capture attributable to the capture event or caused by unknown factors. The total frequency of capture-related mortality (and number) for each species was: moose 0.84% (29), bears 0.99% (13), wolverines 2.14% (12), lynx 3.18% (16), and wolves 2.34% (3). When divided into immediate and post-capture deaths, the frequencies (numbers) were: moose 0.41% (14) and 0.43% (15), bears 0.91% (12) and 0.08% (1), wolverines 1.07% (6) and 1.07% (6), lynx 1.99% (10) and 1.20% (6), and wolves 1.56% (2) and 0.78% (1), respectively.

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Butorphanol, Azaperone and Medetomidine (BAM) for Field Immobilization of Plains Bison

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Seven plains bison were immobilized with a new drug combination, commonly known as BAM, made with concentrated butorphanol (50 mg/ml), azaperone (100 mg/ml) and medetomidine (40 mg/ml) (ZooPharm, Fort Collins, CO). Animals were approached on foot and darted with a Dan-Inject™ JM special rifle with 3 cc Dan-inject™ darts (Fort Collins, Colorado, USA). Four bison were captive animals from a research facility near Saskatoon, SK and three were free-ranging wild bison from Prince Albert National Park, SK. Animals were blindfolded and maintained in sternal recumbency. Mean dosages administered were 0.29 mg/kg for butorphanol, 0.14 mg/kg for azaperone and 0.07 mg/kg for medetomidine. Mean time to sternal recumbency was 14.4 minutes (range 10 to 18 minutes). Bison were non-responsive to stimuli, and quality of anesthesia was similar to neuroleptanalgesia. Oxygen saturation varied from 75% to 96%, arterial oxygen averaged 63.8 mm Hg (range 59.7-69.3, n=3), and arterial CO₂ averaged 52.2 mm Hg (range 49.6-53.5, n=3). Reversal was achieved rapidly with tolazoline (Strathcona Prescription Centre, Edmonton, AB) at a mean dosage of 3.9 mg/kg (half IV and half IM) and naltrexone (0.17 mg/kg IM)(Hawkins Pharmaceutical, Minneapolis, MN). Mean recovery time was 4.4 minutes (range 2.0-8.5 minutes). This combination proved very reliable and repeatable under a variety of field conditions with very small dart volumes (3 cc), which allowed high accuracy of dart placement. Additional analgesia or regional anesthesia would be required for invasive or painful procedures with this combination, but it is very useful for routine non-invasive procedures in bison.

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Avian Filarioid Nematodes of the World: A Synopsis with emphasis on Pathogenic Species

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Filarioids are highly specialized nematode parasites whose adults live in the tissues and tissue spaces of birds, mammals, amphibians, and reptiles. Females produce microfilariae (MF) that enter the host's blood or skin. Synoptic understandings about filarioids in birds, especially their diversity, distributions, and pathogenicity are now available for the first time. Completion of an extensive literature review reveals about 160 described species and 16 valid genera. Only *Pelecitus* occurs in hosts other than just birds and, while considerable host survey work remains to be done, *Pelecitus* also appears to be the most broadly distributed genus with reports from 17 avian orders. *Chandlerella* is known from 13 and *Paronchocerca*, *Splendidofilaria*, and *Cardiofilaria* from 11. With notable exceptions, avian filarioids are not pathogenic, and most cases are associated with adult worms in the heart muscles or lumen, major blood vessels, or brain (e.g. some species of *Sarconema*, *Paronchocerca*, *Chandlerella*, and *Splendidofilaria*) or near joints in the legs and feet (e.g. species of *Pelecitus*). However, the majority of species whose adults live in these sites are not pathogenic. Moreover, a species pathogenic in an individual bird may not be pathogenic in other birds of the same species. And, worms pathogenic in one or more species of birds may not be pathogenic in other species. Pathogenicity is even more rarely reported in association with MF. The normally blood-borne MF of *Splendidofilaria caperata* become trapped and provoke chronic inflammation in tissues near adults in crows. Skin-inhabiting MF of *Eulimdana clava* might be a factor in feather loss in pigeons.

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Pox Virus Outbreak in Magellanic Penguins from Argentine Patagonia

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Avian pox is a slow-developing disease of birds caused by an avi-pox virus which can cause skin lesions (cutaneous form) and/or upper respiratory and digestive tract mucosa lesions (diphtheritic form). Natural poxvirus infection has been reported in about 232 bird species belonging to 23 orders, including penguins and albatrosses. We report a penguin pox outbreak which occurred in Magellanic penguins (*Spheniscus magellanicus*) during the 2007-2008 breeding season at two breeding colonies in Chubut, Argentina. All animals with pox lesions were chicks with apparently healthy parents. A total of 37 live chicks were examined, varying in degrees of infection and general condition. The animals had lesions on their beaks and mouths, in and around their eyes, neck and face, flippers, feet, cloaca, and anal area. Severe lesions were also found on the feet and beaks of two chick carcasses. Cases seemed to occur in clusters and near tourist walkways in the colonies. Histopathology of tissues from 2 animals showed unspecific inflammatory lesions in a number of internal organs, and dermatitis and inclusions consistent with poxvirus infection in skin lesions. A macerate of scabby lesions from 3 infected penguins tested positive for avian pox virus by PCR. Phylogenetic analysis revealed proximity with an albatross pox virus isolated in the Falkland Islands located in the Atlantic Ocean off the shores of Patagonia. This is the first report of pox virus infection in free-ranging Magellanic penguins from Argentine Patagonia.

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West Nile Virus Surveillance in Wild Birds and Mammals from the state of Chiapas, Mexico

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The initial West Nile virus (WNV) outbreak in North America was reported in New York City in 1999. Since then, the geographic range of the disease expanded rapidly across the continent. By 2004, the virus was also detected in Canada, Mexico, the Caribbean, and Central and South America. The ecological consequences of this disease currently are unknown. In addition to the hundreds of humans and thousands of horses killed, WNV outbreaks resulted in the deaths of tens of thousands of birds and a number of mammals and reptiles also have been infected. More than 50% of 317 bird species reported to CDC dying of WNV, are considered Neotropical migrants. While it is likely the disease was transported to Mexico via infected birds or mosquitoes, there are many questions as to how it spread so rapidly throughout the Americas. The role of different wild bird species and mammals on the spread and maintenance of the disease is still unknown. We are conducting an extensive seroepidemiological survey in wild birds and mammals in Chiapas and experimental studies in Mexico City to elucidate the potential reservoir role that Neotropical species may play in the spread of the infection. The study area is located along the Pacific coastal plain in the southwestern portion of the State. It is a coastal ecosystem of mangrove estuaries and mangrove forests where more than 294 species of birds have been identified. We report positive cases in both mammals and birds in a tropical town at the southern Mexican border.

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Lead in Free Ranging Ducks from Argentina Wetlands

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Poisoning of waterfowl due to ingestion of lead pellets is a worldwide problem. No previous studies have assessed exposure of water birds to this heavy metal in Argentina, in spite of intense hunting activity with lead ammunition. As part of an ongoing study, during 2007 and 2008 we collected samples from hunter-killed ducks at several hunting lodges, including 142 gizzards and 119 bones belonging to rosy-billed pochard (*Netta peposaca* NP), fulvous tree duck (*Dendrocygna bicolor* DB), white-faced tree duck (*Dendrocygna viduata* DV), Brazilian duck (*Amazonetta brasiliensis* AB), and silver teal (*Anas versicolor* AV). Lead ammunition occurrence in the gizzards was determined by radiographs followed by pellet retrieval for confirmation. Lead concentration was measured in bones (wet weight). Only NP and DB were evaluated in 2007, with an ingestion prevalence of 31.3% and 28.6% and a mean bone concentration of 13.7ppm (0.01 to 76.3) and 4.21ppm (0.016 to 13.3), respectively. In early 2008, ingestion prevalence for NP, DB, and DV was 18.2%, 4.3%, and 8.3%, with no pellets found in AB and AV. Mean bone concentration was 18.3ppm (0.29 to 76.19), 12.85ppm (0.19 to 87.47), 13.68ppm (2.03 to 47.38), 17.83ppm (0.91 to 123.36), and 5.04ppm (3.25 to 6.82), respectively. Our results indicate substantial lead exposure (recent and chronic), representing the first report in Argentina of a health problem that may pose a threat for waterfowl conservation and for one of the most biodiverse ecosystems of the region.

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Exposure of Black Vulture (*Coragyps atratus*) to Various Viruses in Mississippi*Richard B. Minnis¹, Sherman Jack¹, Danny L. Magee², Amanda Deese¹ and Kyle VanWhy³¹Mississippi State University, Mississippi State, MS, USA; ²Mississippi Poultry Research and Diagnostic Laboratory, Pearl, MS, USA;³USDA/APHIS/Wildlife Services, Columbus, MS, USA

The black vulture, *Coragyps atratus*, is an important scavenger in the Southeast United States. As a scavenger, they have contact with many species, potentially being exposed to numerous diseases. Little research has been conducted on exposure to diseases in black vultures. As part of a damage removal program, 498 birds (19% males, 81% females) were collected from a roost in Columbus, MS in 2007. Birds were sampled and necropsied to determine exposure to pathogens. Forty five randomly selected serum samples from each sex were submitted to the Mississippi Poultry Research and Diagnostic Lab for testing of Newcastle disease virus (NDV), infectious bronchitis virus (IBV), reovirus (Reo), infectious bursal disease virus (IBDV), chick anemia virus (CAV), *Mycoplasma gallisepticum*, and *M. synoviae*. All 498 samples were submitted to the National Wildlife Research Center in Fort Collins for testing of avian influenza, and West Nile virus. Forty (20 each males and females) were also tested for laryngotracheitis. Exposure rates ranged from 0-16%, with all positive samples being from males, except one. A total of 10 birds seroconverted to these diseases, with 3 birds having exposure to 4 diseases (IBV, IBDV, Reo, and NDV), 2 exposed to 2 (IBD and Reo), and 5 others showing titers to 1 pathogen. Multiple exposure individuals mirrored vaccination practices in poultry production. Low numbers of male birds and their higher exposure rates point to a potential sexual selection pressure due to current poultry practices. The impact of this reduced male population needs to be examined.

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Natural Highly Pathogenic Avian Influenza H5N1 Infection of Wild Birds: Species-Related Variations in Severity of the Encephalitic Disease

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Highly pathogenic avian influenza (HPAI) H5N1 virus caused outbreaks of disease and mortality in various species of wild birds in Sweden in 2006. The virus is highly neurotropic and encephalitis is a hallmark of the disease; however, it occurs with varied severity. This study evaluated the severity of the encephalitis in 45 birds of various species infected naturally. Coronal sections representative of the major brain areas were stained with H&E and with special stains. Immunohistochemistry applied pre-treatment with proteinase K and mAbs AI-84 (EVL, The Netherlands). The neuropathology included: multifocal areas of gliosis and inflammatory infiltrate, with a predominance of macrophages/activated microglial cells in the grey matter, neuronal degeneration, neuronophagia, vacuolation of the neuropil, focal necrosis, and perivascular cuffing. Abundant viral antigen was present in the nucleus and cytoplasm of neurons, in macrophages, and in glial cells. The severity and extension of each of the changes, and the amounts of viral antigen were scored semi-quantitatively. The neuropathology was particularly severe in mute swans (*Cygnus olor*) and Canada geese (*Branta canadensis*). Among tufted ducks (*Aythya fuligula*), the degree of encephalitis had a broader variation but it was considered to be severe in more than 30% of the cases. Some of the birds with encephalitis had tested negative at a PCR analysis of the tracheal swab. Even though HPAI-H5N1 virus can target multiple organs, it is postulated that the viral neurotropism and its resulting neuropathology is a key feature in determining the susceptibility of the species to develop severe disease and mortality.

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Molecular Analysis of Temporally Sampled Avian Influenza

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The natural hosts for globally distributed influenza A viruses are wild birds. Typically the virus is found in waterfowl and seabirds. Alaska is uniquely situated along several flyways, and hosts a diversity of bird species. Minto Flats, located in the interior of Alaska, is a large (~500,000 acres) wetland complex supporting high densities of waterfowl, making it an ideal location to monitor influenza infections. Since the summer of 2005, cloacal swabs and faecal swabs from several species of ducks have been screened for influenza A. Positive samples were then grown and subtyped. Here we present the preliminary analysis on the sequence variation and subtype diversity found from Minto Flats waterfowl across the sampling period.

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Spatial Epidemiology of Avian Influenzas in Wild Migratory Waterfowl across the Conterminous United States 2006 – 2007

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A first step in understanding landscape-scale dynamics for any host-pathogen system often involves spatial exploratory data analysis. Identifying how spatial patterns of disease vary with analysis scale can help investigators identify mechanisms that induce spatial structure in the system under study. In conjunction with state, tribe, and laboratory partners, the United States Department of Agriculture collected and tested 124,603 wild bird samples between April 20 2006 and March 31 2007 as part of a national surveillance program targeting the first detection of highly pathogenic avian influenza H5N1 virus. We present results describing spatial and temporal patterns of low pathogenic avian influenza viruses (LPAIV) identified through that surveillance effort. We used spatial statistics to identify patterns in the distribution of LPAIV and found clear geographical and temporal variation, the magnitude of which depended on the scale and extent of analysis. We also examined how the relationship between LPAIV and waterfowl band recoveries varies with analysis scale. Taken together, these analyses highlight clear heterogeneities in the distribution of LPAIV across multiple spatial and temporal scales.

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Seroprevalence against Sin Nombre Virus in Resident and Dispersing Deer Mice

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Through dispersal, deer mice (*Peromyscus maniculatus*) enter peri-domestic settings (e.g., outbuildings, barns, cabins) and expose humans and other deer mouse populations to sin nombre virus (SNV). In June 2004, research on deer mouse dispersal was initiated at two locations in Montana. We accumulated 85,200 trap nights of effort and captured 6,185 individual deer mice a total of 22,654 times over three and half years. During the course of the study, over 12,000 deer mouse movements were recorded, and more than 1,000 of these movements were classified as dispersal movements. Greater than Average SNV antibody prevalence was approximately 11%. Most of the dispersing and antibody-positive individuals were adult males. Among the few sub-adult dispersing mice discovered during the study, none were seropositive for SNV. Our results suggest that dispersal rates are higher in high abundance populations of deer mice and during peak times of dispersal, human exposure to SNV, which commonly occurs in peri-domestic settings, could increase. We were unable to find a clear seasonality to dispersal.

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Cowpox Virus Infection in Eurasian Lynx (*Lynx lynx*) in Sweden***M. Tryland¹, M.-P. Ryser-Degiorgis^{2,3}, M. I. Okeke^{4,5}, C. Hård af Segerstad², and T. Mörner²**

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During the last decades, cowpox virus (fam. *Poxviridae*), once regarded as a zoonotic infection in milking cows and used as a vaccine virus against smallpox, has emerged in humans, cats, and other animal species in Western Europe. Surveys (serology and PCR) have shown that wild rodents and shrews may serve as virus reservoirs, although the virus has never been isolated from these species. Cowpox virus also caused severe dermal lesions in domestic cats, and produced a fatal pulmonary form in captive exotic feline species. We previously detected anti-orthopoxvirus antibodies in 5 of 17 lynx from Sweden and in one of 73 lynx from Finland. In this study, samples of lung, kidney, and spleen from 263 lynx from Sweden were screened for the presence of the conserved orthopoxvirus thymidine kinase (*tk*) gene by PCR. The *tk* gene amplicons (339 bases) were obtained from 14 males and 10 females. The amplicon sequences (21 animals) were all identical among the lynx individuals, as well as with the *tk* sequence from a human cowpox virus isolate (No.H1). Compared with a Norwegian cowpox virus from cat (No.F1) and cowpox virus GRI, one base differed. Compared with two Swedish human cowpox virus isolates, multiple nucleotides differed. It is concluded that the lynx is infected by cowpox virus, reflecting the presence of virus in populations of wild rodents and shrews.

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Disease Surveillance in Wisconsin Free-Ranging Fisher *Martes pennanti****Matt Watrud¹, Julia Langenberg², Nancy Businga²**¹University of Wisconsin School of Veterinary Medicine, Madison, WI, USA; ²Wisconsin Department of Natural Resources, Madison, WI, USA

Fisher (*Martes pennanti*) were reintroduced to the northern forests of Wisconsin in the 1950s after being extirpated in the early 1900s. Though fisher are now regularly harvested in Wisconsin, some regional populations have apparently recently declined. Very little is known about disease occurrence in fisher in Wisconsin or whether disease is a factor in population fluctuations. Fisher are thought to be susceptible to diseases of mustelids (Aleutian mink disease virus), Lyme disease (*Borellia burgdorferi*), as well as some agents associated with domestic carnivores: *Toxoplasma* spp., canine adenovirus, canine parvovirus, canine distemper virus, and *Leptospira* spp.. Blood was collected from 66 trapper-caught fisher from 3 distinct areas of northern Wisconsin. Overall, 12.1% of the fisher were seropositive for Lyme disease, 36.36% for *Toxoplasma*, 40.9% for canine adenovirus, 33.3 % for canine parvovirus, and 13.6 % for canine distemper virus. In the western study area 75%(15/20) of the fisher were seropositive for at least one of the 5 *Leptospira* serovars tested; at the most southern site, 40%(8/20) were seropositive for at least one of the 5 *Leptospira* serovars tested. There was no evidence of exposure to Aleutian mink disease virus. These results suggest that fisher are exposed to common domestic dog pathogens throughout their range in Wisconsin. This study found no significant difference in pathogen exposure between the three study areas, one of which is an area of reported fisher population decline.

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Necropsy Findings in Grey Squirrels (*Sciurus carolinensis*) in Ontario, Canada, 1993-2008**G. D. Campbell, *K.M. Welch and I.K. Barker**

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Two hundred six grey squirrels were examined at necropsy during the period 1993-2008. Trauma, including predation was the leading cause of death (49/206). Verminous encephalitis, likely due to aberrant migration of *Baylisascaris procyonis*, the roundworm of raccoons, was the leading infectious cause of death (20). Other infectious disease conditions included toxoplasmosis (7), West Nile virus (5), poxvirus (9), and sarcoptic mites (3). Poisoning, confirmed or suspected on the basis of clinical and post-mortem findings, was diagnosed in 43 animals (21%). Anticoagulant rodenticides were confirmed in 19 cases and suspected in 21 more. Cholinesterase-depressing insecticides were diagnosed by depressed brain cholinesterase levels in 3 cases. Five animals were left to die in traps. In 40 cases, cause of death was not determined.

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A Previously Unidentified *Chorioptes* Species infesting Outer Ear Canals of Moose (*Alces alces*): Characterization of the Mite and the Pathology of Infestation

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Chorioptes mites were detected frequently in the outer ear canals of moose (*Alces alces*) in Sweden, but neither the taxonomy of the mites nor the lesions associated to the infestation had been investigated. External auditory meatuses from 53 moose were examined for the presence of *Chorioptes*, and samples were taken for histopathological and microbiological examination. A proportion of the mites was identified to species. Mite DNA was extracted, and their ITS-2 sequences were determined and compared phylogenetically to sequences from other *Chorioptes* taxa. *Chorioptes* mites were found in 81% of the moose. The mites had morphological and genetic characteristics distinct from those of *C. texanus* and *C. bovis*, the two species generally accepted within the genus. Skin lesions in the ear canal were characterized by dermatitis with epidermal hyperkeratosis and crust formation. The dermal inflammatory infiltrates consisted of T- and B-lymphocytes, plasma cells, and macrophages, whereas eosinophils were uncommon. *Staphylococcus aureus* was cultured from the infested epidermis of five of 14 examined moose. In conclusion, *Chorioptes* mite infestation in the outer ear canals of moose was a frequent finding and was associated with inflammatory lesions of the external auditory meatus. Our studies indicate infestations with a previously undescribed *Chorioptes* species.

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First Report of Phocine Distemper Viral Infection in Northern Sea Otters (*Enhydra lutris kenyoni*) from Alaska

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The northern sea otter (*Enhydra lutris kenyoni*) in Alaska has been listed as threatened under the endangered species act as a result of a precipitous population decline since the 1980s. Recent evidence of serologic exposure to a phocine distemper-like virus in live free-ranging animals, as well as the high prevalence of a disease usually associated with underlying infection and/or immunosuppression in beach cast otters, resulted in further investigation to ascertain if a morbillivirus could be detected in Alaskan sea otters. Tissues from dead stranded otters (n = 9) examined as a part of the ongoing unusual mortality event, and nasal swabs from live captured otters (n = 83) from the Kodiak Archipelago and the Alaska Peninsula were analyzed by PCR using universal morbillivirus primers directed against the phosphoprotein gene. Morbilliviral RNA was amplified in tissues from three dead stranded otters from Kachemak Bay and from seven nasal swabs from the live captured otters from Kodiak. Sequence analysis confirmed the amplicon as a phocine distemper viral fragment identical to the isolate from the 2002 phocine distemper outbreak in northern Europe. Phocine distemper has caused devastating disease in marine mammals in the Atlantic, but has not been detected in free-living species in the Pacific. Ongoing work is elucidating the correlation between the presence of viral nucleic acid and lesions in tissues from affected otters and defining the association with morbidity and mortality in the population.

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Amyloid-Producing Disseminated Carcinosarcoma in a California Sea Lion (*Zalophus californianus*)*Howard Steinberg¹, Roberta Wallace² and Vickie Clyde²¹University of Wisconsin, Madison, WI, USA; ²Milwaukee Co. Zoo, Milwaukee, WI, USA

A captive 30+-year-old female California sea lion (*Zalophus californianus*) in the Milwaukee County Zoo had progressive appetite decline that progressed to complete anorexia. Following examination and radiographs that revealed multiple pulmonary masses, the sea lion was humanely euthanized. Post mortem examination exposed an emaciated animal. There were hundreds of smooth, raised circular, discrete to multiple cerebriform or verrucous aggregates occasionally pedunculated or umbilicated, firm, cream to tan, well delineated masses, ranging from pinpoint to 4x3x2 cm. present on the pericardium, visceral and parietal pleura, lungs, liver, esophageal serosa, spleen, renal capsules and parenchyma, left adrenal gland, diaphragmatic peritoneal surface, and hepatic hilar lymph node. These were consistent with severe metastatic disease of a carcinoma, most likely adenocarcinoma, which primary source was not determined. Microscopically, the neoplastic masses had two distinct intermixed morphologic forms. They were variably-sized discrete unencapsulated masses comprised of neoplastic epithelial cells rarely forming acinar-like structures. A second cell population with morphologic characteristics consistent with neoplastic mesenchymal cells was interspersed with these neoplastic epithelial cells. There were occasional localized areas with abundant amorphous eosinophilic extracellular matrix suggestive of amyloid. These mixed neoplastic masses were confirmed in liver, spleen, kidneys, lungs, bilateral adrenal glands, bilateral thyroid glands, diaphragm, pericardium, and hepatic lymph node. A diagnosis of amyloid-producing disseminated carcinosarcoma was made based on morphologic features, and immunohistochemical and histochemical staining characteristics.

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Prevalence of Intestinal Helminth Parasites in Rhesus Monkeys of Nepal

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The main objective of this study was to understand the parasite infection in rhesus monkeys of Hindu temples of Kathmandu. A total of 202 fecal samples from *Macaca mulatta* from Kathmandu were collected. The specimens were microscopically examined after concentration for ova of intestinal helminth parasites. Nematodes were the most prevalent (89.5%) and trematodes were the least prevalent (4.8%). Only one species of trematode, *Dicrocoelium* sp., was found. Among nematodes, *Strongyloides fulleborni* was most prevalent (51.6%) whereas *Toxocara canis* (0.8%) and *Cooperia* sp. (0.8%) were the least prevalent. The prevalence of other nematodes were as follows: *Oxyuris* sp. 11.3%, *Ascaris lumbricoides* 10.5%, *Dictyocaulus* sp. 7.2%, *Chabertia* sp. 6.4%, *Toxascaris leonina* 6.4%, *Ostertagia* sp. 6.4%, *Trichuris ovis* 6.4%, *Trichuris trichura* 5.6%, *Trichostrongylus* sp. 4.8%, *Capillaria* sp. 4.0%, *Oesophagostomum* sp. 4.0%, *Ancylostoma duodenale* 2.4%, *Haemonchus contortus* 2.4%, *Cooperia* sp. 0.8%, and *Toxocara canis* 0.8%. Monkeys may also be vectors to human infections. Monkeys should be dewormed regularly to improve their health. Local people of the study area are unaware of many zoonotic diseases which may be transmitted through monkeys, so they should be alerted through awareness programs. More research should be focused in this field because little work has been done in Nepal.

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Disease, Wildlife Research, and the Public's Perception of Risk

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Our continued ability to conduct fieldwork in wildlife biology and train the next generation of field biologists is threatened by social, institutional, and bureaucratic changes that have accelerated over the past decade. These changes include continued decline in field-based natural history studies in the United States and elsewhere, bureaucratic regulations that are increasing in both number and complexity worldwide, increased acceptance of radical animal rights propaganda by our youth, increased fear of nature among our citizens, and poor understanding of risk in an increasingly risk-averse society. These impediments to field research loom especially large in the United States, where scientists find it increasingly difficult to conduct field-based wildlife research. This talk will review the history of the 1993 discovery of the rodent-borne disease Hantavirus Pulmonary Syndrome (HPS) to show how a combination of social, institutional, and bureaucratic forces conspired to influence the U.S. response to the perceived HPS threat. Current U.S. guidelines designed to protect wildlife researchers from HPS rely heavily on knowledge of rodent biology obtained through field-based research. Thus, it is ironic that the excessive stringency of these guidelines, which reflect a deep misunderstanding of risk, may be destroying future opportunities to obtain similarly useful field data.

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Incidence of Hemorrhagic Disease in Virginia is associated with Winter and Summer Climatic Conditions

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The objective of this study was to determine if selected climatic conditions were associated with annual incidence of hemorrhagic disease (HD) in white-tailed deer (*Odocoileus virginianus*) from Virginia. The annual percentages of hunter-harvested deer with hoof wall growth interruptions (a clinical sign of chronic HD) from counties in four climatic divisions east of the Blue Ridge Mountains (HD endemic area) during 1993-2006 were calculated and used as a standardized indicator of annual HD incidence. In addition, data on average temperature (°F) and total precipitation (inches) by month for each of the climatic divisions for the same time period were obtained from the University of Virginia Climatology Office database. Pearson's correlation coefficients between annual HD incidence and temperature or precipitation for each month, as well as for winter (January-February), early summer (June-July), and late summer/fall (August-September-October) seasons were calculated. Strong direct correlations between annual HD incidence and average temperature for winter ($r = 0.39$, $P = 0.003$, $n = 57$), early summer ($r = 0.51$, $P < 0.0001$, $n = 57$), and late summer/fall ($r = 0.42$, $P = 0.001$, $n = 57$) were evident. There was also a strong inverse correlation between annual HD incidence and June precipitation ($r = -0.44$, $P = 0.0006$, $n = 57$). Poisson regression models of the seasonal temperatures and June precipitation to annual HD incidence were also developed. Based on Akaike's Information Criterion with small sample size correction (AICc), the global model was selected as the top model. Higher winter and summer temperatures may increase vector capacity and competence. Further studies at multiple spatial scales that include additional climatic factors are warranted.

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Factors affecting Epizootics of Winter Ticks

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Die-offs of moose (*Alces alces*), associated with, or attributed to, winter ticks (*Dermacentor albipictus*) are widespread and have been reported since the early part of the last century. Extrinsic factors, such as weather and vegetative structure, and host factors, such as moose density and, indirectly, tick-induced damage to the hair coat, were examined in an attempt to predict related problems for moose. The proposal that warmer and shorter winters result in increased survival of adult female ticks dropping off moose in March and April, and increased tick populations on moose the following winter, was generally confirmed. Annual changes in hair damage and loss on moose, which can be documented from the air, coincided with annual changes in numbers of ticks on moose, providing wildlife managers with a survey tool to monitor and estimate changing numbers of ticks. Tick numbers lagged 1 year behind moose numbers in Elk Island National Park over a 12-year period and many moose died when numbers of moose and ticks were high. Several widespread concurrent die-offs and recent information from Isle Royale National Park suggest extrinsic influences play a role, possibly independent of moose density. The lack of objective and continuous data sets should guide future research efforts.

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Evidence of Embryonal Death in Scandinavian Moose (*Alces alces*)

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The moose (*Alces alces*) is considered the most important game species in Scandinavia. Annual bags exceed 120,000 animals in Norway and Sweden combined. Recently, reports by hunters and from the Swedish Association for Hunting and Wildlife Management indicate that reproduction numbers (number of calves per cow in the fall) in local moose populations in southern Sweden are lower than in other areas. To find reasons for the low numbers, we conducted a study on the island of Öland, located in the Baltic Sea east of mainland Sweden. Reproductive organs, spleen, and blood were collected from each animal shot (n=31) during the hunting season of 2007-2008. The observed calf per cow ratio averaged 0.39 during the hunt. In six out of 12 pregnant females, ages varying from 1.5 – 6.5 years, dead embryos were found in the uterus. In some (n=2) one of two twin embryos were dead, and in other (n=4) the only embryo was dead. To our knowledge, this is the first report of embryonal death in moose, and the discovery may be a factor causing lower reproduction numbers. Causes of the embryonal death so far remain unknown, and because of the small sample size, it is not known whether it is a normal finding in moose. Disease or intoxication cannot be excluded, and more studies will be carried out in four more moose hunting areas in 2008-2009 in order to investigate the frequency and possible causes of this discovery.

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Pathological Investigations of the Decline of North Slope Muskoxen

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Sixty-four muskoxen were reintroduced into areas in and near the Arctic National Wildlife Refuge in northeastern Alaska in 1969-70. This isolated population expanded to approximately 800 by 1995, then began declining. Numbers dropped sharply in the refuge beginning in 1999. By 2006 virtually no muskoxen were found in the refuge, and less than 400 animals remained in neighboring areas. Several factors appear to be involved in the decline, including weather and brown bear predation on all age classes. Preliminary investigations suggest that disease, parasitism, and essential trace element deficiencies also had a role. Morbidity and mortality caused by infectious pathogens have been identified, including *Chlamydiophila polyarthritidis*, *Pasteurella trehalosi* pneumonia, and contagious ecthyma. The potential contributions of *Hemophilus* and bovine viral diarrhea also are being pursued with further diagnostics. Hoof lesions and low copper levels in tissues were detected, leading to further studies of essential elements in comparison to other populations of Alaskan muskoxen. Retrospective and prospective serology identified antibodies to additional infectious diseases that were not present pre-decline in this population including: *Brucella suis* serovar 4, leptospirosis, and infectious bovine rhinotracheitis. ELISA and PCR on vaginal and conjunctival swabs as well as IHC on joint cartilage indicated the presence of *Chlamydiophila* in up to 45% of adult female muskoxen, compared to rates of 29% seropositive, 100% PCR-negative for females of similar age/reproductive class in a healthy, increasing population in western Alaska.

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Is Paratuberculosis an Emerging Disease in Spanish Wildlife?

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In Europe, a role of wildlife species as paratuberculosis reservoirs is strongly suspected based on field and molecular epidemiologic evidence. This presentation includes data from Spain at a local and a national scale. At a national scale, we show the first large scale data on ELISA against *Mycobacterium avium* subspecies *paratuberculosis* (MAP) antibodies in red deer (*Cervus elaphus*) from Spain, and test the effect of host and environmental risk factors on antibody levels. A total of 257 of 852 serum samples tested positive, yielding a total seroprevalence of 30.16% (95%CI 27.08-33.24). Sampling locality, presence of cattle, and increasing age explained the variation in the individual ELISA OD results. At a local scale, ELISA combined with PCR and real time PCR testing allowed the study of paratuberculosis epidemiology in Doñana National Park, southern Spain. Prevalences were highest in the areas of highest wild ruminant densities and not in the areas shared with cattle. Our data strongly suggest that deer in Spain are exposed to MAP. While contact with cattle was statistically significant at a large scale, this trend was not confirmed at a local scale. The results support the need of a careful study of MAP prevalence based on culture and molecular tools in order to clarify if deer and other wildlife play a significant role as paratuberculosis reservoirs for livestock, and if paratuberculosis is affecting hunting harvest, trophy quality, or wild animal welfare in Spain.

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Transmission through the Wildlife-Livestock Interface: Foot and Mouth Disease in Mongolia

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Foot and Mouth Disease (FMD) is a highly contagious acute viral disease that affects most ruminant and porcine species, including wildlife. Outbreaks of FMD in Mongolia have caused severe disruptions to the pastoral economy and culture, and threaten the long-term persistence of the Mongolian gazelle (*Procapra gutturosa*), a keystone species on the Mongolian Eastern Steppe. Mongolian gazelles share range with domestic livestock (sheep, goats, Bactrian camels, and cattle) so there is fear that gazelles and other wildlife species may be an effective means for spread of FMD. Consequently, there is a need to understand the potential role of Mongolian gazelles in spreading FMD. In 1998/99, no evidence of FMD exposure was detected during serosurveys of Mongolian gazelles. However, in 2001, antibodies to type O FMD virus were detected in 67% of 33 gazelles. In a follow-up study during 2005-2007, we collected sera from 57 wild Mongolian gazelle calves and 555 adult domestic animals sympatric with the Mongolian gazelle, including sheep, goats, Bactrian camels, and cattle; no evidence of an active outbreak was evident during these years. The episodic nature of FMD outbreaks on the Eastern Steppe, with evidence of FMD exposure in gazelles only during concurrent outbreaks in livestock, strongly suggests gazelles do not form a reservoir for FMD in Mongolia. Consequently, effective management actions such as improving access to veterinary care for livestock on the Steppe and improving vaccination coverage are necessary for improved economics and livelihoods for one of the world's last pastoral cultures, as well as improve prospects for the conservation of the Mongolian gazelle.

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Ecology of Chronic Wasting Disease-Positive and Negative White-Tailed Deer in Wyoming

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Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy of deer (*Odocoileus* sp.), elk (*Cervus elaphus*) and moose (*Alces alces*). It is not known how normal behaviour and ecology of deer is altered by CWD infection. To address this question, we hypothesized that CWD alters normal behaviour of free-ranging white-tailed deer (*Odocoileus virginianus*), producing significant differences between CWD-positive and negative deer regarding landscape use, daily activity, and migration and dispersal rates. The specific research objectives were to compare CWD-positive and negative deer in relation to: 1) annual home range size; 2) migration and dispersal rates; and 3) seasonal daily activity patterns. Deer were captured as fawns (≤ 8 months), tested antemortem for CWD and marked with eartag very high frequency (VHF) radio-transmitters. Deer were re-captured yearly to re-test for CWD and replace eartags with global positioning system (GPS) or VHF collars. Deer were tracked by radio telemetry and GPS technology throughout the year. There was no difference in annual home range size by CWD status. Migration and dispersal rates were lower in CWD-positive (21% and 4%) than negative (39% and 20%) deer. The data suggest CWD-positive deer were more sedentary than negative deer, which may explain locally high CWD-prevalence loci within endemic areas. Male CWD-negative deer were more active than CWD-positive deer at night during fall ($F_{23, 138} = 1.98$, $P = 0.009$). The difference in activity of males during the fall may indicate that CWD-positive males were participating to a lesser extent in the rut.

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Selective Predation and the Control of an Emerging Wildlife Disease: Can Wisconsin Hunters Limit CWD?***Erik E. Osnas**

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Parasites and hosts are part of a larger community that includes predators. If parasites affect the probability that a host will become prey, then predators may experience proportionally more or less infected hosts than the population as a whole. As researchers, we often use samples obtained through predators (human hunters) or act as predators when sampling populations; therefore, our samples may also be biased. I explore these properties using a simple host-parasite model and show that the observed host-parasite dynamics can be very different from the true dynamics and will depend strongly on the intensity of predation, predation bias, transmission rate, and the true prevalence. With increased predation bias, true prevalence can be much lower than in the absence of predation. Finally, I discuss Chronic Wasting Disease, a neurological disease of deer hypothesized to affect susceptibility to hunters, in light of predictions from the model. Specifically, I show that observed prevalence can increase, decrease, or remain relatively unchanged through a hunting season even when infected deer are more vulnerable to hunters. Given these predictions and the spatial, sex, and age-related heterogeneities in Wisconsin CWD prevalence, reliably detecting and interpreting within-season prevalence dynamics will be difficult even when infected deer are much more vulnerable to hunters.

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Deer, Corridors, and Disease: Using Corridor Theory to Project Routes of CWD Spread***Chris Garrett¹, Evelyn Merrill¹, Margo Pybus², David Coltman¹ and Fangliang He¹**¹University of Alberta, Edmonton, AB, Canada; ²Alberta Fish and Wildlife, Edmonton, AB, Canada

Chronic wasting disease (CWD) has been documented in wild deer in Alberta since September 2005 and, despite intensive management actions, new cases continue to emerge and the disease appears to be spreading. Movements of infected deer, such as migration, dispersal, and extra-territorial explorations, may explain part of the pattern of CWD spread. These types of movements are those for which corridors are usually designed, and the goal of our research is to use the principles of corridor theory to identify potential conduits of deer movement as a surrogate for the pattern of CWD spread. To quantify deer movement, we collared deer with global positioning system (GPS) radio collars across a range of landscape patterns in the aspen parkland near Wainwright, Alberta; a current CWD foci along the Alberta-Saskatchewan border. We calculated the home range boundaries of the collared deer using the fixed kernel method and then retained only those movements that were outside the boundaries. Habitat selection during these movements was quantified using a resource selection function, which was used to create a map of preferred deer movement habitat based on the existing landscape. Deer movement in the vicinity of infected areas is then simulated in a GIS environment using a correlated walk approach, with step rejection based on habitat preferences. The result of multiple simulations will be two maps. The first indicates the time at which individuals reach each point, giving an indication of the potential rate of disease spread. The second identifies the number of simulated individuals that have passed through each area, providing an estimate of the probability of disease spread.

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Genetic Analysis of CWD-Infected Deer In Western Canada

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Chronic wasting disease (CWD) is a prion disease now established in herds of wild mule (*Odocoileus hemionus*) and white-tailed deer (*O. virginianus*) in western Canada. We are using population genetic analyses to help predict the spread of CWD in Canadian deer. Both species appear to have very weak genetic structure, indicating high rates of gene flow and potential disease transmission at broad spatial scales. We did not find major geographic barriers to gene flow that might impede further disease spread. At finer spatial scales deer show evidence of social-genetic structure, with pairs of individuals sampled from the same grid coordinates showing elevated genetic relatedness and spatial autocorrelation up to 10km. Pairs of co-infected individuals showed elevated relatedness at longer distances, suggesting that disease transmission within related social groups is an important component of CWD spread. We also tested for association between prion genotype and CWD status by determining RNP gene sequence in 166 CWD- and 83 CWD+ mule deer, and 197 CWD- and 30 CWD+ white-tailed deer. Two variable sites were found in mule deer, and 15 in white-tailed deer. In both species PRNP genotype was associated with CWD status. Mule deer possessing at least one copy of the rare allele at codon 20 were less likely to test positive for CWD than expected given the frequency of this allele in the population. A variant at codon 96 in white-tailed deer also was linked with reduced incidence of CWD. Better knowledge of the genetic sources of heterogeneity in CWD susceptibility may improve our understanding of the CWD epidemic in western Canada.

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Infectivity of Prions following Ingestion and Excretion by American Crows (*Corvus brachyrhynchos*)

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From the first observations of chronic wasting disease (CWD) in mule deer (*Odocoileus hemionus*) and Rocky Mountain elk (*Cervus elaphus nelsoni*) in northern Colorado, USA, the disease has been identified in an increasing geographic area. Mechanisms for the spread of CWD are incompletely understood. We hypothesize avian scavengers have potential to disseminate prions associated with transmissible spongiform encephalopathies (TSEs) like CWD. Our objective was to determine if TSE-positive brain material from mice (mouse-adapted scrapie) could pass through the digestive tract of American crows (*Corvus brachyrhynchos*) and still be infectious to mice. Our experimental design included treatment groups of mice inoculated intraperitoneally with gamma-irradiated feces from crows gavaged with scrapie-infected mouse brain and feces from crows gavaged with normal mouse brain (control.) Our preliminary results indicate feces from each of 20 crows gavaged with infected mouse brain was infectious for mice (proportion of crows=1.00, 95% CI: 0.83-1.00) and average longevity for mice was 213 days (95% CI: 210-216). Most control mice were still alive ≥ 320 days post inoculation with no evident clinical signs of TSE disease. Our results demonstrate that a common, migratory North American scavenger can pass infective prions in feces and, therefore, could play a role in the spatial dissemination of prion disease.

Evaluation of Rectal Biopsy for Preclinical Diagnosis of Chronic Wasting Disease in Free-Ranging Rocky Mountain Elk

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Chronic wasting disease (CWD), a prion (PrP) associated spongiform encephalopathy of cervids, has not previously been diagnosed using a preclinical ante mortem test in free-ranging elk. Live tonsillar biopsy tests for CWD have been successfully applied in captive and free-ranging white-tailed deer and mule deer; however, this technology has not been validated in elk. Recently, biopsy of rectal lymphoid tissue from live domestic sheep, white-tailed deer, mule deer, and captive elk has shown promising results as a preclinical live test for associated prion diseases. In this study, we captured, radio-collared, and collected samples of rectal lymphoid tissue from 136 female elk in Rocky Mountain National Park, Colorado, USA. No clear clinical signs of CWD were observed at the time of capture. Thirteen of 117 diagnostic samples were positive when examined using immunohistochemistry. Positive animals were removed from the population and complete necropsies performed. All had evidence of PrP^{CWD} in the brain and retropharyngeal lymph nodes. Individual PrP genotypes are currently being evaluated. These results show that while rectal biopsy is an intensive tool, it can be used to diagnose preclinical CWD in free-ranging elk.

ABSTRACTS: STUDENT POSTER COMPETITION

P1

Retrospective Identification of Canine Papillomaviruses in Captive African Wild Dogs

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Nearly every mammalian species is susceptible to some form of Papillomavirus, with symptoms ranging from warty lesions to squamous cell carcinomas. Currently, there are 3 genetically characterized forms of this virus in canids with a total of six described in the scientific literature. Due to the large number of Papillomaviruses known for humans and other species, it seems likely that many more forms exist in canids as well. In the spring of 2007, three African wild dogs housed together at the Kansas City Zoo developed wart-like lesions at the base of their ears, cervical skin, and medial thigh. These lesions were biopsied and sent to the University of Missouri for evaluation. Initial sequencing determined that they were the product of a Papillomavirus that did not match any of the three previously sequenced forms. Research will continue through the summer of 2008 attempting to use new primers and long template amplification to further sequence this new strain. As little is known about the occurrence of Canine Papillomaviruses in wild and exotic carnivores, helping to correlate the virulence of different strains with their sequences will help in future studies of transmission, occurrence, and impact of such pathogens in both captive and wild canid populations.

P2

Evaluation of Hematological Values in Free-Ranging African Buffalo

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As part of a large-scale disease screening program, blood samples were collected from 534 African buffalo (*Syncerus caffer*) in South Africa's Hluhluwe-iMfolozi Park in October 2005 and May 2006 to establish age and sex-specific reference intervals for erythrograms and leukograms. Sixty-seven of the animals were positive for bovine tuberculosis (TB), allowing for comparisons between TB positive and TB negative groups. TB positive animals had basopenia and slight lymphopenia compared to TB negative animals. Blood values were compared to those reported for captive African buffalo, American bison (*Bos bison*) and cattle (*Bos taurus*). The free-ranging buffalo sampled in this study had higher white blood cell counts than captive buffalo. Many of the values also differed between the species. Demographic factors strongly affected hematological values in the study population. Many of the hematological values varied significantly between male and female, and across the age groups. Environmental factors, such as season and herd affiliation also had a significant effect on the hematological values. Our results emphasize the need to use species-specific data when interpreting hematological values, and also point to important differences in hematology between captive and free-ranging animals of the same species. Strong variability in hematologic values with animal age and sex, season and herd affiliation, indicates that "normal" hematologic values in wild animals vary throughout their lives and are subject to fluctuating environmental conditions.

P3

Health Assessment of American Oystercatchers (*Haematopus palliatus palliatus*) in Georgia and South Carolina

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The American oystercatcher (*Haematopus palliatus palliatus*) is a large shorebird native to the Atlantic coast of the United States, listed as a species of high concern by the United States Shorebird Conservation Plan. The species feeds primarily on bivalves and is therefore restricted in its range to intertidal shellfish beds. Bivalves are filter feeders that can concentrate toxins and pathogens from the local environment, and so the American oystercatcher may accumulate toxins and be exposed to pathogens in its diet. Oystercatcher population health may reflect contamination of principal food sources and the environment, both of which are shared by humans. The objective of this study was to conduct the first ever health assessment of the American oystercatcher population on the coasts of Georgia and South Carolina. Data were collected from free-ranging American oystercatchers (n=171) captured at five sites in South Carolina and Georgia between 2001 and 2006. We report reference ranges for hematology parameters and blood chemistry profiles, and baseline levels of reproductive hormones and pathogen exposure. Mercury was detected in 32/44 blood samples with a median concentration 0.0855 ppm. Forty-five blood samples tested for organochlorine and polychlorinated biphenyls levels were below detectable limits. This health assessment serves as a reference for continued monitoring and conservation of the American oystercatcher population and coastal ecosystems.

P4

Diseases in Dogs Parapatric to Wolves in Coastal British Columbia

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Little is known about diseases in wildlife from British Columbia's 'pristine' central and north coasts, yet rapid increases in human activity, commercial and tourism, may introduce new diseases or alter existing disease dynamics. To gain baseline data on canine disease in this area, we collected blood and stool samples from 107 dogs in five remote communities with rare to no veterinary services. Therefore, we considered the dogs to be sentinels of disease in parapatric wolves. In addition, we profiled 887 stool samples from wolves for evidence of parasites. Serology revealed that dogs in these communities have been exposed to canine parvo- and distemper viruses, *Bordetella bronchiseptica*, and *Leptospira* serovars *autumnalis* and *pomona*, but not to coronavirus, *Ehrlichia canis*, *Cryptococcus gattii*, *Anaplasma phagocytophilum*, *Borrelia burgdorferi*, or *Dirofilaria immitis*. Seventy-five stool samples from coastal dogs revealed the presence of taeniid tapeworms, nematodes *Toxocara* sp. and *Toxascaris* sp., and protozoans *Isoospora* sp., *Giardia* sp., *Cryptosporidium* sp., and *Sarcocystis* sp. We found no evidence that wolves parapatric with dogs harbored different parasites than did wolves allopatric to dogs, suggesting no 'spillover' of parasites between dogs and wolves. Our results do reveal parasites with zoonotic potential in dogs and wolves in coastal B.C., and this work provides a solid baseline for future disease monitoring.

P5

Qualitative Analysis of Farmed and Wild Cervid CWD Data in Alberta

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While in the past, the transmission of Chronic Wasting Disease (CWD) from farmed cervids to wild populations has been highlighted, it must be remembered that the fence is not a one way barrier and disease transmission may occur in both directions. With more CWD positive cases being found in wild cervids in Alberta along the Saskatchewan border every year, the farmed cervid industry must become more aware of the possibility that wild population can transmit disease to their captive herds. With current work identifying certain geospatial characteristics that facilitate cervid CWD transmission in wild populations, the ability to quantify a risk to farmed cervids is a growing possibility. However, before in depth network analysis can begin, the first logical step is to assess the disease prevalence data with geospatial techniques to plan the direction of further analysis. A number of new GIS and modeling tools exist that can facilitate this and many of them are open source or available from their developers. The tool chosen to conduct the initial qualitative and quantitative analysis in this instance is Biomapper, developed by Dr. Alexandre Hirzel of the Department of Ecology and Evolution at the University of Lausanne, Switzerland. It can be used to develop an ecological niche model of CWD in the province of Alberta and include the geospatial data of the farm locations and habitat characteristic that may facilitate CWD spread. An added benefit to policy makers is that this sort of analysis could have value in the implementation of new or the enforcement of existing disease control policies and surveillance programs.

P6

Endoparasites of Greater Sage-Grouse in Oregon

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A serious dilemma in wildlife conservation is the risk that disease will have deleterious effects on already stressed and shrinking populations. The greater sage-grouse (*Centrocercus urophasianus*) is a galliform of conservation priority, which resides in the sagebrush (*Artemisia* sp.) ecosystems in the western United States, including southeastern Oregon. This species has declined by 33% in North America in the past 30-40 years and been extirpated in five states due to habitat loss and degradation from wildfire, improper grazing practices, and human developments. With the advent of West Nile Virus, the relatively unknown parasitic assemblages of Oregon's greater sage-grouse necessitate examination. Approximately 15 radio-marked greater sage-grouse in central Oregon will be tracked in the first two weeks of July, and fecal and cecal samples will be collected from loafing and roosting sites and flushing flocks. These samples will be evaluated for the presence of parasites at Oregon State University. Morphological and molecular analyses will assist in classifying the genus and species of the helminth eggs and coccidia present in the fecal samples. Fecal egg counts per gram of feces will be determined to estimate the parasitic load in the bird, because they are highly correlative with overall parasitic load. Blood smears will also be examined. This will likely be the most extensive work conducted on greater sage-grouse endoparasites in Oregon, and epidemiological statistical analyses utilizing gender, age, and seasonal variations may reveal intraspecies differences in parasitic incidence and abundance.

P7

Survey for Infectious Agents in Mule Deer in Southern Saskatchewan

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As a part of an ongoing study on the spread of chronic wasting disease (CWD) in wild deer in southern Saskatchewan, a survey was undertaken to determine the prevalence of CWD and other selected infectious agents of mule deer (*Odocoileus hemionus*). During the winter of 2006 and 2007, tonsil biopsies, feces and blood were collected from 210 captured mule deer. Tonsil biopsies were tested for CWD by immunohistochemistry which revealed an overall prevalence of 3.2%. Fecal floatation, Baermann technique, and fluorescent antibody tests identified four species of nematodes; *Trichostrongylus* spp. (31.0%), *Nematodirus* spp. (8.1%), *Skrjabinema* spp. (14.3%) and *Protostrongylus* sp. larvae (36.7%) and 2 species of cestodes; *Monezia* spp. (15.7%) and *Thysanosoma* spp. (11.9%) and 2 species of protozoa; *Eimeria* spp. (13.3%) and *Giardia* spp. (0.7%). Serum neutralization and ELISA tests detected antibodies against infectious bovine rhinotrachitis, parainfluenza-3, bovine virus diarrhea, and *Neospora caninum* with overall prevalence rates of 36.7%, 54.3%, 29.1%, and 17.1%, respectively. Furthermore, 42.1% of the retropharyngeal lymph nodes of 95 hunter-submitted deer heads in 2007 from southern Saskatchewan were positive for a herpes virus by pan herpes PCR. DNA sequencing of the PCR products revealed 98-100% identity to the Type 2 ruminant rhadinovirus of mule deer. Type 2 ruminant rhadinovirus of mule deer is a relatively host-specific, persistent, lymphotropic virus which may be useful in understanding geographic spread of disease in these populations and the effect of management strategies on disease prevalence.

P8

Three Years of Surveillance for Avian Influenza in Hunter-Harvested Waterfowl on the Texas Gulf Coast, What Have We Learned?

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Waterfowl are known reservoirs for type A influenza viruses; however, little is known regarding these viruses on waterfowl wintering grounds. The objectives of this study were to determine what subtypes are present on wintering grounds, focusing on the Texas Gulf Coast, and to identify waterfowl species that may serve as reservoirs in wintering areas. Over 6,000 cloacal swabs were collected from hunter-harvested waterfowl during three consecutive hunting seasons (November 2005–January 2006, September 2006–January 2007, and September 2007–January 2008) at state owned Wildlife Management Areas along the Texas mid-coast. All samples were screened for avian influenza virus (AIV) using real-time reverse transcriptase polymerase chain reaction (rRT-PCR), virus isolation was attempted on all rRT-PCR positive samples and 4047 rRT-PCR negative samples. Year-to-year differences in prevalence and subtypes isolated, as well as differences in prevalence by test method, were observed. AIV prevalence for years one, two, and three were 5.9, 6.5, and 11.5%, respectively, by rRT-PCR; and 0.8, 2.9, and 4.4%, respectively, by virus isolation. One H7 (H7N3) was isolated in January 2007; more interestingly, nine H7 (H7N1, H7N1/4, H7N4, H7N7) were isolated during September and November 2007 and eight H5 (all H5N2 or H5N3) during November and December 2007. Data collected as part of this ongoing project provide valuable information on the prevalence and subtypes of AIV present on the Texas Coast, a previously understudied waterfowl wintering ground. These data are part of the CSREES AICAP “Prevention and Control of Avian Influenza in the US”.

P9

A Pantropic Study of Rabies Virus in Arctic Fox

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Rabies is endemic in arctic fox, *Alopex lagopus*, in Alaska. The occurrence of rabies is cyclic in northern Alaska with outbreaks occurring every 3-4 years. These occur in the winter when foxes move about in search of food and have opportunities for close contact around major food sources, such as animal carcasses and landfills. Unlike warm climates in which the virus is degraded by heat, cold temperatures presumably preserve the virus in infected animal carcasses. Scavenging of fox and other carcasses is very common in the winter as evidenced by the remains of radio-collared animals that died and were retrieved. We hypothesize that scavenging foxes can acquire the disease by feeding on infected carcasses (i.e. soft tissues), which would result in the propagation of the virus and spread of the disease in a fox population. Until now, studies have been lacking to support this hypothesis. Fourteen arctic foxes that tested positive for rabies virus in brain tissue using direct fluorescent antibody analysis are the source of the 13 different tissues being analyzed. Both a direct rapid immunohistochemistry test and a fluorescent antibody test are being used to screen for rabies virus in these various tissues. The results will provide valuable insight into the epizootiology of rabies in arctic and subarctic regions.

P10

Influence of Mercury Toxicity on Hemoparasite Prevalence in *Tachycineta bicolor*

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The link between ecotoxicology and infectious disease has not been widely explored in the literature and this study aims to partially fill that void. Before 1950, the South River in Virginia was contaminated with mercury. Recent work at the South River has shown that tree swallow (*Tachycineta bicolor*) females along the contaminated river had impaired reproductive success compared to those on uncontaminated reference tributaries (Brasso and Cristol 2008). Knowing that mercury contamination impacts their fitness leads to questions regarding its influence on health and disease susceptibility. The specific aims of this pilot study were to assess (a) cell-mediated immunity and (b) hemoparasite prevalence in tree swallows along the contaminated South River in comparison to those on nearby uncontaminated rivers in the same watershed. We hypothesized that tree swallows along the mercury contaminated sites would have a suppressed immune response and an increased prevalence of hemoparasites. Cell-mediated immunity was examined by the phytohaemagglutinin skin test. Hemoparasite prevalence was determined by blood smear examination followed by confirmation with polymerase chain reaction. Results of this study will be presented. Brasso, RL and DA Cristol. 2008. Effects of mercury exposure on the reproductive success of tree swallows (*Tachycineta bicolor*). *Ecotoxicology* 17:133-141.

P11

Population Dynamic Consequences of Impaired Survivorship and Reproductive Success in Deer Mice following Sin Nombre Virus Infection

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While pathogenicity of Sin Nombre virus (SNV) in the deer mouse (*Peromyscus maniculatus*) is unclear, recent evidence suggests reduced survivorship and impaired female reproduction as costs of an infection. As is common with many infections, offspring born to infected deer mice inherit protective maternal antibodies against SNV. Antibody affinity increases with time since infection, while at the same time, and as a consequence of infection, female fecundity may be decreasing. Thus, offspring born to infected mothers may be limited to acquiring low affinity antibodies. Using a two-sex epidemiological model, we explore the consequences of reduced survivorship, in males and females, and the tradeoff between impaired female reproduction and maternal antibody avidity on both host population dynamics and epidemiological dynamics.

P12

Hair Cortisol Concentration: A Potential Non-Invasive Biomarker of Long-Term Stress in Free-Ranging Grizzly Bears

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Human caused environmental change is believed to negatively affect the sustainability of many wildlife populations. In Alberta, grizzly bears live in one of the most populated and heavily exploited landscapes in which the species survives. Long-term physiological stress in individual animals may be the predominant mechanism linking environmental change with impaired wildlife population health. Hair cortisol concentration has recently been validated as a biomarker of long-term stress in non-human primates. We are developing, validating and applying the determination of hair cortisol concentration as a sensitive, reliable and non-invasive measure of long-term stress in free ranging grizzly bears. Preliminary work indicates hair cortisol varies among bears from different regions of Alberta and among different age-sex classes. Hair cortisol does not vary with hair type or body region, is not influenced by short-term stress (capture) or long-term storage (>10 months) and can be reliably measured in as few as 5 guard hairs. Ongoing work involves further laboratory and field validation along with correlation of hair cortisol data with measures of environmental change, individual animal health, and long-term stress determined from blood and skin samples collected from over 150 grizzly bears inhabiting a wide gradient of landscape change in Alberta.

P13

Evaluation of the Elk Brucellosis Test-and-Slaughter Program and Continued Studies on the Epidemiology of Brucellosis in Feedground Elk

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Brucella abortus, the causative agent of bovine brucellosis, has been eliminated from cattle in the United States through a federal/state eradication program that began in 1930s. The disease remains endemic in free-ranging elk and bison in the Greater Yellowstone Area (GYA) of Wyoming, Montana, and Idaho. Annual seroprevalence in adult female elk averages 23.6% on winter feedgrounds in Wyoming within the GYA. Feedgrounds concentrate animals during the peak period of transmission of brucellosis potentially presenting a risk to cattle that winter near these feedgrounds. In an attempt to reduce seroprevalence in elk, the Wyoming Game & Fish Department implemented a five-year pilot test-and-slaughter program. The pilot program began in January 2006 and is focused on the Pinedale elk herd unit with the primary objective to achieve a statistically significant reduction in brucellosis seroprevalence. We are evaluating the success of the test-and-slaughter program in reducing brucellosis seroprevalence in elk, and also continue more general studies on the epidemiology of brucellosis in feedground elk including host and environmental factors that influence intra- and interspecies transmission. Through the first three years of test-and-slaughter a decrease in elk brucellosis seroprevalence has been observed, and epidemiological studies still underway have identified elk abortion and parturition ranges and will be discussed in the context of transmission risks to wildlife and cattle.

P14

Seroprevalence of West Nile Virus and other Arboviruses in Crested Caracaras (*Caracara cheriway*) in Florida

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The crested caracara (*Caracara cheriway*) is a threatened species with a restricted range in the United States. There are populations in Arizona and Texas, and an isolated, resident population in south-central Florida. The biology of Florida's caracaras is well studied, but little is known about exposure rates and effects of arbovirus infection among caracaras. Numerous arboviruses circulate in Florida, including West Nile and St. Louis encephalitis viruses (WNV and SLEV; family Flaviviridae, Genus *Flavivirus*), and eastern Equine encephalitis virus (EEEV; family Togaviridae, Genus *Alphavirus*). We captured individuals throughout the species' range in Florida. In 2007-08, we sampled adults (both breeding and non-territory holding; the latter of which did not attempt to breed), subadults, juveniles, and fledglings (≥ 2 -12 months post-hatch), and tested sera by plaque reduction neutralization test (PRNT). All birds sampled appeared to be in general good health, were flight-capable, and foraging normally when captured. The seroprevalence rate for WNV was higher than for the other viruses, with a rate of 12% (8/68). Only adults of ≥ 3 years of age were WNV antibody positive, with PRNT90 titers ranging from 20-80. Seroprevalence rates of SLEV and EEEV were each 6% (4/68 and 2/35, respectively). The susceptibility of caracaras to adverse effects of WNV, SLEV, or EEEV infection remains unknown. However, our results demonstrate that some individuals survive infection, and remain productive.

P15

Experimental Exposure of Swallow Bugs to West Nile Virus

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Swallow bugs (*Oeciacus vicarius*) are hematophagous ectoparasites that are highly dependent on cliff swallows (*Petrochelidon pyrrhonata*). These bugs use the mud nests of swallows for shelter and swallows serve as their primary source of blood meals. Cliff swallows may be an important reservoir host for West Nile virus (WNV) because they nest in large colonies within areas of high mosquito abundance, and consequently, thousands of swallows are potentially exposed to infectious mosquitoes. Based on field and laboratory studies, swallows have a high rate of exposure to WNV, and appear to be competent reservoir hosts; this suggests that swallow bugs are likely exposed to WNV. Swallow bugs could also serve as a potential overwintering mechanism for WNV because they remain in nests year-round, generally feeding only when cliff swallows are present. We tested the hypothesis that swallow bugs can become infected with WNV by exposing bugs to WNV using two methods: direct abdominal inoculation and allowing bugs to feed on infectious blood. We found that swallow bugs did not maintain or amplify infectious WNV over time, and that viral load decayed rapidly over time, with almost no detectable virus at 15 days post-exposure. We concluded that swallow bugs are not effective vectors of WNV, and are therefore unlikely to play a significant role in WNV disease ecology.

P16

Frequency of Rabies Antibodies in Tropical Bat Communities in Fragmented Landscapes in Puebla, Mexico

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Habitat loss and fragmentation has favored biodiversity loss, changes in species assemblages and changes in the frequency of emerging and re-emerging zoonosis, such as rabies. Rabies virus has been isolated from different species of bats; however, the natural history and the way that the virus is maintained in bat communities remained unknown. The aim of this study is to find out the effects of habitat loss and fragmentation on rabies prevalence in bat communities in different habitat types in fragmented landscapes in Puebla, Mexico. We have compared bat diversity and infection prevalence in three habitat types (forest, edges, and pastures) in large, medium, and small forest fragments. We have obtained blood samples from 20 bats belonging to 6 species and 4 genera. Blood samples were analyzed at the National Center of Veterinary Microbiology, INIFAP and the immunoenzymatic test ELI-Rab was performed. A total of 65% of captured bats were positive. Antibody prevalence at edge sites was 75% followed by grasslands (63%) and forests (60%). Further studies are needed to know the effects of the habitat loss and fragmentation on the bat community assemblages and on the infection dynamics, also to identify the role played by this species in the transmission, and maintenance of the rabies virus in tropical areas where agricultural activities are established. Our results suggest that rabies infection may be increased in fragmented areas where small forest fragments and edge sites are increased.

P17

Effects of Hunting Pressure for Chronic Wasting Disease Control on Movement Patterns of Mule Deer in Southern Saskatchewan

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Since the discovery of chronic wasting disease (CWD) in a free ranging mule deer (*Odocoileus hemionus*) in Saskatchewan in 2000, wildlife managers have attempted to stop the spread of this disease through hunter-based herd reduction in areas of known CWD occurrence. In order for this to be effective, it is important to understand deer movement patterns and how they are influenced by environmental and human factors, including the disease management programs themselves. It has been suggested that deer may congregate in areas of decreased hunter accessibility, higher terrain ruggedness, or greater escape cover to avoid hunting pressure in herd reduction zones. To answer this question, location data from 40 mule deer fitted with GPS collars were analyzed in four study areas near the South Saskatchewan River. Three of these four are areas of known CWD occurrence and are subject to herd reduction through increased hunting opportunities. Location data was divided into hunting and non-hunting seasons and intersected with maps of hunting pressure derived from landowner surveys as well as terrain ruggedness and habitat maps. Analysis was performed to determine whether hunting pressure influenced deer movements. Preliminary results show a significant decrease ($p < 0.05$) in the use of land subject to higher hunting pressure in two study areas, within and outside the herd reduction zone. This trend was not seen in all areas and further analysis is needed before conclusions can be drawn. Analysis regarding changes in the use of rugged terrain and habitat type during the hunting season will also be discussed.

ABSTRACTS: GENERAL POSTER

P18

Longitudinal Studies of Population Cycles and Hantavirus in Montana Voles (*Microtus* spp).

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As part of a continuing longitudinal study on hantavirus in small mammals of Montana, we present data on Montana voles (*Microtus pennsylvanicus* and *M. montanus*). To date, this is the largest data set available for vole populations in Montana. We present data on vole population fluctuations, serum test results for presence of Sin Nombre virus (SNV), and the relationship between population cycles observed in *Microtus* spp. and in sympatric deer mice (*Peromyscus maniculatus*), the primary host of hantavirus. We also examine the relationship between hantavirus infection and prevalence in voles and mice. Live-trapping was conducted on 18 grids, 3 on each of 6 sites throughout Montana for 12 years. Most grids were trapped seasonally, April through September. One site (3 grids) in Cascade, MT, was trapped every month for all 12 years. Using minimum number alive (MNA), vole populations in the Cascade site showed the typical pattern of increases, peaks and declines, as well as synchronicity between grids. This pattern is more difficult to discern in the other sites since they were seasonally trapped; however, there are clear periods of low or no captures, and periods of higher captures in most sites. Statistically, in 'good' to 'great' *Microtus* habitat, MNA and MNI for voles and mice are correlated. MNA correlations may be related to favorable conditions existing for both species, or may be due to voles creating extra nesting sites for mice. MNI correlations may be due to these species occupying similar nest sites. Experimental tests are required to better understand both sets of correlations. Molecular analyses are needed to confirm if the hantavirus detected in *Microtus* serum is SNV.

P19

Canine Distemper Virus discovered in Feces of North American Bobcats (*Lynx rufus*)

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Evaluation of a noninvasive surveillance method among carnivores in eastern North Carolina detected canine distemper virus in the feces of free-ranging North American bobcats (*Lynx rufus*). Fecal reverse-transcription PCR (RT-PCR) assays amplified 2 genotypes of the virus from 6 individuals of the 40 cats surveyed during 2004 and 2005 legal trapping seasons. Concurrent serologic testing revealed that only 1 of 6 (17%) bobcats had CDV-specific IgG antibodies at the time of virus shedding while the overall seroprevalence in the sampled bobcat population was 28% (11/40). Sequence analysis identified one genotype as identical to a commercial canine vaccine strain while the other sequence closely resembled CDV strains recovered in the feces of local species showing clinical signs of the disease, including gray foxes, a raccoon, and a domestic dog. Attempts to amplify the virus from additional target tissues available for some of the fecal-CDV+ bobcats were unsuccessful. Bobcats have not been involved previously in CDV outbreaks among large, exotic felids in North America. Their role in the maintenance of CDV in the environment remains unclear; however, these findings highlight the potential for bobcats to serve as a potential reservoir for this important carnivore disease.

P20

Health Assessment of Steller Sea Lions in Alaska, USA

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One hypothesis for the decline in the endangered western stock of Steller sea lions (*Eumetopias jubatus*) as compared to the threatened eastern stock is decreased pup survival rate. In conjunction with surveys for population dynamics, infectious disease prevalence and toxicologic exposure, methods for evaluating individual and population health are important evaluation tools. An objective, quantitative method of comparing individual and population health was developed as part of an epidemiological assessment of Steller sea lion health in Alaska, USA. Utilizing samples collected between 1998 and 2005 from sea lions aged one to 30 months, “normal” ranges for hematology and blood chemistry parameters (hematocrit, white blood cell counts, total protein, albumin/globulin ratio, total bilirubin, BUN, creatinine, liver enzymes (ALT, AST, GGT), alkaline phosphatase, calcium, chloride, sodium, potassium, phosphorus, CO₂ and glucose) were determined. These ranges were used to score different parameters, incorporating expected age differences and physiological associations (e.g. renal function score based on both BUN and creatinine). A total health score was calculated combining the blood parameters with physical examination findings. Overall, scores did not vary significantly ($p>0.05$) with age and sex, but scores did vary significantly by rookery, with a significant collection year/rookery interaction. No significant difference in pup and juvenile health was noted between the western and eastern stock.

P21

DNA Extraction Method for *Histoplasma Capsulatum* in Soil and Feces

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We have developed a fast one-day method for extracting DNA from the structurally robust fungal spores (i.e., microconidia and macroconidia) of the dimorphic pathogenic fungus *Histoplasma capsulatum* (Hc) found in soil associated with bats and avian roosting areas. This method was used to detect Hc conidia in experimental soil by amplifying a primer-targeted strand of DNA using PCR. Sterilized topsoil was used as an artificial medium for heat inactivated Hc conidia (isolates G186A and G217B, University of California, San Francisco). Soil-Hc suspensions were shaken with solid garnet [(SiO₄)₃] grains in a high-speed mill mixer followed by an extended incubation at 37°C with lyticase before treatment with MoBio UltraClean soil DNA kit. Internal transcribed spacer (ITS) primers, ITS4 (tctcctgattgatatgc) and ITS5 (ggaagtaaaagtcgtaacaagg), were used with a Touchdown PCR after which the PCR product was gel-electrophoresed and visualized under ultraviolet light. DNA extraction from Hc conidia is difficult. Also, PCR can often be inhibited by naturally occurring chemicals found in soil (e.g., humic and fulvic acids). Our method appears to overcome the conidial wall barrier and the complications from PCR inhibitors. We conclude that this extraction and PCR method provides a means to detect conidia in some types of soil. Further testing will be necessary to evaluate the effectiveness of the assay as a detector of Hc conidia in other types of media including, but not limited to, other soil types and plant and animal tissue.

P22

Influence of Previous LPAI Virus Infection on Susceptibility of Wood Ducks to H5N1 HPAI Virus

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In order to evaluate if a pre-exposure to a low pathogenic avian influenza (LPAI) virus provides protective immunity to wood ducks (*Aix sponsa*) challenged with a H5N1 highly pathogenic avian influenza (HPAI) virus, twenty-five 4-month old wood ducks, evenly divided into 5 groups, were inoculated via choanal slit with 10^6 EID₅₀ of the following LPAI viruses: A/mallard/Netherlands/2/05 (H5N2), A/blue-winged teal/LA/B228/86 (H1N1), A/mute swan/MI/451072-2/06 (H5N1), and A/mallard/MN/355779/00 (H5N2). The fifth group was not exposed to a LPAI virus. After 21 days, the birds were challenged with a HPAI virus A/whooper swan/Mongolia/244/05 (H5N1). All four groups infected with a LPAI virus had reduced morbidity and mortality compared to the naïve group, suggesting pre-exposure to a LPAI virus provided some level of protective immunity. The level of protection appeared to vary between LPAI isolates: no LPAI exposure – 100% morbidity, 100% mortality; Netherlands/05 (H5N2) – 80% morbidity, 80% mortality; LA/86 (H1N1) – 60% morbidity, 60% mortality; MI/06 (H5N1) – 20% morbidity, 20% mortality; MN/00 (H5N2) – 0% morbidity, 0% mortality. The cause and mechanism for this protection and variation among isolates need further investigation and will be discussed herein. These results suggest that LPAI viruses naturally circulating in waterfowl populations may influence the susceptibility of wild avian populations to H5N1 HPAI virus.

P23

Detection of Volatiles in the Uropygial Gland Secretions of Gray Catbirds (*Dumetella carolinensis*)

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The uropygial gland of birds produces secretions that are important in maintaining the health and structural integrity of feathers. The gland is located at the base of the tail where birds may easily use their bill to extract the secretions for distribution over the feathers. These secretions are believed to play a number of functions including waterproofing and conditioning the feathers, as well as protection from insect pests, and even predators. Some of the components of the gland secretions, including waxes and lipids, have been described over the past 50 years in several species of birds. However, in 2004 it was discovered that preen gland secretions contain volatile compounds. Such compounds are particularly interesting because of their potential importance in olfactory communication both within and across species. We have used solid-phase microextraction headspace sampling followed by gas chromatography-mass spectrometry to detect and identify volatiles in uropygial gland secretions of Gray Catbirds (*Dumetella carolinensis*). The major analyte class detected with our sampling method is a series of carboxylic acids. The role of these compounds could be important in communication and defense, especially during breeding when birds are especially vulnerable to arthropods such as biting midges and mosquitoes.

P24

Avian Pathology Atlas on the Web

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For scientists and educators around the world to rapidly and accurately identify disease in avian populations, they must have ready access to reference material of both normal and abnormal avian images. We have developed a web-based atlas of these pathologies that will allow rapid search and diagnosis of a large variety of abnormal conditions in wild birds as well as normal anatomy and morphology. An Oracle® database was created to manage the data pertaining to individual cases. The types of data include case histories, radiographs, and both normal and abnormal macroscopic and microscopic images. The database and web site can be searched by species, location, date, morphological diagnosis, causative agent, potential for transmission to humans, and other single or mixed criteria. Links to pertinent literature citations are provided. EPA and our partners are making the Wild Bird Pathology Atlas available to the global scientific community on the EPA.gov public web site. This new tool will aid in the early diagnosis which is the first essential step in timely and effective protective measures for both animals and humans who may be effected by the spread of zoonotic disease.

P25

Thirty Years of Mortality Assessment in Whooping Crane Reintroductions: Patterns and Implications

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We reviewed postmortem data to identify primary causes of mortality in reintroduced whooping cranes (*Grus americana*) and assess their potential for mitigation in future reintroduction efforts. In total, 240 cases from three populations were reviewed for causes of death, including the Rocky Mountain migratory population (n = 24, release dates 1975-1989), the Florida resident population (n = 186, 1993-2005), and the Wisconsin migratory population (n = 30, 2001-ongoing). Traumatic injury was the leading cause of mortality among the reintroduced whooping cranes, most commonly from predation (n = 120 or 50%, range 8-58% per project) or collision with fixed structures such as electrical power lines or fences (n = 22 or 9%, range 3-46%). Disease of infectious etiology (including confirmed cases of bacterial, viral, fungal, and parasitic infection) was the second leading cause of mortality (n = 19 or 8%, range 3-17%). The data were limited by the large number of undetermined causes of death due to scavenging and decomposition of carcasses (n = 64 or 27%, 8-40%). Molting and poor roosting behavior or habitat quality may have increased the risk of predation in these populations. Preventive measures for power line collisions (marking devices) are impractical except at significant roost or migration stopover sites. Health evaluations of release candidates should continue in order to minimize losses from endemic or emerging diseases and prevent the introduction of novel pathogens into native ecosystems.

P26

Use of Genetic Analysis to Evaluate the Alabama River as a Barrier to the Movement of Raccoons and the Raccoon Rabies Virus Variant

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In Alabama, the raccoon rabies variant spread north westward at a rate slower than its spread up the Atlantic seaboard. Alabama is divided from the northeast corner to the southwest corner by the Coosa River and Alabama River system. This system may function as a barrier to spread of rabies virus by restricting raccoon movement. Using gene flow as a record of movement, our objective was to determine if gene flow occurs between raccoon population across the Alabama River. We employed 11 raccoon specific microsatellite markers to obtain individual genotypes. DNA samples from 70 individuals were collected from 5 sampling localities in 3 counties; 2 north of the river in Autauga, 2 south of the river in Lowndes, and 1 northwest in Hale. We tested for significant departures from Hardy-Weinberg equilibrium (HWE) and significant evidence of linkage disequilibria among loci. For population analyses, we estimated population differentiation by estimating F_{ST} and using a coalescent approach in STRUCTURE assuming both admixture and correlated allelic frequencies within populations. There were no significant departures from HWE and no evidence of linkage disequilibrium. From the pairwise F_{ST} estimates, populations on opposite sides of the river were not significantly differentiated, which was supported by the results of STRUCTURE where individuals from either side of the river belong to the same genetic clusters. This suggests that gene flow occurs across the river. Therefore, raccoons do disperse across the river allowing gene flow to occur and possible subsequent rabies transmission.

P27

Population Size, Aggression, and Infection with Sin Nombre Virus (SNV) in Adult Female Deer Mice (*Peromyscus maniculatus*) in Montana

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We examined the relationship between behavioral interactions and potential infection with Sin Nombre virus (SNV) in deer mice (*Peromyscus maniculatus*), the primary reservoir species. SNV is shed from infected individuals in their urine, feces, and saliva. SNV is believed to be transmitted in host populations primarily by intraspecific aggressive encounters. Previous studies indicate that the prevalence of antibody to SNV among male deer mice is at least twice that among females and scarring (used as an index of aggressive encounters) appears associated with antibody prevalence. Since aggression typically increases as population size increases due to increased encounters and conflicts over limited resources, we hypothesize that aggressive encounters involving females will increase during times of higher population numbers. Thus, we should see a positive correlation between the frequency of scarring in females and population size. Consequently, the number of females with antibodies to SNV should also increase during these times. We examined these relationships using long term data collected from four field sites in Montana.

P28

Alopecia in Moose infested with Deer Keds (*Lipoptena cervi*)

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Deer keds (*Lipoptena cervi*) are blood-sucking flies in the family Hippoboscidae. There have previously not been any reports of negative impacts of deer ked on wildlife. In 2006, however, hunters in the south-eastern part of Norway and eastern part of Sweden found several moose (*Alces alces*) cadavers with severe alopecia, and observed numerous moose with extensive hair loss. During the spring of 2007, several affected animals were submitted for examination. The most significant finding at necropsy was alopecia and dermatitis. Large numbers of deer keds were present in the fur. Histological examination revealed moderate, eosinophilic dermatitis and severe, diffuse degeneration of hair follicles and adnexal structures. Our preliminary conclusions are that deer ked infestation probably is the main factor causing alopecia in moose in the affected areas. The dense population of deer ked may be attributed to dense moose populations and favorable climate conditions for deer ked survival.

P29

Epizootic Hemorrhagic Disease Virus in Captive Bison, Elk, White-Tailed Deer, Cattle, and Goats from Colorado

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A captive wildlife research facility in Fort Collins, Colorado experienced mortality in white-tailed deer (*Odocoileus virginianus*) due to epizootic hemorrhagic disease virus (EHDV) infection in late summer and early fall of 2007. Nucleic acid from EHDV was amplified by RT-PCR from the spleen and lung tissues of 2 white-tailed deer with >99% similarity to previously sequenced isolates of EHDV-2. In addition, EHDV was isolated on CPAE cells from the spleens of these 2 deer. Pre- and post-outbreak sera from other species maintained in the same facility, including bison (*Bison bison*), elk (*Cervus elaphus*), domestic cattle (*Bos taurus*), and domestic goats (*Capra hircus*), as well as post-outbreak sera from the surviving deer were assayed by virus neutralization. Pre-outbreak sera from 3 elk and 1 cow, and post-outbreak sera from 2 elk, 7 goats, 1 deer, 3 bison, and 2 cattle neutralized EHDV-2 in all four-virus neutralization replicates. Two elk lost neutralizing antibodies over the time course. No clinical signs were noted in the bison, cattle, or goats during the outbreak. One elk became clinically ill during this time but etiology could not be established. These findings indicate exposure of all species to EHDV-2 before and after the detected outbreak. The possible roles of these species in the epidemiology of EHDV remain unclear.

P30

Role of Gray Catbirds (*Dumetella carolinensis*) in the Overwintering of Eastern Equine Encephalitis Virus

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Eastern equine encephalitis virus (EEEV) is a pathogen of health concern to human and wildlife populations. While many aspects of the ecology of EEEV are well understood, the mechanism by which the virus overwinters and how its annual cycle is reinitiated each spring in temperate regions is not known. One hypothesis is the virus overwinters in the avian reservoir host as a chronic infection and then reactivates the following spring due to some stressful event. We examined the effects of hormones and artificially induced migratory disposition on cryptic EEEV infections in captive gray catbirds. Hatching year catbirds were inoculated with EEEV in October 2007 and then held until January 2008, when birds were either induced to migrate and/or implanted with testosterone, or neither. Both a blood and fecal sample was collected every two days during the experimental period and was tested for presence of EEEV via RT-PCR. During the initial infection peak viremia, one day post-infection, ranged between 5.4 – 8.0 log plaque forming units/ml. During the experimental period we found evidence of recrudescence in fecal samples.

P31

Described Diversity of Influenza Subtypes is Dependent on Amplified Length and Specificity of PCR Primer Sets for Sediment Samples from Alaskan Migratory Bird Ponds

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It is most often assumed that strains of avian influenza are transmitted between birds in the wild through contaminated water or environmental sources, yet little detail is understood about the role of environmental reservoirs in the ecology of virus transmission. While most studies continue to focus on the importance of virus isolated from infected birds, we have previously demonstrated evidence for a diverse and prevalent set of viruses in sediment samples from the perimeter of migratory bird ponds. Using a series of more specific primers amplifying a smaller fragment to identify influenza subtypes, we investigated the possibility that we were not identifying all viral subtypes present in the samples extracted from these ponds. Using RT-PCR and sequencing methodology, we show that the diversity of influenza subtypes for which viral RNA is present in these sediments is even greater than previously thought (at least two additional subtypes). We are examining differences between spring and fall samples and are currently attempting to isolate live virus from these samples. Our results indicate that sampling of environmental sediments can be very informative for disease ecology and is dependent on the reagents used in the study design.

P32

Blood Lead, Cadmium, and Mercury Concentrations in Endangered Marine Species Inhabiting Andaman Sea and the Gulf of Thailand

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Heavy metals can suppress immunity in marine mammals, increase mortality of viral infected animals, and affect function of reproductive system. Evaluation of blood heavy metals is a useful non-lethal method to monitor internal heavy metal accumulation. However, no data in endangered marine species is available in Thailand. In this study, CdB and HgB levels were examined by AAS, while PbB levels were determined using both AAS and LeadCare[®] test kit (ESA Inc., USA) in dolphin, dugong, and sea turtles from July 2006 to October 2007. In the Gulf of Thailand, PbB levels in dolphin were 1.5 µg/dl (LeadCare[®]) and 0.78 µg/dl (AAS), whereas in Andaman Sea they were 0.72 µg/dl in dolphin and 1.18 µg/dl in dugong by AAS. PbB (LeadCare[®]), PbB (AAS), CdB, and HgB average levels were 1.26±1.14, 1.33±0.79, 0.51±0.12, 1.70±0.90 µg/dl in captive and 1.74±0.75, 2.82±1.08, 1.54±0.19, 2.05±0.95 µg/dl in wild sea turtles of the Gulf of Thailand, respectively, and 0.33±0.28, 1.13±0.65, 0.52±0.30, 2.21±1.39 µg/dl and 1.33±1.17, 3.92±1.94, 3.63±2.80, 1.30±1.22 µg/dl in captive and wild sea turtles of Andaman Sea, respectively. Although PbB levels in sea turtles detected by AAS and LeadCare[®] were not exactly the same, both showed similar trend. However, further study with more samples is needed to validate the test kit as a useful rapid tool for these endangered marine species. In conclusion, blood heavy metal levels were likely to be higher in wild sea turtles surveyed except for HgB concentration.

P33

Johne's Disease in a Free-Ranging White-Tailed Deer from Virginia and Subsequent Surveillance for *Mycobacterium avium* subspecies *paratuberculosis*

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Johne's Disease (paratuberculosis) was diagnosed in a 2yr old male free-ranging white-tailed deer (*Odocoileus virginianus*) from Fauquier County, Virginia, based on histopathology and culture for *Mycobacterium avium paratuberculosis*. Clinical and pathologic findings included emaciation; chronic diarrhea; severe, chronic, diffuse granulomatous colitis with intrahistiocytic acid-fast bacilli; moderate, chronic granulomatous lymphadenitis with intrahistiocytic acid-fast bacilli as well as moderate chronic, multifocal, lymphoplasmacytic hepatitis. Findings were consistent with previous reports of Johne's Disease in cervids. Targeted surveillance of ten emaciated deer with diarrhea and 72 asymptomatic deer for *M. avium paratuberculosis* using multiple tissue culture, as well as serologic ELISA optimized for cervid antibody detection, found no additional cases. This appears to be an isolated case of Johne's Disease in a free-ranging white-tailed deer, and infection with the causative agent for Johne's Disease appears to be an infrequent occurrence in deer from this region. The origin of infection was most likely domestic animals as the strain isolated was one typically associated with cattle. Stressors such as high deer population density and low selenium levels may have contributed to the development of clinical disease in this case and warrant further investigation.

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Low-Pathogenic Avian Influenza Detection in Mallards (*Anas platyrhynchos*)

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Avian influenza (AI) is represented by a variety of type A influenza viral subtypes endemic to wild waterfowl and shorebirds. Recently, the U.S. Department of Agriculture developed a strategic plan for detecting avian influenza in the United States. The plan includes sampling live birds, dead birds, and environmental fecal samples. Based on these surveillance efforts, we identified and isolated three common AI subtypes from waterfowl: H3N6, H3N8, and H4N6. The objective of this study was to compare levels, duration, and detection sensitivity of these three LPAI subtypes using cloacal, oral-pharyngeal, fecal, and water sampling in experimentally inoculated domestic waterfowl. We inoculated mallards (*Anas platyrhynchos*) with the three subtypes. All three subtypes resulted in viral shedding 1 day post-inoculation (dpi), continuing through 12 dpi. Peak shedding occurred 1 dpi for oral-pharyngeal, cloacal, and fecal shedding for subtype H3N6 and on 2 or 3 dpi for oral-pharyngeal, cloacal, or fecal shedding for subtypes H3N8 and H4N6. For each subtype, viral concentrations were highest in fecal swabs (peak = $10^{5.4}$ EID₅₀/swab), followed by cloacal swabs (peak = $10^{4.1}$ EID₅₀/swab), and oral-pharyngeal swabs (peak = $10^{3.75}$ EID₅₀/swab). All three subtypes were detected in water used by infected mallards. Our findings are consistent with previous studies of avian influenza detection in wild mallards but we were able to quantify shedding levels and duration of infection with a larger sample than has been previously reported.

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Molecular Ecology of Rabies in the Arctic

***Sara M. Turner and Jonathan A. Runstadler**

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Rabies has likely existed in the Arctic for hundreds of years, but the arctic fox is distinct from its well-documented cousin, the red fox, as a vector of rabies because of its apparent resistance to disease pathology and decreased territorial behavior in the winter season. In the Arctic, rabies is difficult to control, in large part due to the vast amount of pristine wilderness, the seasonal presence of pack ice on the Arctic Ocean on which foxes travel, and a poor understanding of the ecological overlap of arctic and red foxes, both vectors of the disease. The Alaska State Public Health Virology Laboratory routinely monitors rabies within Alaska. We present preliminary data on viruses isolated from both red and arctic foxes from Alaska. In addition, in order to understand the impact of human development on the dynamics of rabies virus in the arctic this study was undertaken to validate molecular tools needed to study the fox vectors of rabies virus in the arctic. We have begun molecular analysis on arctic foxes collected from Alaska using microsatellite markers, mtDNA, and sequences from the major histocompatibility complex (MHC).

P36

Wildlife and Foodborne Zoonoses at the Agriculture/Wildlife Interface

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Human health and safety can be affected by contact or conflict with wildlife in several ways. An increasing but limited proportion of vegetable-borne infection outbreaks are traced to wildlife. For example, leafy vegetables can carry viable zoonotic pathogens because they are usually consumed raw or with minimal preparation. Little attention in vegetable-borne zoonoses is given to whether a wildlife population can actually serve as a reservoir/vector of disease for humans. The emergence/re-emergence of many zoonotic diseases can be linked to anthropogenic factors such as global travel, trade, agricultural expansion, deforestation/habitat fragmentation, and urbanization, increasing the interface between humans (agriculture), domestic animals, and wildlife, creating more opportunities for spillover events to occur. Vegetable-borne zoonoses could represent serious risks to human health in traditional subsistence agriculture communities in poor and developing countries, where land-users rely almost exclusively on livestock, agronomy and/or wildlife; in semi-natural habitats rich in wildlife, often in close proximity to wildlife refuges. The few available reports mainly come from more developed countries where policy schemes and traceability are better established and funded. In these countries, situations where habitats have been simplified, opportunistic/pest/managed wild or free roaming species may become a problem or interact with livestock. This potential zoonosis risk requires specific wildlife disease research and surveillance to understand the links between ecological/epidemiological functions and agricultural practices, for which wildlife, sanitary and agriculture researchers and authorities need common objectives to improve coordination.

P37

Degenerative Cardiomyopathy in Vancouver Island Marmots (*Marmota vancouverensis*)

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Native to select sub-alpine regions of Vancouver Island, the Vancouver Island marmot (*Marmota vancouverensis*) is Canada's most endangered mammal. The population dropped to fewer than 100 animals in year 2000 with ~28 individuals in the wild. Four Canadian institutions (Calgary Zoo, Toronto Zoo, Tony Barrett Mount Washington Marmot Recovery Centre, and Mountainview Conservation Centre) are involved in a captive breeding and reintroduction program. Currently there are 169 marmots in captivity and ~89 in the wild. In captivity, degenerative myocardial changes, including significant myocardial fibrosis, have been identified histologically in ~48% of adult deaths; however, similar changes are rarely identified during histopathological evaluation of wild marmots. No infectious etiology has been identified. In other mammalian species these cardiac changes are most frequently associated with dietary deficiencies in taurine, carnitine, vitamin E, or selenium, and occasionally with deficiencies in copper and zinc. A study is underway to establish baselines of possible serum, cardiac, and hepatic biomarkers for heart disease in captive and free ranging Vancouver Island marmots and to compare levels between normal and diseased animals. If serum or tissue biomarkers for early heart disease are elucidated, or if there is a significant difference in levels between captive and free-ranging marmots, then captive breeding programs will be able to better monitor marmot health, and possibly control the progression of cardiomyopathy through dietary modifications.

P38

“Project Tripwire” – Monitoring Wildlife Health through Wildlife Rehabilitation Centers

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In 2004, the WHO/FAO/OIE issued a joint report on the prevention and control of emerging zoonotic diseases in which they recommended North America needed to develop the capacity for disease surveillance in wildlife. At the present time, established surveillance systems focus on mortality events or target specific diseases however, wildlife morbidity often goes unrecognized and general surveillance of these live moribund animals is not systematically reported. Across North America, there are thousands of organizations and individuals involved in the care of injured and orphaned wildlife. Commonly referred to as wildlife rehabilitation, this field of endeavour seeks to care for these animals and return them to the wild. Where wildlife rehabilitation centers exist, they are essentially the “first responders” to situations involving wildlife health. Project Tripwire will network professionally-staffed wildlife care clinics across North America. By linking the records of these wildlife care centers to a central epidemiological database via the Internet, and creating automated reporting systems, the appearance of any new or unusual wildlife disease events can be more quickly detected and reported. The Tripwire interface will also serve to disseminate information to wildlife rehabilitators with regard to potential disease concerns in their area; personal health and safety protocols, and reportable disease information. This system will also link data from their center to others to determine spatial and temporal associations in disease occurrence. The use of GIS components and a custom designed medical records software system will be employed to better discover and follow these potential disease trends.

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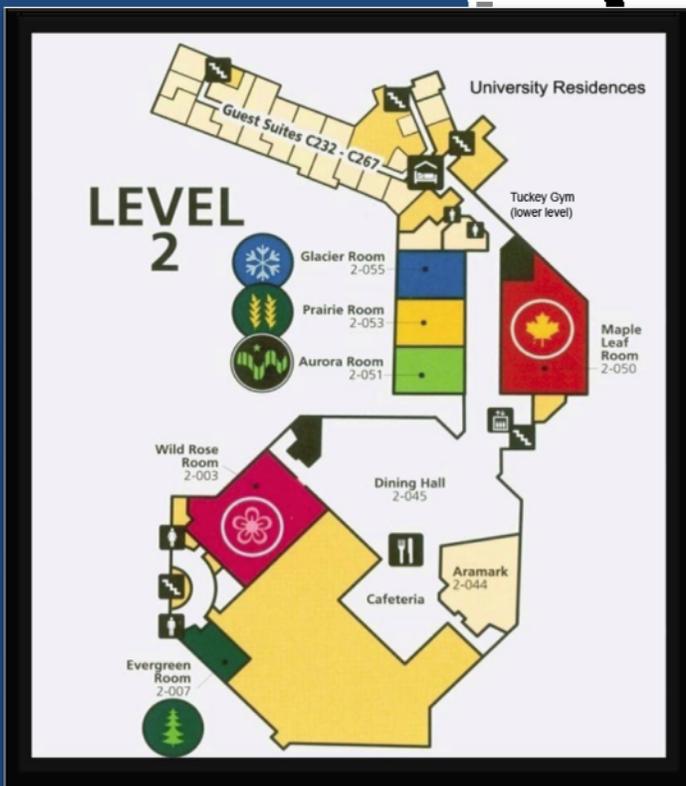
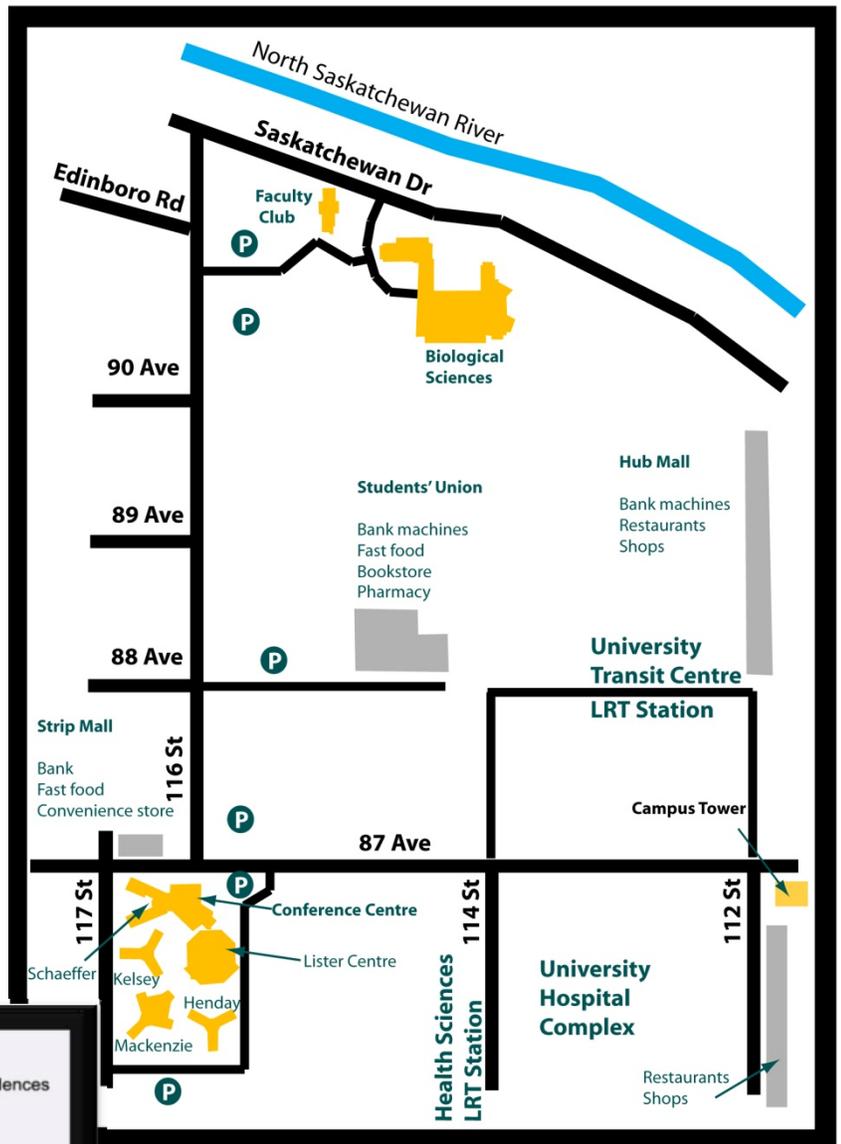
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Making Tracks to LISTER CENTRE

Directions to the Lister Centre



Inside the Lister Centre (2nd Floor)

Program at a Glance

Date	Time	Event	Location
Sunday August 3	8:30 - 12:00	Editorial Board Meeting	Aurora
	1:00 - 5:00	WDA Council Meeting	Aurora
	1:00 - 8:00	Conference Registration	Glacier
	4:30 - 5:45	Student Career Workshop	Wild Rose
	6:00 - 7:00	Student Mentor Kickoff	Wild Rose
	7:00 - 10:00	ALBERTA WELCOME	Wild Rose
Monday August 4	7:30 - 5:00	Registration and Exhibits	Glacier
	8:00 - 8:30	Conference Welcome	Maple Leaf
	8:30 - 12:00	Northern Symposium	Maple Leaf
	1:00 - 4:00	Socio-political Challenges of Disease Management	Maple Leaf
	4:00 - 4:30	Cutting Edge Speaker: Dr. Susan Haseltine	Maple Leaf
	5:00 - 6:45	Student Mixer	Tuckey Gym
	7:00 - 10:00	WDA Evening Poster Session	Tuckey Gym
Tuesday August 5	7:15 - 8:15	Prayer Breakfast	Evergreen
	8:15 - 8:45	Graduate Student Recognition Award: Valarie O'Brien	Maple Leaf
	8:45 - 4:45	Terry Admundson Award: Student Oral Competition	Maple Leaf
	5:00 - 6:00	AAWV Business Meeting	Maple Leaf
	6:00 - 7:00	CAZWV Business Meeting	Maple Leaf
	7:00 - 10:00	WDA Auction	Wild Rose
Wednesday August 6	8:00 - 9:30	Concurrent Sessions: Rabies and Hendra Viruses / Herptiles	Maple Leaf / Aurora
	9:30 - 9:50	Elk Island National Park (EINP) Introduction	Maple Leaf
	10:15 - 5:00	Field Trips	EINP
	5:00 - 10:00	WDA Picnic	EINP
Thursday August 7	8:15 - 9:45	Concurrent Sessions: Avian Diseases I / Wildlife-Domestic Interface	Maple Leaf / Aurora
	10:15 - 11:30	Concurrent Sessions: Tools and Techniques / Genes, Vaccines and Immobilization	Maple Leaf / Aurora
	11:30 - 12:30	WDA Business Meeting	Maple Leaf
	1:45 - 3:45	Concurrent Sessions: Avian Diseases II / Surveys and New Reports	Maple Leaf / Aurora
	4:15 - 5:00	Carlton Herman Lecture: Dr. Mark Hafner	Maple Leaf
	6:00 - 12:00	WDA Banquet and Awards	U of A Faculty Club
Friday August 8	8:30 - 10:00	Contributed: Ungulate Diseases	Wild Rose
	10:30 - 12:00	Contributed: Chronic Wasting Disease	Wild Rose
Friday August 8	1:00 - 5:00	CWD: Presentations	Wild Rose
Chronic Wasting Disease Workshop	7:30 - 10:00	Evening Hospitality	Wild Rose
Saturday August 9	8:30 - 5:00	CWD Workshop: Working Sessions	Wild Rose