63rd Annual
Wildlife Disease Association Conference

One Health:
Transitioning from Theory to Practice

July 27 – August 1, 2014
Albuquerque, New Mexico

Program & Abstracts
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Exhibitors

Visit our exhibitor Sunday – Tuesday in the Puma Room

Continuing education provided by the American Association of Wildlife Veterinarians through the American College of Zoological Medicine
The 63rd Annual WDA Conference is being held in conjunction with the annual meeting of the American Association of Wildlife Veterinarians

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Vice-President .......................................................... Marcela Uhart
Secretary .............................................................. Peregrine Wolff
Treasurer ............................................................... Laurie Baeten
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Christian Gortazar (European Section)

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President .............................................................. Peregrine Wolff
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Margaret Wild
Jenny Powers

Scientific Program Committee
Michael Miller       Ryan Monello       Darby Murphy
Marcela Uhart       Sonia Hernandez   Joni Scheftel
Alan Franklin       Kerry Mower       Kirk Smith
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Dave Jessup         Paul Ettestad     Tegwin Taylor
Kevin Castle        Marilyn Haskell   David Wong

Organizing Committee Co-Chairs
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Dave Jessup

Organizing Committee
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Megin Nichols        Pauline Nol       
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Justin Brown, Chair  Tiggy Grillo       Jose Luiz Catao Dias
Jolianne Rijks      Brant Schumaker    Jennifer Siembieda
Steven van Beurden  Carlos das Neves   

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Margaret Wild        Jose Luiz Catao-Dias Lisa Shender
Jenny Powers         Sonia Hernandez    Dave Hunter
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Katie Brown          Alan Franklin      Scott Bender
Megin Nichols        Lisa Wolfe         Michael Miller
Justin Brown         Kevin Castle       Thierry Work
Jennifer Siembieda  Colin Gillin       Darby Murphy
Carlos das Neves     Peregrine Wolff   

Conference Supporters
Cecily Broomfield provided exceptional administrative support in developing the scientific program; Mike McGovern served as auctioneer and Sportsman’s Warehouse and El Pinto Restaurant generously donated items for the auction; New Mexico Game and Fish staff and student volunteers provided conference support; and Jack Young provided entertaining cultural history. Our sincere thanks to all!

Continuing Education Sponsored by the American College of Zoological Medicine
Conference Logo by Gayle Bone
WDA 2014 WORKSHOPS, FIELD TRIPS, & SOCIAL EVENTS

Pre-conference Workshop and Field Trip
- Student Field Trip to Valles Caldera National Preserve (leaves Saturday, July 26, at 6:45 AM)
- Student Workshop – Field Investigation for Wildlife Mortality (Sunday, 8:30-4:30)

Welcome Reception - Sunday, July 27
A welcome reception Sunday evening at the House of Hummingbird and Oxbow Pool will include a nice assortment of light food including vegetarian choices, sliders, and pizza bites (and a couple drinks of your choice). A cash bar for further drinking will be available. This will be an opportunity to renew old acquaintances and make new ones.

Student-Mentor Mixer – Monday, July 28
Our students and their personal selection of mentors will be going to a mixer to be held at the Kaktus Brewing Company in Bernalillo. Complimentary food and drinks will be provided by the Student Activities Committee and WDA Council. Invitations to this event were sent out in the last 2 weeks and asked for an RSVP. Buses will leave Tamaya at 6 and 6:30 and stop at the Bernalillo train station both going and coming for those staying places other than Tamaya.

One Health Mixer – Monday, July 28
A unique opportunity to promote the One Health theme this year will be a joint mixer with the New Mexico Pediatric Society on the outdoor veranda at Tamaya. A limited number of tickets ($24 each) are available on a first come-first served basis. Heavy appetizers and two drinks will be served. Sign-up at the registration desk for this inter-disciplinary reception for physicians, veterinarians, biologists, ecologists, and other health professionals to meet and discuss potential synergies across disciplines.

WDA Business Lunch – Tuesday, July 29
During the noon break we will be reviewing WDA’s progress over the last year toward a number of goals. A complimentary assortment of salads and green chile corn chowder will be available for attendees and will be provided just outside the Tamaya ballrooms so you can help yourself, eat, and watch the presentations.

Picnic and Auction – Tuesday, July 29
An outdoor Mexican food picnic will take place Tuesday evening at the Cottonwood Event Center on the grounds of Tamaya. Enjoy the short 15 minute stroll from the conference rooms, or catch the shuttle at the “carriage turnaround”. The fiesta will provide an opportunity for informal interaction among registrants in an outdoor setting. Dress in layers for the cool and ever-changing weather.

A silent and live auction will be held indoors at the Cottonwood Event Center following the complimentary dinner and drinks. The WDA auction is always a major source of entertainment at the meeting! It is an opportunity to find that unique item and to support WDA. All proceeds from the auction support student activities.
**Field Trips and Workshops - Wednesday, July 30, afternoon**

All off-site field trips depart from the parking lot west of the hotel. Vehicles will be on-site at 12:30p and depart at 1:00p. Lunch and water will be distributed at the vehicles.

- Basic Forensic Necropsy Workshop
- Sevilleta National Wildlife Refuge
- Bosque Del Apache National Wildlife Refuge
- Petroglyph National Monument & Coronado State Park

A naturalist-led stroll into the Tamaya bosque starting at 1:00p is free and open to all (including children) for those not leaving Tamaya for a field trip.

**Banquet - Thursday, July 31**

The conference banquet will feature crispy pork belly and spanakopita appetizers, salads, grilled corn, fingerling potatoes, grilled tri-tip and assorted vegetarian main dishes and includes two drinks per person and a cash bar. Optional artisanal New Mexico tequila tasting can be signed up for at the registration desk for $14/per person before Wednesday. The banquet will occur at the BioPark (Rio Grande Zoo and Albuquerque Aquarium and Botanical Gardens). Buses leave Tamaya at 6 and 6:30 and will stop at the Bernalillo train station going and coming for those not staying at Tamaya.

Highlights of the banquet, besides the great local cuisine, flora, and fauna, will include a sneak peak of next year’s conference, local color stories, and presentation of major WDA awards. WDA awards include the Ed Addison Distinguished Service Award, the Emeritus Award, the Tom Thorne and Beth Williams Memorial Award, student awards, and the infamous Duck Award to the unfortunate recipient recognized to have made the biggest blunder at the conference!

**LOCATION INFORMATION**

Tamaya means a quiet, peaceful place. Take time to explore the walking trails and other amenities at this hidden oasis. And know that conference attendees have contributed more than $370 toward the rehabilitation of native plants in the Rio Grande cottonwood forest adjacent Tamaya. Tamaya has agreed to apply this amount to our catering costs.

The conference registration desk will be open daily in the Tamaya ballroom foyer or Bear B room. Ask the locals at the conference registration desk or the hotel concierge for information on the surrounding area and how to get around. If you’re giving an oral presentation, be sure to download your Powerpoint file with a student volunteer when you register. Don’t forget to purchase a conference t-shirt, or purchase tickets for the One Health mixer and tequila tasting while you’re there!

Check the schedule for session and meeting locations. Most sessions will be held in the Tamaya Ballrooms E and/or F, G, H. All posters will be on display in the Puma rooms. If you need assistance from WDA staff, a business office will be located in room Bear B, and the speaker ready room is right next door in Bear A.
**SUNDAY, JULY 27**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>8:00a-12:00p</td>
<td>Editorial Board Meeting</td>
<td>Eagle A,B</td>
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<tr>
<td>8:30a-4:30p</td>
<td><strong>Student Workshop</strong></td>
<td>Off-site</td>
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<tr>
<td>10:00a-7:00p</td>
<td><strong>Registration</strong></td>
<td>Tamaya Ballroom Foyer</td>
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<tr>
<td>12:00p</td>
<td>Lunch (Editorial Board and Council)</td>
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<tr>
<td>1:00p-5:00p</td>
<td><strong>WDA Council Meeting</strong></td>
<td>Eagle A,B</td>
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<tr>
<td>6:00p-9:30p</td>
<td>Welcome Reception</td>
<td>House of Hummingbird</td>
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**MONDAY, JULY 28**

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>7:00a-2:00p</td>
<td><strong>Registration</strong></td>
<td>Tamaya Ballroom Foyer</td>
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<tr>
<td>8:00a</td>
<td><strong>Conference Welcome</strong></td>
<td>Tamaya Ballrooms</td>
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<tr>
<td></td>
<td>Thierry Work, President WDA</td>
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<td></td>
<td>Alexandra Sandoval, Director NMDFG</td>
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<td></td>
<td>Zoey Benally, One Health practitioner &amp; poet</td>
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<tr>
<td>8:30a-10:15a</td>
<td><strong>ONE HEALTH</strong></td>
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<td><strong>Moderator: Margaret Wild</strong></td>
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<tr>
<td>8:30a</td>
<td><strong>Steven Osofsky</strong></td>
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<td></td>
<td>[1] Human health impacts of ecological degradation: rethinking public health in the anthropocene</td>
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<tr>
<td>9:00a</td>
<td><strong>Craig Stephen</strong></td>
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<td>[2] One Health in a time of unprecedented environmental change</td>
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<tr>
<td>9:30a</td>
<td><strong>Jonathan Epstein</strong></td>
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<td>[3] A One Health approach to enhancing zoonotic disease surveillance and control</td>
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<td>9:50a</td>
<td><strong>Danielle Buttke</strong></td>
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<td>[4] The role of One Health in wildlife conservation: a challenge and opportunity</td>
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<tr>
<td>10:15a</td>
<td><strong>BREAK</strong></td>
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<tr>
<td>10:45a-12:00p</td>
<td><strong>ONE HEALTH IN PRACTICE</strong></td>
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<td></td>
<td><strong>Moderator: Marcela Uhart</strong></td>
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<tr>
<td>10:45a</td>
<td><strong>Emily Jenkins</strong></td>
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<td></td>
<td>[5] Assessing and communicating risks of toxoplasmosis in wildlife in the Canadian North</td>
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<tr>
<td>11:05a</td>
<td><strong>David Wong</strong></td>
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<td></td>
<td>[6] How can we engage more physicians in One Health? The National Park Service experience</td>
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<tr>
<td>11:25a</td>
<td><strong>Tonie Rocke</strong></td>
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<tr>
<td>11:45a</td>
<td><strong>Paul Ettestad</strong></td>
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<td>[8] Plague in the southwestern United States: epidemiology, surveillance and prevention</td>
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<tr>
<td>12:00p</td>
<td><strong>LUNCH BREAK</strong></td>
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<tr>
<td>Time</td>
<td>Session</td>
<td>Location</td>
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<tr>
<td>1:00p</td>
<td><strong>ONE HEALTH POSTER SESSION – MODERATOR: DARBY MURPHY</strong></td>
<td>Puma Rooms</td>
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<tr>
<td>1:55p</td>
<td><strong>FLAVOR OF NEW MEXICO AND ANNOUNCEMENTS</strong></td>
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<tr>
<td>2:00p-3:00p</td>
<td><strong>ONE HEALTH IN PRACTICE, CONTINUED</strong> – MODERATOR: MEGIN NICHOLS</td>
<td></td>
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</tbody>
</table>
| 2:00p | *Robert Parmenter*  
[9] Hantavirus in the American Southwest: environmental drivers of spatial and temporal dynamics |                     |
| 2:15p | *Gary Simpson*  
[10] One Health discipline: the case for integrating science, medicine, and public health |                     |
| 2:30p | *Leslie McFarlane*  
| 2:45p | *Julia Lankton*  
[12] Diagnosis of West Nile virus in winter mortality of eared grebes (*Podiceps nigricollis*) and bald eagles (*Haliaeetus leucocephalus*) at the Great Salt Lake, Utah |                     |
| 3:00p | **BREAK**                                                                 |                     |
| 3:30p-5:00p | **ONE HEALTH IN ACTION** – MODERATOR: KATIE BROWN |                     |
| 3:30p | *Larisa Vredevoe*  
| 3:45p | *Claire Jardine*  
[14] The potential utility of the red fox (*Vulpes vulpes*) in assessing the risk of *Blastomyces dermatitidis* infection in Southern Ontario |                     |
| 4:00p | *Brian Amman*  
[15] Marburg virus outbreaks: understanding virus spillover from the natural reservoir |                     |
| 4:15p | *Kirsten Gilardi*  
[16] Pathogens detected in human-habituated eastern gorillas (*Gorilla beringei*) in east-central Africa |                     |
| 4:30p | *Marcela Uhart*  
[17] Innovative community-based approach to address lead pollution from hunting in Argentina wetlands |                     |
| 4:45p | *Jean-Michel Heraud*  
[18] Detection of new genetic variants of betacoronaviruses in endemic frugivorous bats of Madagascar |                     |
| 5:00p | **WILDLIFE VETERINARY SECTION MEETING**                                 | Tamaya Ballrooms    |
| 6:00p | **BUSES LEAVE FOR STUDENT/MENTOR MIXER AT 6:00P AND 6:30P**               | off-site            |
| 6:00p | **ONE HEALTH MIXER**                                                    | Tamaya Ballrooms    |
### TUESDAY, JULY 29

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>7:30a-2:00p</td>
<td>Registration</td>
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<tr>
<td>8:00a</td>
<td>Announcements and Introduction</td>
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<td>8:15-10:00</td>
<td><strong>Terry Amundson Award Student Presentations</strong> MODERATOR: JUSTIN BROWN</td>
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<tr>
<td>8:15a</td>
<td>Cristina Hansen <em>Graduate Student Research Recognition Award</em></td>
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<td>[19] Microbial infection as a source of embryo mortality in greater white-fronted geese (<em>Anser albifrons</em>) on the Arctic coastal plain of Alaska</td>
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<tr>
<td>8:45a</td>
<td>Tierra Smiley-Evans</td>
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<td>[20] Field applications of non-invasive saliva collection techniques for pathogen surveillance in non-human primates</td>
</tr>
<tr>
<td>9:00a</td>
<td>Mireya Smith</td>
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<td>[21] Prevalence of <em>Rickettsia africae</em>, <em>Ehrlichia ruminantium</em>, and <em>Theileria</em> spp. in <em>Amblyomma hebraeum</em> from free-ranging African Buffalo, South Africa</td>
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<tr>
<td>9:15a</td>
<td>Lenora Dombro</td>
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<td>[22] Impacts of insecticide plague treatment on populations of deer mice on prairie dog colonies</td>
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<tr>
<td>9:30a</td>
<td>Asha Perera</td>
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<tr>
<td>9:45a</td>
<td>Sarah Leyman</td>
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<td>[24] Amphibian microbiomes as indicators of individual and environmental health</td>
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<tr>
<td>10:00a</td>
<td><strong>Student Poster Session – Moderator: Justin Brown</strong></td>
</tr>
<tr>
<td>10:45a-12:00p</td>
<td><strong>Student Presentations, Continued</strong> MODERATOR: JEN SIEMBIEIDA</td>
</tr>
<tr>
<td>10:45a</td>
<td>Jane Harms</td>
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<td></td>
<td>[25] Molecular epidemiology of avian cholera in northern Canada</td>
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<td>11:00a</td>
<td>Mauricio Seguel</td>
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<td>[26] The effect of hookworm (<em>Uncinaria</em> sp.) infection on the health status of free-ranging South American fur seal (<em>Arctocephalus australis</em>) pups</td>
</tr>
<tr>
<td>11:15a</td>
<td>Stacey Elmore</td>
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<td>[27] <em>Toxoplasma gondii</em> in a terrestrial arctic food web: who brings what to the table and accounting for uncertainty in diagnostics</td>
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<tr>
<td>11:30a</td>
<td>Mohamed Moustafa</td>
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<td>[28] Molecular epidemiological study on <em>Anaplasma phagocytophilum</em> in sika deer (<em>Cervus nippon</em>) in Hokkaido, Japan</td>
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<tr>
<td>11:45a</td>
<td>Laurie Harris</td>
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<td>[29] Investigating adenovirus diversity and the potential for interspecies transmission among endangered mountain gorillas (<em>Gorilla beringei beringei</em>), golden monkeys (<em>Cercopithecus mitiskandti</em>), and people in Rwanda</td>
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<tr>
<td>12:00p</td>
<td><strong>Lunch Break – WDA Business Lunch</strong></td>
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<tr>
<td>Time</td>
<td>Presenter</td>
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<tr>
<td>1:30p</td>
<td>Taya Forde</td>
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<tr>
<td>1:45p</td>
<td>Tristan Burgess</td>
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<td>2:00p</td>
<td>Zoe Grange</td>
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<tr>
<td>2:15p</td>
<td>Danielle Sijbranda</td>
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<tr>
<td>2:30p</td>
<td>Chelsea Himsworth</td>
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<tr>
<td>3:45p</td>
<td>Kathryn Purple</td>
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<td>4:00p</td>
<td>Pratap Kafle</td>
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<tr>
<td>4:15p</td>
<td>Ryan Baker-Branstetter</td>
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<td>4:30p</td>
<td>Andrew Ramey</td>
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<tr>
<td>4:45p</td>
<td>Vanessa Gabriele-Rivet</td>
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<tr>
<td>5:00p</td>
<td>American Association of Wildlife Veterinarians meeting</td>
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<tr>
<td>6:00p</td>
<td>Picnic Fiesta and Auction</td>
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### WEDNESDAY, JULY 30

<table>
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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8:00a</td>
<td>Registration</td>
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<tr>
<td>8:00a</td>
<td>Flavor of New Mexico and Announcements</td>
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<tr>
<td>8:15a</td>
<td>AAWV and WDA/WVS: Field Techniques to Improve Animal Welfare</td>
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<td>Moderators: Sonia Hernandez and Anne Justice-Allen</td>
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<td>8:30a</td>
<td>Dan Mulcahy</td>
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<td></td>
<td>Al Franzmann Memorial Lecture</td>
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<td></td>
<td>[40] Field techniques improving animal welfare</td>
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<td>9:00a</td>
<td>Lisa Wolfe</td>
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<td>[41] Using long acting neuroleptics and other drugs to reduce stress</td>
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<td>associated with large ungulate capture and translocation</td>
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<tr>
<td>9:15a</td>
<td>Kimberly Beckmen</td>
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<td>[42] Evaluation of stress in caribou (Rangifer terandus granti)</td>
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<td>attributed to different capture methods</td>
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<tr>
<td>9:30a</td>
<td>Ole Alcumbrac</td>
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<td>[43] How not to kill pronghorn; a chronology of handling a desert</td>
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<td>subspecies leading to zero mortality</td>
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<tr>
<td>9:45a</td>
<td>Constance Silbernagel</td>
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<td>[44] Effectiveness of the anesthetic Aqui-S 20E in marine finfish and</td>
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<td>elasmobranches</td>
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<tr>
<td>10:00a</td>
<td>Break</td>
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<tr>
<td>10:30a</td>
<td>Ecology of Wildlife Disease</td>
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<td></td>
<td>Moderator: Alan Franklin</td>
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<td>10:30a</td>
<td>Anne Ballmann</td>
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<td></td>
<td>[45] Summer surveillance for Pseudogymnoascus destructans at</td>
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<td>contaminated hibernacula: implications for timing of transmission</td>
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<tr>
<td>10:45a</td>
<td>Shelli Dubay</td>
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<td>[46] Environmental variables that explain exposure of white-tailed</td>
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<td>deer to parainfluenza 3 virus in Wisconsin</td>
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<td>11:00a</td>
<td>Daniel Grear</td>
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<td>[47] Disease transmission at the wildlife-livestock interface:</td>
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<td>multi-species modeling of bovine tuberculosis in Michigan</td>
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<tr>
<td>11:15a</td>
<td>Jill Wilson Bull</td>
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<td>[48] Inability to transmit Borrelia burgdoferi by co-feeding ticks in</td>
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<td>two skink species, Eumeces fasciatus and Plestiodon laticeps</td>
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<tr>
<td>11:30a</td>
<td>Matthew Gray</td>
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<td>[49] From superspreading to amplification hosts: amphibian community</td>
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<td>composition affects ranaviral disease outcomes</td>
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<tr>
<td>11:45a</td>
<td>Announcements</td>
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<tr>
<td>1:00p-5:30p</td>
<td>Field Trips</td>
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### 8:00A - 10:00A CONCURRENT SESSION – DISEASES OF UNGULATES
**Moderator: Lisa Wolfe**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>8:15a</td>
<td>Jacques Godfroid</td>
<td>[50] Spatio-temporal trends in prevalence of anti-Brucella antibodies in barren-ground caribou (<em>Rangifer tarandus granti</em>) in Alaska—an example of enzootic equilibrium</td>
</tr>
<tr>
<td>8:30a</td>
<td>Nancy Boedeker</td>
<td>[51] Screening for exposure to infectious agents in wild takins (<em>Budorcas taxicolor whitei</em>) and domestic yaks (<em>Bos grunniens</em>) from shared summer habitat in Bhutan: management implications</td>
</tr>
<tr>
<td>8:45a</td>
<td>Rick Gerhold</td>
<td>[52] Retrospective study characterizing <em>Parelaphostrongylus</em> species in wild and domestic ungulates from Tennessee</td>
</tr>
<tr>
<td>9:00a</td>
<td>Lee Jones</td>
<td>[53] Hemorrhagic disease in a Nebraska bison herd</td>
</tr>
<tr>
<td>9:15a</td>
<td>Kerry Mower</td>
<td>[54] A mortality event among elk in northern New Mexico during late summer 2013</td>
</tr>
<tr>
<td>9:30a</td>
<td>Hank Edwards</td>
<td>[55] Respiratory disease surveillance in bighorn sheep: linking pathogens and herd health</td>
</tr>
<tr>
<td>9:45a</td>
<td>Mark Drew</td>
<td>[56] Assessment of health status for moose (<em>Alces alces</em>) in Idaho, USA</td>
</tr>
</tbody>
</table>

### 8:15A-10:00A CONCURRENT SESSION – DISEASES OF MARINE SPECIES
**Moderator: Kevin Castle**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>8:15a</td>
<td>Thierry Work</td>
<td>[57] Bacteria are important to coral reef health (but not in the way everybody thought)</td>
</tr>
<tr>
<td>8:30a</td>
<td>Joseph Gaydos</td>
<td>[58] Causes of mortality in a population of marine foraging North American river otters</td>
</tr>
<tr>
<td>8:45a</td>
<td>Tracey Goldstein</td>
<td>[59] Emergence of phocine distemper virus in Arctic and Sub-Arctic pinnipeds in the northeast Pacific off Alaska</td>
</tr>
<tr>
<td>9:00a</td>
<td>Katherine Prager</td>
<td>[60] Leptospirosis in California sea lions (<em>Zalophus californianus</em>): do data from stranded animals accurately reflect trends in the wild population?</td>
</tr>
</tbody>
</table>
### THURSDAY, JULY 31

#### 8:15A-9:45A CONCURRENT SESSION – DISEASES OF MARINE SPECIES, CONTINUED

**MODERATOR: KEVIN CASTLE**

- **9:15a** Jacques Godfroid
  - [61] *Brucella pinnipedialis* hooded seal strain in cell models
- **9:30a** Jacques Godfroid
  - [62] Is *Brucella pinnipedialis* unable to sustain a long term infection in hooded seals (*Cystophora cristata*)?

#### 10:00A-10:45A GENERAL POSTER SESSION – MODERATOR: JENNY POWERS

**PUMA ROOMS**

- **10:45A-12:00P** CONCURRENT SESSION – DIAGNOSTIC TOOLS
  **MODERATOR: COLIN GILLIN**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>10:45a</td>
<td>Anne Justice-Allen</td>
<td>[63] Response of Sonoran pronghorn to vaccination with a multivalent orbiviral vaccine</td>
</tr>
<tr>
<td>11:00a</td>
<td>Jessica Jennings-Gaines</td>
<td>[64] Field techniques for bacterial sample collection and diagnostics: bringing the laboratory to the field</td>
</tr>
<tr>
<td>11:15a</td>
<td>Christine Ellis</td>
<td>[65] Use of volatile organic compound profiles from feces to discriminate between BCG-vaccinated and <em>Mycobacterium bovis</em>-infected white-tailed deer (<em>Odocoileus virginianus</em>)</td>
</tr>
<tr>
<td>11:30a</td>
<td>Pauline Nol</td>
<td>[66] Detection of volatile organic compounds in <em>Brucella abortus</em>-seropositive bison</td>
</tr>
<tr>
<td>11:45a</td>
<td>Jonathan Sleeman</td>
<td>[67] Wildlife health information sharing partnership-event reporting system (WHISPers)</td>
</tr>
</tbody>
</table>

#### 10:45A-12:00P CONCURRENT SESSION – AVIAN DISEASES

**MODERATOR: PEREGRINE WOLFF**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>10:45a</td>
<td>Jennifer G. Chipault</td>
<td>[68] Descriptive epidemiology of avian botulism type E in waterbirds of Lake Michigan, 2010-2013</td>
</tr>
<tr>
<td>11:00a</td>
<td>Susan Shriner</td>
<td>[69] Long-term antibody persistence for low pathogenic avian influenza virus in mallards</td>
</tr>
<tr>
<td>11:15a</td>
<td>David Stallknecht</td>
<td>[70] Role of immunity in regulating avian influenza virus population dynamics</td>
</tr>
<tr>
<td>11:30a</td>
<td>Justin Brown</td>
<td>[71] Understanding the re-emergence of H14 influenza A viruses in ducks</td>
</tr>
<tr>
<td>11:45a</td>
<td>Nabin Rayamajhi</td>
<td>[72] New network for Asian conservation medicine</td>
</tr>
<tr>
<td>Time</td>
<td>Session</td>
<td>Speaker(s)</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife</td>
<td>Susan Kutz</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife</td>
<td>Kristin Mansfield</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife</td>
<td>Karen Fox</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife</td>
<td>Tokuma Yanai</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife</td>
<td>Steven Sweeney</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Wildlife Conservation on Private Lands</td>
<td>Carter Kruse</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Wildlife Conservation on Private Lands</td>
<td>Hanne Small</td>
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<tr>
<td>1:30p</td>
<td>Concurrent Session – Wildlife Conservation on Private Lands</td>
<td>Christiane Wiese</td>
</tr>
<tr>
<td>1:30p</td>
<td>Concurrent Session – Emerging Diseases of Wildlife, Continued</td>
<td>Pauline Nol</td>
</tr>
</tbody>
</table>
### 3:45p-5:00p Concurrent Session – Emerging Diseases of Wildlife, Continued

**Moderator: Pauline NOL**

(Tamaya Ballroom F,G,H)

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>4:00p</td>
<td>Alisa Newton</td>
<td>The pacific coast sea star mortality event: current status of the ongoing investigation</td>
</tr>
<tr>
<td>4:15p</td>
<td>Deborah Fauquier</td>
<td>Dolphin morbillivirus outbreak and the 2013-2014 Mid-Atlantic bottlenose dolphin (<em>Tursiops truncatus</em>) unusual mortality event</td>
</tr>
<tr>
<td>4:30p</td>
<td>Melissa Miller</td>
<td>Cyanotoxin (mirocystin) transfer from land to sea otters</td>
</tr>
<tr>
<td>4:45p</td>
<td>Diane Brown</td>
<td>Morris Animal Foundation’s wildlife research funding opportunities</td>
</tr>
</tbody>
</table>

### 3:45p-5:00p Concurrent Session – Wildlife Diseases of the American Southwest

**Moderator: Scott Bender**

(Tamaya E)

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>3:45p</td>
<td>Paula Kahn-Rivadeneira</td>
<td>The role of wildlife in the transfer of enteric zoonotic pathogens from livestock to leafy green produce fields in the desert southwest</td>
</tr>
<tr>
<td>4:00p</td>
<td>Ivan Castro-Arellano</td>
<td>Climate change, wildlife, and the distribution of <em>Ixodes scapularis</em>, the lyme disease vector tick, in the U.S.-Mexico transboundary region</td>
</tr>
<tr>
<td>4:15p</td>
<td>Amy Gilbert</td>
<td>Natural and experimental infection of big brown bats with rabies virus</td>
</tr>
<tr>
<td>4:30p</td>
<td>Charles van Riper III</td>
<td>Changing climate can greatly affect spring migration routes of passerine birds, and thus have consequences to the potential spread of zoonotic diseases</td>
</tr>
<tr>
<td>4:45p</td>
<td>Carrington Knox</td>
<td>The prevalence of pigeon paramyxovirus 1 and <em>Trichomonas ganninae</em> in band-tailed pigeons, mourning doves, and white-winged doves in Arizona</td>
</tr>
</tbody>
</table>

5:00p  WDA BUSINESS MEETING – ALL ARE WELCOME  Tamaya Ballrooms F,G,H

6:00p  BUSES DEPART FOR BANQUET (6:00p AND 6:30p)  BIOPARK (OFF-SITE)
### FRIDAY, AUGUST 1

#### 8:00a Registration  
WDA Office, Bear B

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<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>8:00a</td>
<td>Registration</td>
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<tr>
<td>8:00a</td>
<td><strong>8:00a-9:45a ANTHROPOGENIC IMPACTS ON WILDLIFE HEALTH</strong> Moderator: Michael Miller</td>
<td>Brian Dykstra</td>
<td>Battle for bats: Surviving white-nose syndrome (a Ravenswood Media film)</td>
</tr>
<tr>
<td>8:30a</td>
<td>Holly Ernest</td>
<td>[92] Mountain lion genetic health: fractured connectivity and low genetic diversity threatens viability of California populations</td>
<td></td>
</tr>
<tr>
<td>8:45a</td>
<td>Jessica Sanchez</td>
<td>[93] Natural and anthropogenic causes of puma mortality in southern California</td>
<td></td>
</tr>
<tr>
<td>9:00a</td>
<td>Sonia Hernandez</td>
<td>[94] Does urbanization impact movement patterns and pathogen prevalence of white ibis (<em>Eucodimus albus</em>)?</td>
<td></td>
</tr>
<tr>
<td>9:15a</td>
<td>Nicole Gottdenker</td>
<td>[95] Species diversity and infection patterns of hemotropic mycoplasmas in raccoons (<em>Procyon lotor</em>) in protected and developed barrier island ecosystems</td>
<td></td>
</tr>
<tr>
<td>9:30a</td>
<td>Marcy Souza</td>
<td>[96] Clean coal? Health effects on raccoons (<em>Procyon lotor</em>) following a coal fly ash spill in east Tennessee</td>
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<tr>
<td>9:45a</td>
<td>Break</td>
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#### 10:15a-11:30a ANTHROPOGENIC IMPACTS ON WILDLIFE HEALTH, CONTINUED  
Moderator: Thierry Work

<table>
<thead>
<tr>
<th>Time</th>
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<th>Speaker</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>10:15a</td>
<td>Gerardo Suzan</td>
<td>[97] Human activities and landscape features influence orthopoxvirus seroprevalence in grey squirrels (<em>Sciurus aureogaster</em>) in Mexico City, Mexico</td>
<td></td>
</tr>
<tr>
<td>10:30a</td>
<td>Elizabeth VanWormer</td>
<td>[98] Tracing <em>Toxoplasma gondii</em> from terrestrial carnivores to marine hosts in coastal California</td>
<td></td>
</tr>
<tr>
<td>10:45a</td>
<td>Sandra Black</td>
<td>[99] Assessment of the health status of narwhal (<em>Monodon monoceros</em>) harvested for consumption by Inuit from Pond Inlet, Nunavut, Canada</td>
<td></td>
</tr>
<tr>
<td>11:00a</td>
<td>Susan Kutz</td>
<td>[100] Complexities in arctic host-parasite interactions in a regime of rapid climate change: the caribou-<em>Ostertagia gruehneri</em> system</td>
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</tr>
<tr>
<td>11:15a</td>
<td>Closing Remarks</td>
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<td>11:30a</td>
<td>Adjourn</td>
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### ABSTRACTS FROM SPEAKER PRESENTATIONS

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<thead>
<tr>
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<th>Abstracts</th>
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<tr>
<td>Moderators: Margaret Wild, Marcela Uhart, Katie Brown, David Wong</td>
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<tr>
<td><strong>Terry Amundson Award Student Presentations</strong></td>
<td>19-39</td>
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<tr>
<td>Moderators: Justin Brown, Jen Siembieda, Carlos das Neves, José L. Catão-Dias</td>
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<td><strong>American Association of Wildlife Veterinarians and WDA Wildlife Veterinary</strong></td>
<td>40-44</td>
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<tr>
<td>Section Session: Field Techniques to Improve Animal Welfare</td>
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<tr>
<td>Moderators: Sonia Hernandez and Anne Justice-Allen</td>
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<tr>
<td><strong>Ecology of Wildlife Disease</strong></td>
<td>45-49</td>
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<tr>
<td>Moderator: Alan Franklin</td>
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<tr>
<td><strong>Diseases of Ungulates</strong></td>
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<td>Moderator: Lisa Wolfe</td>
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<tr>
<td><strong>Diseases of Marine Species</strong></td>
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<td>Moderator: Kevin Castle</td>
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<tr>
<td><strong>Diagnostic Tools</strong></td>
<td>63-67</td>
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<td>Moderator: Colin Gillin</td>
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<tr>
<td><strong>Avian Diseases</strong></td>
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<tr>
<td>Moderator: Peregrine Wolff</td>
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<tr>
<td><strong>Emerging Diseases of Wildlife</strong></td>
<td>73-77 &amp;</td>
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<tr>
<td>Moderators: Lisa Shender and Pauline Nol</td>
<td>83-86</td>
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<tr>
<td><strong>Wildlife Conservation on Private Lands</strong></td>
<td>78-82</td>
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<tr>
<td>Moderator: Dave Hunter</td>
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<tr>
<td><strong>Wildlife Diseases of the American Southwest</strong></td>
<td>87-91</td>
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<tr>
<td>Moderator: Scott Bender</td>
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<tr>
<td><strong>Anthropogenic Impacts on Wildlife Health</strong></td>
<td>92-100</td>
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<tr>
<td>Moderators: Michael Miller, Thierry Work</td>
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The Wildlife Disease Association *Conference Program and Abstracts* booklet is available to all meeting attendees. Abstracts were lightly edited to comply with formatting and space limits, but otherwise were printed as submitted. The Wildlife Disease Association does not regard this *Conference Program and Abstracts* booklet as a publication and abstracts included herein should not be cited in scientific literature.
NOTES
HUMAN HEALTH IMPACTS OF ECOLOGICAL DEGRADATION: RETHINKING PUBLIC HEALTH IN THE ANTHROPOCENE

Steven A. Osofsky

1 Wildlife Health & Health Policy, Wildlife Conservation Society, Bronx, New York, USA

\textit{Homo sapiens} is transforming the structure and function of Earth’s natural systems, including its land cover, rivers, oceans, biogeochemical cycles, and climate system without signs of abatement. There is growing evidence that changes in the state of natural systems will have increasingly numerous impacts on human health, some quite direct and some mediated through complex causal pathways. We urgently need a new branch of environmental health that is focused on characterizing the public health impacts of anthropogenic alterations in the structure and function of Earth’s natural systems, as planetary boundaries are encroached upon and breached: these health impacts simply cannot remain in the realm of vague and poorly quantified externalities, given their increasingly global significance. This envisioned new field is inherently accompanied by an important environmental justice / inter-generational equity issue, in that most of the burdens associated with increased degradation of natural systems will be experienced by the poor and by future generations. In short, we urgently need to develop a body of evidence that addresses the public health implications of changes in the state of natural systems. Employing a \textit{science to policy to action agenda}, earnest and perhaps unprecedented levels of interdisciplinary collaboration must be operationalized to influence the substantial global effort to improve the health of poor populations while simultaneously catalyzing the management of natural systems for goods and services, and for conservation.
ONE HEALTH IN A TIME OF UNPRECEDENTED ENVIRONMENTAL CHANGE

Craig Stephen

Canadian Wildlife Health Cooperative, Saskatoon, Saskatchewan, Canada

Perhaps one of the greatest challenges in the field of wildlife health is figuring how to help animals cope with the multiple interacting threats of everyday life. Wildlife are simultaneously challenged by habitat loss, invasive species, climate change, emerging infections, pollution and more. These problems are becoming more pervasive as the human population continues its exponential growth. The One Health movement has historically been almost exclusively concerned with studying single infectious diseases in isolation; favouring the study of those diseases that put people at risk. One Health, in practice, seems to be “One Disease.” Rather than apply interdisciplinary approaches to a single problem (like an emerging disease) it is time for One Health to adopt a cumulative or “interprobleminary” approach to the biophysical and social spaces that provide wildlife with their resources for health. A cumulative effects perspective aims to track multiple pressures and activities affecting populations in a shared landscape and interpret those changes in the context of population vulnerability and resilience to detect common mechanisms that enhance the ability to adapt and recover from negative change. By examining the interactions and implications of multiple problems and determinants of health that occur simultaneously, it may be possible to identify critical conditions or circumstances that influence and sustain resilience and health. The shift of One Health to creating health (coping capacity) rather than responding to disease is necessary because the emergence of new threats to wildlife seems inescapable. Wildlife health is the result of complex, dynamic socio-ecological interactions. Complex theory tells us that prediction is rarely possible and surprises are natural occurrence. Rather than continuing to react to surprises, it is time for One Health to help wildlife cope with the inevitable next threat that will be added to their life’s challenges and ensure wildlife can be sustained despite the escalating challenges we throw at them.
A ONE HEALTH APPROACH TO ENHANCING ZOONOTIC DISEASE SURVEILLANCE AND CONTROL

Jonathan H. Epstein

1 EcoHealth Alliance, New York, New York, USA

Prevention and control of zoonotic diseases requires an understanding of the pathogen in its natural reservoir as well as in people. Despite an increasing awareness of the interconnectedness of human and animal health by experts, political barriers still remain between human and animal sectors when it comes to surveillance, outbreak response and control at national and global scales. In general, ministries of health are responsible for identifying and responding to outbreaks in people, but rarely engage with livestock departments except in emergency situations. Ministries of agriculture conduct surveillance in livestock, yet almost never conduct disease surveillance in free-ranging wildlife populations; and wildlife authorities rarely have the mandate or resources to conduct disease surveillance in wildlife populations, and have been largely excluded from national disease surveillance and response strategies. Given that the majority of emerging zoonoses originate in wildlife and move into humans either directly or via domestic animal hosts, a unified approach to zoonotic disease surveillance and response that engages all three sectors (human, livestock and wildlife health) can enhance a government’s ability to detect pathogens at earlier stages of transmission and may result in faster response to outbreaks in people. Since the emergence of Nipah virus in 1998, the Government of Malaysia has moved towards enhanced communication and cooperation among these three sectors. Over the past five years, it has further developed national systems for identifying novel and known viral agents in wildlife populations. Here we will present work done under several science, capacity building and policy initiatives in Malaysia, including those under the USAID Pandemic Influenza and other Emerging Threats: PREDICT and the Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL) programs, that have fostered a One Health approach to disease surveillance and control as well as understanding the impact of land use change on disease emergence.
THE ROLE OF ONE HEALTH IN WILDLIFE CONSERVATION: A CHALLENGE AND OPPORTUNITY

Danielle E. Buttke¹², Margaret A. Wild¹, and Daniel Decker³

¹ National Park Service, Wildlife Health Branch, Biological Resource Management Division, Fort Collins, Colorado, USA
² National Park Service, Office of Public Health, Fort Collins, Colorado, USA
³ Human Dimensions Research Unit, Department of Natural Resources, Cornell University, Ithaca, New York, USA

Emerging infectious diseases (EID) are increasingly at the forefront of media headlines and even casual conversation. Numerous EIDs have arisen from or been identified in wildlife, with health implications for both humans and wildlife. In the practice of wildlife conservation, most attention has focused on the threat EIDs pose to biodiversity, particularly the impacts of EIDs on wildlife populations. In the popular media and public eye, however, wildlife is often only portrayed as the cause of EIDs and resultant human health impacts. There is little coverage or conversation on the roles that human-induced habitat destruction or stress on wildlife populations play in EID spread, the negative impacts of disease on wildlife, nor the potential beneficial aspects of wildlife and biodiversity. We urge the wildlife and public health community to focus on a little-studied and seldom discussed concern: how real and perceived risks of wildlife-associated diseases for human and domestic animal health might erode public support for wildlife conservation. We believe that wildlife-associated EIDs and public perceptions of these risks are among the most important threats to wildlife conservation. In light of this concern, we explore the challenges and opportunities for One Health to address this situation by emphasizing the inextricable nature of environmental, human, and animal health and disease.
ASSESSING AND COMMUNICATING RISKS OF TOXOPLASMOSIS IN WILDLIFE IN THE CANADIAN NORTH

Emily Jenkins¹, Nicholas Bachand¹, Craig Stephen², Andy Thompson³, Manon Simard⁴, Brent Dixon⁵, and Asma Iqbal⁵

¹ Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada
² Centre for Coastal Health, Nanaimo, British Columbia, Canada
³ School of Veterinary and Health Sciences, Murdoch University, Murdoch, Western Australia, Australia
⁴ Nunavik Research Centre, Makivik Corporation, Kuujjuaq, Quebec, Canada
⁵ Health Canada, Ottawa, Ontario, Canada

Toxoplasma gondii, a protozoan parasite, is a ubiquitous zoonotic pathogen with a worldwide distribution and a broad range of warm-blooded hosts. Some Inuit communities have a high prevalence of exposure to T. gondii relative to the rest of North America; however, prevalence and risk factors vary greatly among communities. Risk factors for infection with T. gondii in people include the harvesting, preparation, and consumption of marine and terrestrial wildlife. We report on recent reviews and ongoing research on the sources and maintenance of T. gondii in the Canadian North. More information on risk perceptions within communities and a risk analysis framework (including recognition that wildlife species, organ predilection sites, and methods of food preparation vary across the Arctic) are needed in order to determine culturally appropriate and locally specific methods to reduce the risk of exposure to T. gondii in wildlife. This also needs to include consideration of the importance of wildlife as a source of food security, as well as their cultural and economic benefits. Finally, we discuss challenges surrounding communication of the risks associated with T. gondii in Arctic wildlife important for human consumption. Researchers need to plan for knowledge mobilization and to engage with regional public health and within regional Inuit Land Claim Agreements to develop and deliver appropriate messages that address the public health significance of zoonotic diseases linked to wildlife. Translating wildlife disease science into social choice is a key part of One Health and requires consideration of the legal and cultural realities in order to empower people to make wise choices about wildlife consumption.
HOW CAN WE ENGAGE MORE PHYSICIANS IN ONE HEALTH? THE NATIONAL PARK SERVICE EXPERIENCE

David Wong¹

¹ National Park Service, Office of Public Health, Albuquerque, New Mexico, USA

Since the One Health Initiative was established in 2007, support for this interdisciplinary approach has been broad but inconsistent. Physician-champions, in particular, are lacking, thus limiting the potential for One Health to fully engage and transform the human health sector. Using case studies, I will highlight successes and lessons learned from efforts to educate, involve, and inspire my physician colleagues about One Health. Strategies that have worked include: 1) Identifying projects where all partners can make meaningful contributions (Case study: Snakebite surveillance among veterinary and human healthcare providers); 2) Introducing One Health projects to physicians using a physician-liaison (Case study: Surveillance for white-nose syndrome in bats); and 3) Creating opportunities for inter-professional exchange à la cultural exchange programs (e.g. Fulbright) (Case study: One Health sabbatical at the Colorado State University College of Veterinary Medicine and Biomedical Sciences). Gaining acceptance and buy-in among physicians for One Health will be an incremental process that will require creative, ongoing, and effective strategies.
THE ECOLOGY AND MANAGEMENT OF SYLVATIC PLAGUE: CHANGING PARADIGMS

Tonie E. Rocke

USGS National Wildlife Health Center, Madison, Wisconsin, USA

Introduced to North America about 100 years ago, sylvatic plague (*Yersinia pestis*), has contributed to the decline of several species, causing ecological disruptions in mammalian communities throughout the western U.S. Plague outbreaks in rodents were traditionally thought to occur in separate enzootic and epizootic cycles involving different rodent species: more resistant or maintenance hosts (e.g. deer mice - *Peromyscus maniculatus*) and highly susceptible amplifying hosts that suffer high mortality rates (e.g. prairie dogs - *Cynomus* spp.). More recent evidence supports an alternative view that enzootic and epizootic plague cycles can occur in the same rodent species, and that amplification to epizootic levels is triggered by certain environmental conditions and/or increasing densities of rodent hosts and flea vectors. Host resistance in amplifying species, such as prairie dogs, appears to be increasing, most likely evolving as a genetic trait. Our perspective on the role of fleas in driving epizootics in North American rodents and the mechanism by which they transmit plague has also changed. Laboratory studies have shown that prairie dogs fleas (*Oropsylla* spp.) are highly efficient at transmitting the plague bacterium very early in their infection and less so later after blocking, unlike the Oriental rat flea (*Xenopsylla cheopis*), the best known plague vector and the model for most early studies. Methods for managing plague in wild rodents historically relied on flea control through application of pesticides to their burrows and sometimes rodent control. With advances in vaccines for plague, including a bait-delivered vaccine for wild rodents, a more integrated plague management strategy is currently being tested for protecting threatened and endangered species like the Utah prairie dog (*C. parvidens*) and the black-footed ferret (*Mustela nigripes*). This approach would likewise be useful in managing sylvatic plague in parks and other areas where the risk of transmission to humans is highest.
Plague is a flea-borne zoonotic disease (caused by the bacterium *Yersinia pestis*) that affects humans, domestic pets, and various wildlife species. It has caused three historical pandemics, including the Black Death which killed nearly a third of Europe’s population in the 14th century. The third pandemic, the Modern Plague, began in China in the 1860s, appeared in Hong Kong by 1894, and over the next 20 years spread to port cities around the world, carried by rats and their fleas on steamships. From San Francisco in the early 1900s the infection spread from urban rats to sylvatic hosts and by the 1940s had reached its current extent along the 100th meridian of North America. Since the 1970s, the American Southwest has been a focus of plague infection, with over half of the human plague cases in the United States occurring in New Mexico. This talk will highlight several aspects of the ecology and epidemiology of plague in the Southwest and focus on the public health surveillance system used in New Mexico which integrates wildlife, pet, and human surveillance. Specific human cases will be used to emphasize various aspects of this integration, including prevention education. With plague affecting humans, pets, and wildlife and various species of flea vectors, each with their unique ecology, coordination among wildlife, agriculture, public health, medical communities and the general public is essential and provides a unique example of the One Health concept in practice in the southwestern U.S.
HANTAVIRUS IN THE AMERICAN SOUTHWEST: ENVIRONMENTAL DRIVERS OF SPATIAL AND TEMPORAL DYNAMICS

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Since the 1993 discovery in the American Southwest of the zoonotic disease, Hantavirus Pulmonary Syndrome (HPS), the disease agent (\textit{Sin Nombre Hantavirus}) and its rodent host (the deer mouse, \textit{Peromyscus maniculatus}), considerable research efforts have revealed a number of associated environmental variables that appear to drive the spatio-temporal occurrence of disease outbreaks in both rodents and humans. In this presentation, we review the history and current knowledge of hantavirus infections in rodents and humans, along with evidence for our conceptual landscape model linking weather, habitat mosaics and productivity, rodent population densities, demographics and dispersal movements, infection patterns among rodent age-classes, and eventual viral transmission to humans. Field data from New Mexico and the Four Corners Region of the Southwest are used to validate critical portions of our model, and we develop ecological parameter values for forecasting HPS outbreak locations, timing and rates of spread. This model has proven consistent with observed patterns of human HPS outbreaks at both local and landscape scales, and incorporates the tenets of One-Health principles that synthesize environmental conditions, wildlife disease and human health.
ONE HEALTH DISCIPLINE: THE CASE FOR INTEGRATING SCIENCE, MEDICINE, AND PUBLIC HEALTH

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Emerging infectious diseases in the 21st Century have become increasingly complex and unpredictable. Since 85% of emerging infectious diseases in recent decades are zoonotic in origin, the importance of understanding the dynamic interactions of the ecosystems of wildlife, domestic/agricultural animals, and humans has been demonstrated convincingly. Extensive experience with these infectious disease threats has taught that addressing them responsibly requires the collaborative and coordinated efforts of inter-disciplinary, multi-organizational working groups. The example of the initial outbreak of hantavirus pulmonary syndrome will used to illustrate these concepts. The sustained collaborations that resulted from this event will be described. This presentation will focus on applications of the One Health worldview.
A WEST NILE VIRUS OUTBREAK IN EARED GREBES AND BALD EAGLES: A WINTER TRANSMISSION EVENT

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An unusually large wild bird mortality event attributed to West Nile Virus (WNV) occurred November 2013 to February 2014 in areas surrounding the Great Salt Lake, Utah, USA. This event involved between 15,000-20,000 eared grebes (Podiceps nigricollis) and 76 bald eagles (Haliaeetus leucocephalus). WNV, an arbovirus, is typically transmitted by mosquitoes. In Utah, transmission usually occurs soon after emergence of overwintering female mosquitoes, human and animal cases peak in late summer to early autumn, and cease with the first hard freeze. Mass mortality in eared grebes overwintering on the Great Salt Lake was first reported in early November 2013, but could have begun as early as October. Thirty eared grebes collected from November to the end of January 2014 were WNV RT-PCR and/or virus isolation positive. We hypothesize that WNV was the primary contributor to this die-off. Beginning in early December, bald eagles in the area of the Great Salt Lake were observed with neurologic clinical signs, including tremors, limb paralysis, and lethargy, or were found dead. At least 72 bald eagles had died by the end of February. Nine of nine bald eagles examined were confirmed to be infected with WNV. During the late fall, unseasonably warm temperatures may have allowed mosquito transmission of WNV to large numbers of overwintering grebes; due to high concentrations of birds on the lake, some may also have become infected through contact with virus shed by other infected grebes. Active shedding of WNV in grebes was directly demonstrated. The majority of bald eagle deaths occurred during a period when temperatures dropped below freezing and mosquito transmission was not likely. This suggests that bald eagles were infected with WNV via alternative routes such as consumption of infected eared grebes or through oral-fecal transmission at roost sites.
DIAGNOSIS OF WEST NILE VIRUS IN WINTER MORTALITY OF EARED GREBES (PODICEPS NIGRICOLLIS) AND BALD EAGLES (HALIAEETUS LEUCOCEPHALUS) AT THE GREAT SALT LAKE, UTAH

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Two wildlife mortality events occurred on and around the Great Salt Lake, UT in the winter of 2013-2014. The first involved 15,000-20,000 Eared Grebes (Podiceps nigricollis) and the second over 70 Bald Eagles (Haliaeetus leucocephalus). Grebes (n=30) and eagles (n=8) submitted to the National Wildlife Health Center (NWHC) presented with neurologic clinical signs and shared similar gross and microscopic lesions, including necrotizing myocarditis and meningoencephalitis. All birds received tested positive for West Nile Virus (WNV) by RT-PCR and/or virus isolation; no other significant infectious or toxic cause of disease was identified. To our knowledge, this is the first report of WNV in Eared Grebes, the largest single raptor mortality event attributed to WNV in the United States, and the largest suspect WNV-associated wildlife die-off ever reported. In this report, we describe postmortem findings, discuss laboratory results, and consider retrospective data from previous NWHC disease investigations that shed light on this unusual mortality event.
CO-OCURRENCE OF TWO RELAPSING FEVER BORRELIAE IN ORNITHODOROS SPP. TICKS AND WILDLIFE IN A CENTRAL COASTAL CALIFORNIA MIXED AGRICULTURAL WOODLAND LANDSCAPE

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In 2009, a laboratory-confirmed case of human tick-borne relapsing fever (TBRF) was diagnosed in northern San Luis Obispo County, California. The patient had no recent travel history, suggesting the disease agent was locally acquired. This region is an atypical habitat for Borrelia hermsii, the primary agent of relapsing fever in the Western U.S. readily detected by routine clinical laboratory antibody panels, suggesting another species could be implicated. Blood samples from four rodent species and two species of argasid ticks collected at the residence between 2009-2012 were tested for relapsing fever borreliae by various methods, including immunoblotting, transmission attempts from field collected ticks to lab mice, direct blood culture in BSK-H, blood smear slide examination, and PCR. Spirochete transmission occurred after feeding a pool of Ornithodoros parkeri ticks on a lab mouse, leading to subsequent recovery of an isolate identified as Borrelia parkeri by sequencing. Borrelia parkeri infection was also detected in Spermophilus beecheyi and Peromyscus maniculatus rodents collected at the site by immunoblot analysis of serum samples. A second relapsing fever spirochete, Borrelia coriaceae, was detected by PCR in four pools of Ornithodoros coriaceus ticks from the same residence. Additionally, 7/36 blood samples from Odocoileus hemionus columbianus deer obtained from hunter check stations in close proximity to the residence were positive for B. coriaceae by immunoblot analysis and/or PCR. Spirochete 16S rRNA sequences from four of these deer were virtually identical to B. coriaceae detected in O. coriaceus ticks at the site. Immunoblot analyses of two convalescent-phase serum samples from the patient indicates they were both most reactive to a B. coriaceae lysate from northwestern California, as compared to the B. parkeri lysate from the residence and B. hermsii GlpQ, suggesting that this patient may have been infected with a relapsing fever spirochete not previously associated with human disease. Our results indicate that there are at least two independent enzootic transmission cycles of relapsing fever spirochetes at a single site involving different tick vectors and wildlife reservoirs and that B. coriaceae warrants further examination as a potential etiological agent of relapsing fever. The potential inter-relationships between these transmission cycles and periodic cases of relapsing fever in humans deserve further investigation.
THE POTENTIAL UTILITY OF THE RED FOX (VULPES VULPES) IN ASSESSING THE RISK OF BLASTOMYCES DERMATITIDIS INFECTION IN SOUTHERN ONTARIO

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Blastomyces dermatitidis is an emerging fungal pathogen capable of causing fatal infection in a wide variety of mammals, including humans. Transmission is usually via inhalation of conidiophores released from an environmental reservoir (e.g., soil). However, the fungus is not readily recoverable or uniformly distributed within the environment, and therefore it has been difficult to adequately identify outbreak sources and assess infection incidences. Regions with the highest historical blastomycosis prevalence include the Mississippi, Missouri, and Ohio River Valleys of the U.S. In addition, numerous human and dog cases have been reported along southern Canadian waterways, where the incidence appears to be increasing. Although B. dermatitidis is considered endemic in northern Ontario, Canada, it has recently caused disease among humans in urban areas of southern Ontario, as well as Quebec. In addition, blastomycosis was diagnosed in 75 dogs from Ontario at the Animal Health Laboratory (2007-2013), and in six red foxes (Vulpes vulpes) and three wolves (Canis lupus) at the Canadian Wildlife Health Cooperative (CWHC). Subsequently, a 5% blastomycosis prevalence was observed among 20 red fox carcasses submitted by Ontario fur trappers. Due to shared exposure sources with domestic animals and humans, disease detection in wild canids, such as the red fox, may denote regional disease hot spots and signify public health risks. We suggest that additional studies of red foxes within this region will help reveal the potential utility of this species as a sentinel for blastomycosis in southern Ontario and other regions, as well as potential impacts of this disease on red foxes. Red fox natural history traits that would contribute to their potential usefulness include that they are common throughout Ontario and much of Canada and the U.S., have foraging and denning behaviors that readily lead to direct contact with aerosolized soil particles, and have relatively compact home ranges.
Marburg virus (MARV) causes sporadic outbreaks of Marburg hemorrhagic fever (MHF) in Africa. The Egyptian fruit bat (Rousettus aegyptiacus) has been identified as a natural reservoir based most recently on the repeated isolation of MARV directly from bats caught at Kitaka mine and Python Cave, two locations in southwestern Uganda ~50 km apart where miners and tourists separately contracted MHF from 2007-08. A long-term study of R. aegyptiacus at these locations determined that 2-5% of the population was actively infected at any one time and that virus sequences from infected bats and humans were genetically similar. Further, these studies have shown the twice-yearly birthing seasons to produce pulses of juvenile bats that, when ~6 months old, were 5-6 times more likely to be actively infected than adults. These seasonal pulses coincide with the dates of 83% (54/65) of all known MARV bat-to-human spillover events. Together, these data are the first to forecast periods of increased-risk for human infection. Nevertheless, there were still many unanswered questions such as determining the primary routes of virus shedding and the severity of disease, if any, caused by MARV in infected bats. To answer these questions and others, we founded a breeding colony of R. aegyptiacus to generate bats for experimental infection studies with filoviruses under high (BSL4) containment. Thus far, our data show infection profiles consistent with R. aegyptiacus being a bona fide natural reservoir host for MARV capable of infecting humans and other animals.
PATHOGENS DETECTED IN HUMAN-HABITUATED EASTERN GORILLAS (GORILLA BERINGEI) IN EAST-CENTRAL AFRICA

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A majority of the world’s remaining 880 wild mountain gorillas (Gorilla beringei beringei) are habituated to the presence of humans to support robust ecotourism industries and long-term research in Rwanda, Uganda and the Democratic Republic of the Congo (DRC). As well, rapidly declining populations of eastern lowland (or Grauer’s) gorillas (G. b. graueri) in eastern DRC are undergoing human-habituation to facilitate tourism that will generate much-needed revenue to support protection of the parks where eastern lowland gorillas survive. There is great potential for bidirectional pathogen transmission between eastern gorillas and the people with whom they come into direct and indirect contact. Indeed, we have previously demonstrated the close genetic relatedness of some microbial pathogens and parasites found in wild gorillas to those described in humans. More recently, our research has documented clinical disease in eastern gorillas due to infections with human metapneumovirus and human herpes simplex virus. To further characterize the risk of disease transmission among human-habituated gorillas and people, research is currently underway to better understand the epidemiology and pathology of pathogens circulating in eastern gorilla populations. Specifically, we are applying molecular techniques to samples obtained from healthy and ill gorillas to identify viral pathogens, determine their relatedness to known human or non-human primate viruses, and correlate pathogen presence with clinical signs and histopathology. To date, genetic sequences of known and previously unknown viruses in several viral families known to infect and cause illness in people have been detected in eastern gorillas. Our findings will form the basis for recommendations to mitigate disease risk for gorillas in concert with best management practices for tourism and research in the range countries of eastern gorillas.
INNOVATIVE COMMUNITY-BASED APPROACH TO ADDRESS LEAD POLLUTION FROM HUNTING IN ARGENTINA WETLANDS

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For more than fifteen years, Argentina has been an international waterfowl hunting hotspot. Consequently and as expected, we have found high levels of lead from spent gunshot in wetland sediment and in ducks. Given the known toxicity risks for animal and human health, we have successfully capitalized on our findings to advocate for provincial lead shot bans, an unprecedented feat in Argentina and Latin America. However, compliance is poor due to local unavailability of nontoxic alternatives and hunter resistance. Furthermore, hunting sustainability is unknown in the absence of waterfowl population estimates and feeble hunting license records. Thus, the larger environmental health problem remains unsolved. It so transpires that a broader than science approach is needed to address this complex, multi-stakeholder and socially sensitive issue. Here we present an innovative constituency model that involves participatory research with citizens, governments and hunters, combined with community-focused education and sensitization to drive change. As proof of concept, we are using waterbird monitoring to demonstrate the strength of community interventions for conservation and to obtain information on the biology and population status of hunted waterfowl. By sharing our experience we aim to generate discussion within the wildlife health community on ways to more effectively translate science into policy; examine when and how to build on collectively generated ecosystem health knowledge; and, as important, the significance of inspiring and empowering local communities to become stewards of their natural resources.
DETECTION OF NEW GENETIC VARIANTS OF BETACORONAVIRUSES IN ENDEMIC FRUGIVOROUS BATS OF MADAGASCAR

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Bats are amongst the natural reservoirs of many coronaviruses (CoVs) of which some can lead to severe infection in human. To date no CoVs has been identified in endemic bats of Madagascar. We analyzed fecal and throat swabs from 351 frugivorous bats belonging to three species captured in four different regions of Madagascar. We detected 14 coronaviruses from two endemic bats species, of which 13 strains were isolated from Pteropus rufus and one strain isolated from Eidolon dupreanum, giving an overall prevalence of 4.5%. Phylogenetic analysis revealed that the Malagasy strains belong to the genus Betacoronavirus but form three distinct clusters, which seem to represent previously undescribed genetic lineages. Our findings suggest that CoVs, which circulate in frugivorous bats of Madagascar, potentially pose a spillover risk to human populations especially for individuals that hunt and consume infected bats. Possible dispersal mechanisms as to how coronaviruses arrived on Madagascar are discussed.
MICROBIAL INFECTION AS A SOURCE OF EMBRYO MORTALITY IN GREATER WHITE-FRONTED GEESE (ANSER ALBIFRONS) ON THE ARCTIC COASTAL PLAIN OF ALASKA

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Microbial infection contributing to hatching failure could result in avian population declines and has never been studied in an Arctic environment. During the 2011 field season a high number of nonviable eggs were noted in greater white-fronted goose (Anser albifrons) eggs on the Arctic coastal plain of Alaska. The objectives of this study were to identify potentially pathogenic bacteria in contents of nonviable eggs and to determine embryonic mortality potential. During the 2013 hatching season, nonviable eggs from greater white-fronted geese were collected and assessed for bacterial infection using standard culture methods and 16S ribosomal RNA gene sequencing. Isolates recovered were inoculated into fertilized chicken eggs in an attempt to fulfill Koch’s postulates. A Neisseria sp. was isolated from 23 of 36 addled eggs, Macrococcus caseolyticus was isolated from 6 eggs, and Streptococcus uberis and Rothia nasimurium were each isolated from 4 eggs. Other species were isolated from eggs rarely. Chicken egg infections show that between 60-100% of embryos died by 7 days post-infection with these species. 16S rRNA gene sequences from the Neisseria sp. most closely match N. animaloris or N. canis (96-97% identity) but suggest that this might be a new species. Sequences from M. caseolyticus, S. uberis, and R. nasimurium all matched GenBank accessions 99-100%. These isolated bacterial species caused mortality in chicken eggs and are likely causing mortality in greater white-fronted goose eggs on the North Slope of Alaska.
FIELD APPLICATIONS OF NON-INVASIVE SALIVA COLLECTION TECHNIQUES FOR PATHOGEN SURVEILLANCE IN NON-HUMAN PRIMATES

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Pathogen surveillance in free-ranging non-human primates is important for monitoring the health of threatened and endangered species as well as populations in close contact with humans that are a potential source of zoonotic disease. Sample collection from free-ranging primates is logistically challenging and invasive sampling may not be feasible due to difficulties with chemical immobilization in rough terrain and arboreal primate behavior. Moreover, wildlife authorities may strictly limit handling primates, especially when targeting endangered species or those of religious significance. We investigated two non-invasive sampling methods - the distribution of ropes and the collection of discarded forage food, for viral detection in saliva. Optimization of the rope technique was performed by testing paired rope and oral mucosal swabs from captive rhesus macaques (Macaca mulatta) for rhesus cytomegalovirus (RhCMV) and simian foamy virus (SFV) and field applicability was assessed with free-ranging red-tailed guenons (Cercopithecus ascanius), olive baboons (Papio anubis) and L’hoest’s monkeys (Cercopithecus lhoesti) in Uganda and rhesus macaques in Nepal. Optimization of the forage food technique was performed by testing discarded chewed plants from free-ranging human-habituated mountain gorillas (Gorilla beringei beringei) in Rwanda and Uganda for herpes viruses and mammalian beta-actin to determine DNA and RNA virus recovery potential. RhCMV was detected by real-time PCR in 22.2% of saliva samples collected from ropes distributed to captive rhesus macaques and SFV in 40.7%. Gorilla herpes viruses were detected by PCR in discarded chewed plants from mountain gorillas in 21% of samples and beta-actin was detected in 78%. Our study demonstrated that non-invasive saliva collection techniques can be used for detection of both RNA and DNA viruses in multiple free-ranging primate species and, potentially may be used in other wildlife species when invasive sampling techniques may not be possible or appropriate.
PREVALENCE OF RICKETTSIA AFRICAЕ, EHRLICHIA RUMINANTIUM, AND THEILERIA SPP. IN AMBLYOMMA HEBRAEUM FROM FREE-RANGING AFRICAN BUFFALO, SOUTH AFRICA

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Kruger National Park (KNP) in South Africa hosts a large diversity of wildlife, including African buffalo (Syncerus caffer). A common ixodid tick that parasitizes the buffalo is the African bont tick, Amblyomma hebraeum. Our study was conducted to investigate the prevalence and diversity of Rickettsia, Ehrlichia, and Theileria in the salivary glands of A. hebraeum collected from buffalo in KNP. Ticks (n=157) were collected from 18 buffalo (mean 8.7; range 5-14 ticks/buffalo) and the salivary glands were collected via dissection. We hypothesized that the prevalence of E. ruminantium would be low while prevalence and diversity of Theileria spp. would be high based on studies of African buffalo. DNA was extracted from salivary glands (which should not have blood-meal contamination from the buffalo host) and polymerase chain reactions (PCR) that targeted the 17kDa region of Rickettsia spp., the partial pCS20 region of E. ruminantium, and the 18S rRNA region of piroplasms was conducted. A total of 73 (46%) ticks were positive for at least one pathogen (Rickettsia africæ, E. ruminantium, and/or Theileria sp). Single infections were noted in 63 ticks and dual infections were noted in 10 ticks. A total of 54 ticks (34%) were PCR positive for R. africæ, two ticks (1%) were positive for E. ruminantium, and Theileria spp. were detected in 26 (17%) ticks. Sequence analysis indicated that at least five Theileria spp. were detected: 19 were 99% similar to T. mutans-like sp., one was 99% similar to Theileria sp. B15a, two were 99% similar to T. velifera, four were 99% similar to T. parva-like, and two were 99% similar to Theileria sp. ex Syncerus caffer. Our data suggest that A. hebraeum may be an important vector of multiple species of Theileria and supports previous data that it is an important vector of E. ruminantium and R. africæ.
IMPACTS OF INSECTICIDE PLAGUE TREATMENT ON POPULATIONS OF DEER MICE ON PRAIRIE DOG COLONIES

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Plague (Yersinia pestis) is a major threat to populations of prairie dogs (Cynomys spp.) and black-footed ferrets (Mustela nigripes) in western North America. In many black-footed ferret reintroduction sites, deltamethrin is commonly sprayed inside prairie dog burrows to remove plague-carrying fleas (Siphonaptera). This treatment is effective at increasing survival of prairie dogs and potentially reducing plague epizootics. However, the effects of this treatment on non-target wildlife species are largely unknown and concerns have been raised about the impacts of food-source arthropod reductions. We investigated the effects of deltamethrin dusting on populations of deer mice (Peromyscus maniculatus) present on black-tailed prairie dog (C. ludovicianus) colonies at Wind Cave National Park and Custer State Park, South Dakota. Six pairs of treated and untreated grids were established and treated in the summer of 2013. Grids were sampled during four trap sessions, once before treatment and three times after, resulting in the capture of 137 individual deer mice. Upon capture, each animal was individually marked and combed for fleas. To estimate survival, capture-mark-recapture data were analyzed using Cormack-Jolly-Seber models in program MARK. We saw significantly fewer fleas infesting mice on treated grids (mean infestation rate 0.02, 95% CI 0.00, 0.11) than untreated grids (mean infestation rate 0.36, 95% CI 0.21, 0.55). Additionally, there was an increase in capture rates on dusted grids during the final trapping session (estimated proportional effect of dusting on capture rates = 2.86, 95% CI 7.37, 1.12) and evidence for increased survival on treated grids (estimated survival between third and fourth trap session = 0.58, 95% CI 0.19, 0.89) compared to untreated grids (estimated survival = 0.21, 95% CI 0.08, 0.44). Our 2013 results suggest that the overall effect of treatments on mouse populations is neutral or positive; however, there may be additional effects on arthropod food sources.
EVALUATION OF FEATHER CORTICOSTERONE AS AN INTEGRATED MEASURE OF HYPOTHALAMIC-PITUITARY-ADRENAL AXIS ACTIVITY IN LESSER SCAUP (AYTHYA AFFINIS)

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Stressors of moderate to high intensity that occur repeatedly or over prolonged time periods trigger sustained release of high glucocorticoid (GC) levels, resulting in deleterious effects on individual’s health and reproduction. In birds, the major GC produced is corticosterone (CORT). Slow growing keratinized structures such as feathers incorporate amplitude and duration of total CORT secretion during the period of feather growth, thus reflect cumulative energetic costs experienced by a bird during that period. To determine whether feather CORT (CORTf) is an estimate of circulating CORT levels during the time of feather growth, we collected blood and feather samples after implanting captive lesser scaup (Aythya affinis) with synthetic CORT implants (seven-day hormone release). We hypothesized that both serum CORT and CORTf would be higher in treatment birds, and that post-implant CORTf would be positively correlated with serum CORT during the implant-active period. Serum radioimmunoassay revealed that treatment birds had higher serum CORT levels compared to control birds two to four days post-implant, but there was no difference between groups by day 7 post-implant. As predicted, CORTf was higher for back feathers in treatment birds, however this relationship was not observed for tail feathers. Nonetheless, there was a significant positive association between serum CORT and post-implant CORTf for most feather types examined. The shorter hormone-release window for CORT implants than that specified by the manufacturer was likely due to rapid metabolism of implants in birds with higher body temperature compared to mammals for which these implants were designed. The inconsistent relationship between treatment and control birds for the different feather types could have been associated with the variation in growth rates for different feather types.
AMPICBIN MICROBIOMES AS INDICATORS OF INDIVIDUAL AND ENVIRONMENTAL HEALTH

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Amphibians depend on their cutaneous microbial community as a first line of immune defense against disease. However, very few studies have been performed to characterize the bacterial genera found on the skin of different amphibian species and under different water quality conditions. The goal of this study was to classify the bacterial genera present on the skin of two *Lithobates* species living in lakes of highly variant water characteristics on a reclaimed surface mine. A second objective was to develop a baseline frog microbiome library on the site prior to shale gas exploration in order to monitor microbiome changes in association with environmental disturbance. Northern green frogs (*Lithobates clamitans melanota*) and American bullfrogs (*Lithobates catesbeiana*) were caught from 10 different lakes on the Wilds in Cumberland, Ohio, USA. Skin swabs were collected following a sterile saline solution rinse for bacterial characterization and to test for *Batrachochytrium dendrobatiditis* (*Bd*), the etiologic agent of amphibian chytridiomycosis. Pharyngeal swabs were taken to test for ranavirus, another emerging disease of amphibians, and blood samples were collected to assess the heterophil-lymphocyte ratio as an indicator of stress. Water quality parameters were documented and water samples collected for chemical analysis at the time of frog capture for each site. The DNA was extracted from the bacterial swabs and sequenced using 454 pyro-sequencing. At least one frog from each site tested was positive for *Bd*, but no frogs were positive for ranavirus. Water quality among sites varied with regard to pH (4.10 to 8.66), conductivity (137.5 μS/cm to 3.51 mS/cm), ionic content, and dissolved organic carbon (0.13 mg/L to 11.7 mg/L). Our study identified over 300 different genera of microbes representing 68 orders present on frogs on this site. Water quality parameters were found to be associated with differential microbial colonization and physiologic parameters.
MOLECULAR EPIDEMIOLOGY OF AVIAN CHOLERA IN NORTHERN CANADA

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Avian cholera, a bacterial disease of wild birds caused by infection with Pasteurella multocida, remains a leading cause of waterfowl mortality in North America. Avian cholera outbreaks in common eider colonies in the eastern Canadian Arctic were first detected in 2004, and prompted an investigation of the genetic diversity of P. multocida to determine the relatedness of P. multocida strains from the Canadian Arctic to other North American strains. Isolates from live and dead birds from affected eider colonies in Nunavut and Northern Quebec (Nunavik), collected from 2004-2011, were genotyped using two methods and compared to isolates from avian cholera outbreaks across Canada and the United States occurring over the past ~20 years. P. multocida isolates (n=298) were genotyped using repetitive element palindromic polymerase chain reaction (REP-PCR) and 272 of these isolates were also typed using multilocus sequence typing (MLST). REP-PCR fingerprints showed 29 distinct profiles, containing at least two isolates, and MLST grouped the isolates into 15 sequence types and five clonal complexes. Using a cut-off of 90% for REP-PCR, results from REP-PCR and MLST generally corresponded with the P. multocida serotypes, and serotype 4 and 3x4 isolates from Nunavut and Nunavik showed a high degree of relatedness. Serotype 1 isolates from Newfoundland, Saskatchewan, southern Quebec, and the eastern Arctic were related; these isolates also showed some degree of relatedness to isolates from California and Nebraska, but most US isolates were distinct from Canadian isolates. Genotyping also highlighted that serotype 3, 4 and 3x4 isolates from southern Quebec were unrelated to isolates from the eastern Arctic. These results suggest that P.multocida strains may be exchanged among northern outbreaks, and that there may be some connections among P. multocida strains from northern and southern Canada.
THE EFFECT OF HOOKWORM (UNCINARIA SP.) INFECTION ON THE HEALTH STATUS OF FREE-RANGING SOUTH AMERICAN FUR SEAL (ARCTOCEPHALUS AUSTRALIS) PUPS

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Hookworms are highly pathogenic nematodes that parasitize a wide range of mammals, including several species of pinnipeds. At Guafo Island, in the Chilean Patagonia, this parasite reaches 100% prevalence and causes significant mortality in South American fur seal pups. The objective of this study was to evaluate the effects of hookworm infection on fur seal pups by experimental deworming and comparative clinical and anatomic pathology. During the 2014 austral summer, we treated a randomly selected subset of hookworm-infected pups (n=73) with Ivermectin, and compared these treated pups to pups that were clinically infected with hookworms (n=50). Additionally, we performed necropsies on 28 hookworm infected and 20 hookworm free (control) pups. Hookworm-infected pups had marked declines in erythrocytes, hemoglobin, hematocrit and total protein over the first two months of the infection (Student’s t test, p values 0.0006). The number of total leukocytes remained unchanged, despite the severe multifocal necrotizing and histiocytic enteritis that this parasite typically causes in the fur seal pup intestine. Ivermectin-treated pups presented the same drop in hematologic values when compared with the control (infected) groups two weeks after treatment, however they had significantly increased values of all hematological values, including total leukocytes, when compared with the control group 4 weeks after treatment (Student’s t test, p values < 0.0009), suggesting that hookworm infection negatively impacts fur seal pup health by causing severe intestinal damage, severe anemia, hypoproteinemia and moderate immunosuppression by reducing circulating leukocytes.
TOXOPLASMA GONDII IN A TERRESTRIAL ARCTIC FOOD WEB: WHO BRINGS WHAT TO THE TABLE AND ACCOUNTING FOR UNCERTAINTY IN DIAGNOSTICS

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In some regions of the Canadian Arctic, evidence of exposure to *Toxoplasma gondii* is reported at high prevalence in both people and wildlife. However, in most regions, such as the central Arctic terrestrial ecosystem, data are scarce and transmission is enigmatic in the absence of felid definitive hosts. This study examined the occurrence of *T. gondii* in three trophic components from the terrestrial community at Karrak Lake, Nunavut, Canada. To determine where in the food web *T. gondii* occurs, we tested serum and tissues from arctic foxes (*Vulpes lagopus*), Ross’s Geese (*Chen rossii*), Lesser Snow Geese (*Chen caerulescens*), and lemmings (*Lemmus* sp. and *Dicrostonyx* sp.). We analyzed serological data using a multi-state occupancy approach that accounted for imperfect detection of antibodies against *T. gondii*. Arctic foxes within the Karrak Lake ecosystem had a 0.58 probability of being occupied by *T. gondii* antibodies, while Ross’s Geese and Lesser Snow Geese had a 0.36-0.38 probability of seropositivity. DNA of *T. gondii* was detected in brain and heart tissue from both goose species. We did not detect *T. gondii* antibodies in lemming serum samples, but tissue PCR results indicated the presence of *T. gondii* or a closely related organism. These findings suggest that migratory birds are a source of introduction of *T. gondii* in the terrestrial Arctic and a potential source of infection for geese and rodents. These results indicate that these species are potential routes of exposure for arctic carnivores and human harvesters alike. In addition, we demonstrate the utility of an occupancy modeling approach for improving estimates of prevalence in wildlife disease studies, especially in the absence of gold standards and diagnostic tests validated for wildlife.
MOLECULAR EPIDEMIOLOGICAL STUDY ON ANAPLASMA PHAGOCYTOPHILUM IN SIKA DEER (CERVUS NIPPON) IN HOKKAIDO, JAPAN

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The study of tick-borne pathogens (TBPs) has become increasingly important especially those with zoonotic potential. Given the increasing geographic range of tick-borne zoonotic diseases and the potential emergence of pathogens, they are of great concern for public health authorities. However, while we know much about the tick-borne zoonotic diseases, little is known about their prevalence in wildlife. In this study, 239 wild sika deer samples collected in Hokkaido, Japan, were examined to detect \textit{Anaplasma phagocytophilum}. A 770 bp segment of the 16S rRNA gene and a 382 bp segment of the citrate synthase gene (gltA) were amplified by nested PCR using \textit{A. phagocytophilum} species-specific primers. The positive PCR products were sequenced and phylogenetically analyzed. The total prevalence of \textit{A. phagocytophilum} was 51%, and several genetic variants of \textit{Anaplasma} species detected. The probability of infection showed significant regional dependence, yet complete independence from other demographics, including month, gender and age (P≤0.05). The sequences of the 16S rRNA and gltA gene amplicons that were obtained from the positive samples were 98-100% and 90-100 %, similar to \textit{Anaplasma} spp. sequences selected from GenBank, respectively. Phylogenetic analysis suggests the potential existence of novel \textit{Anaplasma} spp. genetic variants in sika deer. This study provides data that will help to understand the epidemiology and genetic diversity of \textit{Anaplasma phagocytophilum} in Hokkaido.
INVESTIGATING ADENOVIRUS DIVERSITY AND THE POTENTIAL FOR INTERSPECIES TRANSMISSION AMONG ENDANGERED MOUNTAIN GORILLAS (GORILLA BERINGEI BERINGEI), GOLDEN MONKEYS (CERCOPITHECUS MITIS KANDTI), AND PEOPLE IN RWANDA

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Human respiratory viruses (e.g. human metapneumovirus) have contributed to fatal respiratory infections in endangered mountain gorillas (\textit{Gorilla beringei beringei}), and recent outbreaks of respiratory illness in mountain gorillas have raised concerns about human-gorilla pathogen transmission. In Volcanoes National Park, Rwanda, mountain gorilla health is monitored by park staff, researchers, and veterinarians. Groups of gorillas and endangered golden monkeys (\textit{Cercopithecus mitis kandti}) are habituated to human presence for research or tourism. Investigating the disease agents and epidemiology of respiratory illness in this system is challenging given the difficulties of obtaining optimal diagnostic samples. We used adenovirus (AdV), a ubiquitous virus found in people and primates, as a model virus to investigate the potential for cross-species viral transmission among mountain gorilla groups and among mountain gorillas, golden monkeys, and people. Voided fecal samples were collected non-invasively from 40 human-habituated golden monkeys and 119 mountain gorillas representing both unhabituated and human-habituated individuals and including animals in both research and tourism groups. Samples were tested by several adenovirus-specific conventional and long-distance PCR assays targeting two genes, and amplified hexon gene fragments were sequenced and compared by phylogenetic analysis. Among gorillas, we found no association between AdV gene sequence and gorilla group (habituated vs. unhabituated or tourism vs. research). Upon initial analysis of short hexon fragments (380 bp), adenoviruses detected in golden monkey samples appeared similar to closely related AdV species from coincident infections in humans and Old World monkeys (e.g. HAdV-41, SAdV-18). Findings may suggest that interspecies transmission of adenoviruses occur in this system; additional long-distance sequencing of golden monkey samples and viral testing of samples from local human groups is underway to further investigate this hypothesis. These results will be used inform management strategies to reduce pathogen spread at this important wildlife-human interface.
GENOME-WIDE CHARACTERIZATION OF *ERYSIPELOTHRIX RHUSIOPATHIAE* CAUSING LARGE-SCALE MORTALITY IN MUSKOXEN IN THE CANADIAN ARCTIC

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The muskox is a keystone species and an important source of food and income for northern communities. Since 2010, mid-summer mortality events involving up to hundreds of muskoxen have occurred in the Canadian Arctic archipelago, raising concerns about the health of these populations. *Erysipelothrix rhusiopathiae*, a zoonotic bacterium never previously reported in muskoxen or in the Arctic, was consistently isolated from multiple tissues of sampled carcasses. As part of the outbreak investigation, we performed whole-genome sequencing of *E. rhusiopathiae* isolated from muskox carcasses (n=11) from three outbreaks on Banks and Victoria Islands (2010-2012), from the bone marrow of a carcass found in Aulavik National Park on northern Banks Island in 2013, and from the tonsil of a healthy, hunter-killed muskox from Victoria Island. These sequences were compared to a wide range of isolates from swine, poultry, marine mammals and wild birds (n=64) on a global scale to provide context within which to evaluate the genetic diversity. Very little variability was found among the *E. rhusiopathiae* isolates from muskoxen, suggesting that these currently circulating strains originated from a recent common ancestor. To estimate how long *E. rhusiopathiae* has been circulating in muskoxen, we used two approaches: first, Bayesian phylogenetic methods were used to estimate the date of the most recent common ancestor of the muskox isolates, and second, archived serum samples collected over a 20-year period were tested using an adapted serology test. We show that *E. rhusiopathiae* has been present in muskox populations since at least the early 1990’s. There was a lack of clustering by host species or geographic location among the other isolates, strongly suggesting that most strains of *E. rhusiopathiae* are not host-specific and can likely cause opportunistic infections in many species. This research is an important first step towards understanding these recent mortality events in muskoxen.
LONGITUDINAL ANALYSIS OF TOXOPLASMA GONDII EXPOSURE IN CALIFORNIA SEA OTTERS SUGGESTS CHANGES IN LOCAL DISEASE RISK

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Protozoal disease is an important cause of mortality in southern sea otters (Enhydra lutris nereis) and the most common pathogens causing protozoal disease, Toxoplasma gondii and Sarcocystis neurona, are of terrestrial origin. Investigations into the land-sea transmission of T. gondii serve as models for terrestrial-origin pathogen pollution and inform conservation actions needed to support sea otter recovery. The aims of this study were to examine long-term trends in exposure of sea otters to T. gondii and to determine if risk factors for exposure have changed over the past 15 years. Serum samples from sea otters captured between 1999-2013 were analyzed for T. gondii antibodies by a validated immunofluorescent antibody test used consistently for sea otter sero-surveys. Serologic data were evaluated in conjunction with demographic data (age, sex, length, weight), diet, and spatial use. In agreement with previous research, consuming a diet rich in marine snails represented a strong risk factor for T. gondii exposure. A declining trend in T. gondii seroprevalence was observed across the study period at Monterey Bay. Female sea otters exhibited a marked decline in T. gondii exposure, but no significant decline was noted among males. Many male sea otters occupy larger home ranges compared with females, often with multiple, widely separated centers of use. Consequently, the health status of female sea otters is considered to be more closely linked to local environmental conditions. This declining trend in pathogen exposure remained significant after accounting for changes in the age distribution of captured animals and other risk factors. A similar declining trend in sea otter seropositivity was not detected at other sites in California, although repeated sampling is sporadic in several locations. Further research is under way, aiming to examine local-scale effects and examine terrestrial inputs of infectious oocysts, which may have declined in the Monterey Bay area.
POPULATION MANAGEMENT INFLUENCES CAMPYLOBACTER CARRIAGE IN AN ENDANGERED POPULATION OF TAKAHE (PORPHYRIO HOCHSTETTERI)

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The intensive conservation management of threatened species often results in individual animals being exposed to altered and artificial habitats, abnormal social structures and physiological stress that are radically different from their natural ecosystems. We hypothesised that intensive conservation management could change the microbial flora of the host species through stresses on their immunity and exposure to diverse microbial ecosystems. Carriage of the bacterial species, Campylobacter, was used to investigate changes in host-microbial dynamics in response to a range of factors that have resulted from the conservation management of the host species. Takahē (Porphyrio hochstetteri) are an endangered flightless bird endemic to New Zealand. Populations have been established within highly modified geographically isolated predator-free reserves, external to the wild population. Subpopulations are linked via regular artificial movements, however extent of connectivity differs between populations. This investigation sampled 118 takahē (~47% of the species) from a range of locations for faecal Campylobacter, via culture and faecal DNA extraction, followed by PCR. The apparent prevalence of Campylobacter was 99%, with three subspecies identified at different carriage rates, C. jejuni (38%), C. coli (24%) and Campylobacter sp. nova 1 (90%), and multiple carriage in 51% of takahē tested. There were significant differences in the carriage of the Campylobacter between takahē sub-populations, with variance in risk associations between Campylobacter subspecies. We highlight the potential role agricultural practices and domestic livestock may play in transmission of organisms to endangered populations, as well as the importance of rearing environment on microflora carriage in adulthood. In conclusion, the intensive management of threatened species in altered environments will result in changes to the microbial flora of the host species. The consequences of these changes are difficult to predict, but may include increased exposure to pathogens of significance to animal and human health.
MOLECULAR TECHNIQUES TO EVALUATE PREVALENCE AND INTENSITY OF INFECTION FOR AVIAN MALARIA IN A MIXED ECOSYSTEM IN NEW ZEALAND

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Avian malaria causes morbidity and mortality in New Zealand’s endemic bird populations. This study was initiated after Plasmodium relictum lineage GRW4 was found in a New Zealand robin (Petroica longipes) during pre-translocation health screening in the Waimarino forest. This area incorporates fragments of remnant native forest, commercial forestry and farmland, with a mixed avifauna of introduced, native and endemic species. New Zealand robins in the Waimarino forest form a potential mainland source population for future robin translocations. The study aims were to evaluate the prevalence of Plasmodium lineages in the Waimarino forest using nested PCR and quantify parasite load using real-time PCR. Results demonstrated the presence of Plasmodium sp. LINN1, Plasmodium (Huffia) elongatum and Plasmodium (Novyella) sp. lineage SYATO5 in this ecosystem. The highest Plasmodium prevalence was found in introduced European species (80.5%), followed by native (19%) and endemic species (3.5%), with a significant difference between these groups ($\chi^2$=117.176, d.f.=2, $p=0$). The relationship between parasite load, haematocrit, and body condition index (BCI) was assessed in blackbirds (Turdus merula), silvereyes (Zosterops lateralis) and NZ robins. Surprisingly, a significant difference in BCI was found between Plasmodium positive- and negative silvereyes, indicating a better BCI in Plasmodium-positive birds ($t=-2.64$, d.f.=31, $P=0.01$), while no difference was found for blackbirds and robins. No significant differences in haematocrit were found between Plasmodium positive and negative birds. Results suggest that, compared to endemic and native bird species, introduced bird- and Plasmodium species might be more co-adapted through longer co-evolution, and that these introduced bird species may act as a reservoir of infection for other species. Quantification of this parasite-host relationship will give new insight in the dynamics of avian malaria infections. This research will provide critical information for the management of native species in the Waimarino Forest, the bordering Wanganui National Park, and other comparable mixed ecosystems.
THE VANCOUVER RAT PROJECT: UNDERSTANDING THE ECOLOGY OF RATS AND RAT-ASSOCIATED ZOONOSES IN AN INNER-CITY NEIGHBOURHOOD

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Urban rats (Rattus spp.) are an important source of zoonotic pathogens, yet there is a paucity of integrated, interdisciplinary, ecosystem-based research on rat-associated zoonoses. The goal of the Vancouver Rat Project was to begin to characterize the public health risks associated with rats by studying the ecology of rat populations and the zoonotic pathogens that they carry in an impoverished inner-city neighbourhood of Vancouver, Canada. By characterizing rat populations within our study area, we were able to identify a number of factors which could influence the ecology of rat-associated zoonoses. We were also able to design a tool to predict rat abundance based on characteristics of the urban microenvironment, which may be useful for predicting pathogen prevalence in the future. Although we found that Leptospira interrogans (a common rat-associated zoonosis) was present in our study area, other zoonoses thought to be endemic in rat populations worldwide (Seoul hantavirus, Rickettsia typhi, and Bartonella spp.) were conspicuously absent. However, rats were found to carry other potentially zoonotic organisms (Clostridium difficile and methicillin-resistant Staphylococcus aureus) for which they are not the ‘traditional’ reservoir. Finally, we found that by integrating data regarding rat ecology and rat-associated zoonoses, we were able to gain a more comprehensive picture of how these pathogens circulate within rat populations. Overall, these results illustrate the importance of a comprehensive and holistic approach for obtaining a better understanding of rat-associated zoonoses, and highlight the need for ongoing research and surveillance. Future research conducted by the Vancouver Rat Project, specifically, will include a serosurvey to detect exposure to rat-associated zoonoses in people and a metagenomic analysis to better understand the full scope of zoonotic risks in rats.
THE PERSISTENCE OF FIVE *TRICHOMONAS GALLINAE* ISOLATES IN SIMULATED BIRD BATHS WITH AND WITHOUT ORGANIC MATERIAL

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*Trichomonas gallinae*, a protozoan parasite, has been implicated in recent mortality events in passerines. However, its persistence in bird baths is unknown and these congregation sites could serve as a nidus of disease transmission. We explored the persistence of five isolates of *T. gallinae* (Cooper’s Hawk, Broad-winged Hawk, Rock Pigeon, Jones-Barn, and House Finch) in distilled water with and without the addition of untreated or autoclaved organic material. We inoculated each container with \(1 \times 10^6\) trichomonads and obtained 500 microliter aliquots at various time points post inoculation. Aliquots were inoculated into Diamond’s media and incubated at 37°C and examined for 5 days for live trichomonads. Persistence of the isolates ranged from 0-16 hours post inoculation. The Cooper’s Hawk isolate persisted up 16 hours post inoculation. Persistence increased with the presence of organic material, autoclaved or untreated. We demonstrated persistence of *T. gallinae* for extended periods in simulated bird baths suggesting that contaminated bird waterers and bird baths may contribute to transmission of *T. gallinae* during outbreaks.
CLIMATE CHANGE AND MUSKOX LUNGWORMS: TRACKING EMERGENCE AND RANGE EXPANSION ON THE CANADIAN ARCTIC

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Umingmakstrongylus pallikuukensis and Varestrongylus sp. nov. are important protostrongylid nematodes of muskoxen in the Canadian Arctic. Previously confined to the westcentral Canadian mainland, they were discovered on the Arctic Archipelago for the first time between 2008 and 2010. Since then, these potentially pathogenic lungworms have substantially expanded their geographical range with increasing prevalence and intensity of infection every year. Previous degree-days mapping based on weather station data suggests that the rapid range expansion for U. pallikuukensis is in part associated with a warming climate, which has now become permissive for a single season completion of the parasite’s life cycle. The present study aims to establish and track the current distribution limit and determine the potential range of both parasite species under past, present and future climatic conditions. Detailed morphological and morphometric studies, confirmed by molecular identification were done to identify and establish the key features which could be used to differentiate the first stage larvae (L1) of the two species. Fecal samples from different areas of the Canadian Arctic (mainland, Victoria and Banks islands) were analyzed for the presence of L1 of these parasites. The survey results support the rapid north-eastward range expansion of U. pallikuukensis on Victoria Island and absence of these parasites on Banks Island. The prevalence and intensity of Varestrongylus sp. nov. on south-east Victoria Island increased from 2009 to 2013, but data are insufficient to comment on its range expansion. Data on temperature dependent larval development for both nematodes will be used along with the satellite surface temperature data to generate the degree day maps for past, current and potential future distribution. This is vital in anticipating areas of potential range expansion. This knowledge contributes to the field of arctic parasitology from diagnostics to wildlife ecology and management.
ROLE OF THE WESTERN GRAY SQUIRREL (SCIRUS GRISEUS) IN THE DISEASE ECOLOGY OF BORRELIA BURGDORFERI ON THE CENTRAL CALIFORNIA COAST

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The ecology of Borrelia burgdorferi genospecies on the central coast of California is poorly understood. Although there are six genospecies of B. burgdorferi sensu lato described from N. America, only B. burgdorferi sensu stricto is routinely isolated and implicated as the cause of human Lyme disease in this region. In San Luis Obispo County, B. bissettii is widespread in several rodent species inhabiting coastal scrub and chaparral. However, B. burgdorferi sensu stricto was not detected in our previous study. In northwestern California, B. burgdorferi sensu stricto has been primarily associated with high populations of Ixodes pacificus tick vectors in dense woodlands or hardwood-conifer habitats, particularly in the western gray squirrel reservoir host, Sciurus griseus. We investigated the role of S. griseus and other associated rodents in central coastal California woodland habitats as potential reservoirs for B. burgdorferi sensu stricto. Rodents were live-trapped in oak and mixed woodland as well as adjacent habitats and sampled by ear punch biopsy for Borrelia burgdorferi genospecies via culture in BSK-H and PCR of the 5S (rrf)–23S (rrl) intergenic spacer amplicon gene. Of 119 captured rodents, 15/16 S. griseus were PCR positive and 3 of these were culture positive. Multiple species of host-associated and questing Ixodes spp. ticks from study sites were also collected and tested for borreliae by PCR. B. burgdorferi genospecies present in rodents and ticks were identified by DNA sequencing. The high infection prevalence in the previously unsurveyed S. griseus in this region of California suggests that this species plays an important role in the disease ecology of Borrelia burgdorferi genospecies in a variety of woodland habitats throughout the state.
OPTIMIZING SURVEILLANCE FOR FOREIGN ORIGIN INFLUENZA A VIRUSES IN WILD BIRDS ALONG THE UNITED STATES GULF COAST

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Relative to research focused on intercontinental viral exchange between Eurasia and North America, less attention has been directed towards understanding the redistribution of influenza A viruses (IAVs) by wild birds between North America and South America. In this study, we sampled blue-winged teal (Anas discors) for IAVs at locations along the Texas and Louisiana Gulf Coast during spring, coincident with northward migration of this species from Neotropical wintering areas to breeding grounds in the United States and Canada, to assess the role of this species in the redistribution of viruses between continents. A total of 46 IAVs were isolated from 1,563 paired oropharyngeal and cloacal swabs tested (2.9%). The relative frequencies of hemagglutinin and neuraminidase subtypes for isolates recovered from spring sampling efforts were different than those recovered from blue-winged teal during summer/autumn sample collections. Genomic characterization revealed no evidence of South American lineage genes in IAVs isolated from blue-winged teal during spring supporting restricted viral gene flow between the United States and southern South America. However, it is plausible that blue-winged teal redistribute IAVs between North American breeding grounds and wintering areas throughout the Neotropics, including northern South America, and viral gene flow is limited by geographical barriers further south (e.g. the Amazon Basin). Surveillance for the introduction of IAVs from Central America and northern South America into the United States may be further optimized through genomic characterization of viruses resulting from coordinated, concurrent sampling efforts targeting blue-wing teal and sympatric species throughout the Neotropics and along the United States Gulf Coast.
ECO-EPIEMIOLOGIC STUDY OF FRANCISELLA TULARENSIS, THE AGENT OF TULAREMIA, IN QUÉBEC

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Francisella tularensis, the etiological agent of tularemia, is a zoonotic bacteria found in over 200 animal species. Tularemia is endemic in Canada, affecting mostly snowshoe hares, muskrats and beavers. Despite numerous studies, knowledge of its ecological occurrence and natural reservoirs is limited. The objectives of the present study were to estimate the prevalence of F. tularensis in snowshoe hares, muskrats and coyotes in 4 regions of Québec and to describe the risk of infection in relation to ecological and host characteristics. In this cross-sectional study, 345 snowshoe hares, 412 muskrats and 385 coyotes were captured by trappers between October 2012 and March 2013. Blood samples were taken from each carcass for micro agglutination tests (MAT). DNA extracts of liver, kidney, lung and spleen from the snowshoe hares and muskrats were tested by real-time PCR. Age was estimated by analysis of the canines of coyotes, molars of muskrats and eye lens of hares. Body condition was measured by the kidney fat index in coyotes and the visual quantity of abdominal fat in hares. Ecological characteristics around the location of capture were extracted from a geographic database. Logistic regression was used to quantify the risk factors for infection. The geographic distribution of infected animals was analyzed. Prevalence of antibody against F. tularensis was 1.3-2.9% in coyotes, 0.3-0.6% in hares and 0% in muskrats, depending on the interpretation threshold. No cross-reaction with Brucella abortus was found. DNA of F. tularensis was not detected by real-time PCR in the pool of 4 organs from muskrats and hares but was detected in individual organs of seropositive hares. Further results will be discussed in the presentation. This study will lead to a better understanding of the ecological cycle of F. tularensis within common reservoir hosts and indirectly, the risk of infection for trappers in Québec.
FIELD TECHNIQUES IMPROVING ANIMAL WELFARE

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The science of animal welfare is relatively new, especially in its application to free-ranging fish and wildlife. However it is growing rapidly, reflected in the large number of scientific publications dealing with fish and wildlife welfare that have appeared in recent years. Society expects the actions of wildlife workers to benefit the wildlife populations and to be beneficial or at least benign to the individual animals being studied. As professionals involved with wild animal work, biologists and veterinarians largely share these goals with members of the public. We must ensure that the data we collect for research and management is of the highest quality. This is possible when we have the least post-interaction effect on the activities and behaviors of the animals being studied. Important reasons for the improvements in animal welfare for fish and wildlife have been technical (e.g., the introduction of chemical immobilization, camera trapping, and non-invasive sampling) and demographic (the involvement of different professions and people). Wildlife professionals can and should promote their pivotal role in the furthering of the welfare of wild animals. In addition they must be pro-active in developing and documenting the effectiveness of new approaches used in wildlife research. Issues that continue to be of paramount concern are the effects of pursuit, capture, holding, handling, sampling, and marking of wild animals. Each of those activities has well documented adverse effects on the animals. The effects may even be trans-generational.
USING LONG-ACTING NEUROLEPTICS AND OTHER DRUGS TO REDUCE STRESS ASSOCIATED WITH LARGE UNGULATE CAPTURE AND TRANSLOCATION

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Capture and translocation are important tools for managing and studying large ungulates in many jurisdictions. Although widely used, many established field practices impose stress on subject animals and can hamper the overall effectiveness and safety of such endeavors. Over the last ~10 years we have been exploring uses of long-acting neuroleptic (LAN) and other tranquilizer combinations as adjuncts to capture and translocation work in Colorado, USA. Our approaches have been tailored to various field applications on a case-by-case basis to facilitate handling, reduce stress, and improve the overall success of capture and translocation for research or management purposes. For capture via darting, a combination of butorphanol, azaperone, and medetomidine (BAM) provides a small-volume alternative to the potent opioids; the immobilizing effects of BAM can be antagonized while still affording short-term tranquilization from azaperone (and butorphanol, as desired). To reduce stress associated with physical capture (e.g., drop net or helicopter netgunning) and mitigate hyperthermia and capture myopathy, combinations of midazolam and azaperone administered immediately upon capture provide transient tranquilization and muscle relaxation during manual restraint and handling. For extended tranquilization (e.g., during transport and overnight holding), long-acting haloperidol provides sustained calming effects for 24–48 hr. In our assessment, appropriate and adaptive use of these drugs and drug combinations stands to benefit treated individuals without impeding the achievement of management or research goals.
EVALUATION OF STRESS IN CARIBOU (*Rangifer tarandus granti*) ATTRIBUTED TO DIFFERENT CAPTURE METHODS

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Caribou (*Rangifer tarandus granti*) are routinely live-captured in Alaska for research and management. Capture methods vary from chemical immobilization with a dart gun from helicopter, net-gunning from helicopter or hand-capture from boats during a river crossing. We evaluated the effect of different capture methods on selected blood constituents known to be influenced by stress. Venous samples were collected from the jugular or cephalic vein, from caribou captured with net-gun (NG, \(N = 28\)), hand-captured (HC, \(N = 20\)) or darted from a helicopter with carfentanil/xylazine (CX, \(N = 54\)), medetomidine/ketamine (MK, \(N = 9\)) or thiafentanil/azaperone/xylazine (TAX, \(N = 8\)). To quantify stress, blood constituents used included lactate and creatine kinase (CK). Use of a hand-held lactate monitor was validated for field use in caribou with a significant correlation to laboratory serum lactate (\(P < 0.05\)). Lactate was increased in all groups, and significantly increased (\(P = 0.001\)) in both NG and HC, compared to chemical immobilization via helicopter darting. Mean±SD (range) for lactate was 4.9±2.7 (1.0 - 13.0) for CX, 4.8±2.0 (2.4 - 7.4) for MK, 4.3±1.1 (2.8 - 6.0) for TAX, all measured in field, and 21.7±5.6 (12.4 - 31.2) for NG and 18.4±7.6 (6.6 - 42.8) for HC both measured in lab. We found a significant correlation (\(P < 0.05\)) between increased lactate values and chase time. CK was increased in all groups, with a trend of highest increase in the hand-captured group. However, this was not proven statistically (\(P = 0.063\)). Physically restrained caribou had lactate levels four times higher than chemically immobilized caribou. This indicates that physical restraint causes more distress for caribou than helicopter darting and thereby may present a higher risk for capture myopathy. Further, our findings show that longer chase times increases lactate, and we recommend that concentrated pursuit of individual caribou be kept <2 minutes.
HOW TO NOT KILL PRONGHORN: A CHRONOLOGY OF HANDLING A DESERT SUBSPECIES LEADING TO ZERO MORTALITY

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The Sonoran pronghorn (Antilocapra Americana sonoriensis) was listed as an endangered subspecies in 1967. Active management began in 2002 when a drought resulted in 19 wild Sonoran pronghorn remaining in the United States. In 2004, seven wild Sonoran pronghorn were transported to a semi-captive breeding pen on the Cabeza Prieta National Wildlife Refuge to recover the subspecies. While pronghorn are a difficult species to immobilize with high mortality risk, managing this semi-captive, non-habituated herd required annual captures, relocations, and releases. Through trial and error using immobilization protocols shown to be successful on other pronghorn, we determined that these procedures resulted in unacceptably high mortality in Sonoran pronghorn. By developing unique protocols, ninety-five pronghorn were handled with zero capture-related mortalities in 2013. The protocol began by baiting the herd into a remote controlled, three-part boma structure. Utilizing a drive-net, six to eight muggers physically captured the pronghorn with two handlers per pronghorn. Animals were immediately removed from the net, held off the ground, and blindfolded. The target animals’ destination determined the next stage of the protocol. Animals selected for return to the breeding pen were tagged, treated, and released. Animals selected for soft release or to be trailered for release received the same treatment with the addition of haloperidol. Animals selected for helicopter transport and release were treated identically to the second group, but were anesthetized with thiafentanil/xylazine intravenously, and maintained with intermittent ketamine along with intravenous fluids and oxygen to reduce temperature and stress for the hour long flight. These animals were antagonized with naltrexone/tolazoline and recovered in special recovery pens at the remote release sites. All animals were observed for two weeks following capture and no mortalities occurred. During the 2013 census, 159 wild Sonoran pronghorn were observed in the U.S., which is largely attributed to these adaptive techniques.
EFFECTIVENESS OF THE ANESTHETIC AQUI-S 20E IN MARINE FINFISH AND ELASMOBRANCHS

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Immersion anesthetics have been used in hatchery settings and by field biologists and laboratory researchers to aid in handling finfish for medical procedures, research purposes, and moderating perceived stress responses. The only FDA-approved anesthetic for food fish, MS-222 (tricaine methanesulfonate), requires a 21-day withdrawal prior to harvest. Aqui-S 20E (10% eugenol), an investigational new animal drug, has been gaining momentum for FDA approval, because of its zero day withdrawal time if fish are not of harvestable size within 72 hours of exposure. Most trials have focused on its use in freshwater finfish. Our marine hatchery performed two trials to determine appropriate anesthetic doses for cultured white seabass and California yellowtail; fish were held in a treated water bath for 10 minutes or until breathing rate slowed to a rate of <2 breaths/minute. Anesthesia was defined as the time when a fish lost its cough reflex and failed to respond to deep palpation of the lateral line. Trials with several species of wild marine finfish and elasmobranchs at a single dosing regime were also performed, with animals held 5-10 minutes in anesthetic baths. Anesthetic dosing of 35-55 ppm provided relatively fast induction and good anesthetic maintenance in cultured and wild finfish. Anesthetic induction times were comparable among yellowtail and white seabass at 35-75 ppm doses, but recovery times were variable, with significant differences between white seabass and other finfish tested. Mortality rates of 20-90% were observed at higher doses (75 and 100ppm, white seabass; 55 and 75 ppm, California yellowtail). The apparent increase in sensitivity of California yellowtail may have been associated with nutritional stress in the fish tested. Anesthetic induction, maintenance and recovery were less predictable in elasmobranchs both within and among species and additional trials are needed to determine optimal dosing.
SUMMER SURVEILLANCE FOR *PSEUDOGYMNOASCUS DESTRUCTANS* AT CONTAMINATED HIBERNACULA: IMPLICATIONS FOR TIMING OF TRANSMISSION

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Persistence of *Pseudogymnoascus destructans* (Pd), the pathogenic agent responsible for white-nose syndrome (WNS), in hibernacula and the continuous or periodic use of some contaminated hibernacula by bats throughout the summer pose a potential risk for exposure from an environmental reservoir. Bats exposed to viable Pd in late summer could transport the fungus to other bats via direct contact or to other locations well-suited for the growth and maintenance of the fungus. In order to explore transmission risks outside of the winter season, this cross-sectional study examined late summer occupants at select hibernacula confirmed to be contaminated with Pd as potential sources for Pd transmission in the fall. Wing swabs from 617 bats, representing eight species, were collected between mid-July and August 2012 at eight hibernacula (six Pd contaminated, two presumably “clean” sites) located in the Ohio River Valley region. Feces were collected opportunistically from 221 individuals. Environmental samples taken from multiple areas within each site confirmed the presence of Pd at the contaminated hibernacula. Pd was detected on bats at both contaminated and “clean” sites and viable fungus was recovered. Feces yielded a higher apparent prevalence of Pd exposure among bats sampled during the summer than wing swabs alone. Low recapture rates of marked bats at all locations on subsequent trap nights suggested a high degree of movement among bats using these sites in late summer and thus, summer-exposed bats may be contributing to pathogen dissemination on the landscape more than previously thought. Finally, demonstration of Pd contamination of research equipment supported the potential for human-assisted movement of the fungus and the risk for cross-contamination of bats associated with late summer/fall trapping activities conducted at hibernacula within the WNS endemic region.
ENVIRONMENTAL VARIABLES THAT EXPLAIN EXPOSURE OF WHITE-TAILED DEER TO PARAINFLUENZA 3 VIRUS IN WISCONSIN

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White-tailed deer (Odocoileus virginianus) are commonly exposed to parainfluenza 3 virus (PI3). In cattle, the virus is transmitted via aerosolization, and contact with cattle and other deer have been proposed as mechanisms for transmission in deer. Our goal was to identify variables that explain exposure of white-tailed deer to PI3 in Wisconsin. We hypothesized that deer would be concurrently exposed to livestock pathogens because natural history would predispose certain deer to concurrent exposure, and that deer from a high-density population would be more commonly exposed to PI3 than deer in a low-density population. Deer were trapped from January to March in Winter and Shiocton, Wisconsin, USA, from 2011 – 2013. Blood samples were taken from deer via jugular venipuncture, and sera were sent to the Minnesota Veterinary Diagnostic Laboratory for testing for antibody against six serovars of Leptospira interrogans using microscopic agglutination, against infectious bovine rhinotracheitis virus (IBR) using serum neutralization, and against PI3 using hemagglutination inhibition. We considered deer titers of 1:100 for Leptospira interrogans, 1:16 for IBR, and 1:20 for PI3 as evidence of exposure. We used logistic regression to model potential intrinsic (e.g., age, sex) and extrinsic (e.g., land type, study site, year, exposure to concurrent infectious diseases) variables that we considered biologically meaningful. We used AIC corrected for small sample size (AICc) for model selection. We specified 14 models: a global model containing seven variables and a subset of a priori models. A model containing exposure to L. i. pomona, exposure to IBR, and trap site was the best-approximating model. Deer trapped in Shiocton that were also exposed to L. i. pomona and IBR were more likely to be exposed to PI3. Deer density near Shiocton is at least twice that near Winter, likely influencing exposure of white-tailed deer to PI3, IBR, and L. i. pomona.
DISEASE TRANSMISSION AT THE WILDLIFE-LIVESTOCK INTERFACE: MULTI-SPECIES MODELING OF BOVINE TUBERCULOSIS IN MICHIGAN

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Disease causing organisms are rarely restricted to a single-host. Multiple host species may be involved as a part of a parasite’s complex life-cycle, as dead-end hosts that are infected but are unsuitable for continuing transmission, or as part of a system of host species with continuous intra- and inter-species transmission. We present a model of transmission of bovine tuberculosis (bTB, Mycobacterium bovis) among a free-ranging white-tailed deer (Odocoileus virginianus) population and a spatially-structured cattle population applied to bTB in Michigan, USA. We ask, can observed bTB dynamics in both species be maintained as if both species are part of a single interacting host population? Or is one species the primary reservoir with directional spillover to the other? We developed a spatially-explicit farm-based susceptible-exposed-infected-removed (SEIR) model of bTB transmission dynamics that includes local farm-farm transmission (such as shared equipment, shared feed, etc.) and long-distance transmission parameterized by the observed cattle transport network. We developed a non-spatial white-tailed deer age-structured SEI model parameterized by disease surveillance and demographic data in Michigan. We found that observed patterns of spatially clustered low-prevalence bTB are unlikely to be generated by separate transmission cycles in cattle and wildlife. Transmission in deer is able to be maintained in a density-dependent manner. Transmission to spatially dispersed areas is unlikely under scenarios with only local-scale transmission among livestock farms and wildlife; a mechanism for dispersal of the disease agent (such as truck transports of animals) is necessary to generate spatial dispersion of the disease. We conclude that bTB in Michigan is adequately described by endemic transmission in deer, but cannot rule-out a system with bi-directional transmission among the multiple hosts species.
INABILITY TO TRANSMIT BORRELIA BURGDORFERI BY CO-FEEDING TICKS IN TWO SKINK SPECIES, EUMECES FASCIATUS AND PLESTIODON LATICEPS

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Although previous studies have assessed the reservoir competency of the agent of Lyme disease, Borrelia burgdorferi, in various lizard species, the potential for co-feeding transmission of B. burgdorferi in lizards has not been examined. Skinks have been shown to be a preferred host for Ixodes scapularis in the southeastern United States anecdotally and a southward moving trend of I. scapularis has been observed. Thus, there is an increasing possibility of skink and I. scapularis interaction and B. burgdorferi transmission. As multiple life stages of tick inhabit a single skink, we sought to assess the potential for B. burgdorferi sensu stricto (s.s.) co-feeding between naturally infected nymphs and larval black-legged ticks (Ixodes scapularis) within two species of skinks. Four five-lined skinks (Eumeces fasciatus) and seven broad-headed skinks (Plestiodon laticeps) were used in the study. Skinks were initially determined to be negative for Borrelia via larval I. scapularis xenodiagnostic testing. To determine co-feeding as a mechanism of transmission, we placed approximately 20 wild-caught I. scapularis nymphs, originating from Lyme borreliosis-endemic regions of the United States, on each lizard. On day 4 post-nymph infestation, approximately 50 B. burgdorferi-negative larvae were placed on each lizard. Seven days post-larval infestation, all attached ticks were removed. All co-fed larvae were PCR negative for Borrelia by polymerase chain reaction (PCR). Of 25 wild-caught nymphs not used for skink infestations and 12 nymphs that were unattached in the skinks’ enclosures, 18.9% (n = 7) were Borrelia PCR positive. However, only 6.5% (n = 2) of skink-fed nymphs were Borrelia PCR positive. These data strongly suggest that co-feeding does not occur in E. fasciatus or P. laticeps.
Superspreading individuals have been found to play a key role in disease epidemics. Superspreading is deemed to occur when <20% of infected individuals are responsible for >80% of transmission. If superspreading occurs for an entire species, they are considered an amplification host. In eastern North America, ranavirus die-offs are often associated with wood frog (Lithobates sylvaticus) tadpoles. We tested whether wood frog tadpoles exhibited superspreading, and if their presence affected transmission dynamics of ranavirus in a typical vernal pool community. Superspreading was tested in controlled laboratory conditions, whereas community-level transmission was observed in outdoor aquatic mesocosms. We found that superspreading of ranavirus occurred in all replicates (n = 20) from one infected wood frog tadpole to nearly all conspecifics with only 6 hours cohabitation. In the aquatic mesocosms, we found that if wood frogs were initially exposed to ranavirus, community-wide mortality was higher than if upland chorus frog (Pseudacris feriarum) or spotted salamander (Ambystoma maculatum) larvae were exposed first. Our results indicate that the presence of wood frogs in an amphibian community could significantly increase the probability of a community-level outbreak of ranavirus. Based on our results, wood frogs could be considered amplification hosts of ranavirus. Wildlife biologists in eastern North America should consider targeting amphibian communities with wood frogs for ranavirus surveillance programs.
SPATIO-TEMPORAL TRENDS IN PREVALENCE OF ANTI-BRUCELLA ANTIBODIES IN BARREN-GROUND CARIBOU (RANGIFER TARANDUS GRANTI) IN ALASKA—AN EXAMPLE OF ENZOOTIC EQUILIBRIUM

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Alaska has approximately 750,000 barren-ground caribou (Rangifer tarandus granti) in 32 herds. Semi-domesticated reindeer (Rangifer tarandus tarandus) were introduced in 1891. Free-ranging descendants of these once numbered over 20,000, but only remnant managed herds of less than 8000 remain on the Seward Peninsula and fewer than 3000 are unmanaged on remote islands. Brucella suis biovar 4, the causative agent of brucellosis in Rangifer tarandus spp., causes bursitis, orchitis, epididymitis, retained placenta, metritis, abortions, and abscesses. Vaccination of semi-domesticated reindeer on the Seward Peninsula against brucellosis started in the mid-1980’s. Of importance, B. suis biovar 4 poses a zoonotic risk. We analysed the spatio-temporal trends in Brucella seroprevalence from 11 caribou herds between 1975 and 2010. The overall pattern over time was a low seroprevalence (average 1.2 %). The Western Arctic Herd (WAH), however, had a decline from 23 to 3 % in seroprevalence in the investigated period (logistic regression estimate of slope, 95 % CI = [-0.09, -0.04]). In the WAH, seropositives were found only among individuals above 23 months. Analysis of a sub-sample of individuals tested by several different serological tests showed good coherence between the tests. The WAH home range overlaps with semi-domesticated reindeer on the Seward Peninsula. While semi-domesticated reindeer could have been a source of B. suis biovar 4 for caribou, efficient management of semi-domesticated reindeer may have reduced the caribou exposure rate. Stochastic severe declines in caribou populations leading to reduced animals densities and thus less exposure on the calving grounds may have reduced further transmission between caribou. Additional reasons for the declining seroprevalence may exist and this warrants further investigation. The severe decline in Brucella seroprevalence in the WAH, however, may indicate a herd reaching an enzootic equilibrium for brucellosis, to the same level of seroprevalence as for the other arctic caribou herds.
SCREENING FOR EXPOSURE TO INFECTIOUS AGENTS IN WILD TAKINS (*BUDORCAS TAXICOLOR WHITEI*) AND DOMESTIC YAKS (*BOS GRUNNIENS*) FROM SHARED SUMMER HABITAT IN BHUTAN: MANAGEMENT IMPLICATIONS

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Infectious diseases and climate change are likely threats to Bhutanese biodiversity. Regional rising mean temperatures expected from climate change will affect exposure to parasites, vector-borne pathogens and other infectious agents. To establish initial baselines, biomaterials were collected from seven domestic yaks and five wild Bhutanese takins in shared Himalayan alpine (elevation ~4000 meters) summer habitat in Jigme Dorji National Park. Diagnostics included hematology, partial biochemistry analysis, serology (*Brucella abortus*, FMD, BVDV, IBR BHV-1, *Fasciola hepatica*, *Leptospira sp*, and *Mycoplasma mycoides*), fecal endoparasite evaluation, skin scrape ectoparasite evaluation, nasal swab influenza A PCR and PCR ectoparasite identification and screening of ticks and blood for vector-borne diseases. Serology revealed one takin as FMD-positive and two yaks *Fasciola hepatica* positive. Four takin tested PCR positive for *Theileria* spp. One takin and one yak tested positive for *Anaplasma phagocytophilum*. *Anaplasma* spp were detected in takin and yak ticks, *Theileria* spp in yak ticks and *Rickettsia* spp in takin ticks. Ticks and blood were negative for *Borrelia, Coxiella, Bartonella, Hepatoplasma, Babesia and Ehrlichia. Anaplasma, Theileria* and FMD have not been previously reported in takins. *A. phagocytophilum* poses a zoonotic risk to yakherders and trekkers. Recent *Cordyceps* harvest legalization has resulted in alterations to regional yak management with yaks now remaining in Tsharjathang valley where they have contact with takins congregating during summer rut. Study results support stricter adherence to existing agreements to exclude yaks from the valley in summer to minimize risks of infection spill-over from reservoir species. Improved infection screening and management of livestock imported to the region should be considered. Further assessment of disease exposure and impact in wild (takin, blue sheep, dhole, fox, snow leopard, marmot) and domestic (yaks, equids, dogs) mammals in the park over time is warranted to optimize adaptive management practices for animal health and biodiversity.
RETROSPECTIVE STUDY CHARACTERIZING PARELAPHOSTRONGYLUS SPECIES IN WILD AND DOMESTIC UNGULATES FROM TENNESSEE

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Parelaphostrongylus tenuis is a nematode commonly found in the meninges of white-tailed deer (Odocoileus virginianus) that causes severe neurological problems in aberrant or dead-end hosts including elk (Cervus elaphus), moose (Alces alces) and numerous other species. Currently, P. tenuis diagnoses are made by histological analysis, but the likelihood of finding a nematode during gross necropsy and/or histology is variable, and therefore diagnoses are often inconclusive. Additionally these lesions may also indicate other neurologic conditions, thus a conclusive test for P. tenuis is critical for proper diagnosis. We histologically examined wild and domestic ungulate formalin-fixed, paraffin-embedded tissues, with case histories and lesions suggestive of P. tenuis, from archived samples at the University of Tennessee’s College of Veterinary Medicine. Sections of paraffin-embedded tissue from these cases were also used in a nested polymerase chain reaction (nPCR) using Parelaphostrongylus-specific primers to determine how PCR results corresponded with histological findings. Histological changes consisted of lesions including acute linear tracks of hemorrhage or perivascular accumulations of hemosiderin-laden macrophages, acute foci of Wallerian degeneration and/or linear glial scars, and perivascular, parenchymal, or meningeal accumulations of eosinophils and/or lymphocytes and plasma cells. Of the 43 samples with histologic lesions consistent with neural larval migrans, 19 were PCR positive; however, only eight were confirmed Parelaphostrongylus by DNA sequencing. One goat was identified with a protostrongylid that had a 97% identity to both Parelaphostrongylus odocolei and a protostrongylid nematode from pampas deer from Argentina. The results indicate that it is possible to extract Parelaphostrongylus DNA from formalin-fixed, paraffin-embedded tissue even if a nematode is not seen in the corresponding histologic sample, but extended fixation presumably can cause DNA crosslinking, which may inhibit amplification for PCR. Furthermore, we detected potential novel protostrongylid DNA from a goat with lesions consistent with P. tenuis infection, suggesting that other neurotropic Parelaphostrongylus species may occur locally.
HEMORRHAGIC DISEASE IN A NEBRASKA BISON HERD

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American plains bison (Bison bison bison) have not traditionally been considered susceptible to epizootic hemorrhagic disease (EHD) or bluetongue virus (BTV), although viremia and subsequent seroconversion have been reported. EHD was suspected in the deaths of three bison examined from three separate herds in South Dakota in 2012. Significant post-mortem lesions were described but oral lesions typically seen in cattle were not found in any of these cases. EHD was also suspected in the death of a single bison in Iowa in 2012 and in a single bison in Montana in 2013. We describe the results from diagnostic investigations from a 2013 disease outbreak that clinically affected most bison in the Fort Niobrara herd in Valentine, Nebraska, USA. Mortality was estimated at 5% and the oldest age classes were disproportionately affected while very few calves died. Clinical presentation was highly variable among individuals and included: lethargy, stiffness, diarrhea, peeling hide most often found near the tailhead, ptyalism, thin to mucoid nasal discharge, thin to mucopurulent ocular discharge, respiratory distress and death. Oral lesions occurred in only one of the first 11 cases and then consistently in the last five. Malignant catarrhal fever was ruled out in all cases. Sixty-nine percent of animals examined contained either EHD serotype 2 (n = 7) or one of 3 BTV serotypes (n = 5) viral RNA, with one animal positive for both. Thirty-nine percent of whole blood samples collected from a portion of the surviving herd contained EHD serotype 2 (n = 8) or one of 3 BTV serotypes (n = 20) viral RNA, including one animal positive for both. Although questions remain about the potential contribution of other pathogens, hemorrhagic disease should be considered a potentially significant disease in bison with a clinical presentation inconsistent with that typically seen in cattle.
A MORTALITY EVENT AMONG ELK IN NORTHERN NEW MEXICO DURING LATE SUMMER 2013

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On the morning of 27 August 2013, two hunting guides discovered a number of elk dead on privately-owned land in Mora County, New Mexico, USA. The guides reported dead elk numbering at least 40. Upon arrival that afternoon, we estimated the elk to have been dead 24 to 36 hours. A thorough count resulted in at least 113 carcasses. All dead elk were cows, young of the year, and yearling males. Carcasses were in ponderosa parkland and were distributed on the open ridgeline and in the shade of the wooded hillside. Signs of paddling were evident at each carcass. Tissues were collected, rumen contents were collected, and water was collected from the nearest water source. A fixed-wing aircraft flight the next morning failed to detect other dead or moribund elk in the area. Except for small hay fields, no agricultural activity was observed and no evidence of chemical or industrial activity was found in the area. No toxic plants were found during walking surveys, and no toxic plants were found in rumen content. Lightning strike data showed no lightning activity in the area. Anthrax was not detected in laboratory testing. Botulinum toxin was presumed present but not confirmed by mouse bioassay. No abnormal histology was reported. Epizootic hemorrhagic disease tests were negative. Cyanobacteria of the genera Anabaena and Coelosphaerium were detected -- anatoxin-A and hepatotoxins are associated with these two cyanobacteria, respectively. We concluded that cyanobacteria in stagnant water troughs appeared to be the cause of this mass mortality.
RESPIRATORY DISEASE SURVEILLANCE IN BIGHORN SHEEP: LINKING PATHOGENS AND HERD HEALTH

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Bacterial pneumonia is a known cause of major population declines in bighorn sheep herds across the west, yet agreement on the true causative agent(s) remains elusive. To better understand the distribution and pathogenicity of these respiratory pathogens, we have initiated a study to link pathogen presence with herd health. Two years into a three year study, we have sampled 187 bighorn sheep from ten herds in Wyoming, USA, via drop net, chemical immobilization and helicopter capture. Blood, feces, and swabs (tonsil, nasal and ears) were collected. Tonsil swabs were immediately plated in the field, then read at 24 and 48 hours; suspect colonies were subcultured and identified via biochemical reactions and polymerase chain reaction. Nasal swabs were placed into enrichment broth within 72 hours, followed by culture and PCR. Most herds were infected with leukotoxigenic Mannheimia haemolytica, M. glucosida, M. rumenalis, and Bibersteinia trehalosi. Pasteurella multocida was endemic in all herds and Mycoplasma ovipneumoniae was identified in eight herds. Three to five year average lamb ratios for these herds range from 21 to 57 (mean 33). At this point in our research, no clear relationship has been identified between a single pathogen or combination of pathogens and lamb ratios. Future research will include similar analysis from bighorn sheep herds in Colorado and Montana.
ASSESSMENT OF HEALTH STATUS FOR MOOSE (ALCES ALCES) IN IDAHO, USA

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Moose (Alces alces) populations in many of the western and Midwestern states are declining. In Idaho, moose populations appear to be stable to increasing. Therefore, this study was undertaken to establish baseline values for the assessment of health for moose in the state. Moose occur in varying densities across most of Idaho, and occupy habitat types that range from agricultural fields, sagebrush steppe, and coniferous forests and elevations from 500 to 8000 feet. Moose in Idaho are managed as a trophy species with bulls as a once in a lifetime opportunity for hunters. In 2013, hunters with moose permits (n=846) were asked to provide blood, feces, and liver samples from harvested animals in all areas of the state except for the southwestern portion. A total of 464 sample kits were received with 292 complete sample sets. Blood in 50 ml tubes was centrifuged and serum harvested and frozen until analysis. Feces for flotation and sedimentation and liver samples for trace mineral analysis were refrigerated or frozen until analysis. Results for 106 animals showed serological exposure to numerous pathogens including Leptospirosis spp. serotypes, IBR, BVD, PI3 and anaplasmosis. Prevalence and geometric mean titers (GMT) varied across the state with low prevalence (10-35%) and GMT (2-2.9) to IBR in the northern half of the state, and low prevalence (3-9%) and relatively high GMT (6-64) to BVD in the eastern half of the state. Prevalence and GMT to PI3 varied from 0-15% and 16-256, respectively with highest prevalence and GMT in the northwest portion of the state. Exposure to anaplasmosis ranged from 70-90% and was essentially equal in all areas of the state which is much different than previous surveys in the state. All animals tested were negative for titers to Brucellosis, BRSV, BT and EHD. Fecal flotation revealed relatively consistent but low prevalence to Nematodirus spp. and strongyle-type ova in the eastern half of state (10-30% and 0%, respectively), but high prevalence (40-60% and 10-40%, respectively) in the northern half of the state. Only two animals had fluke ova identified on sedimentation, but the species is not known. The presence of Taenia spp. cystercerci in the liver was relatively common in all areas of the state, with only two animals with hydatid cysts. Analysis of trace mineral levels in liver are incomplete at the time of abstract submission, but in general, copper, phosphorus and selenium vary greatly across the state and may reflect dietary differences between physiographic regions. Combinations of these mineral levels, especially copper and selenium may have health implications. While individual moose in the state are affected by various disease conditions and pathogens, the disease exposures in this study likely reflect exposure to cattle and do not represent disease risks for moose. Likewise gastrointestinal parasite levels are low. The relatively low levels of some trace minerals are of concern for some moose populations. But collectively, these data suggest that health status of moose harvested by hunters in Idaho is good. These data could be used as a baseline for comparison in those states in which moose populations are in decline.
BACTERIA ARE IMPORTANT TO CORAL REEF HEALTH (BUT NOT IN THE WAY EVERYBODY THOUGHT)

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Coral reefs are highly diverse ecosystems where algal-animal symbioses play a pivotal role. Corals are also dying from disease, and it is widely accepted that bacteria are responsible, yet aside from cyanobacteria, no evidence exists of bacterial-induced pathology at the microscopic level for diseased corals. To clarify potential causes of coral diseases, we have been doing histology on normal and diseased tissue of corals from throughout the Indo-Pacific. Unexpectedly, we found histological evidence of cell-associated bacteria in normal tissues with no associated pathology from healthy and diseased colonies in a diverse array of coral species across a broad geographic range. Prevalence of infection varied among coral genera with \textit{Acropora}, \textit{Porites}, and \textit{Pocillopora} commonly infected whereas \textit{Montipora} were not. Interestingly, three of these genera dominate reef ecosystems in the Pacific. \textit{Acropora} from the Western Pacific were more likely to be infected than those from the Central Pacific whereas the reverse was true for \textit{Porites}. Compared to apparently healthy colonies, normal tissues from diseased colonies were more extensively infected. The close association of bacteria with host cells in numerous species of apparently healthy corals and lack of associated cell pathology reveals an intimate agent-host association. It also appears that this association can be upregulated when corals are diseased, suggesting that these bacteria could be important to coral immunity. We have thus stumbled upon a new facultative secondary bacterial symbiosis in corals that could play an important role in the distribution, evolution, physiology, and immunology of reef corals of the Indo-Pacific.
CAUSES OF MORTALITY IN A POPULATION OF MARINE FORAGING NORTH AMERICAN RIVER OTTERS

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North American River Otters (Lontra canadensis) are widely distributed across North America where they occupy diverse freshwater habitats. From California to Alaska, they also occupy the nearshore marine habitat where they primarily feed on marine invertebrates and fishes and play an important ecological role moving marine nitrogen and phosphorus into nearshore vegetation. In an effort to learn more about diseases that impact marine-foraging river otters, we conducted complete postmortem examinations on 28 river otters that were found sick or dead in the San Juan Islands (Washington State, USA) between 2003 and 2013. These included 15 males and 13 females representing all age classes (<1 year old, 1-4 years old, 4-8 years old, and >8 years old) as determined by dental wear and cementum analysis. The highest mortality was detected in spring and summer months (n=11; 11) as compared to fall and winter (n=3; 3) with an average of 2.5 (±1.2) animals found per year. By far, trauma was the highest cause of mortality (42.9%). Cause of death could not be determined for 25% of cases. Other significant causes of mortality included metabolic (17.9%) and infectious (14.3%) diseases. The high prevalence of trauma in this population of marine-foraging river otters differs from the bulk of published literature on diseases of North America River Otters which focus primarily on toxic and infectious causes of disease, including parasitism.
EMERGENCE OF PHOCINE DISTEMPER VIRUS IN ARCTIC AND SUB-ARCTIC PINNIPEDS IN THE NORTHEAST PACIFIC OFF ALASKA


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Phocine distemper virus (PDV) nucleic acid was detected in live-captured and dead northern sea otters off the coast of Alaska in 2004, the first confirmation of this virus in a Pacific marine mammal. The emergence of this virus in the Pacific highlighted the need to examine its role in the mortality of sea otters and determine viral distribution in Arctic and Sub-arctic marine mammals in the Northeast Pacific. Sequence analysis confirmed the viral fragment was identical to that from the 2002 phocine distemper outbreak that caused large-scale mortality in harbor seals in Europe. Serological surveys prior to 2000 revealed that marine mammals in Alaska had not been exposed to PDV. Thus we hypothesized that virus was transmitted through the Arctic to the North Pacific after the 2002 epidemic by carrier species. A significant reduction in sea ice after 2002 may have altered seal haulout and migration patterns resulting in contact between Atlantic, Arctic, and Pacific Ocean species that was not possible after the 1988 outbreak. Sera (n = 700) were tested by serum neutralization to examine the timeline of exposure, and tissues and nasal swabs (n = 662) were tested by PCR for PDV nucleic acid northern sea otters, Steller sea lions, northern fur seals, bearded seals, ribbon seals, spotted seals and ringed seals from 2004 to 2011 to evaluate infection status. Serology indicated exposure likely first occurred in 2003 as >50% of Steller sea lion pups tested had antibodies against PDV. Positive titers were detected in all species, and the proportion appeared to decrease through 2008 and increased again in 2009. PCR supported the serology results, as positive tissues and nasal swabs were detected in multiple seal and sea lion species. Results indicated that PDV first emerged after 2002 and has been circulating in multiple species across Alaskan waters.
LEPTOSPIROSIS IN CALIFORNIA SEA LIONS (ZALOPHUS CALIFORNIANUS): DO DATA FROM STRANDED ANIMALS ACCURATELY REFLECT TRENDS IN THE WILD POPULATION?

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Since 1970, periodic outbreaks of leptospirosis, caused by Leptospira interrogans serovar Pomona, have caused morbidity and mortality of California sea lions (Zalophus californianus) along the Pacific coast of North America. The Marine Mammal Center (TMMC) has treated and collected data from sea lions stranding along the California coast, and leptospirosis has been a dominant cause of strandings. Mortality in sea lions stranding with leptospirosis is high despite treatment, only ~30% survive to release, and little is known about Leptospira dynamics in the free-ranging population. Since 2010 we have collected data on Leptospira exposure and infection from free-ranging sea lions, both within (Año Nuevo Island: ANI; n=145) and to the south (San Miguel Island: SMI; n=151) of the TMMC stranding range, to determine whether prevalence patterns observed in sea lions at TMMC (n=254) accurately reflect those in the overall population. We assessed evidence of exposure using microscopic agglutination testing for anti-Leptospira antibodies in sera, and active infection and shedding of leptospires in the urine using both PCR and culture. Yearly antibody seroprevalence in stranded sea lions at TMMC ranged from 0.15-0.67. During this same time period, temporal changes of seroprevalence from ANI sea lions (range 0.07-0.49) tracked those seen in stranded sea lions, while seroprevalences from SMI sea lions (range 0-0.03) were significantly lower than those seen in either SMI or stranded populations and showed little variation. Active infection was detected on both ANI (prevalence range 0.12-0.57 from 2010-2012) and SMI (prevalence range 0-0.16 from 2011-2012); however, serum chemistry analysis and clinical examination showed no evidence of renal disease, indicating subclinical infections. Our results suggest that patterns of exposure seen in sea lions stranding within the TMMC range reflect those seen in the free-ranging ANI population, but not those seen in the SMI population, which is south of the TMMC range.
BRUCELLA PINNIPEDIALIS HOODED SEAL STRAIN IN CELL MODELS

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Intracellular survival and replication is the hallmark of Brucella spp infection. Chronicity is often linked to multiplication in macrophages, a feature facilitated by overriding the intracellular response following bacterial infection. A stealthy entry into host cells is essential to avoid detection by the immune system. There are few studies of the mechanisms of bacterial intracellular invasion and multiplication involving marine mammal Brucella spp. Importantly, pathology in association with Brucella infection in seals is not described. Although the zoonotic potential of marine mammal brucellae is largely unknown, reports of human disease exist. Human and murine cell lines, as well as primary cultures from hooded seal (Cystophora cristata), were challenged with B. pinnipedialis strains (reference strain; NTCT 12890 and a hooded seal isolate; B17/17a-1). Our work shows that B. pinnipedialis strains are able to enter macrophages and epithelial HeLa cells in vitro. Although able to survive for up to 96 hr intracellularly, none of the strains were able to multiply in the cell lines tested. Both strains have limited ability to survive within primary cells from hooded seals, thought to be the preferential host species, as well as human/murine cell lines. A lack of, or low, capacity to replicate and survive for prolonged periods within host cells, particularly macrophages, abolishes the ability to produce chronic infections. In conclusion, our results indicate a low zoonotic potential of these B. pinnipedialis strains. Seals may not be the primary host for B. pinnipedialis, but rather a “dead-end” or spillover host susceptible to infection derived from other sources in the marine environment. Future research should aim at identifying the primary reservoir of B. pinnipedialis along with investigating potential virulent traits in marine mammal brucellae that may have implications in the establishment of disease, either acute or chronic, in marine mammals and humans.
IS BRUCELLA PINNIPEDIALIS UNABLE TO SUSTAIN A LONGTERM INFECTION IN HOODED SEALS (CYSTOPHORA CRISTATA)?

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Brucella spp. were first isolated from marine mammals in 1994. Brucella pinnipedialis and Brucella ceti were included in genus Brucella in 2007, with pinnipeds and cetaceans as preferred hosts, respectively. Previous investigations have revealed high prevalences of Brucella-positive hooded seals (Cystophora cristata) in the reduced Northeast Atlantic stock, compared to in the increasing Northwest Atlantic stock. This study evaluated relationships between Brucella-serostatus in seals of the Northeast Atlantic stock and age, sex, body condition and reproductive history (presence of corpus luteum and corpus albicans). No relationship was observed between Brucella-serostatus and sex, body condition or reproductive traits. Pups of the year had a substantially lower probability of being seropositive (4/159, 2.5 %) than yearlings (6/17, 35.3 %), suggesting that exposure is mainly occurring post weaning, during the first year of life. For seals > 1 year, the mean probability of being seropositive decreased with age, with no seropositive animals older than 5 years, indicating loss of antibody titre with either chronicity or clearance of infection. The latter seeming most likely as B. pinnipedialis has never been isolated from hooded seals >18 months. Bacteriological investigation of a range of organ samples from 21 hooded seals revealed one Brucella pinnipedialis isolate from a retropharyngeal lymph node of one animal. Based on the serological age-dependent pattern and the bacteriological findings in the present study we hypothesize an environmental aquatic exposure of hooded seals to B. pinnipedialis early in the hooded seal’s life, rather than a mother-to-pup transmission, with a subsequent clearance of infection. This is in accordance with the behavior of B. pinnipedialis hooded seal strain in various in vitro cell models and in an in vivo experimental infection in mice, where the strain demonstrated an attenuated behavior.
RESPONSE OF SONORAN PRONGHORN TO VACCINATION WITH A MULTIVALENT ORBIVIRAL VACCINE

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Epizootic hemorrhagic disease (EHD) is an orbiviral infection of ungulates which often presents in pronghorn (*Antilocapra americana*) as acute death. As with the related bluetongue virus (BTV), the disease is transmitted by a vector, a midge, most often *Culicoides sonorensis* in Arizona, USA. In 2004, the United States Fish and Wildlife Service and the Arizona Game and Fish Department established a population of Sonoran pronghorn (*A. americana sonoriensis*) in a 640 acre enclosed breeding pen on the Cabeza Prieta National Wildlife Refuge because extreme drought conditions threatened the remaining 21 individuals in the United States population. Sporadic mortalities have occurred within the pen and in several cases lesions consistent with an orbiviral infection were found. In one case, EHD virus was detected with PCR. In an effort to reduce mortalities and improve survival in released pronghorn, a multivalent vaccine containing antigen for BTV 17, EHDV 1, EHDV 2, and EHDV 6 (Newport Laboratories, Worthington, Minnesota, USA) was introduced into the management program in 2010. Before the vaccination program was begun, only 25% of the animal had antibodies to either epizootic hemorrhagic disease or bluetongue virus when tested with agar gel immunodiffusion and enzyme-linked immunosorbent assays, respectively. The strains most commonly identified in serotyping with serum neutralization were EHDV 2 and BTV 2. After instituting vaccination, more than 70% test positive with the same methods. Ten of thirteen animals tested in consecutive years converted from negative to positive, and six animals had titers to EHDV 6, a vaccine strain not previously documented in Arizona. Titer levels after vaccination were significantly higher to the EHD strains included in the vaccine. Concurrently, the number of mortalities in the pen with signs consistent with EHDV or BTV infection has decreased to near zero for the past 2 years.
FIELD TECHNIQUES FOR BACTERIAL SAMPLE COLLECTION AND DIAGNOSTICS: BRINGING THE LABORATORY TO THE FIELD

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Culture and isolation of the common bacterial pathogens responsible for pneumonia in bighorn sheep (Ovis canadensis) can be difficult. Our laboratory increased diagnostic sensitivity for these pathogens by improving field sampling techniques and integrating polymerase chain reaction (PCR) into our laboratory regimen. We optimized sample collection techniques in the field to enhance microbial viability and recovery. Optimization steps included multiple swabs from the tonsillar crypts and immediate inoculation of Columbia Blood Agar (CBA) or Columbia Selective Agar (CSA) plates. Culture plates were placed in a mobile incubator held at 37°C with ~10% CO₂. Phenotypic colonies were removed and recultured every 24 hours until delivery to the laboratory. In addition to optimized field techniques, we used published PCR protocols to screen all the bacterial growth from culture plates for Mannheimia and Bibersteinia spp leukotoxins, followed by Mannheimia spp specific leukotoxin and finally a PCR to detect M. haemolytica. The addition of these PCRs to our standard culture protocol resulted in the identification of 29% more leukotoxin positive Mannheimia spp (including M. haemolytica) than by gross identification of bacterial colonies on CBA or CSA. These improvements in field and laboratory techniques have increased our ability to detect potential pathogens in bighorn sheep populations.
USE OF VOLATILE ORGANIC COMPOUND PROFILES FROM FECES TO DISCRIMINATE BETWEEN BCG-VACCINATED AND MYCOBACTERIUM BOVIS-INFECTED WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS)

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Some wildlife species function as reservoirs for zoonotic diseases, diseases of agricultural significance, and as sources of emerging infectious disease. Disease surveillance in wildlife is problematic, with many wildlife disease surveillance programs reliant upon invasive sampling strategies. Vaccination of wildlife against infectious disease has been proposed as a means to mitigate disease transmission among wild animals, wild and domestic animals, and to prevent spread of zoonoses to humans. As with wildlife disease surveillance, most vaccination monitoring programs involve invasive sampling techniques. Development of non-invasive disease or vaccination detection systems would improve surveillance capabilities for diseases of significance in wildlife. Bovine tuberculosis (bBT), a zoonosis of agricultural concern, is caused by Mycobacterium bovis. This disease is endemic at low prevalence in white-tailed deer (Odocoileus virginianus; WTD) populations in northeastern Michigan, which serve as reservoirs for transmission of bBT to cattle. Detection of disease- or vaccine-specific volatile organic compounds (VOCs) present in breath or feces could allow remote disease surveillance of wildlife. In a pilot study, we demonstrate that it is possible to discriminate between unvaccinated and BCG-vaccinated WTD prior to and 5 months post-experimental challenge with 300-500 CFU M. bovis based on GC/MS analysis to determine fecal VOC profiles. Analysis of these profiles using principle components and linear discriminant analysis demonstrated a high degree of discrimination between the treatment groups prior to and after experimental challenge. Results strongly suggest that development of remote surveillance tools capable of monitoring wildlife populations for disease or response to vaccination is feasible.
DETECTION OF VOLATILE ORGANIC COMPOUNDS IN *BRUCELLA ABORTUS*-SEROPOSITIVE BISON

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Brucellosis is of great public health and economic importance worldwide. This disease is present in many free-ranging wildlife populations globally. Ante-mortem detection of brucellosis currently relies on serologic testing, which requires blood collection, and experiences problems with cross-reactions. Here we present a new method for identifying *Brucella* exposure that is based on profiling volatile organic compounds (VOCs) in exhaled breath. Breath samples from 20 *Brucella abortus* seropositive bison and 18 seronegative controls were collected on Tenax sorbent material. The bison were housed at various locations. The breath samples were chemically analyzed with gas chromatography/mass-spectrometry which demonstrated statistically lower concentration profiles of five tentatively identified VOCs (2-ethyl-1-hexanol, acetophenone, octanal, heptanal, and benzaldehyde) as compared to the negative controls and ambient air samples (Wilcoxon/Kruskal–Wallis test; p < 0.05). In addition, a point-of-care device incorporating an array of 20 nanomaterial-based sensors could identify VOC patterns indicative of *Brucella* exposure based on discriminant factor analysis (DFA). Several potential sensing feature combinations were identified that appeared to distinguish between seropositive and seronegative animals. Overall classification results indicated a sensitivity and specificity of 72% and 90% respectively. Application of the DFA models to separate the animals according to their location was unsuccessful and shows that the patterns were not affected by the animals’ environment. Future work in this area will require much larger sample sizes with confirmation of infection. There is also a need to have access to expanded chemical databases used for identifying VOCs. The *Brucella*-indicative VOCs and collective patterns identified in this pilot study could lead to the development of a novel diagnostic screening test for quickly detecting infected animals chute-side, pen-side, or remotely in populations of free-ranging ungulates.
We previously proposed the creation of a National Fish and Wildlife Health Network designed to build a collaborative, operational framework by which government agencies, tribes, and other stakeholders cooperate to assist tribal, state and federal agencies in their responsibilities to manage wildlife diseases. One of the primary needs for such a Network is improved wildlife health information management and dissemination. The USGS National Wildlife Health Center, in partnership with federal, state, tribal, non-governmental, and academic partners, has developed a web-based system called the Wildlife Health Information Sharing Partnership-Event Reporting System (WHISPers) for tracking basic information about historic and ongoing wildlife mortality and morbidity events. The goal of the system is to provide natural resource management agencies with timely, accurate situational awareness regarding these events. The system is also a searchable archive of historic wildlife mortality and morbidity event data. For nearly 40 years the USGS National Wildlife Health Center has been collecting and distributing information on wildlife mortality events. Quarterly summaries of these data can be viewed at http://www.nwhc.usgs.gov/publications/quarterly_reports/index.jsp. WHISPers represents a significant upgrade, with tools designed to query, map, sort, and download event data. Users will be able to view information about wildlife mortality events and sort and filter records by geographic area, date range, species, or disease of concern. Records can be viewed in a tabular format, or mapped by political jurisdiction (e.g., counties in the U.S.). Users can run compound queries to further refine and download the results. Authenticated partners will have the capability to enter mortality event information into the system, and edit/update those records. The new system, with partner input, will provide a more comprehensive view of wildlife mortality and morbidity events across North America, allowing natural resource management agencies to proactively plan and manage threats to wildlife health.
DESCRIPTIVE EPIDEMIOLOGY OF AVIAN BOTULISM TYPE E IN WATERBIRDS OF LAKE MICHIGAN, 2010-2013

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During 2010 to 2013, waterbird mortality surveillance programs used a shared protocol for shoreline walking surveys performed June to November at three areas around northern Lake Michigan, USA. Detections in 2010 and 2012 were 1,244 total carcasses (0.8 dead birds/km walked) and 2,399 total carcasses (1.2 dead birds/km walked), respectively. Fewer carcasses were detected in 2011 (353 total carcasses, 0.2 dead birds/km walked) and 2013 (451 total carcasses, 0.3 dead birds/km walked). During 3 years, peak detection of carcasses occurred in October and involved primarily migratory diving and fish-eating birds, including long-tailed ducks (Clangula hyemalis; 2010), common loons (Gavia immer; 2012), and red-breasted mergansers (Mergus serrator; 2013). In 2011, peak detection of carcasses occurred in August and consisted primarily of summer residents such as gulls (Larus spp.) and double-crested cormorants (Phalacrocorax auritus). A subset of fresh carcasses were collected throughout each year of the study and tested for botulinum neurotoxin type E (BoNT/E). Sixty-one percent of carcasses (57/94) and 10 of 11 species collected throughout the sampling season tested positive for BoNT/E, suggesting avian botulism type E was a major cause of death for both resident and migratory birds in Lake Michigan. The variety of avian species affected by botulism type E throughout the summer and fall during all 4 years of coordinated surveillance also suggests multiple routes for bird exposure to BoNT/E in Lake Michigan.
LONG-TERM ANTIBODY PERSISTENCE FOR LOW PATHOGENIC AVIAN INFLUENZA VIRUS IN MALLARDS

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Information on long-term antibody persistence in waterfowl is critical to understanding factors associated with avian influenza strain dynamics and appropriately interpreting serology-based surveillance studies. However, very limited experimental information is available on long-term immunity in natural hosts, such as mallards. Therefore, we infected 30 mallards with an H6N2 avian influenza virus to investigate long-term humoral immunity. We collected blood samples from 28 of those individuals for more than 18 months, testing for antibodies to influenza A viruses via ELISA at approximately 4 week intervals. We re-infected the same individuals with the same virus and dose after a year to investigate long-term homosubtypic immunity. After the initial infection, more than half of the ducks exhibited detectable antibodies on day 7 and all ducks were positive on day 10 and remained so through day 28. By day 56, only 39% of ducks were positive by ELISA. Only three individuals had detectable antibodies throughout the year. After the re-challenge, most ducks were antibody positive on day 4, all were antibody positive by day 10, and nearly 70% still showed detectable antibodies on day 140. These results are consistent with an anamnestic response (i.e., a more rapid production of antibodies in greater titers and persistent over a longer time period). Female mallards consistently showed a stronger ELISA response compared to males, but this difference was minor with respect to the percent of positive individuals. Overall, these results indicate antibodies may only be detectable in the short-term in many individuals, but a strong humoral memory may be present. These results have important implications for interpreting surveillance schemes based on serology and shed light on seasonal strain dynamics in mallards.
ROLE OF IMMUNITY IN REGULATING AVIAN INFLUENZA VIRUS POPULATION DYNAMICS

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Many features of pathogen diversification remain poorly explored although host immunity is recognized as a major driver of antigenic evolution, i.e. how pathogen populations evolve and diversify to avoid recognition by host immune systems. Our overall hypothesis is that host population immunity directed at multiple antigens will influence the prevalence, diversity and evolution of Influenza A virus (IAV) populations. Here we carried out experimental infections in mallards to characterize the effects of IAV cross-immunity or heterosubtypic immunity. Mallards were pre-challenged with an H3N8 virus; they were divided into six groups and then 5 weeks later each group was challenged with a different IAV strain or the same H3N8 virus. Heterologous challenge subtypes represented different levels of relatedness between the key antigenic proteins hemagglutinin (HA) and neuraminidase (NA) compared to H3N8. Two additional groups were challenged with the H3N8 virus at weeks 11 and 15 after pre-challenge to evaluate the duration of homosubtypic immunity. Measured responses included: susceptibility (probability of infection), duration and intensity of viral shedding, and characterization of humoral immunity. The outcome of the challenges depended on the genetic relatedness between the HA and NA of infecting strains in successive challenges. Moreover, the mallards were resistant to homologous reinfection 15 weeks after pre-challenge. This suggests that heterosubtypic or cross immunity (i.e. immunity induced by one strain/subtype to other strains) regulates pathogen population dynamics in this IAV system. Thus, measures of strength and duration of immune responses are valuable for interpreting field data. Collectively, these results provide new knowledge of host immunity as a driver of pathogen evolution and maintenance of IAV diversity in wild ducks. Ultimately this can be applied to predicting and managing introductions of influenza in partially immune populations and design efficient vaccination strategies.
UNDERSTANDING THE RE-EMERGENCE OF H14 INFLUENZA A VIRUSES IN DUCKS

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The H14 hemagglutinin subtype of influenza A virus (IAV) was first isolated from mallards in the Soviet Union during 1982. Despite extensive global influenza surveillance efforts, there were no additional reported isolations of this subtype from domestic or wild birds for the next 38 years. However, in 2010, H14 IAVs were isolated from two long-tailed ducks and a white-winged scoter harvested in Wisconsin, USA. Following these detections, H14 IAVs were isolated from a northern shoveler in California in 2011 and multiple blue-winged teal in Guatemala in 2011 and Texas in 2013. These recent detections of H14 IAVs from New World waterfowl provide evidence for expanding host and/or geographic ranges for this subtype. To provide insights into the re-emergence of H14 IAV in ducks, we used genomic analyses and conducted an experimental challenge study in mallards. Genomic characterization of existing New World H14 IAVs revealed high nucleotide identity (≥ 99.9%) among individual gene segments. In contrast, no two strains shared ≥ 92.0% identity across all gene segments compared and multiple neuraminidase subtypes were observed among H14 IAVs. Gene segments of H14 viruses isolated after 2010 shared ancestral genetic lineages with IAVs isolated from wild birds throughout North America. Thus, genomic characterization provided evidence for viral evolution in New World waterfowl through genetic drift and genetic shift since purported introduction from Eurasia. In the challenge study, no clinical disease or lesions were observed among mallards inoculated with A/blue-winged teal/Texas/AI13-1028/2013(H14N5). High concentrations of virus were excreted in the feces, which was associated with replication in the lower intestinal tract and bursa of Fabricius. The infectivity and pathobiology of A/blue-winged teal/Texas/AI13-1028/2013(H14N5) in mallards is consistent with other waterfowl-adapted, low pathogenic IAV strains in ducks. These data suggest that H14 IAVs recently detected in New World waterfowl have evolved and adapted similar to other waterfowl-origin IAVs.
NEW NETWORK FOR ASIAN CONSERVATION MEDICINE

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In order to discuss and find rational solutions to existing and emerging problems associated with wildlife and zoo animals in Asia, expert and subject matter specialists from the Asian region establishment the Asian Society of Zoo and Wildlife Medicine (ASZWM) in 2006. ASZWM meetings have facilitated an exchange of information in wildlife conservation and veterinary medicine, and foster collaboration among Asian countries. Through these ongoing meetings and activities targeting wildlife medicine and conservation, ASZWM has initiated building a network in Asia. Realizing the increasing need of experts in the area of wildlife medicine and conservation, ASZWM started a diploma system for Asian conservation medicine through establishment of Asian College of Conservation Medicine (ACCM) in 2012. These core members then designed and implemented an examination for the ACCM diploma in 2013. The ASZWM has also taken initiative in designing and developing education on zoo/wildlife medicine in representing veterinary colleges in Asia. Plans for editing the common textbook and the joint training course on zoo/wildlife medicine for students will also be introduced in future meetings. With recent progress in understanding the global disease and conservation dynamics, ASZWM has started realizing the need of more inclusive forum and linkage between institutes of each Asian country to have a functional communication on the “One Health” issues. With this realization ASZWM is now considering a broader alliance with other disciplines of common interest like biology, ecology, environmental science, natural sciences, public health and human medicine. The upcoming 7th ASZWM meeting in October at Tam Dao National Park, Hanoi, Vietnam will have experts from all these diverse areas for joint discussion and a holistic approach to work on wildlife conservation/medicine and veterinary education topics in Asia.
Healthy and sustainable wildlife populations are essential for the physical, socio-economic, and cultural health of many aboriginal peoples around the Arctic. Recent emerging parasitic infections and unusual mortality events in muskoxen in the Canadian Arctic Archipelago are thus of great concern to northern communities and businesses. In 2008, the temperature-restricted muskox lungworm, *Umingmakstrongylus pallikuukensis*, was detected for the first time on the southwest corner of Victoria Island. By 2012, this lungworm had expanded its range several hundred kilometers to the northeast on the island. In 2010 and 2011, significant mid-summer mortality events of adult muskoxen were observed on Victoria Island (135,000km$^2$) and similar events occurred across Banks Island (72,000km$^2$) in the summers of 2012 and 2013. *Erysipelothrix rhusiopathiae*, a pathogenic bacterium not previously reported in muskoxen, nor in the Arctic, was consistently isolated from multiple tissues of all animals sampled. Concurrently, recent surveys and anecdotal evidence indicate that muskox populations have experienced significant declines in some of these regions. Similar patterns of mortality have recently been reported for muskoxen and caribou elsewhere in the North American Arctic, but causes of death were not determined. Together, these events suggest broad changes in ecological conditions and cumulative stressors culminating in parasite invasions and range expansion as well as acute disease and mortality with population level impacts. Here we discuss the patterns of pathogen emergence in muskoxen, historic mortality events, and data derived from analyses of archived serum and fecal samples. This information is used to evaluate the direct and indirect roles of climate and other ecological factors in the recent and widespread emergence of pathogens in the Arctic.
ASSOCIATION BETWEEN *TREPONEMA* SPP. AND SEVERE HOOF DISEASE IN WASHINGTON ELK

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Reports of elk (*Cervus elaphus*) with lameness and severely deformed or missing hooves increased dramatically in southwest Washington during the late winter and early spring of 2008. The geographic distribution of reports of the disease has continued to expand since then, and at this time is estimated to encompass a core area of approximately 10,500 km\(^2\) (4,000 mi\(^2\)). A diagnostic investigation to determine the cause was initiated in 2009. Radiography, bacteriology, virology, serology, and trace mineral analysis failed to reveal a cause of the disease. Histopathology and silver staining of lesions from affected hooves demonstrated the presence of deeply invasive spirochetes accompanied by significant inflammation. Furthermore, *Treponema phagedenis*-like and *Treponema medium*-like spirochetes were isolated from diseased elk hooves. These isolated *Treponema* represent two of the three phylotypes known to be highly associated with hoof diseases in domestic animals: bovine digital dermatitis in cattle and contagious ovine digital dermatitis in sheep. Based on findings to date, it appears that *Treponema* spp. may have a causal role in the emergence of a significant disease of free-ranging elk in the Pacific Northwest of North America.
BIGHORN SHEEP SINUS TUMORS ARE ASSOCIATED WITH CO-INFECTIONS BY POTENTIALLY-PATHOGENIC BACTERIA IN THE UPPER RESPIRATORY TRACT

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Previously, we described a novel disease in bighorn sheep (Ovis canadensis) characterized by hyperplastic to neoplastic masses of the paranasal sinuses (sinus tumors), and we have proposed a retroviral etiology for this disease. Grossly, bighorn sheep sinus tumors expand the sinus lining, obstruct the sinus cavities, and exude abundant mucus. We suspect that these features may interfere with the normal clearance of bacterial pathogens from the upper respiratory tract. The purpose of this study was to explore whether or not the presence of sinus tumor features (tumor score) affected the likelihood of detecting potentially-pathogenic bacteria from upper respiratory sinus lining tissues in bighorn sheep. We developed a PCR assay for the detection of leukotoxigenic Pasteurellaceae bacteria, suitable for use with DNA extracted directly from tissue samples. We used this assay, and an existing PCR assay for the detection of Mycoplasma ovi pneumoniae, to screen sinus lining tissues from 97 bighorn sheep for the presence of these potentially-pathogenic bacteria. Using logistic regression analysis we found that, for predicting the detection of potentially-pathogenic bacteria in sinus lining tissues, a model that included tumor score was clearly more likely than a model excluding tumor score (evidence ratio>1000). These findings add to our understanding of possible mechanisms for maintenance and shedding of bacterial agents from the upper respiratory tracts of bighorn sheep.
EQUINE HERPESVIRUS 9 (EHV-9) AS AN EMERGING INFECTIOUS AGENT IN ZOO ANIMALS

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EHV-9, the newest member of the equine herpesvirus family, is a highly neurotropic herpesvirus first described in an outbreak of disease in Thomson’s gazelles (Gazella thomsoni) that died of fulminant encephalitis. Serologically, EHV-9 is most closely related to EHV-1, but its DNA fingerprint is different from that of EHV-1. Natural hosts of EHV-9 might be African equidae like zebras. Recently, EHV-9 was detected in a polar bear with progressive encephalitis as well as in a giraffe, raising fears of emerging infections in zoo animal species. EHV-9 was proved to be infective for wide range of susceptible hosts including mice, rats, hamsters, goats, pigs, dogs and cats and common marmosets. Although EHV-9 was shown to infect a broad range of animals, it remains unknown how the virus travels from the nasal cavity to the brain, or how long this progression takes. To accurately detect and stage the kinetics of viral infection from the nasal cavity to the brain, a suckling hamster model was developed so that precise sagittal sections of nasal and cranial cavities including the brain could be processed. At 12-24 hr after intranasal infection, the virus propagated in the olfactory epithelium, and infected adjacent epithelial cells. At 48 hr, the viral antigen extended into the olfactory bulb and nerve. These results indicate that EHV-9 rapidly invades the brain via the olfactory route after intranasal infection. Encephalitis has also been induced in hamsters with different inoculation routes like oral, peritoneal and ocular routes. There are many populations of equidae including zebras imported from Africa, which may be possible reservoirs of EHV-9. Zoo veterinarians should consider possible infection by EHV-9 if symptoms related to central nervous system are observed in zoo animals with history of close contact with African equidae.
MYCOPLASMA BOVIS – AN EMERGING PATHOGEN OF RANCHED BISON

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Mycoplasma bovis (M. bovis) is an emerging bacterial pathogen of ranched bison (Bison bison) in North America. Unlike in cattle, M. bovis in bison seems to be a primary pathogen, causing severe disease among animals in feedlots and in breeding-age cows and bulls on pasture. Mortality rates in adult bison have been as high as 25%, resulting in significant economic losses to producers. Clinical expressions of Mycoplasma bovis disease in bison have been variably reported as caseonecrotic pneumonia, pharyngitis, polyarthritis, dystocia and abortion, with lesions disseminated to various organ systems. Affected animals may be alert at the onset of disease, but lag behind the rest of the herd due to lameness and exercise intolerance. Eventually, M. bovis-affected bison become emaciated and weak, usually leading to death or euthanasia. It is unknown to what extent epizootics of M. bovis in bison are influenced by geographic and environmental variables, or by differences in bacterial strains or disease resistance among herds. Potential risk factors for M. bovis disease in bison include introduction of new arrivals into herds, movement of bison to feedlots or among pastures, unusually hot or cold weather, seasonal decline in forage quality, stress of lactation, and excessive parasite loads. Immunological strategies to protect bison from M. bovis outbreaks have yielded mixed results. Canadian and U.S. researchers have launched diagnostic and epidemiological studies of M. bovis disease in bison to explore some of these important topics.
COLLABORATIVE EFFORTS TO RESTORE AQUATIC SPECIES ON PRIVATE LAND: A STORY OF GENETICS, HABITAT, DISEASE, AND SWEAT

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The Turner organization is guided by a philosophy of conserving and restoring biological diversity within an economically sustainable land management framework. While we emphasize the role private lands must play in native species conservation, relationships and collaboration with public agencies and other conservation organizations are critical. Interior cutthroat trout (*Oncorhynchus clarkii*) have been a focal conservation species on Turner lands, and collaboration between the Turner organization and state and federal resource management agencies has led to the implementation of two of the largest stream restoration projects ever attempted. These projects - Cherry Creek in Montana and Costilla Creek in New Mexico, USA - are the foundation of a goal to catalyze conservation or preservation of cutthroat trout in over 400 km of habitat on private and public lands. Parallel to efforts on behalf of cutthroat trout are projects to conserve and restore other imperiled members of the native aquatic community, such as western Pearlshell mussel (*Margaritifera falcata*) or Rio Grande sucker (*Catostomus plebeius*). Fundamental to these projects is the availability and selection of genetically suitable, genetically pure, and disease free source stocks for introduction into restored habitats. Here we discuss the mechanics of cutthroat trout restoration and the important, sometimes counteracting roles that habitat, genetics, disease, and related policy can play in determining whether a restoration project succeeds or fails.
THE CHIRICAHUA LEOPARD FROG: THE TRIAL AND TRIBULATIONS INVOLVED WITH THE CONSERVATION OF A DESERT AMPHIBIAN

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The mission of the Turner Endangered Species Fund (TESF) is to conserve imperiled species and biodiversity, particularly on private lands. The conservation program for the Chiricahua leopard frogs (*Lithobates chiricahuensis*), a federally threatened species found in Arizona and New Mexico, USA, is an important example of how TESF is advancing this mission. The species has been lost from much of their historical range, with the most prevalent reasons being the amphibian fungal disease Chytridiomycosis (*Batrachochytrium dendrobatidis*), drought, habitat loss, and invasive species. The Ladder Ranch supports the most robust population of *L. chiricahuensis* in New Mexico, and since 2001 TESF has implemented a multifaceted conservation program. The success of this effort has relied upon close collaboration with state, federal, and other non-profit stakeholders as part of the New Mexico Chiricahua Leopard Frog Conservation Working Group. The major goals on the Ladder Ranch are to 1) conserve a secure and sustainable wild population on the Ladder Ranch, 2) maintain captive assurance colonies of frogs from imperiled populations across the species’ range, and 3) support range-wide recovery efforts through captive breeding of individuals for introductions or augmentations to restored habitats range-wide. To this end, TESF activities include habitat restoration, ecological research, breeding, disease testing, population surveys, behavioral and dispersal studies, and a captive breeding program. We will discuss the mechanisms being used for restoration and population conservation, our recovery efforts on expanding wild and captive populations of the frog, the management of parasites and other invasive threats, and efforts to maintain a Chytrid-free environment.
RESTORATION OF A PLEISTOCENE RELICT: THE BOLSON TORTOISE IN SOUTHERN NEW MEXICO

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The ‘endangered’ Bolson tortoise (\textit{Gopherus flavomarginatus}) is the largest and rarest of the five North American tortoise species in the \textit{Gopherus} genus. It is prehistorically endemic to most of the Chihuahuan desert, but the only extant wild population is found in the Mapimi region in north-central Mexico. Due to a suite of political, social, economic, and personal safety issues, the current status of the Bolson tortoise in the wild is largely unknown. The last population count estimated fewer than 10,000 animals alive in the early 1980’s. Since then continued habitat degradation and loss make it likely that this number has decreased significantly, highlighting the urgency with which we need to establish independent “assurance” colonies (among other, \textit{in situ} conservation approaches) that counteract the foreseeable extinction of this keystone species. A group of 24 adult Bolson tortoises collected and bred over a period of \(~\)30 years by the late Ariel Appleton was donated to the Turner Endangered Species Fund (TESF) in 2005, and the tortoises were moved to a semi-captive environment on the Armendaris Ranch in southern New Mexico, USA in the fall of 2006. The goal of TESF’s Bolson Tortoise Project is to use this unique colony as a starting point to establish two independent, viable populations in the U.S. in the northern portion of its prehistoric range. We began by focusing on two key questions: 1) Are the New Mexico habitats on the Armendaris and Ladder Ranches suitable for Bolson tortoise growth and fecundity? And 2) Can we develop and establish a breeding program that generates sufficiently large cohorts of releasable animals? Regular surveys for tortoise health, growth and egg production since 2006 show that both juveniles and adult tortoises thrive in the desert grassland habitat of the northern Chihuahua desert with minimal or no management. Further, reproduction is vigorous: the adult females produce up to three clutches of eggs per year (typically 1-2), and clutch size ranges from two eggs for the smaller to nine eggs for the larger tortoises. We have developed a robust (albeit currently labor-intensive) breeding program that typically generates cohorts of \(>50\) new hatchlings per year. Maximizing the number of hatchlings born each year is an important step in generating an independent Bolson Tortoise population in New Mexico. We are using genetic analyses to ensure that our management strategies maintain the genetic diversity of the parental group. We are using carefully controlled constant-temperature incubation of the eggs combined with endoscopy to reveal sex allowing us to determine and manipulate sex ratios of the offspring cohorts. We initially protect juvenile tortoises inside predator-proof enclosures until they can safely be released. Our current studies focus on testing different release strategies as well as determining minimal size and shell hardness that result in high survivorship. Furthermore, we are using modeling to optimize repatriated population size and growth strategies.
The desert bighorn sheep (*Ovis canadensis mexicana*) has been the focus of conservation efforts in New Mexico, USA for the last several decades. In 1995 Turner Enterprises began a close collaboration with New Mexico Department of Game and Fish (NMDGF) to establish a herd to the Fra Cristobal Mountains (FCM) on the Armendaris Ranch. The collaboration led to the release of 37 of these New Mexico ‘endangered’ bighorn sheep to FCM before the end of 1995. The Turner Endangered Species Fund (TESF) assumed a lead role with the restoration effort in the summer of 1997 and by Fall another seven bighorn were released. Following those releases staff from the TESF and Armendaris Ranch intensively monitored the sheep and also the local cougar population on a near daily basis to promote survival. Controlling cougars to minimize predation on bighorn was the principal management activity during that time. To ensure success, TESF and the Ranch successfully employed remote, motion sensitive cameras to improve detection of cougars on the mountain and to determine the threat they posed to bighorn sheep. By May 2011 the population that inhabited the FCM included 200 to 220 sheep and had given rise to a second population on the nearby Caballos Mountains that included 65 to 75. This “meta-population” of 265 to 295 bighorn sheep was the largest in state, included over 40% of all sheep in the state, and was the principal reason that New Mexico State Game Commission removed the species from the state list of endangered species in November 2011. Prior to that on October 30 the TESF, Armendaris Ranch, and NMDGF recognized the success of the project by translocating 16 ewes from the FCM to suitable habitat to further secure the species’ future. The translocation represented the first time that desert bighorn sheep have been restored to private property and managed so successfully that the herd grew to sufficient size to serve as a “donor population”. This presentation will consider the various aspects of this 17-year restoration effort.
MEXICAN WOLF RECOVERY: MANY MATTERS OF CONFUSING CONCERN

Mike Phillips

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Since at least the middle of the 20th century the Mexican wolf (Canis lupus baileyi) has been one of the most critically endangered carnivores in the world. This is curious since the species is the most genetically unique wolf in North America and has been protected under the federal Endangered Species Act since the early 1970s. During the last few decades other gray wolf subspecies, that were always common in Canada and Alaska and never actually threatened with extinction, have benefited from successful recovery programs. Remarkably, Mexican wolf recovery has languished for what appears to be a lack of focus and chronic opposition from socio-political forces that oppose the subspecies’ recovery. Progress with Mexican wolf recovery has been so modest that the only approved recovery plan for the subspecies was authorized in 1982, did not present specific recovery criteria, and has never been updated. The Turner Endangered Species Fund has been actively promoting Mexican wolf recovery since 1998 when we opened the nation’s only private captive breeding and pre-release facility for the subspecies at the Ladder Ranch in southwestern New Mexico, USA. Additionally, TESF staff has served on all three Mexican wolf recovery teams that have been convened by the U.S. Fish and Wildlife Service since 1995. This presentation will consider the problems and opportunities in recovering the Mexican wolf (including those related to wolf-livestock interactions), the importance and significance of large predators and why restoration is appropriate, and the roles of private individuals and organizations in biodiversity conservation and how such efforts can integrate with governmental efforts.
**OPHIDIOMYCES OPHIODIICOLA IS ASSOCIATED WITH CASES OF SNAKE FUNGAL DISEASE ACROSS THE EASTERN UNITED STATES**

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Snake fungal disease (SFD) is an emerging disease in certain populations of snakes in the eastern U.S. that is characterized by invasion of the skin (and in some instances, underlying tissue) by a fungal pathogen. Many cases of SFD in captive snakes have been attributed to *Ophidiomyces ophiodiicola*, and this fungus has recently been detected in populations of wild snakes with severe skin infections in the northeastern and midwestern U.S. However, little is known about the suite of fungi that may cause SFD, the distribution of *O. ophiodiicola*, or whether *O. ophiodiicola* represents a native or introduced pathogen. Using a culture-based approach, we characterized the fungi associated with lesions on snakes with SFD (n=22) and fungi associated with healthy skin collected from snakes without clinical signs of SFD (n=14). *Ophidiomyces* was reliably isolated from snakes with skin lesions (90.9%), but was not cultured from snakes without clinical signs of skin infection. The association between *O. ophiodiicola* and SFD was further supported by histopathologic analyses that demonstrated invasion of the skin by a fungus morphologically consistent with *O. ophiodiicola*. The fungus appears to have a broad host range among serpents and was widely distributed, being recovered from snakes in nine states east of, or bordering, the Mississippi River. We next sequenced the internal transcribed spacer and intergenic spacer regions of the genomes of 43 isolates of *O. ophiodiicola* collected from wild snakes across the eastern U.S. and found a pattern of genetic diversity consistent with the fungus being native to North America. This work demonstrates for the first time that *O. ophiodiicola* is commonly associated with cases of SFD in wild snakes, is widely distributed in eastern North America, and likely represents a native pathogen that may be emerging due to host- or environmental-related factors.
THE PACIFIC COAST SEA STAR MORTALITY EVENT: CURRENT STATUS OF THE ONGOING INVESTIGATION

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A large scale mortality event affecting 12 species of sea star (Asteroidea) on the Pacific Coast of North America began in June of 2013 and continues to present (March 2014). First detected in Ochre sea stars (\textit{Pisaster ochraceus}) along the outer coast of Washington State, the event has been observed in at least 240 subtidal and intertidal locations extending from Southeastern Alaska to San Diego, California. \textit{Pisaster}, \textit{Pycnopodia} and \textit{Evasterias} are the most affected genera and mortality approaches 100% in select species at some locations. Concurrently, multiple Pacific Coast public aquaria and teaching centers that use ‘open’ water systems experienced severe mortalities in both resident and recently collected sea stars. The progression of clinical signs includes: 1) loss of body turgor (deflation) and weakness; 2) foci of epidermal pallor and tissue loss; 3) sloughing of multiple rays and/or rupture of the body wall with evisceration; 4) death. Samples of affected and unaffected sea stars from wild locations in California, Washington and Vancouver, British Columbia and from affected aquaria were collected for pathologic and molecular investigation. Consistent histologic changes include: 1) epidermal degeneration, necrosis and ulceration; 2) dermal edema, necrosis and inflammation. The presence and diversity of viruses and bacteria in affected and unaffected sea stars were compared by metagenomics and quantification of constituent genotypes. Community fingerprinting and bacterial metagenomics identified three candidate disease-associated bacterial families including \textit{Bacteroidetes, Gammaproteobacteria} and \textit{Spirochaetes}. Viral metagenomics identified several candidate disease-associated metazoan viruses. Links between the histologic lesions and candidate disease-associated organisms are under investigation by transmission electron microscopy, in-situ hybridization, immunohistochemistry and infectivity studies. Evaluation of environmental data from long-term monitoring sites continues. Body wall composition analysis and advanced histologic and electron microscopic techniques are being pursued to clarify the pathogenesis of the clinical body wall dissolution that characterizes ‘sea star wasting syndrome’.
DOLPHIN MORBILLIVIRUS OUTBREAK AND THE 2013-2014 MID-ATLANTIC BOTTLENOSE DOLPHIN (TURSIOPS TRUNCATUS) UNUSUAL MORTALITY EVENT

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Dolphin morbillivirus (DMV) has caused previous outbreaks of disease in bottlenose dolphins (Tursiops truncatus) in the Mid-Atlantic region of the United States east coast (1987-1988), the Gulf of Mexico (1992, 1994), and in striped dolphins (Stenella coeruleoalba) in the Mediterranean (1990-1992, 2007-2008). An Unusual Mortality Event (UME) was declared by the National Marine Fisheries Service on August 8, 2013 due to increased numbers of bottlenose dolphin strandings documented in New York, New Jersey, Delaware, Maryland and Virginia during the months of July and August. Since that time strandings have remained elevated and the geographic scope of the event extends from New York to northern Florida (through Brevard County) with the UME still on-going. From July 1, 2013 to March 17, 2014, >1100 bottlenose dolphins stranded within the UME area with approximately 18% of animals stranding alive or fresh dead, and 82% of the carcasses in moderate to advanced states of decomposition. Gross necropsy findings included dermal, oral, joint, and pulmonary lesions. Consistent histopathology findings included bronchointerstial pneumonia and/or pulmonary fibrosis, lymphoid depletion, syncytial cells and viral inclusions. Tissue samples from 209 dolphins were tested for morbillivirus via polymerase chain reaction and/or immunohistochemistry with 96% being positive (200 of 209) and of these, 90% (175 of 195) had results confirmed by sequencing. Serum from 15 DMV-positive bottlenose dolphins was tested for morbillivirus neutralizing antibody titers, which ranged from 32 to 8,192. Virus isolation was successful on 13 animals to date. Preliminary whole genome sequencing of the dolphin morbillivirus genome in five bottlenose dolphins has found the sequences to be 99.9% similar to each other. Research is ongoing to better understand the impacts of this large scale outbreak on bottlenose dolphin populations and affected coastal stocks.
CYANOTOXIN (MICROCYSTIN) TRANSFER FROM LAND TO SEA OTTERS

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Cyanobacteria, or “blue-green algae”, thrive in warm, nutrient-enriched watersheds worldwide. Under optimal conditions, these primitive bacteria can form super-blooms with release of potent toxins (cyanotoxins) into lakes, rivers and estuaries. Over the past 30 years, an exponential increase in the distribution, severity and duration of toxic blooms has occurred, concurrent with coastal urbanization, increased water impoundment and withdrawal, global climate change and nutrient pollution of lakes and rivers. Once formed, these toxins are environmentally persistent, can magnify through food webs and spread from their point of origin, killing downstream animals and posing human health risks. One of the most concerning is the potent liver toxin, microcystin. Until recently, microcystin was considered to be a problem only of freshwater lakes, rivers and ponds, affecting domestic livestock, pets, and occasionally, humans. However, in 2007, at least 11 Southern sea otters, a state and federally protected threatened marine mammal, were poisoned, and microcystin was detected in several rivers flowing into the Monterey Bay National Marine Sanctuary. Affected sea otters exhibited icterus, hepatomegaly and coagulopathy. At present, at least 34 Southern sea otters have tested positive, and additional otters are suspected to have died from microcystin poisoning. Poisoning is also common in pet dogs, but many cases go unrecognized and untreated. Careful review of clinical signs and lesions for microcystin-poisoned sea otters will aid case recognition by veterinarians and medical doctors. Preliminary data also suggests that medical treatment may be possible and cost-effective. Our data suggest that sea otters are poisoned through contact with microcystin-contaminated freshwater runoff, or through consumption of marine shellfish that can bioconcentrate microcystin. Spatial connections have been identified between microcystin-poisoned sea otters and microcystin- and nutrient-impaired freshwater outflows, highlighting the potential for anthropogenic activity to enhance toxin production by freshwater and marine algae.
THE ROLE OF WILDLIFE IN THE TRANSFER OF ENTERIC ZOONOTIC PATHOGENS FROM LIVESTOCK TO LEAFY GREEN PRODUCE FIELDS IN THE DESERT SOUTHWEST

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The desert southwest is home to some of the most productive soil in the U.S. for growing leafy green produce. Neighboring some of these agricultural fields are concentrated animal feeding operations (CAFOs). Worldwide, it is well documented that cattle maintained at CAFOs actively shed a number of enteric zoonotic pathogens in their feces. There is concern that these pathogens can be transferred to nearby produce fields by wildlife where they may contaminate the crops and ultimately cause human illness. In order to determine if rodents and birds carry enteric zoonotic pathogens from CAFOs to nearby produce fields, we tested cow, bird, and rodent fecal samples for \textit{Salmonella}, \textit{Escherichia coli} O157 (\textit{E. coli} O157), and non-O157 shiga toxin-producing \textit{Escherichia coli} (STEC), all of which have been implicated in outbreaks of human foodborne illness. From July 2013 to February 2014, we tested samples at CAFOs in southern California and Arizona from 450 cows, 87 birds, and 42 rodents. Our preliminary findings revealed that none of the birds or rodents carried STEC, including \textit{E. coli} O157, despite 40.0\% of cows actively shedding STEC and 9.8\% actively shedding \textit{E. coli} O157. However, 2.3\% of birds and 9.5\% of rodents tested positive for \textit{Salmonella}, while 8.7\% of cattle samples tested positive. \textit{Salmonella} isolates will be subtyped to determine if wildlife and cattle share genetically related strains. Radio telemetry is also being used to assess bird movements and the potential spread of pathogens, including evaluation of the industry recommended 400 ft set-back from a CAFO to the edge of a leafy green crop. Knowledge gained from this study will be shared with growers, ranchers, buyers, regulators, conservation groups, and other stakeholders to improve best practices relating to livestock-wildlife risks near produce fields.
CLIMATE CHANGE, WILDLIFE, AND THE DISTRIBUTION OF IXODES SCAPULARIS, THE LYME DISEASE VECTOR TICK, IN THE U.S.-MEXICO TRANSBOUNDARY REGION

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Disease risk maps are important tools that ascertain exposure likelihoods to specific infectious agents. The bacterium Borrelia burgdorferi causes Lyme disease (LD) and it is transmitted to humans and other mammalian hosts through the bite of infected Ixodes ticks. Understanding how climate change may affect tick habitat suitability will improve the accuracy of risk maps for tick-borne pathogen transmission to humans. Lyme disease risk maps in the transboundary region between the U.S. and Mexico are lacking. Our study area includes Texas, USA and a portion of northeast Mexico. The objective of this study is to forecast the distribution of the tick vector Ixodes scapularis in this region. Tick samples were obtained from various vertebrate hosts and from vegetation in different localities within the studied area. Ticks identified as I. scapularis were processed to obtain DNA and to determine if they were infected with B. burgdorferi using PCR. A maximum entropy approach (MAXENT) was used to forecast the present and future (2050) distribution of I. scapularis in the Texas-Mexico transboundary region by correlating geographic data with climatic variables. Of the 1,235 tick samples collected, 109 were identified as I. scapularis. Infection with B. burgdorferi was detected in 45% of the I. scapularis ticks collected. The model presented here indicates a wide distribution for I. scapularis, with higher probability of occurrence along the Gulf of Mexico. The model also predicts that suitable habitats for I. scapularis in the Texas-Mexico transboundary region will remain relatively stable until 2050. Consequently, the Texas-Mexico transboundary region may be part of a continuum in the pathogenic landscape of LD. Forecasting the effect of climate change in I. scapularis distribution and LD transmission risk provides crucial information for the implementation of strategies aimed to mitigate the impact of LD in the near future in the Mexico-U.S. transboundary region.
NATURAL AND EXPERIMENTAL INFECTION OF BIG BROWN BATS WITH RABIES VIRUS

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Big brown bats (Eptesicus fuscus) are a natural reservoir of rabies virus in North America. They are a peridomestic species and can roost in dense aggregations, but populations can vary in genetic structure and ecology across their geographic range. This species has also been implicated in spillover events of rabies virus into wild carnivores in the United States, notably in Flagstaff, Arizona. Outbreaks of natural infection have been shown to occasionally occur within captive colonies of this species. Prior captive experimental rabies infections have demonstrated that big brown bats can develop immunity to repeated rabies virus infection. In this experiment, bats were taken into captivity and housed in two cages. Two cases of natural rabies infection were observed in one cage during the quarantine period, separated in time by 76 days. Seroconversion of cagemates was observed during the outbreak, suggesting nonlethal exposure of bats to rabies virus within a cage. However, the colony was observed for over one year without any additional rabies cases. During the outbreak, rabies virus was isolated from the salivary glands of one rabid bat, with a titer of $10^{3.8}$ TCID50/ml. The surviving colony was experimentally challenged with the salivary gland isolate 509 days after the last case of natural rabies infection in the colony. The mean incubation period of bats developing rabies from experimental infection was 25 days (range: 18-40 days). Seropositive bats were more resistant to experimental infection compared to bats that were seronegative throughout the captive period (17% versus 73% mortality, respectively). Infrared thermographic images were also taken of bats prior to and daily until day 60 following experimental infection, and changes in facial temperatures correlated with clinical outcomes of individual bats will be discussed.
CHANGING CLIMATE CAN GREATLY AFFECT SPRING MIGRATION ROUTES OF PASSERINE BIRDS, AND
THUS HAVE CONSEQUENCES TO THE POTENTIAL SPREAD OF ZOONOTIC DISEASES

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We have found that the timing and location of bird migration in western North America, and thus routes of potential zoonotic disease movement, are closely tied to climate patterns. Migrating passerine birds were found to respond to plant phenology patterns, which respond to climatic, geographic, and elevation factors. Lowland riparian areas are known to be important migration corridors and stopover sites in the American southwest, and are thus the primary locations for potential zoonotic disease movement. However species distributions and habitat associations of en route migratory birds across upland habitats are poorly understood, particularly in arid mountain regions. The Madrean Archipelago of southeast Arizona provides vital "stepping stones" of relatively rare upland vegetation communities between the mountains of Mexico and the United States and Canada. We will discuss research that 1) examined the timing, distribution, abundance, and diversity of migratory birds during spring migration in mixed conifer forest, pine-oak woodland, oak woodland, mesquite bosque, and lowland riparian forest of southeast Arizona, 2) identify phenological, structural, and compositional habitat associations of migratory bird selection of stopover habitat, and 3) will discuss models of climate change scenarios and their potential impacts on zoonotic disease movement in migratory passerine birds. This information is important for a better understanding of the epidemiology of wildlife disease movement by passerine birds, and for land managers working to conserve neotropical migratory bird species of western North America.
THE PREVALENCE OF PIGEON PARAMYXOVIRUS 1 AND TRICHOMONAS GALLINAE IN BAND-TAILED PIGEONS, MOURNING DOVES, AND WHITE-WINGED DOVES IN ARIZONA

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Pigeon Paramyxovirus 1 (PPMV1) is an emerging disease of concern to native wild bird species in Arizona, USA. This disease is often associated with the invasive Eurasian collared dove. First identified in the state in the 2001 Christmas bird count, Eurasian collared dove range has extended to include most of the state and now overlaps with that of the band-tailed pigeon. The objective of this study was to determine the prevalence of PPMV1 in band-tailed pigeons, mourning doves, white-winged doves, and Eurasian collared doves by serologic and molecular methods. *Trichomonas gallinae* has caused several epizootics in dove and raptor populations in Arizona. Coinfection with *T. gallinae* and PPMV1 could increase the severity of a mortality event. Presence of *T. gallinae* infection was determined by examination of cultures. Band-tailed pigeons (n = 25), mourning doves (n = 143), white-winged doves (n = 45), Eurasian collared doves (n = 59), and rock pigeons (n = 1) were sampled in 2012 and 2013. Prevalence in Eurasian collared doves was significantly higher than mourning doves, 44.1% and 1.4 % respectively (OR = 55.5455 P < 0.0001). The majority of birds positive for PPMV1 (75.0%) were found in the Phoenix metropolitan area. All of these cases were associated with large scale mortality events during 2012 and 2013 with an estimated total mortality of 1,500 birds. The overall prevalence for *T. gallinae* for 2012 and 2013 in the birds examined was 19.8% (n = 197). Eurasian collared doves (n = 14) and white-winged doves (n = 44) had a significantly greater number of infections, 6 and 44, respectively than mourning doves with 19 positive of 118 (OR_{ECDO} = 3.908, P = 0.0220; OR_{WWDO} = 2.432 P = 0.0299). Very few live birds tested positive suggesting an acute course of infection with little opportunity for the development of immunity.
MOUNTAIN LION GENETIC HEALTH: FRACTURED CONNECTIVITY AND LOW GENETIC DIVERSITY THREATENS VIABILITY OF CALIFORNIA POPULATIONS

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Mountain lions (Puma concolor) in California, USA live amongst habitat mosaics spanning a range between extremes of urbanized fragmented coastal environments and vast montane wild lands in the north state and inland. Coast regions extending between San Francisco, Los Angeles, and San Diego have burgeoning human populations while the North Coast Range, Sierra Nevada, and Modoc Plateau encompass vast sections of intact puma habitat less impacted by human developments. In order to assess population connectivity and genetic health of California mountain lions across these extremes, we conducted a detailed appraisal of the genetic diversity, relatedness, and population structure of California puma populations using 354 samples, including those from three long-term telemetry projects, and a 46-locus microsatellite DNA panel. This study follows up on work conducted 10 years ago and employs an expanded genetic tool set and larger coast region sample size. We evaluated and compared levels of genetic diversity, inbreeding, relatedness, and effective population sizes, and tested whether genetic data supported hypotheses of recent bottlenecks in key populations including the Santa Cruz Mountains (n=78), Santa Monica Mountains (n=26), Santa Ana Mountains (n=42) and adjacent Peninsular Ranges (n=55). We found that coast populations near large urban centers had much lower genetic diversity than inland populations such as those in Sierra Nevada. Specific instances of repeated inbreeding and signs of potential genetic defects were detected. These findings raise major concerns about the current health status of California coastal mountain lions, and the longer-term outlook for puma population viability in southern and central coastal California. In particular, the findings highlight the urgency to maintain – and enhance – what connectivity remains for pumas (and presumably numerous other species) across human barriers including multilane highways and developments. We are hopeful that these new genetic results, coupled with the demographic findings, will motivate greater conservation focus and effective outcomes.
NATURAL AND ANTHROPOGENIC CAUSES OF PUMA MORTALITY IN SOUTHERN CALIFORNIA

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We monitored 76 collared pumas (Puma concolor) from 2001-2013, and investigated 258 mortalities from 1981-2013, to assess puma health and disease in the rapidly urbanizing landscape of Southern California, USA. Demographic and genetic analyses showed that Interstate 15, a 10-lane freeway carrying >300,000 vehicles/day, effectively created two puma populations (east, west). Annual survival rates were low in both populations (55.8-66.5%), and most mortalities were caused by humans (vehicle collision, depredation) rather than natural causes such as disease. All pumas tested (n = 31) were positive for anticoagulant rodenticides, some with levels known to cause mortality. Coccidiodomycosis and Salmonella sepsis were fatal in two collared animals, and puma lentiviruses (both A and B clades), feline foamy viruses, and novel gammaherpesviruses were isolated from healthy animals. Serologic testing revealed exposure to Yersinia pestis, Toxoplasma, Bartonella, and feline leukemia virus; however, none of these pathogens were linked to disease or mortality. Leptospira spp. was detected in animals with evidence of non-fatal renal pathology. Habitat fragmentation and high mortality rates raise doubts about the long-term persistence of pumas in this urban area, particularly for the small, inbred, western population. To mitigate human caused mortality in this region, transportation authorities recently funded fencing and road modifications to minimize mortalities of pumas and other wildlife.
DOES URBANIZATION IMPACT MOVEMENT PATTERNS AND PATHOGEN PREVALENCE OF WHITE IBIS (*EUDOCIMUS ALBUS*)?

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Urbanization causes wildlife declines and biodiversity loss, but some species benefit from resources offered by human-altered habitats. Yet, if hosts change their behaviors, aggregate near food sources and interact with novel species, “resource provisioning” can increase contact rates and exposure to pathogens. Urbanization may also impact public health when it promotes novel or more frequent interactions between people and wildlife hosts infected with zoonotic pathogens. We examined the recent urbanization of white ibis (*Eudocimus albus*) in Florida to ask: 1) how do urban resources affect patterns of movement and aggregation? 2) does resource provisioning affect the prevalence of pathogens? We predicted that the use of urban environments by ibis would reduce their movements and alter their susceptibility to infection. Our current radio telemetry results (n=28; captured at urban sites) show that daily foraging and nightly roosting movements took place in urban habitats and ibis use only natural areas immediately adjacent to urban sites to breed. We found an overall prevalence of *Salmonella* spp infection of 12% (32/261) across sites, where there was a tendency for the prevalence to be higher at urban sites than natural sites. Of the *Salmonella* spp serotypes isolated (n=20), the most frequent were Rubislaw, Anatum, Bareilly, Newport, Saint Paul, San Diego and Florida. For all isolates, we found 100% matches of their Pulse Field Gel Electrophoresis (PFGE) patterns with human isolates in the PulseNet database, of which a significant portion came from the state of Florida. We found a high seroprevalence against avian influenza and paramyxovirus (89 and 75% respectively; n=273) in urban ibises when compared to ibises captured in natural environments, but we have not isolated either virus to date (n=298). These results show that the behavior and pathogen prevalence of white ibis is influenced by their consistent utilization of urban habitat.
SPECIES DIVERSITY AND INFECTION PATTERNS OF HEMOTROPIC MYCOPLASMAS IN RACCOONS (PROCYON LOTOR) IN PROTECTED AND DEVELOPED BARRIER ISLAND ECOSYSTEMS

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Raccoons are successful urban adapters that can actively interact with domestic and wild animals, potentially leading to cross-species pathogen transmission. This study identifies novel hemotropic Mycoplasma species in raccoons and their association with habitat type, and compares hemotropic mycoplasmas identified in urban raccoons to those of sympatric cats. Blood samples from free-ranging raccoons (n=37, urban; n=58, natural) and feral cats (n=37, urban) were collected in two Georgia, USA coastal islands with different habitat types, St. Simons Island (urbanized) and St. Catherines Island (protected native habitat). The total DNA was extracted from blood samples and 16S rRNA genes of hemotropic mycoplasmas were directly amplified using different combinations of the universal and species-specific primers. The partial RNA polymerase beta subunit (rpoB) and the DNA gyrase subunit B (gyrB) genes were also amplified for some hemoplasmas. Hemoplasma infection rates were 35.1% and 17.9% in raccoons and feral cats from the developed habitat, respectively, whereas 67.2% of raccoons from the relatively undisturbed natural habitat were hemoplasma positive. All mycoplasmal amplicons from blood samples were sequenced for species identification. Three species, M. haemofelis, Candidatus M. haemominutum and Candidatus M. turicensis, were detected in blood samples of the feral cats. In raccoons, the total of six hemotropic Mycoplasma species were identified in populations from both habitat types, although there were habitat-related differences in infection patterns of hemotropic mycoplasmas in raccoons. Based on the analysis of the 16S rRNA gene, the detected species were phylogenetically closely related to several published hemotropic mycoplasmas. However, due to low levels of genetic similarity of these raccoons' hemoplasmas to the previously described hemoplasmas and the mammalian host in which these novel hemoplasmas were detected, we propose that five of these six hemoplasmas definitely represent novel hemotropic Mycoplasma species, suggesting that raccoons can be a reservoir host of several novel hemotropic Mycoplasma species.
CLEAN COAL? HEALTH EFFECTS ON RACCOONS (*PROCYON LOTOR*) FOLLOWING A COAL FLY ASH SPILL IN EAST TENNESSEE

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In December 2008, approximately 5.4 million cubic yards of coal fly ash and water spilled from the Kingston Fossil Plant (Kingston, Tennessee, USA) into the Emory River. Raccoons were collected in 2009 and 2010 from the spill site and unexposed areas to determine what health effects occurred and if metal accumulation was present in various tissues. A complete blood count, plasma biochemistry panel, and histopathology of select tissues were performed on each animal (n = 30). Select tissues were analyzed for the presence and concentration of 26 metals/metalloids. Results were analyzed by year and location. No clinically important differences were seen on complete blood counts or plasma biochemistry panels. Abnormalities seen on gross necropsy included gastrointestinal parasites (n=10), fractured teeth (n=5) and nodules in the lungs (n=1). Pulmonary anthrocosis (n=19), eosinophilic pneumonia (n=11), hepatic portal fibrosis (n=16), gonadal hypertrophy (n=11), and pulmonary fibrosis/granuloma (n=7) were observed but there was no difference in the prevalence of the different lesions in exposed compared to unexposed animals. Although significant differences in metal concentrations occurred, only arsenic in hair, iron in muscle, nickel in hair, selenium in hair and muscle, strontium in hair, and vanadium in hair and liver were elevated in exposed animals compared to unexposed animals in either one or both years. The concentrations of metals and metalloids detected in this study were not associated with any gross or microscopic lesions. Continued monitoring of exposed populations for the previously mentioned metals was recommended. For raccoons, baseline concentrations of most of the metals/metalloids measured were not available in the literature, and this research may provide information to aid future research.
HUMAN ACTIVITIES AND LANDSCAPE FEATURES INFLUENCE ORTHOPOXVIRUS SEROPREVALENCE IN GREY SQUIRRELS (SCIURUS AUREOGASTER) IN MEXICO CITY, MEXICO

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Orthopoxviruses (OPXV) have been isolated from wild rodents worldwide. OPXV outbreaks have been reported in the Old World affecting some species of rodents and represent a conservation and public health concern. In North America, endemic OPXV have been reported in rodents and little is known about OPXV on synanthropic species in urban landscapes. The Mexican grey squirrel (Sciurus aureogaster), an opportunistic rodent, lives in close proximity with humans, representing an ideal model to assess the effects of urbanization on disease dynamics. Our main goal was to analyze the influence of habitat patch structure, host population attributes, and human activities on OPXV seroprevalence in S. aureogaster; we additionally analyzed the influence of host individual traits on OPXV seropositivity. From February to June 2011, we captured 366 grey squirrels in 18 urban parks in southwestern Mexico City. Oral swabs, 1 ml of blood, and skin lesions or scabs were collected from individuals. A modified enzyme-linked immunosorbent assay was used for detection of anti-OPXV immunoglobulins. DNA was extracted from oral swabs (n=366) and from skin lesions or scabs (n=65) to determine whether the serologic reaction was due to a previously described North American OPXV. DNA was screened with the North American OPXV Real Time-PCR assay. DNA samples were all negative. Our serologic data (prevalence = 30%) provides the first evidence of OPXV antibodies in Mexican wildlife. The generalized linear model (GLM) showed that patch structure was the best variable to explain differences in seroprevalence; in particular, populations living close to other squirrel populations exhibited higher OPXV prevalence (P= 0.014). Body index was partially significant (P = 0.09), indicating that heavier individuals were less likely to be seropositive. Our results suggest that some landscape features and individual attributes may influence the prevalence of the virus in the population.
TRACING *TOXOPLASMA GONDII* FROM TERRESTRIAL CARNIVORES TO MARINE HOSTS IN COASTAL CALIFORNIA

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Environmental transmission of the zoonotic parasite *Toxoplasma gondii*, which is shed only by felids, poses risks to human and animal health in diverse ecosystems. Atypical *T. gondii* genotypes have been linked to severe disease in people and the threatened population of Southern sea otters. To investigate land-to-sea parasite transmission, we screened 373 carnivores (feral domestic cats, mountain lions, bobcats, foxes, and coyotes) for *T. gondii* infection and examined the distribution of genotypes in 85 infected animals sampled near the California sea otter range. Nested PCR-RFLP analyses and DNA sequencing at six independent polymorphic genetic loci were used to characterize *T. gondii* strains in infected animals. Strains consistent with Type X, a novel genotype previously identified in over 70% of infected sea otters and four terrestrial wild carnivores along the California, USA coast, were detected in all sampled species. Odds of Type X infection were 14 times higher (95% CI: 1.3-148.6) for wild felids than feral domestic cats. However, discovery of Type X in coastal domestic cats suggests that they may play an important role in marine infection, as their populations are substantially larger than those of wild felids. A spatial cluster of Type II infection (P=0.04) was identified in developed lands bordering an area of increased risk for sea otter Type II infection. Two spatial clusters of animals infected with strains consistent with Type X (P<0.01) were detected in less developed landscapes. Differences in *T. gondii* genotype prevalence among carnivores, as well as the spatial distribution of genotypes, suggest co-existing domestic and wild *T. gondii* transmission cycles that likely overlap at the interface of developed and undeveloped lands. Anthropogenic development driving contact between these cycles may increase atypical *T. gondii* genotypes in domestic cats and facilitate transmission of potentially more pathogenic genotypes to humans, domestic animals, and wildlife.
ASSESSMENT OF THE HEALTH STATUS OF NARWHAL (MONODON MONOCEROS) HARVESTED FOR CONSUMPTION BY INUIT FROM POND INLET, NUNAVUT, CANADA

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The Canadian Arctic, home to well over half of the world’s narwhals (Monodon monoceros), is being profoundly and rapidly affected by global climate change and increased anthropogenic activities. Dramatic changes in sea ice cover, range expansion of temperate marine mammals and their pathogens, altered host-parasite interactions, and the potential for disease emergence in naïve populations are all of concern. As an ice-associated apex fish-eating predator, and as a major food source for subsistence Inuit, the narwhal is an ideal sentinel for the health and resilience of the Arctic marine ecosystem. To understand climate change-related effects on narwhal health, sustainability and food security, a benchmark of population health is required. In August 2013, tissue samples were collected from hunter-harvested narwhals in collaboration with the Pond Inlet Hunters and Trappers Association, along Milne Inlet on the north coast of Baffin Island, a principal summer calving and feeding habitat. Eight whales were sampled representing both sexes and an age range from sub-adult to advanced age. Full necropsies were conducted after harvesting of muktuk and meat by the hunters. Samples from all body systems were collected for histopathology, virology, bacteriology and serology. Initial results support the use of these animals as a safe and healthy food source. Parasitic infections were a consistent finding in younger animals while two distinct neoplasias were identified in adults. Results of bacterial culture, serology for a panel of pathogens of significance to animal and human health (Influenza A, morbillivirus and Brucella ceti) and histopathology are presented. This is the initial step in identifying primary drivers of health, stress and potential population vulnerabilities with the goal of improving protective measures and informing government policy affecting the Arctic marine ecosystem to ensure sustainability of this important resource for the socio-cultural and physical health of Inuit people.
COMPLEXITIES IN ARCTIC HOST-PARASITE INTERACTIONS IN A REGIME OF RAPID CLIMATE CHANGE: THE CARIBOU—OSTERTAGIA GRUEHNERI SYSTEM

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³ Ecology and Evolutionary Biology, Princeton University, Princeton, New Jersey, USA

Widespread climate change is having profound impacts on physical and ecological processes across the Arctic. Our studies on Ostertagia gruehneri, a common and pathogenic abomasal nematode of caribou, demonstrate complex interactions between parasite life history strategies, host migratory behavior, and climate warming. Using complementary field studies, laboratory experiments, and modeling frameworks incorporating the Metabolic Theory of Ecology, we have described the life history of O. gruehneri in caribou and investigated the impacts of climate change on host-parasite interactions. We found that 1) the transmission dynamics are highly seasonal where host winter migration spatially and temporally separates caribou from their parasites, and parasites ‘counteract’ this by focusing their reproductive output to the summer; 2) tundra surface temperatures now and in the future frequently exceed the upper tolerances of free-living stages of O. gruehneri; and 3) changing physical barriers (sea ice patterns) may alter the caribou-O. gruehneri transmission dynamics substantially. Our results counter-intuitively indicate a mid-summer trough in transmission because of high temperatures, but that this loss in transmission may be counteracted by a prolonged transmission season in spring and fall and a decreasing propensity for larval hypobiosis in the caribou. Overlaying this are shifting migratory patterns. Together these studies highlight the value of integrated ecological, laboratory, and modeling studies and emphasize the critical importance of understanding the complex interactions between the physical environment, host behavioral ecology and parasite life history strategies and tolerances.
Abstracts from Poster Presentations
All posters will be presented in the Puma Rooms

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The Wildlife Disease Association Conference Program and Abstracts booklet is available to all meeting attendees. Abstracts were lightly edited to comply with formatting and space limits, but otherwise were printed as submitted. The Wildlife Disease Association does not regard this Conference Program and Abstracts booklet as a publication and abstracts included herein should not be cited in scientific literature.
NOTES
Presentation Schedule for Posters
One Health Poster Session
Monday, July 28, 2014
1:00-2:00pm

Justice-Allen
[101] Chlamydophila mortality in rosy-faced lovebirds with a case of human illness in Arizona

Botzler
[102] Assessing chytrid infection in local amphibian communities through citizen science, Humboldt County, California

Buchholz
[103] Feral swine *Leptospira* serology in Hawaii

Driscoll
[104] "Still crazy after all these years" - 15 years of "One Health" in Maryland

Harms
[105] Emaciation and ulcerative ingluvitis in two golden eagles: a role for lead?

Keatts

Kinani

Lankau

Garland-Lewis
[109] Occupational health of wildlife health professionals: moving towards best practice in a One Health framework

McConnell
[110] *Trypanosoma cruzi* infection in New Mexico: wildlife disease, interdisciplinary approaches, and One Health

Mortenson
[111] *Cryptococcus gatti*: where is environmental exposure occurring?

Nicholson
[112] Occurrence of "*Neoehrlichia lotoris*" in raccoons (*Procyon lotor*) and other hosts in northwestern Missouri

Nymo
[113] Validation of an indirect ELISA for the detection of anti-*Brucella* antibodies in *Rangifer tarandus* spp.

Palamar
[114] Public preference towards rabies pet vaccination and rabies information dissemination in Greensboro, North Carolina

Pedersen
[115] Widespread detection of *Leptospira interrogans* antibodies in feral swine in the U.S.

Pennington
[116] Emerging technologies for One Health
Rizzoli [117] Understanding the impact on human and wildlife health of the invasive alien mosquito species *Aedes albopictus* in northern Italy


Tauer [119] Epidemiology of skin lesions in a population of gorillas (*Gorilla gorilla gorilla*) at Langoue Bai, Ivindo National Park, Gabon and possible zoonotic health implications

Torres [120] Parasitological findings of five species of Ecuadorian primate: preliminary data

Tsubota [121] Molecular epidemiological study on *Anaplasma phagocytophilum* in sika deer (*Cervus nippon*) in Hokkaido, Japan

Ward [122] Salmonella infection in feral pigs in remote northwest Australia and implications for co-grazing beef cattle

Webeck [123] Domestic canine-associated human rabies outbreak investigation and response, Kenya
A population of rosy-faced lovebirds (*Agapornis roseicollis*), an invasive avian species, became established in the Phoenix metropolitan area of Arizona more than 25 years ago. They are frequent visitors to backyard feeders in the Phoenix area, and have been observed roosting and nesting in ornamental palms and native saguaro cacti. In spite of their predilection to displace other species from nesting sites, no negative impacts by lovebirds to native species have been documented. In late August 2013, a mortality event involving lovebirds was reported to the Arizona Game and Fish Department by a Mesa resident. Several carcasses were collected and submitted to the USGS National Wildlife Health Center for diagnostic evaluation. Gross lesions consisted of yellow exudate at the nares, red lungs, and hepatosplenomegaly. *Chlamydophila psittaci* was detected by PCR in four of four birds tested. Tests were negative for avian paramyxovirus, West Nile virus, and avian influenza. Follow-up communication with the resident revealed that the individual had sought treatment at a medical clinic for a febrile illness with respiratory symptoms and was not improving with amoxicillin clavulanate treatment. After being advised of the cause of the mortality in the lovebirds, she revisited her physician and her medication was changed to doxycycline. Within three days, her symptoms began improving. A single convalescent titer taken by Maricopa County Department of Public Health in late September was positive for exposure to *C. psittaci* by microimmunofluorescence testing. Wild birds species implicated in transmission of psittacosis to humans include fulmars, green Amazon parrots, pigeons, ducks, and turkeys. Recently, transmission of chlamydia to humans from psittacines kept as pets has been more common. With increasing numbers of invasive populations of psittacines identified around the world, the public health implications of native and non-native urban populations of psittacines should be considered by physicians and wildlife veterinarians.
ASSESSING CHYTRID INFECTION IN LOCAL AMPHIBIAN COMMUNITIES THROUGH CITIZEN SCIENCE, HUMBOLDT COUNTY, CALIFORNIA

Ecoclub Amphibian Group,¹ Greta Wengert,² Janet Foley,³ and Richard G. Botzler¹,⁴

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Learning of its world-wide importance, the Bilingual McKinleyville Ecoclub (ages 4 to 16 years) chose to assess the prevalence and distribution of the chytrid fungus, Batrachochytrium dendrobatidis, among amphibians of Humboldt Bay National Wildlife Refuge (HBNWR) and Redwood National and State Parks (RNSP), Humboldt County, California (USA); habitats varied from redwood forest to salt marsh. All appropriate collecting permits were completed. Following required educational workshops by disease researchers held at the Community Garden in McKinleyville, 18 youth and 13 supervising adults made sampling trips to HBNWR and RNSP between May 2013 and January 2014. Skin swabs from 68 metamorphosed amphibians and buccal swabs from 5 tadpoles were collected at HBNWR, RNSP, and the Community Garden. Using a real-time polymerase chain reaction test, 14 (19%) of 73 samples were positive for B. dendrobatidis. Among metamorphosed animals this included 8/30 Pacific chorus frogs (Pseudacris regilla) (Hylidae); 0/11 Western toads (Anaxyrus (Bufo) boreas), (Bufonidae); 2/17 northern red-legged frogs (Rana aurora), 4/9 foot-hill yellow-legged frogs (Rana boylii) (Ranidae); and 0/1 rough-skinned newt (Taricha tenebrosis) (Salamandridae). None of the 5 tadpoles were positive with buccal swabs. At HBNWER, 6 of 40 (15%) amphibians were positive, compared to 4 of 26 (15%) at RNSP, and 4 of 7 at the Community Garden. Estimated chytrid zoospore intensities generally were low among positive samples (median = 3; range 1-33). Eleven of 41 (27%) amphibians sampled by youth <12 years old were positive, compared to 3 (10%) of 30 amphibians sampled by participants over 12 years of age; the difference was not significant ($X^2$ =2.13, p>0.10). The Ecoclub results are comparable to other chytrid studies of the region and reflect that the field techniques of the youth were comparable to those of professional scientists; these findings support the potential value of involving children and youth in citizen science projects.
FERAL SWINE LEPTOSPIRA SEROLOGY IN HAWAII

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Serum collected from feral swine for disease surveillance by hunters and USDA/APHIS/Wildlife Services staff was tested by microscopic agglutination test (MAT) using a panel of 20 Leptospira serovars at the Centers for Disease Control and Prevention. One hundred forty-four serum samples collected on the islands of Oahu, Hawaii and Maui from January to December 2009 were tested. The overall prevalence of antibodies to Leptospira at a titer of 100 or greater was 34% (49 of 144 samples). Samples collected from swine on Oahu had a seroprevalence of 31% (33 of 106). Serum samples from Maui had a seroprevalence of 40.5% (15 of 37). One sample was collected on Maui and was positive at a titer of 100. L. interrogans serovar Bratislava was the most common serovar that reacted with the serum samples, with 67% (33 of 49 samples) demonstrating a titer of 100 or greater. Eight of 49 samples, or 16%, had titers of 100 or greater to L. interrogans serovar Icterohaemorrhagiae. One of 49 samples (2%) had a titer of 400 to L. interrogans serovar Djasiman, and 2 of 49 (4%) samples had a titer of 100 to L. interrogans Autumnalis. Two cases each had equal titers for serovars Bratislava/ Icterohaemorrhagiae and Bratislava/ Autumnalis and one case for Bratislava/ Australis. The range in MAT antibody titer was 100-1600. Twenty-two of 46 (48%) animals of known sex with Leptospira infections were female and 24 of 46 (52%) were male. L. interrogans serovar Bratislava is commonly associated with Leptospira infections of domestic swine. Additional studies of leptospirosis in feral swine may lead to strategies to mitigate the risk for human and domestic animal exposure. While MAT studies provide information on exposure to Leptospira, the infecting serovars usually cannot be determined and culture isolates are necessary for definitive identification. Hence, continued research is needed to identify Leptospira culture isolates from feral swine samples.
“STILL CRAZY AFTER ALL THESE YEARS” – 15 YEARS OF “ONE HEALTH” IN MARYLAND

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Veterinarians are expected to communicate and cooperate with each other and state agencies; however that does not always happen. Before the current state veterinarians were hired in Maryland, agencies communicated, but it usually was limited to emergency situations. Efforts to bring disparate interests to the table were met with lukewarm receptions. In the early days, university, human health and animal agencies met periodically and agreed to stay connected, though no single effort drew us together for anything other than a superficial collegiality. The efforts of One Health advocates changed the way we all look at animal (both domestic and wildlife), human and environmental health issues. In the past 15 years, when veterinarians were hired in key government positions in our state the possibilities now seemed endless. Communication flowed, and information concerning important issues was shared. In 2010 we began to discuss how our small state could better address these issues and started the development of a monthly bulletin. The Maryland One Health Bulletin (MOHB) is now distributed to over 4000 individuals in MD and beyond. While initially intended as a tool to inform practicing veterinarians of disease outbreaks, it has grown to incorporate public health practitioners, wildlife biologists and government agencies. It includes topics such as important legislation that can affect all One Health partners as well as timely alerts distributed immediately when diseases are imminent. Some of the disease outbreaks have included tularemia, rabies, harmful algal blooms, avian botulism, and canine influenza. Other addressed problems have included legal issues such as pentobarbital poisoning of eagles from improper disposal of euthanized animals, the accreditation renewal process, and licensed or authorized marine mammal and sea turtle stranding rescue. We are happy to share our template for this bulletin with other states and hope to expand the reach of One Health.
EMACIATION AND ULCERATIVE INGLUVITIS IN TWO GOLDEN EAGLES: A ROLE FOR LEAD?

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Two sub-adult male golden eagles presented to a wildlife rehabilitation facility in May 2013. The first eagle was found near Haines Junction, Yukon, the second eagle was found 8 days later approximately 150 km east of the first eagle. Both eagles were depressed and unable to fly. Twelve days after being admitted, the first eagle was found dead; the second eagle died 2 days after being admitted. Gross and histological examination revealed similar lesions in both cases; including emaciation with severe atrophy of skeletal muscles and absence of fat stores; severe, multifocal, ulcerative ingluvitis; and multifocal, partially healed lacerations on the neck, feet and legs. The heart of the second eagle was characterized by multifocal areas of mild fibrosis and adhesions. High-normal lead levels were detected in the livers of both eagles (0.78 and 1.67 ppm wet weight, respectively). Culture of tissues detected Escherichia coli in the lung and kidney and Staphylococcus spp. in the lung and crop from the first eagle, and Mucor spp. and E. coli in the kidney and crop of the second eagle. Although the lead levels do not indicate toxicity in these eagles, lead may have played a role in their morbidity through reduced immune function and starvation. Lead-contaminated offal from big game hunts is proving to be a significant source of dietary lead exposure for scavenger birds. Lead fragments in the tissues of harvested game also have important implications for the health of people who consume wildlife shot with lead bullets. A pilot surveillance program to examine lead levels in avian scavenger species in Yukon was initiated to determine if scavenger birds are exposed to lead and to explore the possible role of lead bullet fragments; this program may also provide an indicator of the potential impacts on human health.
A ONE HEALTH APPROACH TO SURVEILLANCE FOR ZOONOTIC DISEASES AT WILDLIFE-HUMAN INTERFACES IN CAMBODIA, LAO P.D.R AND VIETNAM

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Greater than 60% of emerging zoonoses have reservoirs in wildlife. In order to predict the emergence of novel infectious diseases in humans, pathogens must be identified at their source. This requires targeted, informed surveillance along high-risk transmission pathways with strategic selection of geographic locations and species demanding a One Health approach. Southeast Asian countries are high in biodiversity and are key sources, conduits and consumers of wildlife. Rapid economic development over the past decade has seen dramatic large-scale land-use change for extractive industries and agriculture. These factors have increased the number of interfaces between humans, domestic animals and wildlife, increasing opportunities for pathogen spillover. The USAID PREDICT project has brought together animal and human health, agriculture, forestry, education, laboratory and environmental sectors across Lao P.D.R, Cambodia and Vietnam to conduct collaborative surveillance and novel diagnostic screening to better identify higher risk interfaces. In Lao P.D.R where wildlife is traded openly in markets, 86 markets were surveyed over 3 years, recording a snapshot of trade that included >14,000 wild birds, >7000 rodents, >3000 bats. In Cambodia, wildlife including primates, is consumed in many rural communities; commercial trade has moved underground requiring surveillance to target middle-men and confiscated wildlife; increasing numbers of bats are being farmed for guano; and large numbers of economic land concession grants are leading to large-scale deforestation in and around the country’s protected areas. In Vietnam, wildlife consumption is increasing, driven by increasing purchasing power of a burgeoning middle-class, and farming of various species from porcupines to crocodiles to civets is growing in popularity, though many farm stock are still sourced from the wild. Surveillance at these interfaces can advise policy-driven One Health preventative actions that are needed in the immediate future to reduce activities that threaten biodiversity and increase the risk of disease spillover from wildlife to humans.
RESPIRATORY DISEASE AMONG MOUNTAIN GORILLA IN THE VOLCANOES NATIONAL PARK, RWANDA, 2005-2011

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The mountain gorilla, found only in Rwanda, DRC and Uganda is one of the most endangered species. Due to its great genetic similarity with humans (> 98%), gorillas are susceptible to human illnesses like respiratory diseases. This study was conducted to establish the prevalence of respiratory diseases and describe the patterns associated with it among mountain gorillas in the Volcanoes National Park. Occurrence of respiratory disease among the gorillas was recorded from 2005-2011. Respiratory infection was defined by a three day cough with nasal discharge, lethargy or sneeze. Key variables on demographics, season and habitat were collected using structured tools. Data analysis was performed using STATA 1 and statistical associations between respiratory disease and selected variables determined. Multivariate analysis was done using stepwise logistic regression. Record review was done in health facilities around the park to establish trends of respiratory diseases among humans. From 2005 to 2011, 129 of 282 (45.7%) mountain gorillas were reported with respiratory disease. Respiratory diseases were the leading (52%) cause of morbidity and the fifth cause of mortality (8.6%). Juvenile gorillas (OR: 3.26, 95% CI: 1.16-9.07) and silver back gorillas were more likely to develop respiratory diseases than infants (OR: 2.86, 95% CI: 1.16,7.04). Respiratory diseases were more likely to be reported during the main dry season (OR: 6.31, 95% CI: 2.34-16.95), coinciding with the period of greatest human respiratory disease activity in the health-facilities around the park. Respiratory diseases among mountain gorillas were very high but mortality relatively low probably due to early reporting and treatment. We recommended enhancing of control measures to reduce risk of cross-contamination between humans and mountain gorilla.
PUBLIC HEALTH IMPLICATIONS OF CHANGING RODENT IMPORTATION PATTERNS – UNITED STATES, 1999-2013

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The United States imports a large volume of wildlife species; these animals pose a demonstrated zoonotic disease risk. Rodents are imported for multiple purposes including scientific research, zoo exhibits, and the pet trade. Current U.S. public health regulatory prohibitions on rodent importation, enacted in 2003, pertain only to those of African origin. We evaluated rodent importations from 1999-2013 by shipment origin, taxonomy and source (wild vs. captive bred) to better understand disease importation risks. Following the 2003 ban, African-origin imports declined, becoming sporadic under the federal permit process. Total rodent imports increased from 2,737 animals during 1999 to 173,761 animals during 2013, an overall 63-fold increase. The proportion of wild-captured imports declined from 75% during 1999 to less than 1% during 2013. Imports from Europe and other North American countries increased substantially, with European imports peaking in 2007 at over 400 times 1999 levels and North American imports in 2011 at 33 times 1999 levels. Furthermore, shipment number and size steadily increased from 12 shipments in 1999 with a median of 5 animals per shipment (range: 1-150) to 63 shipments in 2013 with a median of 150 (range: 1-450). The predominant purpose of importation for all years was commercial. Specific rodent taxa driving these increases included gerbils and hamsters from Europe and chinchillas, guinea pigs, and hamsters from North America. Overall, these patterns suggest a shift to large-scale captive rodent breeding for commercial imports. This shift may alleviate risks of importing infectious diseases present in wild populations, such as monkeypox, but also may elevate exposure risks for zoonotic diseases associated with high-density rodent breeding, such as lymphocytic choriomeningitis or salmonellosis. Regulatory considerations must balance the potential economic benefits of rodent trade against public health risks associated with these emerging patterns of increased density and shipment volume.
OCCUPATIONAL HEALTH OF WILDLIFE HEALTH PROFESSIONALS: MOVING TOWARDS BEST PRACTICE IN A ONE HEALTH FRAMEWORK

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Wildlife health professionals are at unique risk for occupational illness and injury, yet there are no widely accepted models for preventative occupational health services for this population. Additionally, such persons may not consider themselves part of an organized workforce, which may in part explain why occupational health services for this group is less formalized than for many other occupational groups. Our objective is to review occupational disease and injury risks for wildlife health professionals in order to propose best practices for occupational preventative services, with a One Health framework in mind. A systematic survey of biomedical literature and review of available protocols for occupational health of wildlife workers was carried out using online databases and communication with wildlife health professionals. Animal-related injuries were the most commonly reported issue among wildlife health workers, with a number of zoonotic disease issues identified as well. Issues such as allergy and skin reactions were also reported. Best practice recommendations include: baseline screening of workers, training in hazard identification and control, periodic monitoring and medical surveillance, identification of sentinel health events, and acute injury/illness management. Additionally, since medical providers may not be aware of risks, training of human health care workers to better understand occupational risks and exposures in wildlife health workers is imperative in this field. Wildlife health professionals have unique risks requiring unique occupational health programs. One of the challenges of occupational health in the wildlife setting is managing the health of workers as well as the health of animals in a wide variety of environments. Such interrelationships require a comprehensive One Health approach to maximize human, animal and environmental health. Organized programs that combine human health care providers, veterinarians, conservation biologists and safety are a key component of developing strong occupational health services for wildlife workers.
TRYPANOSOMA CRUZI INFECTION IN NEW MEXICO: WILDLIFE DISEASE, INTERDISCIPLINARY APPROACHES, AND ONE HEALTH

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Biosurveillance of vector-transmitted emerging diseases from wildlife hosts creates challenges that require an increasing number of interdisciplinary collaborations. Historically, a “mono-culture” approach to disease research has prevented effective infectious disease research, because discipline-specific disease indicators often do not transcend to other disciplinary concepts. To help advance new concepts in approaches to zoonotic, infectious diseases, the Geo-Epidemiology Research Network (GERN) was founded in 2010 to bring together experts representing various disciplines and a common interest of infectious disease and to utilize emerging technologies to their fullest advantage. An initial focus of New Mexico GERN identified Chagas’ Disease as a potential challenge to the public health of New Mexico residents. Chagas’ Disease, caused by the parasite Trypanosoma cruzi and vectored through triatomine bugs, is a primary example of a neglected disease that resides latent in humans for decades, yet remains poorly understood in the southwestern United States. A pilot study conducted in 2011 re-confirmed the existence of T. cruzi in New Mexico that closely matched southern Texas and Arizona. Additionally, during Spring/Summer of 2013, community collection efforts yielded 82 Triatoma specimens from local dwellings and peridomestic areas. Full analysis is forthcoming. Because the identification of Triatoma protracta in New Mexico is consistent with expected distributions in southern Texas and Arizona, the range of reservoir hosts for the parasite may now be compared with parasite incidence, geography and habitat. This information may then be used in concert with vegetation/rainfall remote sensing to understand how the natural environment may contribute to zoonotic diseases. Integrating new surveillance strategies with emerging technologies such as the Virtual Learning Commons (VLC), ELSEWeb and ZORN 3.0 will lead interdisciplinary approaches toward translational infectious disease research. By expanding parameters from different disciplines through technologies, effective public health outreach programs may be created to reduce risk of exposure and maintain healthy populations.
CRYPTOCOCCUS GATTI: WHERE IS ENVIRONMENTAL EXPOSURE OCCURRING?

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The fungal pathogen Cryptococcus gatti was first described in North America on Vancouver Island, British Columbia, Canada in 2002. Since then, a wide range of species have been identified with C. gatti infections including humans, domestic animals and wildlife. Many studies have documented the extensive fungal colonization of tree bark and soil among other substrates on the southern end of Vancouver Island and transmission is considered primarily via air-borne environmental spores. Infections occurring in humans and animals from Oregon have been identified since 2006. Early on, these infections were considered related to northern travel, but now thought to be locally acquired due to infection in non-migratory animals and humans with no travel history. Previous published efforts to detect C. gatti from tree swabs and soil samples in Oregon have been unsuccessful. We were interested in locations where humans and animals shared space as possible sites of exposure to C. gattii. We combined this concept of shared local places with the knowledge of C. gattii colonization of specific tree species and decided to survey urban parks. This study was conducted to determine the presence of C. gattii in selected urban parks of Oregon cites within the Willamette Valley where both human and animal cases of C. gattii have been diagnosed. Two of 500 environmental samples taken from 64 parks were positive for C. gattii. One park had a positive tree bark sample and another park, 60 miles away, had positive bark mulch samples from a walkway. Genotypic subtypes identified included C. gattii VGIIa and VGIIc, both considered highly virulent in murine host models. Given the increasing number of confirmed C. gatti infections, local environmental exposure is not yet identified in Oregon.
OCCURRENCE OF “NEOEHRlichia Lotoris” IN Raccoons (PROcyon Lotor) AND OTHER HOSTS IN NORTHWESTERN MISSOURI

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Raccoons (Procyon lotor) and opossums (Didelphis virginiana) were collected using Tomahawk live traps from multiple sites in northwestern Missouri over a period from April 2012 to September 2013. Whole blood was collected into EDTA tubes for molecular testing. Bacterial DNA was detected by using a real-time PCR assay targeting the 16S rRNA of the family Anaplasmataceae, and any positive amplicons sequenced to determine species identity. Blood samples from several other species of animals collected in the same area were also tested. Of the 93 raccoons tested, 54 (58%) of them were found to be infected with “Neoehrlichia lotoris”, a newly described, yet informally named, taxon in the bacterial family Anaplasmataceae. Of the other animals tested, 1/37 Virginia opossums, 1/9 eastern cottontails, and 1/7 wild turkeys were positive for the agent. However, none of the 14 white-tailed deer or 4 fox squirrels were positive for “N. lotor” DNA. This organism had only previously been detected in raccoon populations from Florida, Georgia, and South Carolina. This agent was prevalent from multiple sites in northwestern Missouri and may be more widely distributed in other states. The mode of transmission has yet to be determined, but tick transmission is highly suspected. This organism is closely related to “N. mikurensis”, which has been found to be pathogenic to humans in multiple countries in Europe and Asia. Further studies will be needed to determine the distribution of “N. lotoris” in the United States and evaluate its importance to animals and humans.
VALIDATION OF AN INDIRECT ELISA FOR THE DETECTION OF ANTI-BRUCELLA ANTIBODIES IN RANGIFER TARANDUS SPP.

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Infection with Brucella suis biovar 4 causes brucellosis in Rangifer tarandus spp. in Canada, Alaska and Russia. Brucellosis in R. tarandus spp. is characterized by bursitis, orchitis, epididymitis, retained placenta, metritis, abortions and abscesses; it also poses a zoonotic risk. For the detection of anti-Brucella antibodies in R. tarandus spp. a validation of the serological method, by isolation of B. suis biovar 4, is a prerequisite. The aim of this study was to validate an in house indirect ELISA (iELISA) for the detection of anti-Brucella antibodies in Rangifer tarandus spp. When tested with the Rose Bengal Test (RBT), all the semi-domesticated reindeer from Norway (R. t. tarandus, n=304) which previously tested negative for antibodies against Brucella spp., were confirmed seronegative. Likewise, all the B. suis biovar 4 bacteriology positive barren ground caribou (R. t. groenlandicus, n=34) were seropositive. The cut-off for the iELISA was calculated as the mean value of the samples from the seronegative reindeer plus 2.58 standard deviations, providing a cut-off of 1.13 percent positivity (%P = percentage of the reactivity of a positive control). All caribou samples were positive in the iELISA. Two Norwegian sera were classified as weak positives (<2.0 %P), but they were seronegative when tested with classical tests. Receiver Operator Characteristic (ROC) analysis of the iELISA results, using the bacteriology-positive caribou as true positives, showed an area under the curve of 0.99 (95% CI: 0.99–1.00), a sensitivity of 100.0%, and a specificity of 99.3%, yielding 99.4% of the animals being correctly classified. The results obtained with the iELISA were thus consistent with the bacteriological gold standard and the iELISA was validated as a highly sensitive and specific serological method for the detection of anti-Brucella antibodies in Rangifer tarandus spp.
PUBLIC PREFERENCE TOWARDS RABIES PET VACCINATION AND RABIES INFORMATION DISSEMINATION IN GREENSBORO, NORTH CAROLINA

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Urban environments can host high densities of wildlife species because of higher reproduction rates and increased survival. This, combined with specific human behaviors towards wildlife, increase the risk of disease transmission such as terrestrial rabies in urban environments. Pet vaccination, wildlife vector management and public health education may be the most efficient ways to prevent a rabies epidemic in urban environments. Ethnic minorities, particularly Latinos, are increasing throughout the United States and becoming critically important for wildlife management and outreach programs. Therefore, we conducted a bilingual (English/Spanish) survey of people residing in Greensboro, North Carolina to determine their compliance with pet vaccination and use of low cost rabies vaccination clinics, understanding of rabies reporting requirements and ways they would like to receive rabies information in the future. We interviewed 301 people, 23 Spanish speaking; half of them pet owners and 85% indicated they vaccinated their pets. Our results show that pet owners know that they should vaccinate their pets, but in reality fail to do so. Most African Americans and Latinos were not aware of low cost rabies vaccination clinics. Most respondents would call to report rabid animals but did not have the appropriate number. Half of the white respondents would like to receive future rabies information through internet, but Latinos and African Americans preferred postal mail. Different segments of the population use different information outlets depending on ethnicity, income and education. Variances in risk perception and communication of diverse segments of the population influenced by ethnicity, economic and educational status may have great impact on message decoding and interpretation, and should be considered for public health campaigns. Novel communication methodologies such as mobile phone messaging should be evaluated as an important tool to reach people of all ages and levels of education or income with public health information.
WIDESPREAD DETECTION OF *LEPTOSPIRA INTERROGANS* ANTIBODIES IN FERAL SWINE IN THE U.S.

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As feral swine continue to expand their geographic range and distribution across the U.S., their involvement in crop damage, livestock predation, and pathogen transmission likely also will increase. Despite the relatively recent discovery of feral swine involvement in the etiology of a variety of pathogens, their propensity to transmit and carry a wide variety of pathogens is disconcerting. We examined sera from 2,055 feral swine for the antibody presence to six serovars of *Leptospira interrogans* that can also infect humans, livestock or domestic animals. Approximately 13% of all samples tested positive for at least one serovar suggesting that *Leptospira interrogans* infection is common in feral swine. Further studies to identify the proportion of actively infected animals are needed to more fully understand the risk they pose.
EMERGING TECHNOLOGIES FOR ONE HEALTH

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A challenge in One Health initiatives is finding and integrating relevant data, models, and methods across disciplinary and stakeholder groups. Next generation internet technologies (called Semantic Web) are being developed in collaboration with the Geo-Epidemiology Research Network (GERN) to tackle these issues. GERN was founded in 2010 to bring together experts representing various disciplines and a common interest of zoonotic infectious disease and to utilize emerging technologies to their fullest advantage. This presentation will introduce three Semantic Web technologies being developed at the Cyber-Share Center of Excellence at University of Texas at El Paso that are designed to support geo-epidemiology research initiatives. The Earth, Life, and Semantic Web (ELSEWeb) enables earth science data to be easily discovered, transformed and input into species distribution models, allowing various stakeholders to engage in analysis of wildlife distributions as well as the potential impact of future environmental and landscape change scenarios on those wildlife distributions. The Virtual Learning Commons (VLC) works in conjunction with ELSEWeb, supporting learning about the methods, models and tools developed in different disciplines and communities that might be relevant for a particular geo-epidemiology problem, resulting in robust community discussions around those resources. ZORN 3.0 enables stakeholders to discover potential zoonotic infectious disease risks in their area, model them with ELSEWeb and explore recommended actions. ZORN 3.0 also enables citizens to contribute back to the VLC and ELSEWeb with their own data, observations, questions and comments. This presentation will include brief demos of these technologies, a discussion of ways we envision how they support One Health investigations of zoonotic infectious disease and how such approaches respond to the calls for open data and translational research in the scholarly community.
UNDERSTANDING THE IMPACT ON HUMAN AND WILDLIFE HEALTH OF THE INVASIVE ALIEN MOSQUITO SPECIES *Aedes albopictus* IN NORTHERN ITALY

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*Aedes albopictus* is among the most widespread alien species in the world and its introduction and spread in northern Italy has been documented since 1990. While its impact on human health is well known in this area not only for its nuisance but also for being the most important vector involved in the 2007 epidemics of Chikungunya (CHIKV), its role as a bridge vector of infections impacting both human health and wildlife is less understood. In fact, extensive epidemics of West Nile virus (WNV) and Usutu Virus (USUV) have been recently documented within the study area. Although referred to as an anthropophilic species, there is evidence of its relative ornithophily. To better understand its role as bridge vector for human and wildlife diseases in Italy, we carried out mosquito samplings within two regions (Trentino and Veneto) from 2011 to 2013. A total of 4613 unfed female and 1976 males were screened for Flaviviruses, while 86 fed females were screened to identify the host used by the mosquito for its blood meal. The virological screening identified the occurrence of *Aedes flavivirus* (AeFV) in a significant number of pools tested (14.6% in Trentino and 19.3% in Veneto) while no positive samples were obtained for West Nile virus or Usutu virus. Blood meal analysis of the engorged females identified the following host species: *Homo sapiens* (88.3%), *Erinaceus europaeus* (2.3%), *Coturnix japonica* (1.2%), *Passer montanus* (1.2%) and *Turdus merula* (1.2%). These preliminary finding indicate the ability of this species to feed also on non-human hosts and thus act as an additional potential bridge vector of pathogens among wildlife and humans, although in this study we could not identify West Nile or Usutu virus in our samples.
THE IMPORTANCE OF A COMPLETE NECROPSY IN NEGATIVE HUMAN/ANIMAL INTERACTIONS: A CASE REPORT OF A FREE-RANGING GRAY WOLF (CANIS LUPUS) CONFIRMED IN A HUMAN/WOLF CONFLICT INCIDENT

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An intact male free-ranging gray wolf (Canis lupus) was submitted to the University of Minnesota Veterinary Diagnostic Laboratory for post-mortem investigation by the Minnesota Department of Natural Resources. The wolf was trapped and euthanized near a northern Minnesota campground following a report that a 16-year-old boy was injured in an apparent gray wolf bite incident. DNA analysis confirmed that the trapped wolf was indeed the wolf involved in the incident and was also not a wolf hybrid. The wolf was severely emaciated and exhibited dental, skeletal and central nervous system deformities and abnormalities from the frontal brain region through the rostrum. We hypothesize that the wolf suffered injury at an early age. Compromise in the detention and/or bite of a wolf can have direct negative consequence to food procurment and social behavior. Location and severity of brain atrophy in this wolf provides evidence that the wolf suffered behavior modifying neuronal and olfaction deficits. Well-documented reports of aggressive wolf encounters show that few have led to serious human injury and tend to involve extenuating circumstances (e.g., unhealthy or tame wolf, extensive intrusion by the human). Human/wildlife encounters are inevitable with continued urban expansion and the public’s interest in outdoor recreation. A 2011 United States Fish and Wildlife Service (USFWS) survey indicated that 90.1 million Americans age 16 and older participate in wildlife related recreation. This case demonstrates the importance of a complete post-mortem examination in the circumstance of negative human/animal interactions to assist in understanding the dynamics of the situation.
EPIDEMIOLOGY OF SKIN LESIONS IN A POPULATION OF GORILLAS (GORILLA GORILLA GORILLA) AT LANGOUÉ BAI, IVINDO NATIONAL PARK, GABON AND POSSIBLE ZOONOTIC HEALTH IMPLICATIONS

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The prevalence of skin disease was evaluated in a population of western lowland gorillas (Gorilla gorilla gorilla) in Ivindo National Park, Gabon. Of particular interest was the prevalence of a syndrome that is similar to the human infection yaws (Treponema pallidum pertenue). Dermatopathy, including alopecia, scarring, erosions, ulcerations, abrasions, and scaling were present in 78.9% (15/19) adults of the population. No lesions were observed in the juvenile (n= 3) and infant population (n=6). Adult gorillas had a prevalence rate of 47.3% that fit the case definition for a yaws-like syndrome (YLS). There is evidence to suggest that cross species infection (human and non human primates) may occur, and further research is required to elucidate the ecology of this disease in gorillas, confirm microbiologically the pathogen causing clinical signs and determine the public health implications.
PARASITOLOGICAL FINDINGS OF FIVE SPECIES OF ECUADORIAN PRIMATE: PRELIMINARY DATA

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In Ecuador, expansion of agricultural border and residential and commercial development are threats for the conservation of primates. Thus, possible transmission of parasites between primates, men and domestic animals could happen. In order to know the parasitological state of five species of Ecuadorian primates with conservation status, parasite profiles were evaluated. Free ranging primates that entered rescue centers of Pastaza Province, Puyo City and free–ranging primates which livein the urban area of Misahuallí County, Napo Province were evaluated; all places were located in the northeastern Ecuadorian Amazon. Fecal samples were obtained of Cebus albifrons (23), Ateles belzebuth (8), Saimiri sciureus (6), Saguinus fuscicollis (4) and Lagothrix poeppigii (7). Samples were collected in the day, directly off of the soil. Feces were collected, refrigerated and analyzed by means of the sedimentation technique (Hoffmann-Pons-Janner) with the Paratest® (Freyma Representations, Ecuador). Results in C. albifrons showed mild presence of Strongyloides spp. (39.13%, 9/23) and high infection but low percentage of parasites with zoonotic potential as Taenia spp. (4.35%,1/23). A similar situation was reported in A. belzebuth with mixed infection of Strongyloides spp. and Balantidium coli (25%, 2/8). In S. sciureus, mild to moderate infections of Strongyloides spp. were more representative (4%, 2/6). In S. fuscicollis severe infection of Prosthenorchis elegans was detected (50%, 2/4); this parasite can cause severe and fatal pathologies and has been identified as a major cause of illness or death in captive primate colonies. An individual died, adult P. elegans was reported in necropsy. In L. poeppigii a few samples were positive with mild and moderate infections of Strongyloides spp. (28-58%, 2/7). In this study, basic tests were performed to assist future studies of identification, which could improve the state of the knowledge surrounding the effects of fragmentation and habitat loss on the parasitological profile of neotropical primates.
MOLECULAR EPIDEMIOLOGICAL STUDY ON *ANAPLASMA PHAGOCYTOPHILUM* IN SIKA DEER (*CERVUS NIPPON*) IN HOKKAIDO, JAPAN

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The study of tick-borne pathogens (TBPs) has become increasingly important, especially those with zoonotic potential. Given the increasing geographic range of tick-borne zoonotic diseases and the potential emergence of pathogens, they are of great concern for public health authorities. However, while we know much about the tick-borne zoonotic diseases, little is known about their prevalence in wildlife. In this study, 239 wild sika deer samples collected in Hokkaido, Japan were examined to detect *Anaplasma phagocytophilum*. A 770 bp segment of the 16S rRNA gene and a 382 bp segment of the citrate synthase gene (*gltA*) were amplified by nested PCR using *A. phagocytophilum* species-specific primers. The positive PCR products were sequenced and phylogenetically analyzed. The total prevalence of *A. phagocytophilum* was 51% and several genetic variants of *Anaplasma* species detected. The probability of infection showed significant regional dependence, yet complete independence from other demographics, including month, gender and age (P≤0.05). The sequences of the 16S rRNA and *gltA* gene amplicons that were obtained from the positive samples were 98-100% and 90-100%, similar to *Anaplasma* spp. sequences selected from GenBank, respectively. Phylogenetic analysis suggests the potential existence of novel *Anaplasma* spp. genetic variants in sika deer. This study provides data that will help to understand the epidemiology and genetic diversity of *Anaplasma phagocytophilum* in Hokkaido.
Wildlife populations have been implicated in recent disease emergencies, yet our understanding of how such diseases are maintained in wildlife populations is poor. Feral pigs are an invasive species in Australia that cause agricultural, economic and environmental damage. Limited research has been conducted in Australia (or internationally) to investigate disease epidemiology in feral pigs. Salmonella infection in a geographically-isolated population of feral pigs in northern Australia and associated grazing beef cattle was studied to gain insights into pathogen maintenance and the wildlife-domestic animal interface. Feral pigs in a core habitat area were sampled via helicopter harvesting and recreational hunter surveys. Co-grazing cattle herds were selected via aerial surveys. Faeces were collected from feral pigs post mortem and fresh faeces from cattle herds were collected directly off the ground. Samples were cultured for *Salmonella* spp. and presumptive colonies were serotyped and genotyped via pulsed-field gel electrophoresis (PFGE). Overall 651 feral pigs at 93 locations were sampled and 496 fecal samples were collected from 32 mobs of beef cattle. The prevalence of *Salmonella* infection based on faecal culture was 36.3% (95% CI 32.1–40.7%) in feral pigs (29 serotypes), versus 2.02% (95% CI, 1.03–3.80) in cattle (9 serotypes). Six serotypes were shared in common by feral pigs and grazing cattle. In general, serotypes isolated from pigs were genotypically (PFGE) more similar (range 69–96%) than cattle isolates (range 71–83%). Study results suggest that this population of feral pigs is highly endemic for *Salmonella* and that *Salmonella* is transmitted from older to younger pigs and from males to females, perhaps associated with landscape features such as water. Cattle *Salmonella* isolates were more common in areas without feral pigs and from high density cattle populations on artificial water. This combined with serotyping and genotyping suggests that feral pigs are not a reservoir for cattle infection within this ecosystem.
DOMESTIC CANINE-ASSOCIATED HUMAN RABIES OUTBREAK INVESTIGATION AND RESPONSE, KENYA

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In February–March 2012, in Nyanza Province, Kenya, two children died from rabies. Review of hospital records indicated that visits for dog bites had increased 57% in one Nyanza Province district during November 2011-January 2012, compared with August–October 2011. We investigated to determine the extent of the outbreak and to prevent additional cases. We reviewed district veterinary records to identify rabid animals and persons with known exposures, queried district animal bite registries on March 19, 2012 to identify persons who experienced an animal bite on or after December 1, 2011 and could potentially benefit from rabies postexposure prophylaxis (PEP), and conducted a rabies vaccination campaign during April 5–9, 2012 followed by a house-to-house survey to determine pet vaccination status. Based on veterinary records, during January 1–March 31, 2012 six canines tested positive for rabies; three had bitten humans. Among the 12 persons exposed to confirmed rabid dogs, eight were successfully contacted and provided with PEP. Among 378 animal bites identified through the registries 93 (25%) were successfully contacted. Among the 64 with PEP indications 54 (84%) completed at least 1 dose. During the rabies vaccination campaign, we vaccinated 7,630 animals (6,616 dogs; 1,014 cats) in the 10 district sublocations with the highest rabies incidence. The house-to-house survey revealed rabies vaccination coverage of 49% (range, 25%–73%), which is below the target 70% for rabies outbreak control. During the outbreak, we developed a rabies surveillance system that integrated medical, public health and veterinary services, and trained health care personnel to detect and investigate rabies cases. During the 2 years since this response, no further human rabies cases have been reported in this district. We recommend continued promotion of animal rabies vaccination, increased community rabies and dog bite prevention education and further enhancement of rabies surveillance activities.
Student Poster Session
Tuesday, July 29, 2014
10:00-10:45am and 2:45-3:45pm

Richardson
[124] Dirty possums and their TB – A look at superspreading and supershedding, infectious disease transmission, emergence and persistence

Hartwig
[125] Chikungunya virus in non-mammalian species: a possible new reservoir

Griff
[126] Evaluating mercury concentrations relative to the microanatomy of grey whale (Eschrichtius robustus) epidermis as a biopsy use optimization effort

Goldsmith
[127] Population structure of artic foxes (Vulpes lagopus) in Alaska is correlated with geographically restricted strains of rabies virus

Dunham
[128] Evidence of an Oxyspirura petrowi epizootic in northern bobwhites (Colinus virginianus) from the rolling plains of Texas

DeVivo
[129] Microevolution of a mule deer population affected by high chronic wasting disease prevalence in southeast Wyoming

Dent
[130] Prevalence of zoonotic ascrid ova (Baylsascaris procyonis, Toxocara canis, and Toxocara cati) in Columbus city parks

Curry
[131] Public perceptions of urban birds and disease dynamics in Palm Beach County, Florida

Coker
[132] Prevalence and diversity of Haemoproteus in the American white ibus Eudocimus albus from southern Florida

Catalano
[133] First report of Taenia arctos (Cestoda: Taeniidae) in North American bears: further evidence for an ancient host-parasite association

Bogomolni
[134] Quantifying differences in species susceptibility to phocine distemper virus in northeast U.S. seals

Berger
[135] Impacts of exotic lice on the severity of hair loss syndrome and body condition of California mule deer fawns

Benvenuto
[136] Evaluation of metabolomics as a novel tool for assessing stress in wild birds

Brown
[137] Evaluation of pathogenesis of Francisella tularensis in cottontail rabbits

Winnett
[138] Bats: important reservoirs for zoonotic disease and the implications for public health

Williams
[139] Connecting tabanid relevance and prevalence with elaeophorosis in Wyoming moose
Whitmer [140] Physical effects of chemically dispersed oil on common murres (*Uria aalge*)

Verant [141] Epidemiology of white-noes syndrome in hibernating bats and relationships to environmental reservoirs within hibernacula

Taylor [142] Unusually high prevalence of a tumor in a captive colony of the endangered Perdido Key beach mouse (*Peromyscus polionotus trissylepsis*)

Schwartz [143] Multihost pathogens in domestic hunting dogs of Nicaragua’s Bosawás Biosphere Reserve - the value of a One Health approach


Ogdee [145] Are *Baylisascaris procyonis* eggs potentially exposed to temperature lethal limits at common raccoon latrine sites?

Mejía-Salazar [146] Paparazzi-ing mule deer to unravel environmental prion contamination

Lott [147] Crickey! Crocodile farming and *Paratrichosoma* infection dynamics in northern Australia

Wong [148] Antibodies to influenza A virus in snow geese (*Chen caerulescens*) along the Texas coast

Kovacs [149] An unusual bird and fish mortality event in Wood Buffalo National Park, Alberta
DIRTY POSSUMS AND THEIR TB — A LOOK AT SUPERSPREADING AND SUPERSHEDDING, INFECTIOUS DISEASE TRANSMISSION, EMERGENCE AND PERSISTENCE

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The brushtail possum (Trichosurus vulpecula) is the key wildlife maintenance host of bovine tuberculosis (TB) in New Zealand. With TB being rapidly killed in the environment and the notion that possums are highly anti-social animals, this raises questions about how the disease persists within possum populations. We are currently exploring TB transmission in possum at the Orongorongo Valley east of Wellington, New Zealand by conducting a three year mark and recapture study monitoring TB symptoms and secondary infections that occur in four possum subpopulations. Cage trapping grids (each comprising 100 traps over 16 ha) were initially set in March 2012 and 16 possums were experimentally challenged with TB during the first two trapping seasons (season one July and November/ season two November). Here we present our primary findings to date, of initial and secondary infections determined to be present in possums by way of visual cases, swab results and end of season necropsies.
CHIKUNGUNYA VIRUS IN NON-MAMMALIAN SPECIES: A POSSIBLE NEW RESERVOIR

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Chikungunya virus (CHIKV) is an arbovirus distributed widely in tropical regions of the world that causes a febrile and often painful disease in adults and children. Recent outbreaks of CHIKV infection in the Caribbean have raised concerns about establishment of this virus in North America. A significant question about the transmission cycle of CHIKV is whether non-human reservoir hosts are important in maintenance or transmission of the virus. We conducted experimental infections with CHIKV and discovered that several reptiles and amphibians developed viremia of sufficient magnitude to possibly serve as reservoir hosts. One or two strains of CHIKV were inoculated into a variety of ball pythons, Burmese pythons, northern garter snakes, American alligators, green iguanas, painted turtles, leopard frogs, Bufo species toads and cane toads. Viremia was not detected in alligators or cane toads but all other species developed viremia at variable magnitude. Peak viremia in the other species varied from 2.8 (Burmese pythons) to 4.7 (leopard frogs) log10 pfu/ml. We also conducted experiment to evaluate the effect of ambient temperature changes to monitor the “over wintering” capabilities of CHIKV in snakes. Northern garter snakes were inoculated a South African strain of CHIKV at temperatures of 16C versus 26C and tested for viremia. The snakes kept at 26C developed a short term viremia, whereas in snakes kept at 16C, the virus was maintained for a longer period and viremia titers as high as 7.2 log10 pfu/ml were achieved when animals were subsequently slowly warmed to 26C.
EVALUATING MERCURY CONCENTRATIONS RELATIVE TO THE MICROANATOMY OF GREY WHALE (ESCHRICHTIUS ROBUSTUS) EPIDERMIS AS A BIOPSY USE OPTIMIZATION EFFORT

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Grey whale (Eschrichtius robustus) epidermis can be morphologically and functionally divided into three distinct layers: the protective top layer, stratum corneum; the middle layer, stratum spinosum; and the regenerative layer, stratum basale. The objective of this study was to evaluate baseline measurements of grey whale epidermis based upon age, sex and season collected. These evaluations will then be used in a comprehensive study to compare environmental contaminants (e.g., mercury) concentrations and chemical feeding ecology values (stable isotopes of C and N) in the various layers as part of optimization of use of full thickness epidermis biopsies. We used archived, frozen grey whale epidermis subsamples (n=16) collected from stranded animals along the western coast of the USA. The subsamples were fixed in 10% formalin and routinely processed for viewing by light microscopy. Preparations were photographed and analyzed using Image J image analysis software. We determined that the stratum corneum may be thicker in calves than subadults or adults and the ratio of spinosum without basale to spinosum with basale may increase with age. These preliminary data indicated the need for standardized sampling to better ascertain cohort-specific differences with respect to epidermis based assays. As expected, the layers appear thicker in the winter versus summer but a standardized sampling regime is required to investigate this further. Preliminary testing suggests that total mercury (THg) concentrations vary by layer. These baseline parameters give us insight into the histology of cetacean epidermis and can be used in determining contaminant distribution in the body and to improve future sampling and use of biopsy samples.
POPULATION STRUCTURE OF ARCTIC FOXES (VULPES LAGOPUS) IN ALASKA IS CORRELATED WITH GEOGRAPHICALLY RESTRICTED STRAINS OF RABIES VIRUS

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Researchers from the CDC have identified three distinct variants of rabies virus localized to three regions of coastal Alaska (Kuzmin et al., 2008), while the Alaskan interior region and south-central Alaska are devoid of endemic rabies. Rabies is maintained as an endemic infection in Alaskan wildlife, primarily in the Arctic fox population, and the presence of endemic rabies corresponds to the range of the Arctic fox (Vulpes lagopus) in Alaska. Arctic foxes are a circumpolar species, but population structure in Alaska has not been addressed. Mitochondrial DNA and microsatellite analysis were used to describe the population genetics of Arctic foxes in Alaska. A Bayesian clustering program assigned Arctic foxes to two groups, North Slope and western Alaska, however, a Bayesian clustering program that accounts for spatial variation divides the foxes into three populations: North Slope, Seward Peninsula, and southwestern Alaska. This indicates that long distance movements documented for Alaska’s Arctic foxes do not necessarily result in dispersal. Moreover, those three geographic areas correspond to the distributions of the three strains of rabies virus present in Alaska. We hypothesize that a lack of movement of foxes among populations serves to keep rabies strains geographically restricted. Replacement of Arctic foxes by red foxes (Vulpes vulpes) throughout their mainland range in Alaska, likely due to climate change, may serve to change the host-pathogen dynamics of rabies in Alaska and potentially alter the geographic distribution of the virus.
EVIDENCE OF AN *OXYSPIRURA PETROWI* EPIZOOTIC IN NORTHERN BOBWHITES (*COLINUS VIRGINIANUS*) FROM THE ROLLING PLAINS OF TEXAS

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There is unequivocal evidence that northern bobwhites (*Colinus virginianus*) are declining throughout their range. While the causes are unclear, many have pointed to extremes in rainfall patterns, declining quality of habitat and habitat fragmentation. Often overlooked is the potential impact of parasites and diseases. The eyeworm *Oxyspirura petrowi* has received recent interest in the role it may play in negatively impacting gamebirds. Anecdotal reports have occurred of eyeworm-infected bobwhites found dead after flying into buildings and other anthropogenic structures while others have reported infected bobwhites behaving erratically. These reports have lead to speculation that eyeworms may be causing visual obstruction. One hundred and ten northern bobwhites were captured and/or hunter donated from Mitchell County, Texas from June 2013 – February 2014 and examined for the presence of eyeworms. Recovered were 1,045 eyeworms from 101 of 115 bobwhites (88% prevalence); infections ranged from 1–69 worms and mean abundance of 9.1±11.2 (SD). It is suspected that several previous studies may under-report prevalence and abundance due to only examining the eye surface and nictitating membrane and not thoroughly examining eye-associated tissue, ducts, glands or sinuses. Based on our finding of eyeworms in the nasal-lacrimal-orbital tissue and observing eyeworms connected to orbital tissue ingesting blood, high numbers of *O. petrowi* can cause inflammation and localized petechiae/spot hemorrhaging to the lacrimal duct. Insufficient examinations may result in erroneous conclusions that infections are inconsequential when they could very well be a contributing factor in the bobwhite’s decline.
MICROEVOLUTION OF A MULE DEER POPULATION AFFECTED BY HIGH CHRONIC WASTING DISEASE PREVALENCE IN SOUTHEAST WYOMING

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High chronic wasting disease (CWD) prevalence of mule deer (Odocoileus hemionus) (approximately 30% in females and 50% in males) was observed in southeast Wyoming, where the population has declined to half its size since 2000. Other studies have shown that mule deer with phenylalanine (F) at codon 225 on the prion protein gene (PRNP) were less susceptible to CWD than deer with serine (S) at the same position. We hypothesized that 1) CWD-positive deer experience lower annual survival compared to CWD-negative deer, 2) 225SS deer would be over-represented in CWD-positive samples, and 3) frequency of less susceptible genotypes (225SF/FF) in the population would increase over time due to their decreased likelihood of dying as a result of CWD. Our objective was to determine whether mule deer in southeast Wyoming experience divergent CWD susceptibilities based on their PRNP genotypes, thus greater survival of less susceptible genotypes. We captured, radio-collared, CWD tested, and genotyped 73 adult mule deer. Survival was adversely affected by CWD, whereby annual survival of CWD-negative deer and CWD-positive deer was 0.76 (95% CI = 0.68, 0.85) and 0.32 (0.21, 0.47) (χ² = 41.2, df = 1, P < 0.001), respectively. Twelve percent (n=17) of 225SF deer were CWD positive compared to 55% (n = 56) of 225SS deer. Additionally, 225SS deer were over-represented in our CWD-positive group (χ² = 21.8, df = 1, P < 0.01). Furthermore, genotype 225SF frequency in the population increased from < 2% in 2003 to > 23% in 2012. These results support our hypotheses and 225SF deer appear to live longer without CWD-infection, allowing them to recruit more fawns into the population that possess the 225SF genotype. Our findings suggest microevolution is occurring in this mule deer population as a result of CWD exerting selective pressure for less susceptible genotypes.
PREVALENCE OF ZOONOTIC ASCARID OVA (BAYLISASCARIS PROCYONIS, TOXOCARA CANIS, AND TOXOCARA CATI) IN COLUMBUS CITY PARKS

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Zoonotic ascarids present an important veterinary public health issue as it involves animal, human, and environment. This perfect storm is brought together in the playground, as it encourages humans and animals to interact in the same environment. A handful of prevalence studies on zoonotic ascarids in playgrounds have been published throughout the US, but none in Ohio. The objectives of the study were to determine the prevalence of zoonotic ascarid ova in soil in the Columbus city parks and to identify potential risk factors associated with the presence of this parasite in playgrounds in these parks. There are a total of 220 parks in Columbus, of those only 127 parks had playgrounds and qualified for the study. Of the 127 parks with playgrounds, a subset of 30 parks was chosen. Ten soil/ground cover samples, as well as fecal samples (if present), were collected from each park (30 parks total) and analyzed for zoonotic ascarid ova. The prevalence of zoonotic ascarids ova in soil/ground cover in the Columbus city parks was found to be 0.3\% of the samples (1/289 samples) and 3.4\% of the parks (1/29 parks), the thirtieth park was omitted. This low prevalence suggests that contamination of playgrounds in the central Ohio areas is not as large of a risk as in other locations in the country. This low prevalence may be due to multiple factors such as the type of ground cover used in playgrounds, time of year of sampling (late summer), or the spatial distribution of reservoir hosts in central Columbus (including wildlife and feral or domestic dogs/cats). This study will help to better inform the community of the potential risk of zoonotic ascarids ova in Columbus playgrounds and give public health professionals a baseline for future studies and recommendations.
PUBLIC PERCEPTIONS OF URBAN BIRDS AND DISEASE DYNAMICS IN PALM BEACH COUNTY, FLORIDA

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Bird watching and feeding provides an opportunity for people in cities to connect to nature. However, artificial provisioning can increase aggregation, inter-specific contact and exposure to environmental pathogens, with implications for avian health and disease transmission. Traditional research has focused on host-pathogen relationships. However, understanding human dimensions of urban wildlife disease is paramount to the management of urban wildlife and public health. For example, people may change detrimental behaviors more readily if they care about urban birds and understand how and why to mitigate negative impacts of feeding. We investigated disease dynamics and public perceptions of birds and disease risk in Palm Beach County, Florida (2010-2013). In a separate study of urbanized white ibis (Eudocimus albus) we demonstrated a high prevalence of pathogens relevant to public and wildlife health. We have additionally demonstrated highly variable stress levels and immune function in urban ibis, suggesting site-specific implications for ibis health and disease transmission. We assessed public perceptions by administering surveys addressing socio-demographic characteristics of urban park visitors, their attitudes towards birds, whether and why they feed birds, and if their interaction with urban birds would change if they understood implications to their health or the health of birds. Approximately 73% of respondents intentionally watch birds, 49% feed birds in general, and 28% fed birds during their visit. Of those that feed birds, 78% would likely stop feeding birds given risk of disease transmission among birds and 83% would likely stop given risk of disease transmission to people. This suggests that most people do not currently perceive existing disease risks to wildlife or public health. Inclusion of human dimensions in wildlife disease investigation will help directly inform disease management programs that seek to alter public behaviors to protect wildlife and public health while maintaining positive attitudes toward and support of urban wildlife.
PREVALENCE AND DIVERSITY OF *HAEMOPROTEUS* IN THE AMERICAN WHITE IBIS (*EUDOCIMUS ALBUS*) FROM SOUTHERN FLORIDA

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Rapid urban development along the Florida coast has major implications for wetland dependent avifauna. It is estimated that the Florida everglades have declined in area by 31% in the past century. Changes in habitat quality and use can alter the exposure of animals to pathogens and possibly change their role in the epidemiology of diseases. The American white ibis (*Eudocimus albus*), a common bird species in Florida, has become increasingly urbanized with many populations relying heavily on urban and suburban habitats. The parasites of ibis, especially haemosporidians, are understudied. Blood parasites can cause a wide range of impacts on birds, including decreased reproductive success or mortality. Because southern Florida is subtropical and has a high diversity of vectors, we hypothesized that there will be a high prevalence and genetic diversity of haemosporidia in ibis and differences would be associated with variable land uses. Ibis from three counties (Palm Beach, Lee, and Broward) in southern Florida were sampled during concurrent studies or on admission to rehabilitation centers. A blood sample was collected from each bird and Giemsa-stained thin blood smears were examined for haemoparasites. Additionally, DNA was extracted from whole blood and tested for haemoparasites using a nested PCR targeting the cytochrome b gene. To date, 68% of 95 birds from Palm Beach County were PCR positive for *Haemoproteus*. Only a single novel genetic haplotype was detected among 30 sequences analyzed, and was most similar (99%) to a *Haemoproteus* sp. from West Africa. No *Plasmodium* was detected. Parasitemias of this *Haemoproteus* were very low (<1%). Results from Lee and Broward Counties are pending. Additional research is needed to determine if this parasite has subclinical effects on ibis health and if additional haplotypes infect ibis in other regions in southern Florida.
FIRST REPORT OF *TAENIA ARCTOS* (CESTODA: TAENIIDAE) IN NORTH AMERICAN BEARS: FURTHER EVIDENCE FOR AN ANCIENT HOST-PARASITE ASSOCIATION

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The tapeworm *Taenia arctos* (Cestoda: Taeniidae) was recently described at its adult stage in the small intestine of brown bears (*Ursus arctos arctos*) from Finland, and at its larval stage in the skeletal muscle of Eurasian elk (*Alces alces*) from Finland, moose (*Alces americanus*) from Alaska, USA, and a muskox (*Ovibos moschatus wardi*) from west Greenland. We isolated taeniid specimens at necropsy from the small intestine of one grizzly (*Ursus arctos horribilis*) and three black bears (*Ursus americanus*) from western Canada. Morphological analysis of the rostellar hooks did not allow the discrimination between *T. arctos* and *Taenia krabbei*, to which previous reports of tapeworm infections in North American bears were largely ascribed. Molecular analysis of the mitochondrial DNA cytochrome c oxidase subunit 1 gene confirmed the identity of *T. arctos* and the first report of this taeniid species from definitive hosts in North America. Given the morphological similarity between *T. arctos* and *T. krabbei*, the present study underlines the potential for misidentification of *Taenia* spp. in previous parasitological reports from bears and moose across North America. The marked overlap in the number, size and shape of the rostellar hooks between *T. arctos* and *T. krabbei* made the application of molecular tools necessary for the unequivocal identification of the tapeworm species. Our findings confirm the Holarctic distribution of *T. arctos* and potentially expand its geographic range to ecosystems of North America where bears and moose are sympatric. The historical biogeography of the ancestors of the modern black bears, grizzlies, and moose suggests an ancient association between *U. arctos, Alces* spp., and *T. arctos*, and a relatively recent host-switching event in *U. americanus*. However, the occurrence of *T. arctos* in a muskox from west Greenland remains enigmatic, and possibly suggests a more complex ecology and history for this taeniid species.
QUANTIFYING DIFFERENCES IN SPECIES SUSCEPTIBILITY TO PHOCINE DISTEMPER VIRUS IN NORTHEAST U.S. SEALS

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In 2006, gray seal (\textit{Halichoerus grypus}) and harbor seal (\textit{Phoca vitulina}) mortalities in New England were confirmed to be the result of a North American isolate of phocine distemper virus (PDV USA 2006), representing the first cases of clinical disease and death associated with an isolated strain of PDV in North American seals. In contrast to the European mortality events, grey seals in the U.S. were notably affected. Evidence from natural pinniped population exposures to PDV 2006 and PDV strains in 1988 and 2002 suggests that a difference exists in seal species susceptibility to infection. In order to experimentally determine if differences in species susceptibility exist, peripheral blood mononuclear cells (PBMCs) were isolated and in-vitro infection by PDV USA 2006 was carried out until 11 days post infection. RNA was isolated and virus quantified by multiplex real time RT-PCR in lymphocytes, monocytes and supernatant fractions. Tissues from dead stranded seals during the 2006 unusual mortality event (UME) were also obtained to quantify virus loads in tissues from known PDV positive, PDV negative and PDV unknown animals. Tissues from 22 seals of three species: harbor seal, harp seal (\textit{gphoca groenlandica}), and gray seal revealed that virus was detectable from tissues in all three species. Virus was present equally between species and harbor seal tissues carried the highest quantity of PDV. In PBMC infection experiments, differences were apparent in the three cell fractions and between species throughout the 11-day experiment. These results suggest that there are differences in the quantity of virus present in tissues of different seal species during the time course of infection. Differences in the course of infection of lymphocytes and monocytes together with the frequency, distribution and intensity of infection in different tissues may affect the outcome of PDV infection in different species of seals.
IMPACTS OF EXOTIC LICE ON THE SEVERITY OF HAIR LOSS SYNDROME AND BODY CONDITION OF CALIFORNIA MULE DEER FAWNS

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Hair loss syndrome (HLS) is a seasonal condition affecting mule deer (Odocoileus hemionus) in western North America. Signs of HLS include loss of pelage, increased grooming, and poor body condition. Infestations of exotic lice, Damalinia sp. and Bovicola tibialis, have been associated previously with HLS. Fawns are most susceptible to HLS and show higher rates of overwinter mortality than do other demographic groups. Twenty-four of 48 mule deer fawns captured in the winter of 2012-2013 were treated for lice using a Cydectin® pour on (0.1 cc/kg) and a PYthon® insecticide cattle ear tag containing Zetacypermethrin insecticide. Physical examinations were conducted and samples of whole blood, feces, hair and ectoparasites were collected. HLS was quantified using a standardized scoring system and lice were counted within ten, 10 cm² evenly dispersed sampling areas. Body condition was calculated as a scaled mass index using mass (kg) and total body length (cm). Three of five recaptured treated fawns showed signs of hair loss despite no lice being found, and none of three recaptured controls showed signs of hair loss despite the fact that all were infested with exotic lice. Body condition at recapture was negatively correlated with the number of lice found in sampling areas (r = -0.816, n = 8, p = 0.013). These results suggest that infestation by exotic lice is not necessary for deer to develop HLS in this population, and that the intensity of a louse infestation may impact the body condition of deer.
EVALUATION OF METABOLOMICS AS A NOVEL TOOL FOR ASSESSING STRESS IN WILD BIRDS

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Stress responses play an essential role for animals to adapt to changing conditions within the environment. However, sustained increases in corticosterone (the primary glucocorticoid in birds) in response to long term environmental changes, may lead to immunosuppressive effects that increase risk of infection and disease. Metabolomics is a novel cutting edge technique involving a systems approach to studying the small, endogenous metabolites in biological samples, particularly biofluids (e.g., blood, plasma, serum, urine) or tissue. Metabolomics techniques have recently been used to investigate stress in a number of different species including salmon, rats and cattle. However, these techniques have not been used in avian species. Here we describe the use of ¹H Nuclear magnetic resonance (NMR) spectroscopy to examine metabolite changes in semi-captive lesser scaup implanted with synthetic pellets that released corticosterone compared to those implanted with placebos. The use of NMR techniques will assist us in understanding the physiological mechanisms associated with chronic stress responses in free-ranging birds, will help to identify individuals and populations that are responding to stressful conditions and will ultimately allow us to investigate the fitness consequences associated with chronic stress in wildlife, particularly in response to large scale environmental changes.
EVALUATION OF PATHOGENESIS OF *FRANCISELLA TULARENSIS* IN COTTONTAIL RABBITS

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*Francisella tularensis* is a highly virulent, zoonotic bacterium that causes significant natural disease and is also of concern as an organism for bioterrorism. Serologic testing of wildlife is frequently used to monitor spatial patterns of infection and quantify exposure. Cottontail rabbits are a natural reservoir for this bacterium in the U.S., although very little work has been done experimentally to determine how these animals respond to infection; thus, information gathered from field samples can be difficult to interpret. The objective of this study was to provide an initial characterization of clinical disease, bacteremia, pathology and antibody kinetics of desert cottontail rabbits (*Sylvilagus audubonii*) experimentally infected with five strains of *F. tularensis*. We infected rabbits with four field strains, including MA00-2987 (A1b strain), WY96-3418 (type A2), KY99-3387 and OR96-0246 (type B strains), and with SchuS4 (type A1a strain), a widely used virulent laboratory strain. The results clearly indicate that infection with different strains of the bacterium resulted in significantly varied patterns of disease as well as gross and histopathology. We also characterized the long term humoral immune responses and the ability of cottontail rabbits to clear infection of Type B strains of *F. tularensis*. Understanding *F. tularensis* infection in a natural reservoir species can guide serosurveillance projects as well as generate new insights into environmental maintenance of this pathogen.
BATS: IMPORTANT RESERVOIRS FOR ZOONOTIC DISEASE AND THE IMPLICATIONS FOR PUBLIC HEALTH

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Bats are one of the most diverse and abundant mammals on earth, compromising 20% of all mammal species and have been implicated as reservoirs for a variety of diseases. With approximately 70% of emerging and re-emerging infectious diseases being zoonotic in origin, bats have become an animal of interest as they serve as a reservoir for a variety of diseases, currently 81 virus species and parasites being isolated and detected within this group of mammals. Understanding what makes bats such good candidates for carriers of disease are still poorly understood, but research interest is gaining and pointing to unique biological traits bats possess compared to other mammal species. Public health implications for understanding biology of bats are important in preventing future outbreaks of disease, such as increased wildlife surveillance and communication between wildlife biologist, veterinarians, physicians and public health practitioners. This paper will review current literature with public health implications regarding bats as reservoirs for disease.
CONNECTING TABANID RELEVANCE AND PREVALENCE WITH ELAEOPHOROSIS IN WYOMING MOOSE

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Many moose herds across North America have experienced decreasing population trends. Several factors such as marginal habitat, increases in minimum and maximum temperatures, parasites and predators, have been implicated as detrimental to moose fitness and population growth. In Wyoming, several moose herds have concurrent decreased calf:cow ratios and population trends. In addition to the above factors, the arterial worm *Elaeophora schneideri* has recently been found in many moose herds throughout Wyoming. Prevalence has increased from 0% to 25% and 48% in two Wyoming counties, with a prevalence as high as 82.6% in one southwest Wyoming herd. Elaeophorosis causes morbidity and mortality in abnormal hosts such as moose and has been found to depress population growth in elk. To better understand what drives the prevalence of *E. schneideri* in Wyoming moose, we examined the tabanid vector and its relationship with potential ungulate hosts. We hypothesize that prevalence of *E. schneideri* among Wyoming moose herds is related to the distribution of relevant vectors and host preferences of tabanids. From field-collected horse flies, there were differences in the species composition among four study sites, with two species comprising 70% of the entire collection. After testing horse flies for *E. schneideri* larvae using real-time PCR, we expect that differences in species composition of flies will correlate with the prevalence of *E. schneideri* among the 18 different species of horse flies identified. In addition, mammalian DNA was found in 6% of flies tested using real-time PCR. We will determine if moose are being selected for blood meals more than other animals on the landscape using species-specific primers and a combination of real-time and conventional PCR. The results from this study will help researchers better understand the dynamics of *E. schneideri* transmission and the conditions that lead to elaeophorosis in Wyoming moose.
PHYSICAL EFFECTS OF CHEMICALLY DISPERSED OIL ON COMMON MURRES (URIA AALGE)

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Chemical dispersants are used in marine oil spill response to disperse oil particles into the water column. Their use is assumed to reduce impacts of spilled oil to seabirds by decreasing exposure; however, few data actually exist as to the physical effects of chemical dispersant and chemically dispersed oil on seabirds (Addassi & Farout-Daniels, 2005; Natural Resource Council, 2005). Thirty-six wild-caught common murres (Uria aalge) were randomly assigned to a control group or one of seven treatment groups exposed to increasing concentrations of dispersant (Corexit 9500, Nalco Energy), crude oil or dispersed oil in water. After exposure, changes in behavior, body temperature, body surface heat loss and water penetration through plumage were assessed over the course three, 40-minute free-swim periods in uncontaminated water. Significant differences were detected in mean body temperature change, water penetration and behavior both across treatment groups and within treatment groups over time. Effects of exposure to oil, dispersant or dispersed oil included decreased body temperature, increased water penetration and loss of buoyancy with associated behaviors such as treading water with the wings. Effects were more pronounced in groups exposed to higher contaminant concentrations. Without intervention, severely impaired buoyancy would likely have resulted in mortalities during the first swim period in the high concentration groups. After the third swim period, there was no significant difference in mean body temperature change or water penetration in groups exposed to dispersant only as compared to the control, suggesting that preening activity may have mitigated effects of contamination in those groups. By contrast, significant differences in behavior and water penetration were detected in groups exposed to oil and dispersed oil as compared to the control after the third swim period. This study provides data to evaluate assumptions regarding benefits of chemical dispersant use with regard to seabirds during oil spill response.
EPIDEMIOLOGY OF WHITE-NOSE SYNDROME IN HIBERNATING BATS AND RELATIONSHIPS TO ENVIRONMENTAL RESERVOIRS WITHIN HIBERNACULA

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Since emergence in 2007, white-nose syndrome (WNS), caused by the fungus \textit{Pseudogymnoascus destructans} (\textit{Pd}), has devastated hibernating bat populations across eastern North America. Disease spread has been well-documented in bats at the hibernaculum level. Additionally, viable \textit{Pd} has been isolated from sediment and walls of WNS-affected hibernacula, demonstrating that environmental reservoirs play a likely role in pathogen transmission. However, gaps exist in our understanding of dynamics of pathogen spread and establishment of environmental reservoirs within hibernacula. We used qPCR to quantify loads (intensity) of \textit{Pd} on bats (\(N=558\)) and in environmental substrates (\(N=1050\)) within five hibernacula over two years. To define relationships between \textit{Pd} infections in bats and environmental loads of the fungus during establishment of a WNS endemic state, hibernacula were categorized based upon the length of time (WNS years) since WNS was first confirmed in bats at each site. Preliminary results indicated that prevalence and intensities of \textit{Pd} on bats were lowest in WNS year-1 hibernacula and highest (prevalence approaching 100\%) in WNS years-3 and -4 sites. Fungal intensities on bats in hibernacula during WNS years-5 and -6 were lower than observed peak intensities, but prevalence remained near 100\%. Additionally, there were differences in infection rates and intensity between co-located species, with greatest amounts of \textit{Pd} first detected on little brown bats (\textit{Myotis lucifugus}). Detections of \textit{Pd} in environmental substrates lagged behind detections on bats. Once detected, however, environmental fungal loads increased across subsequent WNS-years but remained lower than fungal intensities on bats within each site. These results suggest that \textit{Pd} spreads differentially across bat species within a hibernaculum and that establishment of environmental reservoirs is driven primarily by bats. Increased understanding of pathogen spread in bat populations and environmental reservoirs in hibernacula will help inform surveillance strategies and identify critical control points for disease management.
UNUSUALLY HIGH PREVALENCE OF A TUMOR IN A CAPTIVE COLONY OF THE ENDANGERED PERDIDO KEY BEACH MOUSE (PEROMYSCUS POLIONOTUS TRISSYLEPSIS)

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The Perdido Key beach mouse (Peromyscus polionotus trissylepsis) is a critically endangered subspecies for which there is currently less than 10 miles of remaining beach dune habitat. There are just three captive colonies (all located in Florida), which are occasionally used to support reintroduction efforts by the U.S. Fish and Wildlife Service and the Florida Fish and Wildlife Conservation Commission. In the colony maintained at the Santa Fe College Teaching Zoo, which has previously been reported to have decreased genetic diversity compared to the wild population, we have identified a high prevalence of a rare and aggressive, malignant tumor among deceased mice. Evidence of the tumor was found in 18% (9/50) of the cases necropsied from 2007 through January 2014, and in 2013 alone, 28.6% (6/21) of necropsied mice had evidence of the tumor. This unusually high prevalence of a tumor in a population with low genetic diversity strongly indicates the potential for a heritable predisposition. After definitive identification of the type of tumor, candidate gene mutations will be examined in hopes of identifying the predisposing factor.
MULTIHOST PATHOGENS IN DOMESTIC HUNTING DOGS OF NICARAGUA’S BOSAWÁS BIOSPHERE RESERVE–THE VALUE OF A ONE HEALTH APPROACH

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For subsistence-based societies worldwide, hunting wild game is an important source of nutritional augmentation. Domestic hunting dogs are often valued hunting partners, as is the case in the indigenous Mayangna and Miskito communities of Nicaragua’s Bosawás Biosphere Reserve. These dogs interact closely with humans, livestock and wildlife in the isolated and autonomous Bosawás region, placing them at the nexus of these populations. Because of their central position within this interface, domestic hunting dogs may not only represent a potential vector for multihost and zoonotic pathogens, but also represent a feasible sentinel for assessing the presence of disease in this remote landscape. Leptospirosis in particular has been recognized as an important disease in Nicaragua. Additionally, domestic canine populations have recently been implicated in the transmission of diseases to wild carnivores, highlighting a conservation concern. In Bosawás, jaguar predation is a common cause of dog mortality, illustrating that direct contact does occur between dog and wild carnivore populations. We examined and sampled 77 dogs in June 2013 and found evidence of exposure to multiple multihost and zoonotic pathogens. At least one dog was actively shedding leptospires. Seroprevalence of canine distemper virus was 82%, canine parvovirus was 94%, Trypanosoma cruzi was 18.5% and Anaplasma phagocytophilum was 4%. All of these pathogens have the potential to infect livestock, wildlife and/or human populations, emphasizing the need for a One Health approach to healthcare in this isolated area of Nicaragua. Further investigation of disease prevalence is warranted in assessing risk for human populations and wildlife conservation.
ORGANOCHLORINES IN CALIFORNIA SEA LIONS: TEMPORAL TRENDS AND ASSOCIATION WITH CANCER AND INFECTIOUS DISEASE

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Organochlorine contaminants (OCs) are widespread in the marine environment; and because marine mammals readily accumulate them in their lipid rich blubber layers, are long lived and feed at high trophic levels, they are good sentinels for OCs in the environment as well as of potential health effects on mammals. A retrospective study was conducted on lipid normalized OC levels, specifically polychlorinated biphenyls (PCBs) and dichlorodiphenyltrichloroethane (DDTs), in blubber samples from California sea lions (Zalophus californianus) off the coast of California. Temporal trends and association of OCs with sex, age and presence of cancer or fatal infectious disease were investigated. Stranded sea lions (n=310) as well as healthy males (n=60) and females (n=46) sampled during live captures from Puget Sound and San Miguel Island were included in the study. Adult males had higher mean blubber concentrations of PCBs and DDTs in comparison to levels in adult females and juveniles of both sexes. Concentration of the OCs in adults decreased over time (adjusted for sex). Cancer was almost 5 times more likely in animals with higher summed PCBs and DDTs of 1000 μg/gm, compared to lower levels of 100 μg/gm (95% CI 3.85-6.52 and 3.40-5.53 respectively), after adjusting for sex. Fatal infectious diseases were also twice as likely in animals with similar higher OC levels compared to lower contaminant burdens (95% CI 1.55-2.73 and 1.67-2.90 respectively). Mean contaminant loads were significantly higher in stranded sea lions than in healthy live captured animals (p<0.001). Our study indicates that environmental OC contamination has significant health implications for California sea lions, increasing risk of cancer and fatal infectious disease. Thus, despite decreasing levels in recent years, their presence in the environment warrants concern for animal health, including humans eating contaminated seafood.
ARE *BAYLISASCARIS PROCYONIS* EGGS POTENTIALLY EXPOSED TO TEMPERATURE LETHAL LIMITS AT COMMON RACCOON LATRINE SITES?

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*Baylisascaris procyonis* is a large zoonotic nematode that occurs in the small intestine of raccoons (*Procyon lotor*), of which the larvae can cause visceral, ocular and neural larva migrans within intermediate hosts. However, eggs of *Baylisascaris procyonis* dessicate and die at 65 C (150 F). Humans, especially children, have become infected through contact with raccoon latrines, which commonly include tree crevices, woodpiles, barns and attics. Therefore, we placed temperature and humidity data loggers on the ground in full sun and in the shade, in attics with and without exhaust fans, in woodpiles, in barns, in tree crevices and in closed cars parked in the sun in southern Texas. Data loggers recorded temperature and humidity every 30 minutes during 2012 to determine the likelihood of survival of *Baylisascaris procyonis* eggs at the various potential latrine sites. The hottest month during 2012 was August with a maximum temperature of 42 C (107 F) and 15 days where temperatures exceeded 38 C (100 F; \( \bar{x} = 2.2 \text{ hrs/day}; \text{ range } 0.5 - 6 \text{ hrs/day} \)). However, no potential latrine site exceeded 65 C at any time throughout the year. A car parked in the sun came the closest to the lethal limit (i.e., 62 C, 144 F) but only for 1 hour. Southern Texas is one of the furthest southern locations in the contiguous United States and has one of the warmest known climates. Unfortunately, it is not hot enough for an extended period to kill eggs of *Baylisascaris procyonis*, making it possible for such eggs to accumulate within an environment.
PAPARAZZI-ING MULE DEER TO UNRAVEL ENVIRONMENTAL PRION CONTAMINATION

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Chronic wasting disease (CWD) is a complex disease affecting mule deer, white-tailed deer and elk in Saskatchewan. Control efforts so far have been unsuccessful and prevalence is increasing in endemic zones; therefore, there is an urgent need to develop management strategies. Our research group has developed a system dynamics model to evaluate scenarios for CWD control in wild mule deer in Saskatchewan. In addition to direct transmission between animals, models evaluating control measures must consider the impact of environmental prion deposition and transmission. However, there are no currently effective tools for quantifying CWD prions in soil and water to provide data for model development. Alternatively, we deployed a system of triggered-by-movement cameras at 8 different environmental site types to investigate the patterns of visitation by mule deer as a proxy for environmental prion contamination. We assessed whether the relative probability of visiting each site type differed by mule deer sex and age category during different seasons of the year. We also evaluated differences in behaviours with a high risk for environmental transmission (deer demonstrating behaviours that are likely to contaminate the environment with prions, such as urinating, defecating, salivating or in which the ingestion of prions from the environment is more likely, such as eating from the ground). We demonstrated that human-made sites (e.g., feeding stations, salt licks, waterholes) are preferentially visited by mule deer. We discuss how these findings not only enhance the knowledge of deer biology, but can be used in the construction of disease models that aid in the evaluation of different management activities to control the transmission of CWD, and other infectious diseases.
Crocodile farmers in northern Australia report a parasite characterized by a series of zigzag scars on the abdominal scales of infected animals. These distinctive lesions are presumed to be caused by nematodes of the genus *Paratrichosoma*, though their presence has never been verified by direct observation or genetic analysis. Sections of abdominal skin displaying symptoms of *Paratrichosoma* infection were collected from four crocodiles euthanized at Darwin Crocodile Farm. Skin tissue was shredded under a dissecting microscope to recover adult nematodes. The heart, lungs, liver, stomach, intestines and deeper muscle tissue were also examined for parasitic helminths. While no adult nematodes were recovered from the epidermis, DNA was obtained from eggs present in the skin tissue of the host. Phylogenies derived from analysis of the small subunit (SSU) 18S rRNA gene supported taxon identify as *Paratrichosoma* and revealed high genetic diversity at the population level (2.6%). This may indicate that the observed skin conditions are a consequence of infection by multiple distinct species or sub-species. Additionally, as an understanding of epidemiology is essential for effective parasite control, crocodiles of grow-out size (n=800) were examined for symptoms of *Paratrichosoma* infection at monthly intervals. While current data suggest a weak positive correlation between incidence and temperature, no significant seasonal variation was found in prevalence, incidence or infection intensity.
ANTIBODIES TO INFLUENZA A VIRUS IN SNOW GEESE (*CHEN CAERULESCENS*) ALONG THE TEXAS COAST

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¹College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA
²Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA

Wild waterfowl in the order Anseriformes are recognized reservoirs for influenza type A viruses (IAVs); however, prevalence of infection can vary greatly by species. Few isolates of IAV have been reported from snow geese (*Chen caerulescens*), and generally they have not been regarded as an important component of this reservoir. In February 2013, 151 combined cloacal and oropharangeal swabs and 147 serum samples were collected from snow geese overwintering on the coast of Texas. None of the swab samples tested positive by virus isolation, but antibodies to IAV were detected in 87 (59%) birds tested by competitive blocking ELISA (bELISA). To further characterize these detected antibodies, positive samples were tested by virus neutralization (VN) for antibodies to viruses representing 12 hemagglutinin subtypes (HA1 - HA12). By VN, antibodies to H1 (*n* = 41; 47%), H5 (*n* = 32; 37%), H6 (*n* = 49; 56%), H9 (*n* = 50; 57%), and H12 (*n* = 24; 28%) were detected. Snow geese have become an overabundant species in North America, and their grazing behaviors on agricultural lands provide a potential indirect source of IAV infection for domestic poultry. This potential, as well as the detection of antibodies to HA subtypes H5 and H9 that are not well-represented in other waterfowl species, suggests that further snow geese surveillance is indicated.
AN UNUSUAL BIRD AND FISH MORTALITY EVENT IN WOOD BUFFALO NATIONAL PARK, ALBERTA

Monica Kovacs¹, Padraig Duignan¹, Manigandan Lejeune Virapin¹, and Susan Kutz¹

¹ Canadian Cooperative Wildlife Health Centre, University of Calgary Veterinary Medicine, Calgary, Canada

During the summer of 2013 the Canadian Cooperative Wildlife Health Centre was called upon to investigate a mortality event of fish and birds in the Peace-Birch-Athabasca Delta within Wood Buffalo National Park, Alberta. One of the principle rivers, the Athabasca, drains the Alberta oil sands and flows through areas of intensive industrial oil extraction. Thus, there was public concern that the mortality was caused by industrial contamination of the environment after heavy rainfall. Our investigation, three weeks after the first reported death, uncovered over 250 dead or moribund birds at Galoot lake but no dead fish. All dead birds were young of the year Franklin’s gulls in various stages of decomposition. There were no adult Franklin’s gulls present; however, numerous other seeming healthy avian species were observed, along with abundant, apparently healthy aquatic invertebrates, amphibians and fish. Consistent necropsy and histopathology findings in the gulls included severe emaciation and metabolic bone disease consistent with a phosphorous deficiency. Lake water sampled at the gull breeding colonies was negative for both cyanobacteria and hydrocarbons. Tissue samples were negative for botulism toxin, circovirus and excess aluminum levels. Several fish species, collected and frozen at the peak of the event, were necropsied and, while the state of preservation was poor, a consistent finding was that they were large fish in excellent body condition and had severe silt impaction of the brachial arches. Field observations and laboratory findings suggest that this was a naturally occurring flood event associated with unusually heavy rainfall leading to flooding and siltation of the rivers. Decreased oxygen carrying capacity and siltation resulted in acute fish mortality of the larger fish. The floods hit at the peak of gull nesting season and as the colonies flooded the adults appeared to have abandoned the area leaving the nestlings to starve to death.
### General Poster Session
#### Thursday, July 31, 2014
10:00-10:45am and 2:45-3:45pm

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DEVRIESEA AGAMARUM INFECTION AMONG A FREE-RANGING POPULATION OF ENDANGERED LESSER ANTILLEAN IGUANAS (IGUANA DELICATISSIMA)

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Since April 2011, endangered Lesser Antillean iguanas (Iguana delicatissima), also known as West Indian iguanas, on the French Caribbean island of St. Barthélemy have been observed with large, hard nodules and abscesses on the body, predominantly occurring on bite-prone areas of the legs, tail, back and neck. These lesions had not been previously observed in this population during monitoring efforts by St. Barthélemy Nature Reserve biologists who estimated approximately 10% of the male population at multiple locations around the island were involved. In addition, several affected males were found dead. Frozen and formalin-fixed samples of affected tissues from two freshly dead individuals were submitted to two independent laboratories (USGS-National Wildlife Health Center and The Pasteur Institute) for diagnostic evaluation. The actinobacterium Devriesea agamarum, identified by partial nucleic acid sequencing, was consistently isolated from multiple lesions. Dermatitis caused by D. agamarum is an emerging bacterial disease in captive reptiles, particularly among Old World agamid species, that can lead to fatal septicemia if untreated. This is the first report of D. agamarum in free-ranging iguanids. The origin of its introduction to St. Barthélemy remains uncertain although the invasive common iguana (Iguana iguana) is believed to play a role and the occurrence of the bacterium appears to be spreading among the island’s native iguana population through territorial fighting.
PASTEURELLA MULTOCIDA CAUSES MARINE BIRD MORTALITY IN THE BERING STRAIT REGION OF ALASKA

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Avian cholera has long been documented as one of the most significant infectious diseases of wild birds throughout the lower 48 United States and Canada, causing large scale mortality in waterfowl and other water birds. The disease is caused by the highly contagious bacterium Pasteurella multocida. Here we describe an unusual mortality event in marine birds along the northern coast of Saint Lawrence Island, Alaska, caused by infection with Pasteurella multocida. The event occurred in late November 2013 and involved Crested Auklet (Aethia cristatella), Thick-billed Murre (Uria lomvia), Northern Fulmar (Fulmarus glacialis) and Common Eider (Somateria mollissima). This mortality event was the first confirmed report of avian cholera in Alaska involving these species. Other species may have been involved but evidence (carcasses) could not be obtained. The closest geographical avian cholera outbreak was reported on Banks Island, Northwest Territories, Canada, and involved Lesser Snow Geese (Chen caerulescens) (1995-1996). Other outbreaks have been reported in Common Eiders (Somateria mollissima) on East Bay Island, Nunavut, Canada, (2005) and in the Baltic Sea (1998). The disease was also reported in Common Murre (Uria aalge) in the Baltic Sea (1998). Many marine birds, including the world population of threatened Spectacled Eiders (Somateria fischeri) overwinter around Saint Lawrence Island. Native Alaskans from the remote communities of Savoonga and Gambell who rely almost exclusively on marine wildlife, including seabirds, for food were the first to report and respond to this event. They collected specimens for diagnostic evaluation and documented the size and scope of the mortality event. They surveyed a total of 21 km of shoreline and recorded 912 bird carcasses. By extrapolation to the immediate area, a conservative estimate of 7,000 birds died, but mortality may have been considerably higher than this given weather and shoreline conditions during the survey.
EVALUATION OF THIAFENTANIL DOSING IN MIXTURES FOR CHEMICAL CAPTURE OF FREE-RANGING CARIBOU (RANGIFER TARANDUS GRANTI)

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For many years, carfentanil/xylazine (CX) has been the drug combination used for immobilizing free-ranging ungulates in Alaska. However, carfentanil is extremely hazardous for humans. The new drug of choice is expected to be thiafentanil (A-3080), which has a higher safety index. This motivated a drug trial to determine efficacious doses for free-ranging caribou calves (Rangifer tarandus granti). Data collected in April 2010, on free-ranging calves darted with thiafentanil/azaperone, suggested the addition of a sedative for muscle relaxation. Subsequent trials on captive adult caribou indicated thiafentanil/azaperone/medetomidine provided good levels of immobilization. However, field trials conducted in October 2013 on free-ranging caribou calves, found the combination too potent, causing respiratory arrest and one mortality. The protocol was revised to thiafentanil (5 mg), azaperone (25 mg) and xylazine (20 mg) (TAX), with good results. The mean ± SD (range) induction time for TAX was 3.3±1.6 (2.0 - 7.0) minutes vs 2.8±1.5 (1.5-5.2) for CX. To further compare TAX with the previous CX protocol, a physiological evaluation was performed on 5 animals immobilized on CX and 8 animals on TAX. Arterial blood was collected after induction, and again after 10 minutes of nasal O₂ supplement (1 L/min). Both groups had a significant (P < 0.001) increase in PaO₂ after oxygen treatment. However, only the CX group had a significant (P = 0.019) increase in PaCO₂, suggesting better ventilation in the TAX group. Based on our current results, we found that TAX proved to be a safe and efficient drug protocol for free-ranging caribou calves. Additional trials using CX, TAX and TX during April 2014 are expected to further refine the most efficacious protocol.
ORAL SYLVATIC PLAGUE VACCINE UPTAKE BY NON-TARGET SMALL RODENTS ON PRAIRIE DOG COLONIES

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Plague, caused by the bacterium *Yersinia pestis*, is a potentially fatal disease for humans and animals. In the western United States plague is endemic and frequently decimates prairie dog colonies. Prairie dogs (*Cynomys* spp.) are a keystone species of the grassland ecosystem and crucial in the recovery of the endangered black-footed ferret (*Mustela nigripes*). In 2013, field efficacy trials for a prairie dog oral sylvatic plague vaccine (SPV) started on 29 blind placebo controlled pairs in seven US states. In addition to those trials, this study assesses the direct and indirect impact of SPV on non-target small rodents in the grassland ecosystem. We selected 12 paired study sites; six pairs on black-tailed prairie dog (BTPD) colonies (2 in South Dakota, 4 in Montana) and 6 on Utah prairie dog (UTPD) colonies (2 low-elevation and 4 high-elevation). During the summer of 2013, each pair was sampled 3-4 nights, over 1160 unique animals were caught and approximately 1400 fleas were collected for *Y. pestis* analysis. The UTPD colony pairs had higher small rodent abundance and species richness than the pairs on BTPD colonies. Bait uptake levels were highly variable (17-100%) and further analysis is warranted to determine if this is multifactorial or predominantly due to prairie dog densities, small rodent abundance or forage availability. The results confirm that small rodents consume the bait, thus the vaccine could modify the enzootic plague cycle directly. In addition to annual small rodent trapping and flea collection on the SPV sites, further studies are required to assess the direct impact of the vaccine on the different non-target species.
GENOTYPIC CHARACTERIZATION OF STREPTOCOCCUS PHOCAE ISOLATES FROM NORTHERN (ENHYDRA LUTRIS KENYONI) AND SOUTHERN SEA OTTERS (ENHYDRA LUTRIS NEREIS)

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Streptococcus phocae is a commonly-isolated bacterial agent in a variety of infectious disease processes in both northern and southern sea otter populations. Previously published work has demonstrated that Streptococcus infantarius ssp. coli isolates from sea otters with infective endocarditis and/or septicemia demonstrate a high degree of relatedness with the majority falling into 1 of 2 genogroups. The genetic relatedness of S. phocae isolates within and between sea otter populations is not known. Pulsed-field gel electrophoresis was performed in order to characterize the genotypes of S. phocae isolated from cardiac, systemic (e.g. blood or brain), wound and lymph node samples from both northern and southern sea otter populations. A total of 48 isolates were examined. Among the isolates from cardiac or other systemic tissues, 15 different PFGE types (patterns) were observed in 20 different isolates. When lymph node or wound isolates were examined, a total of 16 PFGE types among 28 S. phocae isolates tested. There was no association of PFGE type with tissue of origin. Although some PFGE types were found only in southern sea otter isolates, there was no strong association of genotype with geographic region. Overall, there appears to be large genetic variation in S. phocae isolates from northern and southern sea otters as determined by PFGE. These findings suggest that the majority of these infections are opportunistic rather than the result of a single or few virulent strains.
ANTHROPOGENIC LESIONS ON HUMPBACK WHALES FROM THE ABROLHOS BANK, BRAZIL, USING PHOTOGRAPHIC ANALYSIS

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Scars or lesions derived from anthropogenic causes (e.g., boat propeller wounds, fishing gear or other entanglement) were investigated through photographs of photo-identified humpback whales (*Megaptera novaeangliae*) in the Abrolhos Bank (16°40’–19°30’S, 37°25’–39°45’W), Brazil. Data were collected during boat based expeditions from 2008 to 2012, and scars and marks were classified according to standardized protocols from the literature. From 2765 sightings, over 21,000 images identified 909 individuals through unique ventral fluke coloration patterns and were examined for the presence of fishing gear or entanglement scars and propeller wounds. For systematic estimates of non-lethal entanglement, only photographs of the lateral view of caudal peduncle were evaluated. In total, 17.7% (26/147) of individuals with lateral peduncle photographs had a high likelihood of prior entanglement. An additional 9 animals had evidence of entanglement on the dorsum, dorsal fin and peduncle. Wounds likely caused by a propeller were observed in 0.9% (6/622) of the cases with dorsal photo coverage. Considering only fluke photographs, 0.4% (4/909) had severed tails consistent with propeller laceractions. Combining all cases (one case had lesions both in the dorsum and fluke), a total of 9 animals had propeller wounds leading to; partial amputation of the fluke (44%, 4/9), deep cuts in the dorsum (55%, 5/9) or deep cuts to the peduncle (11%, 1/9). The proportion of individuals that survived entanglement is similar to other baleen populations, while prevalence of vessel collision is lower. However, these data demonstrate that conflict exists between humans and this humpback whale population. Given that the study covers animals that survived such interactions, our results offer conservative estimates of the actual boat or entanglement encounter rate for this humpback whale population and must be interpreted with caution given the exploitation of natural resources has been intensified along the Brazilian coast and may lead to increased anthropogenic pressure on the marine ecosystem.
WHICH SPECIES OF HEMOSPORIDIANS CAN INFECT PENGUINS? PROSPECTIVE STUDY AND META-ANALYSIS

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Haemoproteus, Leucocytozoon and Plasmodium infections have been reported in penguins. The two latter parasites may cause significant disease leading to morbidity and mortality of penguins, and are therefore potential conservation threats. It is not clear, however, which of the 143 Haemoproteus spp., 60 Plasmodium spp. and 36 Leucocytozoon spp. can infect penguins. In this study we examined the phylogenetic relationship between hemosporidian lineages identified in Magellanic penguins (Spheniscus magellanicus) undergoing rehabilitation in Brazil and lineages identified in penguins elsewhere. We used a nested PCR targeting the cyt-b gene of Haemoproteus and Plasmodium to test blood and tissue samples from 547 rehabilitated Magellanic penguins. Hemosporidian lineages were identified through blood smear examination and sequencing of PCR products. Cyt-b sequences obtained in this study were aligned with sequences from published penguin-infecting lineages and sequences deposited at the MalAvi database. Maximum likelihood phylogenetic analysis was conducted using the model General Time-Reversible + Gamma, with nearest-neighbor interchanges and 1000 bootstrap replications. Several lineages within the Haemamoeba and Novyella subgenera were reported in penguins, as well as multiple records of P. elongatum (subgenus Huffia). The morphologically-defined subgenera Bennettinia, Novyella and Giovannolaia are not monophyletic; as a result it is difficult to determine to the subgenus of several Plasmodium lineages identified in this study. Our findings of P. cathemerium and P. nucleophilum are novel for penguins and have been confirmed through blood smears. Overall, the occurrence of diverse and unrelated Haemoproteus and Plasmodium lineages in penguins indicate that these infections are opportunistic and not host-specific, reflecting the diversity of hemosporidians in the avifauna from each region. Conversely, Leucocytozoon lineages identified in yellow-eyed penguins from different locations were closely clustered and belonged to at least two slightly different lineages.
NEW DATA ON THE PREVALENCE AND GEOGRAPHIC DISTRIBUTION OF *ECHINOCOCCUS* IN WOLVES (*CANIS LUPUS*) AND ARCTIC FOXES (*VULPES LAGOPUS*) IN ALASKA

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*Echinococcus* cestodes are important zoonotic tapeworms that have the ability to produce significant cystic or alveolar hydatid diseases in humans. Worldwide, these tapeworms are estimated to affect more than two million people and approximately 200,000 new cases are diagnosed each year. The tapeworms thrive in both sylvatic and domestic cycles with humans serving as aberrant intermediate hosts. Due to public health concerns, it is necessary to understand the current distribution and prevalence of these parasites. Although extensive research was conducted in the 1950s and 1960s, little is currently known about the prevalence, distribution, and transmission ecology of these tapeworms in wild canids in Alaska. Given climatic changes occurring in Alaska, we sought to give an update regarding the current prevalence and geographical distribution of echinococcus tapeworms in wild canids in Alaska. From the years 1999 to 2010, the North Slope Borough Department of Wildlife Management and Veterinary Clinic and Alaska Department of Fish and Game conveniently sampled wolf (N=81), arctic fox (N=72), red fox (*Vulpes vulpes*) (N=3), and coyote (*Canis latrans*) (N=1) carcasses. We performed fecal flotation and multiplex PCR analysis on DNA extracted from fecal samples and proglottids for a variety of intestinal parasites, including *Taenia* spp. and *Echinococcus* spp.. *Echinococcus multilocularis* was found in 12.5% of arctic foxes, and not found in any of the other canids. *Echinococcus granulosus/canadensis* was present in 37% of wolves, and within the one coyote collected. We detected *Taenia* spp., but not *Echinococcus* spp., in the red foxes. We intend to use these updated data to further examine the role that climate change and other ecological factors will have in the future distribution, prevalence and public health consequences of echinococcus tapeworms in Alaska.
RANAVIRUS COULD CAUSE A THREATENED TOAD SPECIES TO GO EXTINCT

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Ranaviruses are known to infect and cause disease in common amphibian species such as the wood frog (Lithobates sylvaticus). However, there is increasing evidence that rare amphibians may also be affected negatively by this emerging pathogen. For example, Mississippi gopher frogs (L. sevosus) and Chinese giant salamanders (Andrias davidianus) are highly susceptible to ranavirus. Wild populations of the boreal toad (Bufo boreas) have been declining for over 20 years, and pathogens are believed to play a role. To date, no studies have been performed to explore the susceptibility of boreal toad tadpoles and metamorphs to ranavirus. Thus, we exposed boreal toad tadpoles and metamorphs to an environmentally relevant concentration (10³ PFU/mL) of two Frog Virus 3 (FV3)-like isolates (n=20 tadpoles per isolate) in water and monitored survival for 21 days. Tadpoles began dying at five days post-exposure and 100% mortality and infection was documented after eight days for both isolates. Similarly during the metamorph stage, by day 5 post-exposure, mortality and infection was 90% and 95% for both isolates. These results indicate that multiple life stages of the boreal toad are highly susceptible to ranavirus. Additionally, population-simulations of wood frogs exposed to ranavirus during the larval or metamorph stage, indicated extinction can occur as fast as 5 years, if exposed every year. Such models suggest that ranavirus infection can seriously impact the federally threatened boreal toad. Future pathogen surveillance and conservation planning should consider ranavirus as a threat to this species.
ASSessment of Viral Pathogens in Svalbard Reindeer (Rangifer tarandus platyrhynchos): An Example of Ecological and Geographical Driven Viral Extinction?

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Svalbard reindeer (Rangifer tarandus platyrhynchos) are the only ruminant species inhabiting the remote Arctic archipelago of Svalbard (around 10,000 animals). Even though focus on climate change in the Arctic has been increasing, reindeer have not received the same attention as other species even if they represent a central part of the Arctic ecosystem. Recent surveys in other reindeer populations across the Arctic revealed a variety of viral agents known to cause different diseases in other ruminants. Because of an ongoing increase in the population, which may lead to higher chances of transmission, and given that no recent information on health status was available, it was decided to assess for the presence of several viruses. A total of 250 serum samples (2003-2012) from several locations on Svalbard were screened for alphaherpesvirus, pestivirus and gammaherpesvirus. Of these, 150 were further analyzed for bovine respiratory syncytial virus, bovine parainfluenza virus 3, bovine adenovirus and bovine coronavirus. Nasal and ocular swabs from reindeer (n = 82; 2010-2012) were screened by PCR or RT-PCR for alphaherpesvirus, gammaherpesvirus and pestivirus. Nasal and ocular swab samples from 23 animals were further screened by next-generation sequencing methods for identification of hitherto unknown viral sequences. No antibodies or viral DNA were identified in any animal and next-generation sequencing failed to identify any mammalian viruses. These results make Svalbard reindeer the only reindeer population in the Arctic so far screened to be completely free of these viruses. This may have an important significance when discussing viral extinction mechanisms. Ecological and geographical isolation, as well as lack of other reservoirs/hosts for viruses, lack of predation, or absence of other diseases are examples of drivers commonly associated to the extinction of viruses from a given population that should be considered and further studied in this population.
2013-2014 MARYLAND AND MID-ATLANTIC BOTTLENOSE DOLPHIN UNUSUAL MORTALITY EVENT

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In July 2013 the Maryland Department of Natural Resources - Marine Mammal and Sea Turtle Stranding Program at the Cooperative Oxford Laboratory began receiving increased reports of dead-stranded bottlenose dolphins in the Chesapeake Bay. Given air temperatures were warm, dolphins were found decomposed in remote islands of the Bay or floating and generally inaccessible. However, stranding network staff members accessed carcasses from land and by boat to document the unusual stranding circumstances. Within a few weeks, dolphins were being reported along the coast. Concurrently, Virginia, Delaware, New Jersey and New York were also inundated with dolphin strandings. Once the federal agency with jurisdiction for strandings, the U. S. Department of Commerce, National Oceanic and Atmospheric Administration, National Marine Fisheries Service realized that large numbers of dolphins were being found dead along mid-Atlantic coast states, an “Unusual Mortality Event” / UME was officially declared. As of March 2014, nearly 1200 bottlenose dolphins have been documented during this event. A similar UME occurred in 1987-88 along the Atlantic Coast when 770 dolphins were found dead. In both circumstances the etiology was determined to be a morbillivirus. Morbilliviruses are known to affect both cetaceans and pinnipeds along the Maryland and Atlantic coasts. Based on serologic screenings and stranding patterns, the first documented epizootic was probably in Florida in the Indian and Banana Rivers in 1982. In both the 1987 and 2013 events – the first reports were in early summer months and continued through the winter in southern latitudes. Naive populations are especially susceptible to the introduction of this virus and timing of the strandings coincided with known calving areas of the mid-Atlantic. As of March 2014, 74 bottlenose dolphins have been documented along Maryland shores during this UME. The current mortality event is expected to continue as dolphins again move north this spring.
INFLUENCE OF ECOLOGICAL FACTORS ON PREVALENCE OF MENINGEAL WORM IN SOUTH DAKOTA

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Meningeal worm (*Parelaphostrongylus tenuis*) is a nematode parasite that commonly infects white-tailed deer (*Odocoileus virginianus*; WTD) throughout the deciduous forest biome and deciduous-coniferous ecotone of eastern and central North America; the species is not known to occur west of the grassland biome of central North America. We used logistic regression and county-specific prevalence data previously collected by Jacques and Jenks (2004) to evaluate potential effects of landscape (e.g., wetland cover, grassland cover, acreage of irrigated farmland) and climatological (e.g., temperature, precipitation) factors on prevalence of infection of *P. tenuis* in white-tailed deer populations throughout South Dakota. We documented no difference (*t*64 ≤ 0.439, *P* ≥ 0.567) in mean (1991–2000) spring temperature, summer temperature, fall temperature, spring precipitation or winter precipitation between eastern and western South Dakota, where prevalence of *P. tenuis* was 25.3% (*n* = 2,271 white-tailed deer) and 1.2% (*n* = 577 white-tailed deer), respectively. Our analyses indicated that probability of infection with meningeal worm decreased 0.91 between eastern and western South Dakota. In contrast, probability of infection with meningeal worm increased by 1.14 and 2.15 for each 1 °C increase in mean spring temperature and 1 cm increase in summer precipitation, respectively. Our analyses suggested that the Missouri River acted in part, as a physical barrier that limits movement of meningeal worm to the western region of South Dakota. Though the probability of infection with *P. tenuis* in western South Dakota remains low, evaluating potential effects of distribution and density of intermediate hosts, deer density and deer feeding activities and habitat use on spatial distribution of meningeal worm in counties where the parasite has not been documented is warranted.
A REVIEW OF DERMATOLOGIC DISEASE IN WILD TURKEYS IN THE SOUTHEASTERN UNITED STATES FROM 1975-2013

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Skin lesions of wild turkeys are a common cause of concern to wildlife biologists and observant citizens, and consequently a frequent reason for consultation or submission for diagnostic examination. The purpose of this retrospective review is to evaluate the causes, incidence and pathology of dermatologic diseases in wild turkeys in the southeastern United States. Among 660 wild turkeys submitted to SCWDS from 1975 to 2013, dermatologic lesions were diagnosed in 32% (n=209) of cases, and were the primary cause of disease in 27% (n=177) of cases. Avian pox was the most frequent diagnosis among turkeys with primary dermatologic disease, accounting for 62% (n=130) of cases, followed by bacterial dermatitis (21%, n=43), parasitic dermatitis (2.8%, n=6), fungal dermatitis (2.3%, n=5) and cutaneous neoplasia (2.3%, n=5). Other rare causes of dermatologic disease include epidermal or follicular cysts, and trauma. Avian pox represents the most common cause of dermatologic disease in wild turkeys and a common cause of morbidity overall (21% of all cases). Though gross evaluation of most skin lesions is insufficient to determine the etiology, the distribution of lesions and temporal occurrence of certain diseases may offer some insight into likely causes. Avian pox infections are observed more frequently in the fall and winter, whereas other causes of dermatologic disease occur with similar frequencies across all seasons. The vast majority of avian pox cases have lesions over the unfeathered portions of the head and neck (94%, n=122). Cases with lesions involving only the feet, legs and feathered skin were more likely to have bacterial or other non-avian pox etiology (OR = 16.25). This retrospective study will provide a useful diagnostic reference to biologists and citizens when evaluating wild turkeys with skin lesions.
REGIONAL VARIATION IN *OXYSPIRURA PETROWI* INFECTIONS IN TEXAS NORTHERN BOBWHITES

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*Oxyspirura petrowi* is an indirect lifecycle nematode that occurs under the nictitating membrane and within the conjunctival sacs and nasolacrimal ducts of gallinaceous birds. *Oxyspirura petrowi* has been reported in northern bobwhites (*Colinus virginianus*) from the Rolling Plains of Texas, but it is uncertain whether this species occurs elsewhere due to the lack of helminth surveys in other regions. Several ongoing studies have suggested that *O. petrowi* may cause visual impairment leading to negative impacts of infected birds. Because the bobwhite is an economically and ecologically important game bird in the Rolling Plains and South Texas regions, the objective of this study was to compare prevalence, intensity and abundance of *O. petrowi* in bobwhites from the Rolling Plains (n=128) and South Texas (n=125) using hunter-shot birds from October 2012 to February 2013. Bobwhites collected in the Rolling Plains had a mean intensity of 14.2 ± 1.6 worms (range 1–67), whereas in South Texas mean intensity was 2.6 ± 0.2 (SE) (range 1–7). Prevalence of *O. petrowi* was higher in the Rolling Plains (66%) than in South Texas (8%) (P<0.0001). Abundance of *O. petrowi* was higher in the Rolling Plains (9.3 ± 1.2) than in South Texas (0.2 ± 0.1 worms) (P<0.0001). Based on our results, future studies are needed to explain the major differences in *O. petrowi* occurrence and abundance between the 2 regional bobwhite populations.
OCULAR LESIONS IN APPARENTLY HEALTHY WILD COMMON MURRES FROM SANTA CRUZ, CALIFORNIA

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Forty common murres (Uria aalge) were captured in Monterey Bay near Santa Cruz, California over the course of 6 nights for a dispersant exposure study. Murres underwent a brief veterinary exam after capture, then were housed in net-bottom pens and transported to a pool facility the following morning. All birds were in good to excellent body condition and appeared to be in good health at the time of capture. On day 7, a veterinary ophthalmologist examined a subset of 31 birds using phenol red thread tear tests (PRTT), fluorescein staining, slit lamp and rebound tonometry. Mean PRTT was 18 ± 4 mm. Mean intraocular pressure was 22 ± 3 mmHg. Twelve of 31 (39%) birds had corneal ulcers, some of which had evidence of chronicity. Ten of 31 (32%) birds had mild to moderate conjunctivitis which was bilateral in 80% of the cases. Twenty-five (81%) birds and 36 (72%) eyes had corneal scars, and 11 (31%) of these represented full thickness lacerations. Nine birds had cataracts, the majority of which were anterior cortical. Visible anterior uveitis was present in 3 birds. Although raptors admitted to rehabilitation centers have a high prevalence of ocular lesions, the number of corneal ulcers seen in this apparently healthy population was surprising. Corneal scarring indicates that wild murres are frequently exposed to ocular trauma and the body condition scores indicate they appear to remain successful predators despite some vision compromise.
WILDLIFE HEALTH DATA FROM BRITISH COLUMBIA: INSIGHTS INTO THEIR USEFULNESS AND SIGNIFICANCE FOR ONGOING MONITORING

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Over the past several decades increased efforts to monitor wildlife disease have led to the establishment of comprehensive databases. Such datasets provide valuable information on baseline wildlife health and disease prevalence, though are often considered inherently biased and observational rather than research driven. To address the usefulness of such databases, we analyzed a long-term dataset from British Columbia. This highlighted how such data can prove useful in directing ongoing monitoring and providing a platform to base future efforts that will increase our understanding of cumulative effects of anthropogenic disturbances as it relates to wildlife health and disease. The wildlife health database from British Columbia has a total of 5269 cases of wildlife mortalities or sampling events from 2006 to present. Of these, approximately 4000 are considered “active surveillance” for reportable diseases. An additional 832 cases have been necropsied and submitted for diagnostic tests as part of a “passive surveillance” effort to monitor wildlife health across British Columbia. GIS-based analyses of spatial data for all cases indicate a geographically biased sampling effort focused in southern British Columbia. Based on these analyses, we make recommendations for general improvements to data collection for wildlife health datasets, including increased and directed sampling efforts in under represented areas and species coupled with a reallocation of resources in locations with established baselines of wildlife health. In conclusion, though wildlife health databases are often considered biased, we highlight their usefulness in providing guidance in designing monitoring efforts for wildlife disease. Furthermore, such baseline health data will serve to direct surveillance efforts that monitor the cumulative effects of ongoing anthropogenic environmental disturbances through a specific, data-driven sampling design.
PARASITIC INFECTIONS OF AVIAN HOSTS IN NORTHERN CALIFORNIA

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Parasite infections have a significant impact on their host, for example \textit{Ribeiroia ondatrae} encysts in the limb buds of tadpoles and can cause extra or missing limbs which make them more susceptible to predation. Birds are the most relevant wildlife host to survey because not only do they serve as the definitive host for most taxa of parasites with complex lifecycles, but have extensive migratory ranges and affect the transmission and landscape level distribution of a variety of diseases. The helminthes of birds have been well studied in most parts of the United States; however, there are no studies that examine birds from the San Francisco Bay area of California and few elsewhere along the Pacific flyway. Our study addresses this knowledge gap by surveying the adult parasitic infections of birds within the flyway. Our previous research of larval stages found in snails, amphibian, fish and aquatic invertebrates indicate that a high diversity of parasites exist in these ecosystems. We obtained the intestinal tract of 68 birds samples sacrificed from organizations such as airports, wildlife rescues, and wildlife refuges. Our bird samples represent 22 different species from the following families: Accipitridae, Anatidae, Ardeidae, Charadriidae, Laridae, Podicipedidae, Rallidae, Recurvirostridae and Tytonidae. We performed morphological analysis and detailed molecular analysis using a combination of the following gene fragments: 28S, internal transcribed spacer including 5.8S, and COX1 of select specimens. Using this combination of analyses, we have discovered a high diversity of parasites, with approximately 50 different identified genera. We found an average parasite species richness of 2.7. We have not identified \textit{R. ondatrae} despite finding \textit{R. ondatrae} highly prevalent as larval stages in several different host species including \textit{Helisoma trivolvis}, amphibians and fish. However, we have found species from the Echinostomatidae, Strigeidae, and Diplostomatidae, which were also previously found as larval stages.
FIRST HEALTH ASSESSMENT OF JUVENILE WHOOPING CRANES IN WOOD BUFFALO NATIONAL PARK, CANADA

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During the summers 2010-2012, 31 pre-fledging, juvenile whooping cranes (Grus americana) were captured for satellite tagging and health assessment at Wood Buffalo National Park (WB), NT, Canada. All birds were in good to excellent condition, with normal body weights and morphological measurements for birds 40-70 days of age. Each bird exhibited a normal response to capture. Feather condition was generally good and no external parasites were observed. Preliminary analysis of laboratory data revealed differences in the hematology, clinical chemistry, trace element and serum protein electrophoresis values of WB versus age-matched captive-reared juveniles, likely due to increased exposure to potential antigens compared to captive birds and dietary differences between the two populations. Two of 21 (10%) birds were positive for the protozoan parasite Hemoproteus sp. Four of 30 (13%) birds were seropositive for West Nile virus, and 11 of 28 (39%) were seropositive for Infectious Bursal Disease virus. All birds tested were seronegative for Inclusion Body Disease of Cranes, and all RT-PCR tests of cloacal swabs were negative for avian influenza virus. Moderate to heavy growths of E. coli were isolated from cultures of cloacal swabs; no Salmonella sp. or Campylobacter sp. was isolated. Minor morbidity was associated with capture in 4 birds. Twelve post-release mortalities have been confirmed from this sample population. These birds’ mean ± SD survival time following capture was 212 ± 174 d (range 3-496 d). Two causes of death could be determined from diagnostic necropsies: predation was confirmed in the bird banded 3 d prior to death, and a systemic enteric bacterial infection with Klebsiella oxytoca was a causal factor in the death of a 6 mo old juvenile in Texas following fall migration. This study provides the first in situ measurements of numerous health parameters and outcomes of endangered whooping cranes.
EVALUATION OF MYCOPLASMA AGASSIZII TREATMENT PROTOCOLS

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Mycoplasma agassizii has been well documented as causing upper respiratory tract disease in desert tortoises. We evaluated four treatment protocols using M. agassizii ELISA positive tortoises with nasal discharge for at least five of seven days prior to the start of the study. Treatment protocols evaluated were as follows: 1) Enrofloxacin 5 mg/kg IM SID x 14 days plus a dilute solution of enrofloxacin/ dexamethasone/ saline intranasally once daily for 5 days then every other day for 3 more treatments; 2) Enrofloxacin 5 mg/kg IM SID x 14 days; 3) Tulathromycin 5 mg/kg IM repeated in 7 days; and 4) Tulathromycin 5 mg/kg IM once only. This was a randomized trial with fifteen tortoises in each treatment group plus six animals in the untreated control group. Nasal lavage samples were collected just prior to treatment and seven days after the completion of the specified treatment protocol. Quantitative PCR for M. agassizii was performed on all samples and analysis of covariance (ANCOVA) was used to compare differences in the absolute post-treatment copies of M. agassizii DNA across treatment and control groups, while controlling for pre-treatment copies of DNA. Treatments 1 and 2 significantly reduced the number of copies of Mycoplasma agassizii DNA when compared to the untreated control group and Treatments 3 and 4. Treatments 1 and 2 were not significantly different from each other. Treatments 3 and 4 showed no significant reduction of DNA copies when compared to the untreated control group and were not significantly different from each other. Treatments 1 and 2 were also the only treatments to significantly reduce the mean number of days post-treatment where clinical signs were present. There were no significant differences in mean percent weight change across treatment groups when compared to the untreated controls.
ANESTHESIA IN PACIFIC MARTENS (MARTES CAURINA): KETAMINE AND MIDAZOLAM

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Field studies documenting anesthesia protocols for martens have focused on the use of cyclohexamines combined with alpha-2 adrenergic tranquilizers or induction with inhalation gas. The cyclohexamine ketamine can be combined with midazolam, a benzodiazepine tranquilizer. Both drugs are considered fast acting, inexpensive, injected intramuscularly and quickly metabolized – all beneficial qualities for field use. The use of midazolam with ketamine has not been reported for North American martens, but has been used successfully in several mustelids. Pacific martens (\textit{Martes caurina}) were trapped and anesthetized in Lassen National Forest (Northern California). Our goal was to assess anesthesia with ketamine used at 18 or 25 mg/kg in combination with 0.2 mg/kg of midazolam. We compared induction, return to consciousness and recovery time durations, plus physiological parameters post-anesthetic induction. No reversal was used for the midazolam portion of the anesthetic. Mean (±SD) induction for both dosages was 1.9±1.0 and 1.7±0.8 min, respectively. The interval from induction returning to consciousness, but not fully mobile (anesthetic depth 2) was longer for the 25 mg/kg ketamine dosage (mean difference = 9.4 min, p < 0.001). Full recovery was also longer for the 25 mg/kg ketamine dosage (mean difference =11.6 min, p < 0.001). Physiological parameters were consistent for both ketamine dosages. Low oxygen saturation levels were noted and supplementation is advised. Age, gender, month of capture, and ambient temperature were not statistically related to induction, return to consciousness or recovery time durations. In conclusion, the combination of ketamine, at both dosages, and midazolam provided reliable field anesthesia for martens and the 25 mg/kg ketamine dosage allowed extended handling time.
HISTORY AND SPREAD OF CHRONIC WASTING DISEASE AMONG MULE DEER AND ELK IN NEW MEXICO

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Chronic wasting disease (CWD) was first detected in New Mexico from an emaciated deer that died at the Cantonment of White Sands Missile Range (WSMR) in early spring 2002. Surveillance effort was increased afterwards, and public interest was high. Hunters cooperated by bringing harvested animals to wildlife officials for testing. CWD seemed limited to WSMR and adjacent Organ Mountains, and then CWD was detected in an emaciated deer from the Sacramento Mountains in 2004. In 2005, CWD was detected among elk in the Sacramento Mountains. A single deer was found with CWD in 2006 at the extreme north end of WSMR near the Stallion gate. That deer is yet the sole case from the Stallion area. In 2007, CWD was found among deer south of the Sacramento Mountains. Deer from the New Mexico and Texas border were found with CWD leading to its detection in Texas in 2012. The geographic range of CWD appears to expand each year slowly. The single case at the north end of WSMR might have been an iatrogenic transmission. Public and hunter interest in CWD has waned and fewer hunters now cooperate. Cases in new areas are usually abnormal animals reported to wildlife officials.
MYCOPLASMA COROGYPSI–ASSOCIATED POLYARTHRITIS IN A BLACK VULTURE (CORAGYPS ATRATUS) FROM CONNECTICUT, USA

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Mycoplasma corogypsi was first reported in a free-living black vulture (Coragyps atratus) from Alabama, USA, in 1993. Since its identification, M. corogypsi has been associated with polyarthritis in free-living black vultures from Virginia, USA, in 2009 (n=1) and North Carolina, USA, in 2013 (n=3). This report describes a case of M. corogypsi-associated polyarthritis in a free-living black vulture from Connecticut, USA. The vulture was found on the ground unable to fly and was admitted to the Tufts Cummings School of Veterinary Medicine Wildlife Clinic. The bird was lame on its left leg and displayed a droop of the left wing. Physical examination revealed flocculent swellings of the left tibiotarsal-tarsometatarsal (hock) and elbow joints. Radiographs revealed soft tissue swellings at these joints as well as periosteal reaction at the distal left tibiotarsus and proximal left tarsometatarsus. A complete blood count showed anemia and an elevated white blood cell count. As the prognosis for recovery and release was determined to be poor, the vulture was humanely euthanized. Histopathologic examination confirmed synovitis, tendonitis, and osteoarthritis of both joints. PCR performed on a sample of joint capsule identified M. corogypsi. This report extends the documented range of M. corogypsi-associated polyarthritis in black vultures to the northeastern United States.
THE BILIARY TREMATODE *PSEUDAMPHISTOMUM TRUNCATUM* IS PATHOGENIC FOR OTTERS (*LUTRA LUTRA*)

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*Pseudamphistomum truncatum* is an opportunistic biliary trematode of fish-eating mammals, including humans. Historically reported from Russia and Eastern Europe, this parasite recently emerged in grey seals (*Halichoerus grypus*) in Sweden and in wild mustelids in the United Kingdom and Denmark. The first probable case in an otter (*Lutra lutra*) in Sweden was described in 2006. However, the pathological significance of *P. truncatum* for otters has not been clearly demonstrated. Here we report parasitism resulting in, or contributing to, death in four otters in Sweden. All were found dead in the winter months of November, December or January, in 2012 or 2013. All were emaciated. Otters 1-3 were icteric and had shrunken gallbladders with markedly thickened walls and intraluminal 1-2 mm long trematodes morphologically consistent with *P. truncatum*. These otters also had severely enlarged (up to 20% of body mass) livers with moderately to severely thickened bile ducts. Severe, chronic, cholangiohepatitis was seen microscopically. Otter 1 also had evidence of acute, sublethal trauma. The gallbladder of otter 4 was identical to those of otters 1-3 and had evidence of a chronic rupture. Concurrent, chronic peritonitis with intraperitoneal pigment and trematode eggs was seen, supporting a gallbladder rupture secondary to parasitic infection. Otters are listed as a vulnerable species in Sweden following a severe population decline in the 1960s and 1970s. *P. truncatum* can cause severe debilitation and death in otters and further investigation into reasons for its emergence and significance for final hosts, including otters and humans, is warranted.
GAPS AND CHALLENGES IN MODELING PATHOGEN TRANSMISSION AT THE INTERFACE OF WILDLIFE, LIVESTOCK AND POULTRY POPULATIONS

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Many diseases of animal health concern occur in both free-ranging wildlife and domestic populations. The complexity with which wildlife and domestic animal host populations interact, habitat heterogeneity, variation in host response and the potential for multiple host species are just several of the components contributing to the challenges of disease prevention, surveillance and management at the wildlife-livestock interface. Simulation models can be valuable tools to characterize disease systems and to support animal health decision-making. Although models are being used increasingly to study transmission within domestic or wildlife host species, models of transmission at the interface remain limited due to the complexity of these systems. During a recent workshop, we brought together experts in ecology, veterinary medicine and animal disease modeling to discuss novel, science-based methods to address disease concerns at the wildlife-livestock interface. Outcomes of this workshop included a new compilation of the gaps in our knowledge and challenges modeling transmission at the interface between wildlife and domestic populations. Here we present this review and a qualitative analysis of these gaps in several focal pathogen systems of great importance to animal health.
PHYLOGENETIC ANALYSIS OF FULL LENGTH GENOMES OF EPIZOTIC HEMORRHAGIC DISEASE VIRUS-6

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Epizootic hemorrhagic disease virus (EHDV) is an Orbivirus (family Reoviridae) that infects domestic and wild ruminants. Until 2006, only two serotypes had been reported in North America; EHDV-1 and EHDV-2. However, in 2006 an exotic virus, EHDV-6, was isolated from a white-tailed deer in Indiana. With the exception of 2011, we have isolated this virus every year since its original detection. Although confirmed cases have come from both captive and wild deer in Arkansas, Indiana, Illinois, Michigan, Missouri, and, and Texas, large-scale mortality events associated with EHDV-6, have not been documented. The annual occurrence suggests that these viruses, like other arboviruses, are overwintering as opposed to regularly being reintroduced. In order to assess the evolutionary relatedness of these isolates from different geographic locations within the United States, we sequenced 10 full length genome EHDV-6 isolates from a three year period, 2009, 2010, and 2012 to genetically characterize these viruses and compare them to the index strain from Indiana CC-304-06.
EMERGING VIRAL DISEASES OF THE MACROPODOIDEA

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Viruses within the families Herpesviridae and Reoviridae have emerged as important pathogens of the Macropodoidea in recent decades. A detailed understanding of the epidemiology of these viruses is lacking despite significant virus associated morbidity and mortality in both free-ranging and captive macropodoids. Within the Herpesviridae the following macropodid herpesviruses (MaHV) have been characterized: MaHV-1, associated with mortalities in Parma wallabies (Macropus parma); MaHV-2 associated with mortalities in dorcopsis wallabies (Dorcopsis muelleri) and quokkas (Setonix brachyurus); MaHV-3 associated with ulcerative cloacitis and respiratory disease in eastern grey kangaroos (M. giganteus); and MaHV-4 associated with respiratory disease in eastern grey kangaroos. Additionally potoroid herpesvirus 1 (PotHV-1) has been recently identified from clinically normal eastern bettongs (Bettongia gaimardi). Neutralizing antibodies to MaHV-1 and MaHV-2, or related viruses, have been demonstrated in numerous species of free-ranging and captive macropodoids suggesting wide spread exposure to these viruses. However the host species, mode of transmission and the circumstances under which disease occurs remain to be elucidated. Within the Reoviridae members of the Orbivirus genus have also been associated with significant mortality events in free-ranging and captive macropodoids. Orbiviruses of the Wallal and possibly the Warrego serogroups were identified as the cause of an outbreak of choroid blindness in free-ranging kangaroos, principally western grey kangaroos (M. fuliginosus) in the mid-1990s. Since 1998 recurring epizootics of sudden death associated with orbiviruses of the Eubenangee serogroup have occurred in captive colonies of tammar wallabies (M. eugenii). The maintenance host(s), vector(s) and the factors precipitating disease outbreaks associated with viruses of the Eubenangee serogroup remain unknown.
PREVALENCE, TRANSMISSION, AND GENETIC DIVERSITY OF BLOOD PARASITES INFECTING TUNDRA-NESTING GEESE IN ALASKA

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A total of 842 blood samples collected from five species of tundra-nesting geese in Alaska were screened for haemosporidian parasites using molecular techniques. \textit{Leucocytozoon}, \textit{Haemoproteus}, and \textit{Plasmodium} parasites were detected in 169 (20\%), three (<1\%), and zero (0\%) samples respectively. Occupancy modeling was used to estimate \textit{Leucocytozoon} parasite prevalence and assess variation relative to species, age, sex, geographic area, year, and decade. Species, age, and decade were identified as important in explaining differences in \textit{Leucocytozoon} parasite prevalence. \textit{Leucocytozoon} parasites were detected in goslings sampled along the Arctic Coastal Plain using both historic and contemporary samples which provided support for transmission in the North American Arctic. In contrast, lack of detection of \textit{Haemoproteus} and \textit{Plasmodium} parasites in goslings (n=238) provided evidence to suggest that the transmission of parasites of these genera may not occur among waterfowl using tundra habitats in Alaska, or alternatively, may only occur at low levels. Five haemosporidian genetic lineages shared among different species of geese sampled from two geographic areas were indicative of interspecies parasite transmission and supported broad parasite/vector distributions. However, identical \textit{Leucocytozoon} and \textit{Haemoproteus} lineages on public databases were limited to waterfowl hosts suggesting constraints in parasite host range.
BURMESE STAR TORTOISE (GEOCHELONE PLATYNOTA) HEALTH SCREENING AS PART OF SPECIES RESTORATION TO THE WILD IN MYANMAR

Bonnie L Raphael¹, Tracie Seimon¹, Robert Ossiboff³, Marisa Ostek¹, Brian Horne¹, Steven G. Platt², Kalyar Platt²,³, Tint Lwin³, Paul Gibbons⁴, Heather Mohan-Gibbons⁴, Andrew D. Walde⁵, and Angela M. Walde⁵

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⁴ Turtle Conservancy, Ojai, California, USA
⁵ Walde Research & Environmental Consulting, Atascadero, California, USA

The Burmese star tortoise, G. platynota, is endemic to the dry zone of central Myanmar. Population surveys, conducted by the Wildlife Conservation Society (WCS) from 1999 through 2005, documented the rapid range-wide decline of G. platynota as a result of intensive, illegal harvest for international pet markets. Subsequent surveys concluded that the species is functionally extinct with no viable wild populations of G. platynota. Pursuant to a survey in late 2011, a reintroduction plan was developed that included detailed protocols for returning G. platynota, captive bred in Myanmar, to the wild. These protocols addressed biological issues, health concerns, and cultural dimensions of a reintroduction program and were implemented in 2013. After education and outreach was performed in surrounding communities, health assessments were performed on tortoises (n=150) from one breeding facility in Myanmar. Those animals were also tattooed on their shells with Buddhist iconography to discourage hunting for the pet trade. Health screening consisted of physical examination, molecular PCR testing for mycoplasma, ranavirus and herpesviruses, complete blood count, and opportunistic fecal examination. All testing was done in Myanmar using portable laboratories. Results of all molecular testing were negative and all individuals were robust with CBC’s within normal limits compared to other Geochelone sp. Many of the tortoises had transmitters and temperature recorders attached to their carapaces to track movements and behaviors. These animals subsequently were placed into soft release pens. In addition, 50 tortoises at one other breeding facility in Myanmar underwent the same testing; the results were similar. Additional testing will be performed at the breeding facilities during the coming year to further assure that they are free of known infectious diseases. Testing of chelonians rescued from the illegal wildlife trade in Myanmar is planned to ascertain what threats they may pose to the chelonian fauna of Myanmar.
ASSESSING THE RISK OF PATHOGEN POLLUTION: A PRELIMINARY TEST OF CO-EVOLUTION BETWEEN RANAVIRUS AND WOOD FROGS

Patrick N. Reilly\textsuperscript{1,2}, Matthew J. Gray\textsuperscript{1}, Rebecca P. Wilkes\textsuperscript{2}, Jordan C. Chaney\textsuperscript{1}, Rachel D. Hill\textsuperscript{1}, and Debra L. Miller\textsuperscript{1,2}

\textsuperscript{1} Center for Wildlife Health, University of Tennessee, Knoxville, Tennessee, USA
\textsuperscript{2} College of Veterinary Medicine, University of Tennessee, Knoxville, Tennessee, USA

Hosts that co-evolve with pathogens presumably have a greater immune response to endemic strains. Ranaviruses are an emerging pathogen and have been associated with die-offs in wood frog (\textit{Lithobates sylvaticus}) populations from Georgia, USA, to Northwest Territories, Canada. We hypothesized that pathogenicity of ranavirus would increase as distance between isolate and host population locations increased. We are testing pathogenicity of two FV3-like ranaviruses isolated from ranavirus die-offs in Minnesota and Tennessee, USA, among four populations of wood frog tadpoles collected from Tennessee, Michigan, Manitoba Canada, and Minnesota, USA. Inasmuch as temperature affects amphibian immune response and viral replication, we are performing our experiments in environmental chambers at 15 and 25 C. If our predictions hold true, pathogenicity of the Tennessee isolate should decrease in the following order: Manitoba, Minnesota, Michigan and Tennessee populations. Similarly, pathogenicity of the Minnesota isolate should decrease in the following order: Manitoba, Tennessee, Michigan, and Minnesota populations. We anticipate that pathogenicity will be greater in the 25 C treatment, because ranavirus replication and tadpole development increase with temperature. With the Tennessee population completed, initial data show that tadpoles exposed to the MN isolate experienced 100% mortality in a 2-day period compared to 5 days for the TN isolate, with the median day to mortality being a half-day faster with the MN isolate. Mortality also was much later in the 15 C chamber as compared to the 25 C chamber. Experiments for the remaining populations are ongoing, and results will be presented in our poster. Our results have potential implications in host-pathogen evolutionary theory and conservation relevance regarding the transport of amphibians sub-clinically infected with ranavirus across large geographic distances (i.e., threat of pathogen pollution). Additionally, our temperature results may provide insight into possible effects of global climate change on ranavirus emergence.
DOES GEOGRAPHIC DISTANCE BETWEEN HOST POPULATION AND ISOLATE LOCATION EQUATE TO RANAVIRUS PATHOGENICITY?

Patrick N. Reilly\textsuperscript{1,2}, Matthew J. Gray\textsuperscript{1}, Rebecca P. Wilkes\textsuperscript{2}, Jordan C. Chaney\textsuperscript{1}, Debra L. Miller\textsuperscript{1,2}, and Rachel Hill\textsuperscript{1}

\textsuperscript{1} Center for Wildlife Health, University of Tennessee, Knoxville, Tennessee, USA
\textsuperscript{2} College of Veterinary Medicine, University of Tennessee, Knoxville, Tennessee, USA

Hosts that coevolve with pathogens presumably have a greater immune response when infected. Ranaviruses are an emerging pathogen and have been associated with die-offs in wood frog (\textit{Lithobates sylvaticus}) populations from Georgia to Alaska, USA. We hypothesized that pathogenicity of a ranavirus would increase as distance between isolate and host population locations increased. We are testing pathogenicity of two FV3-like ranaviruses isolated from morbid amphibians in Minnesota and Tennessee, among four populations of wood frog tadpoles collected from Tennessee, Michigan, Manitoba Canada, and Alaska. Inasmuch as temperature affects amphibian immune response and viral replication, we are performing our experiments in environmental chambers at 15 and 25 C. If our predictions hold true, pathogenicity of the Tennessee isolate should decrease in the following order: Alaska, Manitoba, Michigan and Tennessee populations. Similarly, pathogenicity of the Minnesota isolate should decrease in the following order: Alaska, Tennessee, Manitoba and Michigan populations. We anticipate that pathogenicity will be greater in the 25 C treatment, because ranavirus replication and tadpole development increase with temperature. By the time of the symposium, we will be completed with the Tennessee, Michigan and Manitoba experiments. Our results have potential implications in host-pathogen evolutionary theory and conservation relevance regarding the transport of amphibians sub-lethally infected with ranavirus across large geographic distances. Additionally, our temperature results may provide insight into possible effects of global climate change on ranavirus emergence.
ROCK DOVES EXHIBIT LIMITED VIRAL SHEDDING OF LOW PATHOGENIC AVIAN INFLUENZA VIRUSES

Susan A. Shriner\textsuperscript{1}, J. Jeffrey Root\textsuperscript{1}, Nicole L. Mooers\textsuperscript{1}, Jeremy W. Ellis\textsuperscript{1}, Heather J. Sullivan\textsuperscript{1}, Kaci K. VanDalen\textsuperscript{1}, and Alan B. Franklin\textsuperscript{1}

\textsuperscript{1}U.S. Department of Agriculture, APHIS, National Wildlife Research Center, Fort Collins, Colorado, USA

We conducted experimental inoculation studies of wild-caught pigeons with low pathogenic H5N8 and H4N6 avian influenza viruses. Results from the experimental inoculation studies indicate pigeons shed virus and seroconvert at relatively low rates. Viral RNA was primarily detected in oral swabs with no shedding evident in cloacal swabs and very limited shedding in fecal swabs. Thirty percent of the pigeons inoculated with the H5N8 and 22\% of the pigeons inoculated with H4N6 virus showed no detectable viral RNA in any oral, cloacal or fecal swab across the seven days of the two studies. These results indicate that while pigeons are commonly associated with poultry operations, they are unlikely to play a significant role in transmission of these viruses.
HEALTH AND DEMOGRAPHICS OF AFRICAN BUFFALO (*SYNCERUS CAFFER*) IN RUAHA NATIONAL PARK, TANZANIA

Annette Roug¹, Epaphras A. Muse², Woutrina Smith¹, Jonna Mazet¹, Rudovick Kazwala³, Goodluck Paul³, Paul Banga², and Deana Clifford¹,⁴

¹ Wildlife Health Center, One Health Institute, School of Veterinary Medicine, University of California, Davis, California, USA
² Ruaha National Park, Tanzania National Parks, Iringa, Tanzania
³ Department of Veterinary Medicine and Public Health, Sokoine University of Agriculture, Morogoro, Tanzania
⁴ California Department of Fish and Wildlife, Rancho Cordova, California, USA

The African buffalo (*Syncerus caffer*) population of Ruaha National Park is thought to be declining, but little information is available about the population. Seasonal drying of the park’s water source due to upstream irrigation may have caused loss of dry season habitat, increased pressure on remaining water sources, and possibly increased contact between wildlife and livestock at the park borders. The Health for Animals and Livelihood Improvement project and Ruaha National Park are collaborating to investigate the health and population status of African buffaloes in Ruaha. In 2011, 10% (3/30) buffaloes from a single herd were found positive for bovine tuberculosis, and 11% (2/19) were seropositive for *Brucella* spp. Demographic surveys, fecal egg counts and parasite identifications were conducted in September of 2011 and 2013. In 2011, three out of four large buffalo herds had age and sex ratios as well as body condition scores within what would be expected in the dry season for stable buffalo populations in eastern and southern Africa, whereas one herd had poorer body condition and no calves. In 2013, the herd composition was more varied, with most herds appearing to be in good health but with fewer calves than observed in 2011. The mean herd level egg counts ranged from 83–140 and 28–113 eggs/g feces in 2011 and 2013, respectively, and with *Haemonchus, Nematodirus, Cooperia*, and *Oesophagostomum* sp., and coccidian oocysts detected in one or more herds. Overall, the two surveys showed mixed results, with most herds appearing to be in good health while some had lower than expected reproductive parameters. A September 2013 aerial total count revealed a reduction in buffalo numbers compared to 2004. Continued monitoring of herd health and demographics parameters are needed to understand population demographic trends, health and potential conservation threats of buffaloes in Ruaha.
MONITORING FOR CULICOIDES SPP. AT SITES OF PREVIOUS EPIZOOTIC HEMORRHAGIC DISEASE OUTBREAKS IN SOUTHERN MICHIGAN

Mark G. Ruder¹, Michelle Rosen², Stephen M. Schmitt², Stacey Vigil³, Joseph L. Corn³, and Robert S. Pfannenstiel¹

¹ Arthropod-Borne Animal Diseases Research Unit, USDA, Agricultural Research Service, Manhattan, Kansas, USA
² Wildlife Disease Laboratory, Michigan Department of Natural Resources, Lansing, Michigan, USA
³ Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA

Epizootic hemorrhagic disease (EHD) virus (EHDV) infects numerous wild and domestic ruminants and is a significant pathogen of white-tailed deer (WTD; Odocoileus virginianus). Additionally, reports of EHD in cattle are increasing. Although historically rare, the frequency of EHD epidemics in the upper Midwest and other northern areas (USA) have increased over the past decade. Michigan EHD outbreaks have occurred in 1955, 1974, 2006, and 2008-2013 and while most were localized, the 2012 epidemic was widespread in southern Michigan, resulting in high mortality among WTD. The increasing frequency of EHD in northern areas exposes our incomplete understanding of EHD epidemiology, especially concerning overwintering mechanisms and competent vector populations. Culicoides sonorensis is the only confirmed EHDV vector in North America, although other Culicoides spp. are suspected vectors. It is unclear whether C. sonorensis occurs in Michigan and entomological surveillance is needed to identify relevant vectors in this region. To address this need, we initiated light trap surveys for Culicoides during September 2012 in areas of previous EHD outbreaks in southern Michigan with the goal of identifying the resident Culicoides species complex. At each site, CDC UV-LED traps were set overnight at 2-3 week intervals July-September. Insects were trapped into ethanol, manually sorted, and morphological identifications of Culicoides were made. During 2012, four traps collected Culicoides in Allegan, Calhoun, Ionia and St. Joseph counties. The 2013 sites were located in Branch, Cass, Ionia, Livingston and Muskegon counties, where trapping will continue during 2014. During 2012-2013, we collected and identified C. arboricola, C. biguttatus, C. crepuscularis, C. haematopotus, C. nanus, C. stellifer, and C. venustus. Culicoides stellifer is a suspected vector of EHDV. While basic, Culicoides surveillance is essential to understand EHDV transmission and these data will help provide a baseline for future surveillance efforts and will inform targeted studies to incriminate vectors.
THE IMPORTANCE OF CONTINUED PRION RESEARCH: AN ENIGMATIC CASE OF CHRONIC WASTING DISEASE IN A CAPTIVE RED DEER (CERVUS ELAPHUS)

Marc D. Schwabenlander¹, Marie R. Culhane¹, S. Mark Hall², Sagar M. Goyal¹, Paul L. Anderson³, Michelle Carstensen⁴, Scott J. Wells⁵, William B. Slade⁶, and Aníbal G. Armién¹

¹ University of Minnesota, College of Veterinary Medicine, Veterinary Diagnostic Laboratory, St. Paul, Minnesota, USA
² U.S. Department of Agriculture, APHIS, National Veterinary Services Laboratories, Ames, Iowa, USA
³ Minnesota Board of Animal Health, St. Paul, Minnesota, USA
⁴ Minnesota Department of Natural Resources, St. Paul, Minnesota, USA
⁵ University of Minnesota, College of Veterinary Medicine, Center for Animal Health and Food Safety, St. Paul, Minnesota, USA
⁶ North Oaks Farms LLC, North Oaks, Minnesota, USA

A 22-month-old, female red deer (Cervus elaphus) was found positive for the chronic wasting disease (CWD) abnormal prion protein in the obex and the retropharyngeal lymph node (RPLN) by immunohistochemical staining. Microscopic lesions of spongiform encephalopathy and immunohistochemical staining patterns and intensity were similar to those in CWD-positive elk and experimentally infected red deer. Western blot and enzyme-linked immunosorbent assay were positive for a TSE consistent with CWD. The red deer was in good body condition and the only clinical sign observed was recumbency the day of death. The red deer did not appear to demonstrate advanced clinical signs of CWD infection despite severe CWD prion accumulation within the brain and RPLN and widespread distribution throughout multiple other tissues. An epidemiological investigation was completed on the captive herd from which this red deer originated with no obvious biosecurity deficiencies revealed. Approximately 70% of the herd, including this red deer’s life-long enclosure cohorts, has tested negative for CWD prion infection via immunohistochemical staining methods on obex and RPLN. Certain aspects of this case are enigmatic including the young age of this red deer in correlation with the severe and widespread CWD prion accumulation, the fact that none of the lifelong cohorts were infected, and the source of the infection. CWD and other prion diseases are not completely understood. Spontaneous prion disease has been described in bovine spongiform encephalopathy (BSE) in cattle, scrapie in sheep, and creutzfeldt-jakob disease (CJD) in humans. The methods for spontaneous classification in BSE, scrapie, and CJD have not produced evidence of spontaneous CWD. Continued research in CWD prion disease is warranted for sound protection and management of captive herds, free-ranging herds and human health.
EVALUATION OF DYNAMICS OF VIRAL AGENTS WITH IMPACT ON POULTRY FARMS IN WILD BIRDS OF CENTER-EAST ZONE OF COLOMBIA

Diego Soler-Tovar¹, Laura Vargas-Castillo¹, Andrés F. Santander¹, Diana C. Álvarez¹, and Arlen P. Gomez¹

¹ Facultad de Ciencias Agropecuarias, Universidad de La Salle, Bogotá, Colombia

Colombia has reported circulation of pathogenic viral agents in poultry, causing concern in the poultry industry by the presence of wild birds in the facility and the possible transmission of these diseases between species. The aim of this study was to evaluate the circulation of Newcastle disease virus (NDV), Gumboro disease (IBDV), avian infectious bronchitis (IBV) and avian infectious laryngotracheitis (ILTV) by serological and molecular techniques in wild birds; additionally, bird species were identified and staff perceptions regarding contact between wild and domestic birds was established. The presence of wild birds was established in nine poultry farms in the center-east zone of Colombia (Fómeque, Cundinamarca) in 2012 and 2013; oral and cloacal swabs were collected from wild birds to detect the virus by RT-PCR and PCR, and blood samples were taken to detect antibodies. Six orders, 17 families, 30 genera, 32 species and 417 individuals were identified, capturing a greater number of individuals of the order Passeriformes, Columbiformes and followed by fewer Apodiformes, for a total of 48 birds in close contact with poultry; additional data provided by farm staff affirms the presence of small birds near the storage warehouses, on the tiles or fruit trees, and larger birds flying above farms. All samples were negative by virus genome assessed using molecular techniques. In the serological results titres against NDV were detected in pooled sera from two of the nine farms. These results demonstrate the close proximity of wild birds with domestic poultry and suggest a possible contact of wild birds with commercial birds that had antibodies to NDV strains. However, in wild birds evidence of a variety of pathogenic viruses was not detected.
ESTABLISHMENT OF A HEALTH ASSESSMENT FOR THE WEST INDIAN MANATEE (TRICHECHUS MANATUS) IN COLOMBIA

Alejandra Vega Llach\textsuperscript{1}, Leonardo Arias Bernal\textsuperscript{2}, and Diego Soler-Tovar\textsuperscript{3}

\textsuperscript{1} La Salle University, Bogotá, Colombia
\textsuperscript{2} Scientific Director Park Zoo Jaime Duque, Bogotá, Colombia
\textsuperscript{3} Agricultural Sciences and Research, La Salle University, Bogotá, Colombia

The West Indian manatee (Trichechus manatus) is categorized as endangered in Colombia and as vulnerable in the IUCN and Red List. The species is distributed throughout eight departments and eight rivers in Colombia and is considered a sentinel for environmental and human health. Manatees can provide vital information about the ecosystems they inhabit and also help in keeping them free of pathogens. For these reasons, monitoring their health is important in order to identify clinical signs that can occur due to environmental and anthropogenic changes, among others. The objective of this project was to develop a protocol for monitoring the health of Trichechus manatus in Colombia, by increasing knowledge of veterinary parameters. The methodology used implied compiling protocols available in print and electronic literature and extracting factors applicable to captive and free-ranging manatee experts from Fundacion Omacha, Dolphin Discovery and Colegio de la Frontera Sur. Protocol validation was done using the Agree protocol platform. The overall result was acceptance of the new protocol to facilitate the work of veterinarians and other professionals working with the species. The protocol was considered a useful tool for monitoring the health of manatees in Colombia and is the first attempt to standardize a health assessment protocol for aquatic mammals in Colombia.
CONTINUING EDUCATION CERTIFICATION

Annual International Conference of the Wildlife Disease Association
CE Sponsored by the American Association of Wildlife Veterinarians
July 27- August 1, 2014
Albuquerque, New Mexico

This is to certify that ________________ [print name] attended the Annual International Conference of the Wildlife Disease Association during July 28-August 1, 2014 in Albuquerque, NM. S/he is eligible to receive the following continuing education credit (one lecture hour = one CE unit):

<table>
<thead>
<tr>
<th>Date</th>
<th>Maximum Lecture Hours Attainable</th>
<th>Lecture Hours Attended</th>
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</thead>
<tbody>
<tr>
<td>Sunday, 07/27/2014</td>
<td>Field Investigation of Wildlife Mortality 7.0</td>
<td></td>
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<tr>
<td>Monday, 07/28/2014</td>
<td>One Health 3.0</td>
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<tr>
<td></td>
<td>One Health in Action 1.5</td>
<td></td>
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<tr>
<td>Tuesday, 07/29/2014</td>
<td>Terry Admundson Award Student Presentations 4.5</td>
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<tr>
<td>Wednesday, 07/30/2014</td>
<td>Field techniques to improve Animal Welfare 1.75</td>
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<tr>
<td></td>
<td>Ecology of Wildlife Disease 1.0</td>
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<tr>
<td></td>
<td>Forensics workshop 4.00</td>
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<tr>
<td>Thursday, 07/31/2014</td>
<td>Diseases of Ungulates 1.5</td>
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<td>Diseases of Marine Species 1.5</td>
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<td>Diagnostic Tools 1.25</td>
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<td>Avian Disease 1.25</td>
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<tr>
<td></td>
<td>Emerging Disease of Wildlife 2.5</td>
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<td></td>
<td>Wildlife Conservation on Private Lands 1.0</td>
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<td>Wildlife Conservation of the American Southwest 1.25</td>
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<tr>
<td>Friday, 08/01/2014</td>
<td>Anthropogenic Impacts on Wildlife Health 2.5</td>
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<tr>
<td>Total CE units:</td>
<td>35.5</td>
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</table>

I am a licensed veterinarian and am therefore qualified to obtain Continuing Education credit for my attendance at this meeting, and I confirm that I attended the lecture hours as specified above:

______________________________ (Signature required)

Peregrine L. Wolff, DVM
President, AAWV

Kay A. Backues, DVM, DACZM
Secretary, American College of Zoological Medicine

CE Provider Approval: American College of Zoological Medicine

Disclaimer: The ACZM is a registered veterinary specialty college of the American Veterinary Medical Association for sponsoring of continuing education credits. Individual States may have different laws or policies on acceptability of conferences, meetings or courses to qualify for continuing education (CE) credit. You are advised to check with the State(s) in which you are
# Wildlife Disease Association Conference Schedule at a Glance

<table>
<thead>
<tr>
<th>Day</th>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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</thead>
<tbody>
<tr>
<td>Saturday</td>
<td>6:45a</td>
<td>Student field trip to Valles Caldera National Preserve</td>
<td>Eagle A, B</td>
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<td>July 26</td>
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<tr>
<td>Sunday</td>
<td>8:00a – 12:00p</td>
<td>Editorial Board Meeting</td>
<td>Eagle A, B</td>
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<td>July 27</td>
<td>8:30a – 4:30p</td>
<td>Student Workshop</td>
<td>Off-site</td>
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<td>10:00a - 7:00p</td>
<td>Registration</td>
<td>Tamaya Ballroom Foyer</td>
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<td>1:00p – 5:00p</td>
<td>WDA Council Meeting</td>
<td>Eagle A, B</td>
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<td></td>
<td>6:00p – 9:30p</td>
<td>Welcome Reception</td>
<td>House of Hummingbird</td>
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<tr>
<td>Monday</td>
<td>8:00a – 8:30a</td>
<td>Conference Welcome</td>
<td>Tamaya Ballrooms</td>
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<td>July 28</td>
<td>8:30a – 10:15a</td>
<td>One Health</td>
<td>Tamaya Ballrooms</td>
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<td></td>
<td>10:45a – 12:00p</td>
<td>One Health in Practice</td>
<td>Tamaya Ballrooms</td>
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<td></td>
<td>1:00p – 2:00p</td>
<td>One Health Poster Session</td>
<td>Puma Rooms</td>
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<tr>
<td></td>
<td>2:00 – 5:00p</td>
<td>One Health in Action</td>
<td>Tamaya Ballrooms</td>
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<tr>
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<td>5:00p – 6:00p</td>
<td>Wildlife Veterinary Section Meeting</td>
<td>Tamaya Ballrooms</td>
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<td>6:00p &amp; 6:30p</td>
<td>Buses leave for Student/Mentor Mixer</td>
<td>Off-site</td>
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<td></td>
<td>6:00p – 8:00p</td>
<td>One Health Mixer</td>
<td>Tamaya Ballrooms</td>
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<tr>
<td>Tuesday</td>
<td>8:00a – 10:00a</td>
<td>Terry Amundson Award Student Presentations</td>
<td>Tamaya Ballrooms</td>
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<tr>
<td>July 29</td>
<td>10:00a – 10:45a</td>
<td>Student Poster Session</td>
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<td>Tamaya Ballrooms</td>
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<td>12:00p - 1:30p</td>
<td>WDA Business Lunch</td>
<td>Tamaya Ballrooms</td>
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<td>Terry Amundson Award Student Presentations</td>
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<td>2:45p – 3:45p</td>
<td>Student Poster Session</td>
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<td>3:45p – 5:00p</td>
<td>Terry Amundson Award Student Presentations</td>
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<td>5:00p – 6:00p</td>
<td>American Association of Wildlife Veterinarians</td>
<td>Tamaya Ballrooms</td>
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<td>6:00p – 10:00p</td>
<td>Picnic and Auction</td>
<td>Cottonwoods</td>
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<tr>
<td>Wednesday</td>
<td>8:00a – 10:00a</td>
<td>Field Techniques to Improve Animal Welfare</td>
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<td>July 30</td>
<td>8:30a – 9:00a</td>
<td>Al Franzmann Memorial Lecture</td>
<td>Tamaya Ballrooms</td>
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<td>10:30a – 11:45a</td>
<td>Ecology of Wildlife Disease</td>
<td>Tamaya Ballrooms</td>
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<td>1:00p – 5:30p</td>
<td>Field Trips</td>
<td>Various</td>
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<tr>
<td>Thursday</td>
<td>8:00a – 10:00a</td>
<td>Diseases of Ungulates</td>
<td>Tamaya Ballroom F,G,H</td>
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<td>July 31</td>
<td>8:00a – 9:45a</td>
<td>Diseases of Marine Species</td>
<td>Tamaya E</td>
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<td>10:00a – 10:45a</td>
<td>General Poster Session</td>
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<td>10:45a – 12:00p</td>
<td>Diagnostic Tools</td>
<td>Tamaya Ballroom F,G,H</td>
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<td>10:45a – 12:00p</td>
<td>Avian Diseases</td>
<td>Tamaya E</td>
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<tr>
<td></td>
<td>1:30p – 2:45p</td>
<td>Emerging Diseases of WildLife</td>
<td>Tamaya Ballroom F,G,H</td>
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<td></td>
<td>1:30p – 2:45p</td>
<td>Wildlife Conservation on Private Lands</td>
<td>Tamaya E</td>
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<td>2:45p – 3:45p</td>
<td>General Poster Session</td>
<td>Puma Rooms</td>
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<tr>
<td></td>
<td>3:45p – 5:00p</td>
<td>Emerging Diseases of WildLife, Continued</td>
<td>Tamaya Ballroom F,G,H</td>
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<td>3:45p – 5:00p</td>
<td>Wildlife Diseases of the American Southwest</td>
<td>Tamaya E</td>
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<tr>
<td></td>
<td>5:00p – 6:00p</td>
<td>WDA Business Meeting</td>
<td>Tamaya Ballroom F,G,H</td>
</tr>
<tr>
<td></td>
<td>6:00p &amp; 6:30p</td>
<td>Buses depart for Banquet</td>
<td>BioPark (off-site)</td>
</tr>
<tr>
<td>Friday</td>
<td>8:00a – 11:30a</td>
<td>Anthropogenic Impacts on Wildlife Health</td>
<td>Tamaya Ballrooms</td>
</tr>
<tr>
<td>August 1</td>
<td>11:45a</td>
<td>Adjourn</td>
<td></td>
</tr>
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