58th Annual International Conference of the Wildlife Disease Association

Wildlife Health from Land to Sea: Impacts of a Changing World

Program and Abstracts
August 2—7, 2009
Blaine, Washington
THANK YOU TO OUR SPONSORS

Oregon Department of Fish and Wildlife Platinum Sponsor $10,000
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Wild Sheep Foundation $750
Idaho Department of Fish and Game $500
U.C. Davis, School of Veterinary Medicine, Wildlife Health Center in-kind
Washington Department of Fish and Wildlife in-kind
Nevada Department of Wildlife in-kind
Wildlife Conservation Society in-kind

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Back Cover Photo: Colin Gillin

Centers for Disease Control and Prevention (CDC) funded the printing of this year’s program
58th Annual International Conference of the Wildlife Disease Association

August 2-7, 2009
Semiahmoo
Blaine, Washington
Program & Abstracts
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Christine Kreuder Johnson Dolores Gavier-Widén

STUDENT MEMBER OF COUNCIL
Terra Kelly

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Europe...............................................................Paul Duff
Nordic.................................................................Erik Ågren
Wildlife Veterinarian..............................................Jonathan Sleeman

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Kevin Keel

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Elizabeth Crawford  Semiahmoo Event Organizer
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Sonja Lapinski  Oregon State University
Nadia Rifat  UC Davis
Michelle Barbieri  UC Davis
And many other volunteers!
CONTINUING EDUCATION

Continuing education for this conference was set up by the American Association of Wildlife Veterinarians through the American College of Zoological Medicine. CE forms can be acquired at the conference registration desk.

The Program and Abstracts booklet is distributed to all WDA Conference attendees. The Wildlife Disease Association does not regard this Conference Program and Abstracts booklet as a publication. It is used only as an information and reference guide for conference participants. Abstracts included in this program should not be cited in any scientific literature or peer-reviewed publications.

This conference is officially referred to as the Annual International Conference of the Wildlife Disease Association.
WDA 2009 Conference Greening Information

The Conference Committee added “greening” to this year’s event. We contracted with Calyx~ Sustainable Hotel & Tourism Consultants to work with the resort to reduce the amount of waste produced by our conference and provide ideas on decreasing our carbon footprint. They worked directly with the resort staff to address more environmentally sustainable actions involving the resort’s management and operations (who makes decisions, support of environmental initiatives, communication), energy, water, purchasing, and food and beverage. Several of the many ideas generated are listed below and we invite you to help us green our conference with the following ways you can help:

- If you drink coffee or tea, please bring a hot beverage container with you since there will be both on and off-site opportunities to use it.
- Please bring a reusable water bottle of your choice. Using your own reusable water bottle will help reduce waste, save on the energy costs associated with transporting bottled waters, and help the WDA save money on conference expenses.
- This year, we will not provide conference tote bags with conference materials to help reduce our conference costs.
- Conference attendees were asked to provide their own writing materials.
- Although the hotel provides individual shampoos and conditioners in small plastic bottles which are replaced daily, these are not biodegradable and half or more of the contents is usually wasted. To avoid using these individually packaged personal amenities, we request that you please bring your own shampoo and conditioner.
- If you don’t need the newspaper, please inform the front desk when you check in and the newspaper will not be delivered to your door. Complimentary newspapers will always be available in the lobby if you should change your mind on any given day.
- Cell phones, MP3 players and laptops are real energy drains. The most energy efficient way to charge these devices is to charge them after the last session of the day and unplug them before you go to bed.

Many thanks on behalf of the organizing committee for helping us meet our goals of greening this conference by participating in all, or as many of our requests as possible.

Suggestions for next year’s conference will be greatly appreciated.

This program is printed on recycled paper
The conference logo for the 2009 meeting was created by Ashley Wolff, a renowned children’s book illustrator and artist. More information on Ashley Wolff can be found on her website http://www.ashleywolff.com/newsite/index.html.

Totem poles are an ancient tradition of the Indians of the Pacific Northwest coast. The totem figures and symbols have been represented for thousands of years and were originally carved on combs, boxes, masks and walking sticks. After contact with Europeans in the 1700s, and the subsequent acquisition of metal tools, large poles carved from mature cedar trees began to appear. Totem figures are not gods and totem poles were not worshipped. Instead they represented, through the placement of the animals and symbols on the totem pole, a coat of arms or seal for the family or clan. This represented a symbolic history for members related by blood, kinship, or shared experience. Totems placed at the entrance of the family longhouse were symbols of honor to ancestors and the clan.

The animals chosen for the Semiahmoo totem represent the spirit of this meeting and a symbolic history of our WDA clan. The central animal is the Raven who represents Creation and knowledge – the “bringer of the light”. Within his left wing swims Killer Whale representing the Traveler and guardian – the “bringer of good” and in his right wing prowls Bear who brings Strength, learned humility, motherhood, and teaching.
WDA 2009 CONFERENCE EVENTS & PROGRAM

Welcome Reception – Sunday, August 2 (7:00 -10:00)
The welcome reception of conference participants will begin Sunday evening in the Semiahmoo Ballroom. Hors d’oeuvres and complimentary local beer and wine will be served with a cash bar available. The event will begin with a tradition, the student/mentor only reception from 5:30-7:00 followed by an all conference participant gathering to renew old acquaintances and meet new colleagues.

Picnic – Monday, August 3 (7:00-10:00)
The Monday evening Salmon Cook-Out will take place beachside at the resort with Pacific Northwest fare and complementary brews and wine. The weather in August makes the outdoor setting at Semiahmoo the place to be with volleyball, kayaking, and other outdoor resort activities including a nightly beach bonfire.

Auction – Tuesday, August 4 (7:00-10:00)
Tuesday night’s auction, held in the Semiahmoo Ballroom, will be every bit as entertaining as any of memory. Complementary local beers and wine, a cash bar and hors d’oeuvres will be served to get everyone in a cheerful bidding mood. Proceeds from this year’s auction will be applied to student activities including student awards.

Excursions – Wednesday, August 5 (12:30 – 5:00)
As is customary for the WDA Conference, the afternoon of Wednesday August 5th has been set aside for conference attendees to relax, play, and experience some of the unique flavors of the conference venue. With that in mind, the WDA 2009 Conference organizers have arranged an afternoon of excursions to give attendees a taste of the Pacific Northwest.

Rafting - This afternoon with Wild and Scenic River Tours rafting the north fork of the beautiful Nooksack River promises an exciting ride, with opportunities for wildlife watching, fossil finding, and spectacular views of nearby Mount Baker. A riverside deli lunch including smoked salmon and other delicacies is planned. No experience necessary, though you must be at least 10 years of age to participate. Bring your bathing suit, sandals, and a change of clothes!

Salmon Fishing – Join Captain Frank Dickerson of Riptide Charter for an afternoon of salmon fishing in the fertile waters of the Puget Sound. Pink salmon are running, and we may come across King, Sockeye, or Coho. Your catch is cleaned and packaged on board, ready for the BBQ. Captain Dickerson’s 15 years of experience on Puget Sound, promises to make this a memorable afternoon of sun, sea, and salmon.

Whale Watching - Hop aboard the 99 ton Island Explorer III for a six hour cruise around the San Juan Islands in search of orcas. Orca pods J and K are year-round residents of the waters of the San Juan and Gulf Islands, so chances are very good that we will
encounter them. Our host, Island Adventures, is a well-established whale watching operation and a member of the Whale Watch Operators Association Northwest, dedicated to research, education and responsible whale watching, so we can rest assured that our presence will have minimal impact on the whales, seals, river otters, seabirds and other wildlife we’re likely to encounter. We will be accompanied by an experienced naturalist with information and presentations to add to our experience, and to top off the afternoon we will be treated to a beautiful Pacific sunset on the return trip.

**Inaugural Polar Bear Challenge - Thursday, August 6 (6:00 AM)**
Since this is the first you won’t want to miss it. Torsten Mörner is set to lead a pack of bleary-eyed WDA members on a sunrise dip into the cool waters of Puget Sound. Plenty of rewards for on-lookers and swimmers alike, and with this much water this activity has the potential for spawning this year’s much anticipated Duck Award!

**Banquet - Thursday, August 6 (7:00-10:00) Pre-banquet mixer (6:00-7:00)**
The Semiahmoo conference banquet offers complementary local beers and wine and cash bar with a meal featuring Pacific halibut. WDA awards are the focus of this annual event including the presentation of the Distinguished Service Award, the Emeritus Award, and the much awaited Duck Award given for the most notable conference gaffe sure to produce a guffaw!
# 58th Annual International Conference of the Wildlife Disease Association
Semiahmoo, Blaine, Washington USA 2009

## SUNDAY AUGUST 2, 2009

### Pre-Conference Events

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>7:00 - 7:00PM</td>
<td>Registration</td>
<td>Pre-function Area</td>
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<tr>
<td>8:30 - 12:00</td>
<td><strong>Workshop: Hot Topics in Marine Mammals</strong></td>
<td>San Juan – Lopez Pender Room</td>
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<tr>
<td>8:30 - 12:00</td>
<td><strong>Student Workshop: Wildlife Disease Career Building Topics</strong></td>
<td>San Juan – Salt Spring Saturna Room</td>
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<tr>
<td>8:30 – 12:00</td>
<td>Journal of Wildlife Diseases Editorial Board Meeting</td>
<td>Victoria Room</td>
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<tr>
<td>12:00</td>
<td>Lunch (Editorial Board &amp; Council)</td>
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<tr>
<td>1:00 - 5:00</td>
<td>WDA Council Meeting</td>
<td>Victoria Room</td>
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<tr>
<td>1:00 - 4:30</td>
<td><strong>Workshop: Field Investigation of Wildlife Mortalities</strong></td>
<td>San Juan-Lopez Pender Rm.</td>
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<tr>
<td>1:00 - 4:30</td>
<td><strong>Workshop: Oiled Wildlife Care and Response</strong></td>
<td>San Juan – Salt Spring Saturna Room</td>
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<tr>
<td>5:30 – 7:00</td>
<td>Student Mentor Kick-off</td>
<td>Pre-function Area / Semiahmoo Ballroom</td>
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<tr>
<td>7:00</td>
<td><strong>Pacific Northwest Welcome Reception</strong></td>
<td>Semiahmoo Ballroom</td>
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## MONDAY AUGUST 3, 2009

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>7:00</td>
<td>Continental Breakfast</td>
<td>Pre-function Area</td>
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<tr>
<td>7:00 – 10:30AM</td>
<td>Registration</td>
<td>Pre-function Area</td>
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<tr>
<td>8:00</td>
<td><strong>Conference Welcome</strong></td>
<td>Semiahmoo Ballroom</td>
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<tr>
<td>8:30 – 10:00</td>
<td><strong>Wildlife Health from Land to Sea: Impacts of a Changing World</strong></td>
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<td>Session Chair: Dave Jessup</td>
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<tr>
<td>8:30</td>
<td>1. KILLER FOAM: LARGE MARINE BIRD STRANDING EVENT DUE TO HARMFUL ALGAL BLOOM PRODUCING NOVEL PROTEIN SURFACTANT</td>
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<td></td>
<td>David Jessup</td>
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<tr>
<td>8:45</td>
<td>2. SHIPWRECKS LEAD TO UNHEALTHY CORAL REEFS: A CASE STUDY AT PALMYRA ATOLL NWR</td>
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<td></td>
<td>Thierry Work</td>
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<td>9:00</td>
<td>3. LANDSCAPE EPIDEMIOLOGY IN A CHANGING ENVIRONMENT: THE INFLUENCE OF LAND USE PATTERNS AND VIRAL PROPERTIES ON THE</td>
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<td>9:15</td>
<td>4. EMERGENCE OF TICK-BORNE DISEASE ASSOCIATED WITH BIODIVERSITY AND FOREST CHANGE IN THE WESTERN US</td>
<td>Janet Foley</td>
</tr>
<tr>
<td>9:30</td>
<td>5. THE ECOLOGY OF EMERGING DISEASES AMONG POPULATIONS OF WILD FISH</td>
<td>James Winton</td>
</tr>
<tr>
<td>9:45</td>
<td>6. BAT WHITE-NOSE SYNDROME: AN EMERGING FUNGAL PATHOGEN?</td>
<td>David S. Blehert</td>
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<tr>
<td>10:00</td>
<td>Break</td>
<td>Pre-function Area</td>
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**10:30 – 12:00 Contributed Papers: Wildlife – Domestic Animal – Human Interface**  
*Session Chair: Delores Gavier-Widen*

<table>
<thead>
<tr>
<th>Time</th>
<th>Paper Title</th>
<th>Speaker</th>
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<tbody>
<tr>
<td>10:30</td>
<td>7. ONE HEALTH</td>
<td>Tracee Treadwell</td>
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<tr>
<td>10:45</td>
<td>8. AN INFECTIOUS DISEASE MODEL FOR MOUNTAIN GORILLAS: EPIDEMIC AVOIDANCE BY POPULATION DISPERAL</td>
<td>Christopher Whittier</td>
</tr>
<tr>
<td>11:00</td>
<td>9. FARM VISITATION BY WHITE-TAILED DEER (<em>ODOCOILEUS VIRGINIANUS</em>): IMPLICATIONS FOR MITIGATION OF BOVINE TUBERCULOSIS TRANSMISSION</td>
<td>Ryan S. Miller</td>
</tr>
<tr>
<td>11:15</td>
<td>10. THE ROLE OF BATS IN LYSSAVIRUS EVOLUTION AND EMERGENCE: RABIES IN FLAGSTAFF, ARIZONA</td>
<td>Charles Rupprecht</td>
</tr>
<tr>
<td>11:30</td>
<td>11. CHANGES IN FEEDING GARDEN BIRDS IN ENGLAND WITH WIDESPREAD SALMONELLA INFECTION IN OTHER SPECIES VIA ENVIRONMENTAL CONTAMINATION</td>
<td>James Paul Duff</td>
</tr>
<tr>
<td>11:37</td>
<td>12. POULTRY BRED IN OPEN RANGE AND WILD WATERFOWL: ARE THE LIAISONS DANGEROUS?</td>
<td>Marc Artois</td>
</tr>
<tr>
<td>11:44</td>
<td>13. NECROPSY FINDINGS IN PERIURBAN WILD RODENTS (<em>SCIURUS CAROLINENSIS, TAMIASCIURUS HUDSONICUS, EUTAMIAS STRIATUS, MARMOTA MONAX</em>) IN ONTARIO, 1976-2009</td>
<td>Douglas Campbell</td>
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### 11:51 – 12:00

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>11:51</td>
<td>Lunch</td>
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<td></td>
<td>Garden Terrace Pavilion under the Tent</td>
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</table>

### 1:00 – 4:00 Contributed Papers: Marine/Aquatic Health

Session Chair: Frances Gulland

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<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Speaker</th>
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<tbody>
<tr>
<td>1:00</td>
<td>15. EVIDENCE OF MORBILLIVIRUS INFECTIONS IN SEA OTTERS IN WASHINGTON STATE</td>
<td>Nancy Thomas</td>
</tr>
<tr>
<td>1:15</td>
<td>16. THE ROLE OF WILDLIFE COLLECTION AND CARE IN OIL SPILL RESPONSE: THE COSCO BUSAN CASE STUDY</td>
<td>Michael Ziccardi</td>
</tr>
<tr>
<td>1:30</td>
<td>17. PERFLUOROOCTANESULFONATE (PFOS) AND PERFLUOROOCTANESULFONYLAMIDE (PFOSA) IN BOTTLENOSE DOLPHINS (TURSIOPS TRUNCATUS): AN INVESTIGATION INTO TWO UNUSUALLY HIGH MORTALITY EPIZOOTICS</td>
<td>Romona Haebler</td>
</tr>
<tr>
<td>1:45</td>
<td>18. CULTIVATION OF A HERPESVIRUS THAT PROBABLY CAUSES BENIGN GENITAL PLAQUES IN BOTTLENOSE DOLPHINS (TURSIOPS TRUNCATUS)</td>
<td>Thijs Kuiken</td>
</tr>
<tr>
<td>2:00</td>
<td>19. DISEASES AND WILDLIFE TRANSLOCATIONS: ENDANGERED LAYSAN DUCKS AS AN EXAMPLE</td>
<td>Thierry Work</td>
</tr>
<tr>
<td>2:15</td>
<td>20. IMPACT OF RANAVIRUS IN FINFISH IN THE MURRAY-DARLING BASIN RIVER SYSTEM OF AUSTRALIA</td>
<td>Richard Whittington</td>
</tr>
<tr>
<td>2:30</td>
<td>21. EMACIATION/MALNUTRITION SYNDROME IN STRANDED HARBOR SEAL PUPS FROM SAN JUAN COUNTY, WASHINGTON</td>
<td>Joe Gaydos</td>
</tr>
<tr>
<td>2:37</td>
<td>22. FEATHER-LOSS DISORDER IN CHICKS OF TWO SPHENISCUS PENGUIN SPECIES</td>
<td>Olivia Kane</td>
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<td>2:44</td>
<td>23. CRYPTOCOCCOSIS IN OREGON WILDLIFE</td>
<td>Rob Bildfell</td>
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<td>2:51</td>
<td>24. CHRONIC LYMPHOCYTIC LEUKEMIA IN A CAPTIVE FEMALE NORTHERN X</td>
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<tr>
<td>3:00</td>
<td>Break</td>
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</table>
| 3:30   | 25. UNUSUAL SOUTHERN RIGHT WHALE MORTALITY EVENTS AT PENINSULA VALDES, ARGENTINA  
       | Marcela Uhart                                                          |
| 3:45   | 26. HARMFUL ALGAL BLOOMS (HAB) IN THE ST. LAWRENCE ESTUARY (SLE): IMPLICATIONS FOR SPECIES AT RISK  
       | Lena Measures                                                           |
| 4:00   | AAWV Cutting Edge Speaker                                               |
| 4:45   | WDA 2010 Argentina! Marsela Uhart                                        |
| 5:30 – 7:00 | **WDA Poster Session, Student Poster Competition and Snappies**     |
|        | Semiahmoo Ballroom                                                     |
| 7:00 – 10:00 | **Picnic Beachside** (Volleyball, Bocce Ball, Kayaking)               |
| 9:30   | Nightly Beach Bonfire                                                  |
| 7:00   | Prayer Breakfast                                                       |
| 7:00   | Continental Breakfast                                                  |
| 8:00 – 5:00 | **Student Program – Kevin Keel Presiding**                            |
| 8:00 – 8:30 | **WDA Graduate Research Recognition Award Presentation**               |
|        | 28. INVASION ECOLOGY OF BLACKLEGGED TICKS AND LYME DISEASE IN THE MIDWESTERN UNITED STATES  
       | Sarah Hamer                                                            |
| 8:30 – 12:00 | **Terry Amundsen Student Oral Competition**                          |
| 8:30   | 29. MANIPULATIVE EXPERIMENTS EXPLORING TRANSMISSION OF A ZOOONOTIC PATHOGEN IN ITS HOST POPULATION  
<pre><code>   | Karoun H. Bagamian                                                    |
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<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Speaker</th>
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<tr>
<td>8:45</td>
<td>30. SEASONALITY AND SEX-STRUCTURE IN THE EPIDEMIOLOGY OF SIN NOMBRE VIRUS IN DEER MICE (P. MANICULATUS)</td>
<td>Sean Laverty</td>
</tr>
<tr>
<td>9:00</td>
<td>31. IMMUNOHISTOLOGICAL EVALUATION OF DEVIL FACIAL TUMOUR DISEASE AND IDENTIFICATION OF A BIOMARKER FOR DISEASE DIAGNOSIS</td>
<td>Cesar Tovar</td>
</tr>
<tr>
<td>9:15</td>
<td>32. MOLECULAR EPIDEMIOLOGY OF RABIES IN THE CENTRAL GREAT PLAINS: DO HOST ECOLOGY AND LANDSCAPE INFLUENCE VIRAL EMERGENCE?</td>
<td>Heather Barton</td>
</tr>
<tr>
<td>9:30</td>
<td>33. EFFECT OF AGE ON SHEDDING OF AVIAN INFLUENZA VIRUS IN MALLARDS (ANAS PLATYRHYNCHOS)</td>
<td>Taiana P. Costa</td>
</tr>
<tr>
<td>9:45</td>
<td>34. AVIAN INFLUENZA INFECTION DYNAMICS AMONG SHOREBIRD HOSTS AT THE DELAWARE BAY SPRING MIGRATION STOPOVER SITE</td>
<td>Angela M. Maxted</td>
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<tr>
<td>10:00</td>
<td>Break General Poster Session - Pre-function Area /Semiahmoo Ballroom</td>
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<td>10:30</td>
<td>35. EVALUATION OF CANADA GEESE (BRANTA CANADENSIS) AS SENTINELS FOR DETECTING LOCAL TRANSMISSION OF AVIAN INFLUENZA VIRUSES</td>
<td>Whitney Kistler</td>
</tr>
<tr>
<td>10:45</td>
<td>36. INVESTIGATION OF AN OUTBREAK OF BOVINE TUBERCULOSIS IN THE HOOK LAKE WOOD BISON RECOVERY PROJECT HERD</td>
<td>Chelsea Himsworth</td>
</tr>
<tr>
<td>11:00</td>
<td>37. SEX-SPECIFIC CONTACT RATES: POTENTIAL ROUTES OF DISEASE TRANSMISSION IN ELK (CERVUS ELAPHUS)</td>
<td>Eric Vander Wal</td>
</tr>
<tr>
<td>11:15</td>
<td>38. BRUCELLOSIS IN BARREN-GROUND CARIBOU ON SOUTHAMPTON ISLAND, NUNAVUT</td>
<td>Jane Harms</td>
</tr>
<tr>
<td>11:30</td>
<td>39. THE ELK BRUCELLOSIS TEST-AND-SLAUGHTER PROGRAM: DOES IT WORK?</td>
<td>Laura Meadows</td>
</tr>
<tr>
<td>11:45</td>
<td>40. CHARACTERIZATION OF MALIGNANT CATARRHAL FEVER VIRUSES IN TENNESSEE CERVID POPULATIONS UTILIZING REAL-TIME POLYMERASE CHAIN REACTION</td>
<td>Robin L. Cissell</td>
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<td>12:00</td>
<td>Lunch</td>
<td>Garden Terrace Pavilion under the Tent</td>
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<td>1:00</td>
<td>Terry Amundsen Student Oral Competition</td>
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<td>41. APPLICATION OF SPATIAL GENETIC ANALYSES TO REVEAL CORRELATIONS BETWEEN WHITE-TAILED DEER DISPERSEL AND CHRONIC WASTING DISEASE SPREAD IN WISCONSIN</td>
<td>Stacie J. Robinson</td>
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<tr>
<td>1:15</td>
<td>42. INFLUENCE OF BIOTIC AND ABIOTIC FACTORS ON MARINE MAMMAL STRANDINGS IN THE SAINT-LAWRENCE ESTUARY AND GULF OF ST. LAWRENCE (1994 TO 2008)</td>
<td>Marie-Hélène Truchon</td>
</tr>
<tr>
<td>1:30</td>
<td>43. PREVALENCE OF POTENTIALLY PATHOGENIC BACTERIA IN THE FECES OF STRANDED AND WILD HARBOR SEALS (PHOCA VITULINA) IN CENTRAL CALIFORNIA</td>
<td>Denise Greig</td>
</tr>
<tr>
<td>1:45</td>
<td>44. THE PHYSICAL EFFECTS OF CHEMICALLY AND PHYSICALLY DISPERSED OIL ON WILDLIFE</td>
<td>Rebecca Duerr</td>
</tr>
<tr>
<td>2:00</td>
<td>45. BREVETOXIN INDUCED MORBIDITY AND MORTALITY IN STRANDED SEA TURTLES AND SEA BIRDS IN FLORIDA</td>
<td>Deborah Fauquier</td>
</tr>
<tr>
<td>2:15</td>
<td>46. THE ECOLOGY OF ASPERGILLOSIS IN SEABIRDS: BRIDGING THE GAP BETWEEN ENVIRONMENT AND DISEASE VIA MICROSATELLITE ANALYSIS</td>
<td>Julia Burco</td>
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<td>2:30</td>
<td>47. EVIDENCE OF LEAD EXPOSURE IN A FREE-RANGING POPULATION OF KEA (NESTOR NOTABILIS)</td>
<td>Jennifer McLelland</td>
</tr>
<tr>
<td>2:45</td>
<td>48. BUILDING A BRIDGE BETWEEN SCIENCE AND SOCIETY: THE IMPLICATIONS OF SPENT LEAD FROM AMMUNITION</td>
<td>Luis Cruz-Martinez</td>
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<tr>
<td>3:00</td>
<td>Break</td>
<td>General Poster Session - Pre-function Area /Semiahmoo Ballroom</td>
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<tr>
<td>3:30</td>
<td>CYLICOSPIRURA SPECIES (NEMATODA: SPIROCERCIDAE) AND STOMACH NODULES IN COUGARS (PUMA CONCOLOR) AND BOBCATS (LYNX RUFUS) IN OREGON</td>
<td>Jayde A. Ferguson</td>
</tr>
<tr>
<td>3:45</td>
<td>49. SURVEY AND MOLECULAR SEQUENCING OF SARCOCYSTIS SPP. FROM SKELETAL MUSCLE OF FREE-RANGING FISHERS FROM PENNSYLVANIA</td>
<td>Jayde A. Ferguson</td>
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Richard Gerhold

4:00  51. NICHE PARTITIONING AND SEASONALITY OF TICKS IN FREE RANGING AFRICAN BUFFALO (SYNCERCUS CAFFER)
      Kadie Anderson

4:15  52. THE ROLE OF NATURAL ANTIBIOTICS IN IMMUNOLOGICAL PROTECTION OF ALTRICIAL YOUNG OF THE AUSTRALIAN PLATYPUS (ORNITHORHYNCHUS ANATINUS)
      Camilla Whittington

4:30  53. MICROSATELLITE MARKERS DEVELOPED FOR THE STUDY OF LEPROSY IN NINE-BANDED ARMADILLOS
      Leah Chinchilla

4:45  54. THE POTENTIAL ROLE OF COLLARED PECCARIES IN THE TRANSMISSION OF INFLUENZA A VIRUSES
      Paul Oesterle

5:00  Wrap-up comments - Kevin Keel

6:00 – 7:00  AAWV Business Meeting  San Juan – Lopez Pender Room

6:00 - 7:00  CAZVW Business Meeting  San Juan – Salt Spring Saturna Room

7:00 – 10:00  WDA Auction  Semiahmoo Ballroom

9:30  Nightly Beach Bonfire

WEDNESDAY August 5, 2009

7:00  Continental Breakfast  Pre-function Area

8:00 - 1:00  Contributed Papers: Disease Ecology: International and Special Topics  Session Chair: Richard Whittington

8:00  55. CONSUMPTION OF BAITS CONTAINING RACCOONPOX-BASED PLAGUE VACCINES PROTECTS PRAIRIE DOGS AGAINST PLAGUE INFECTION
      Tonie E. Rocke

8:15  56. SALMONELLA IN RACCOONS (PROCYON LOTOR) IN ONTARIO, CANADA
      Claire Jardine

8:30  57. A NETWORK MODEL OF DISEASE RISK ALONG A GRADIENT IN RESERVOIR HOST BIODIVERSITY
      Christopher Brooks
### 8:45
58. HISTOPATHOLOGICAL AND EPIZOOTIOLOGICAL INVESTIGATIONS ON IDIOPATHIC CARDIOMYOPATHY IN FREE-RANGING EURASIAN LYNX (LYNX LYNX) FROM SWITZERLAND
Marie-Pierre Ryser-Degiorgis

### 9:00
59. EPIDEMIOLOGY OF HPAI IN WILD BIRDS IN MONGOLIA
Damien Joly

### 9:15
60. IMMUNIZATION OF TASMANIAN DEVILS AGAINST DEVIL FACIAL TUMOUR DISEASE TUMOUR CELLS
Alexandre Kreiss

### 9:30
61. INVESTIGATION OF WILD AND FERAL CARNIVORES AS RESEVOIRS OF ALEUTIAN DISEASE VIRUS
Mark Drew

### 9:45
62. EBOLA IN GREAT APES IN NORTHERN CONGO: AN UPDATE FROM THE FIELD
Kenneth Cameron

### 9:52
63. EXCHANGE OF GASTRO-INTESTINAL HELMINTH SPECIES AMONG FOUR SPECIES OF KANGAROOS AND WALLABIES IN WESTERN VICTORIA, AUSTRALIA
Ian Beveridge

### 9:59
64. ARE PYRENEAN CHAMOIS INFECTED WITH BORDER DISEASE VIRUS PERSISTENTLY INFECTED ANIMALS?
Ignasi Marco

### 10:06
65. WILDLIFE DISEASES OF CONCERN IN CHINA
Hongxuan He

### 10:15 – 10:45
**Break**

### 10:45 – 12:15
**Contributed Papers: Toxicological Effects of Metals and Poisons on Wildlife**

**Session Chair: Åsa Fahlman**

#### 10:45
66. LEAD OBJECTS INGESTED BY COMMON LOONS IN NEW ENGLAND
Mark Pokras

#### 11:00
67. HEAVY METALS AND ORGANIC CONTAMINANTS: SILENT KILLERS OF MIGRATORY WATERFOWL IN LATIN AMERICA
Alonso Aguirre

#### 11:15
68. SOURCES OF LEAD AND RECOMMENDATIONS TO REDUCE EXPOSURES IN WASHINGTON STATE
Holly Davies
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| 11:30 | 69. EFFECTS OF ENVIRONMENTAL METHYLMercury EXPOSURE ON REPRODUCTION IN WHITE IBISES (EUDOCIMUS ALBUS)  
Nilmini Jayasena                                      |
| 11:45 | 70. THE EFFECT OF BRODIFACOUM ON JAPANESE QUAIL (COTURNIX JAPONICA) COAGULATION: A MODEL FOR ASSESSMENT OF EXPOSURE IN WILD BIRDS  
Kendal Elizabeth Harr                                    |
| 12:00 | 71. BIOCHEMISTRY RESULTS OF BLOOD SAMPLES OF ORYX AND GAZELLES SHOW INCREASING CARDIAC AND LIVER PROFILE ENZYMES  
Saud Anajariyya                                              |
| 12:07 | 72. INTOXICATION OF NONTARGET WILDLIFE WITH RODENTICIDES IN NORTHWESTERN KANSAS  
Mark Ruder                                                   |
| 12:45 | **Box Lunch: Excursions or On-Your-Own tours & hikes**  
Buses leave for field trips (Lobby Pickup / Drop-off Area) |
| 7:00 - 9:00 | **Student-only mixer on the beach**                                          |
| 7:00 – 9ish | WDA Council Meeting Continued  
Victoria Room                                           |
| 9:30  | Nightly Beach Bonfire                                                             |
|       | **THURSDAY, August 6, 2009**                                                       |
| 6:00  | Inaugural Polar Bear Club Challenge  
Beachside                                                  |
| 7:00  | Continental Breakfast  
Pre-function Area                                           |
| 8:00 – 9:40 | **Contributed Papers: Topics in Avian Disease Ecology**  
Session Chair: J. Paul Duff |
8:45  76. ECOLOGICAL CORRELATES OF BUGGY CREEK VIRUS INFECTION IN HOUSE SPARROW NESTLINGS
       Valerie A. O'Brien

9:00  77. VOLATILE COMPONENTS OF UROPYGIAL SECRETIONS IN THE GRAY CATBIRD (DUMETELLA CAROLINENSIS)
       Mary Garvin

9:07  78. LYMPHOPROLIFERATIVE DISEASE VIRUS IN A WILD TURKEY IN SOUTHERN ARKANSAS
       Andrew Cartoceti

9:14  79. REOVIRUS-ASSOCIATED NECROTIZING ENTERITIS IN AMERICAN CROWS
       Carol Meteyer

9:21  80. PATHOGENS OF GREATER SAGE-GROUSE (CENTROCERCUS UROPHASIANUS)
       Cheryl A. Mandich

9:28  81. URBANIZATION EFFECTS ON PARASITIC INFECTIONS IN SONG BIRDS
       Carin Williams

9:35  82. RANGE EXPANSION OF ALCATAENIA LONGICERVICA (EUCESTODA: DILEPIDIDAE) COMPLEMENT CHANGES IN THE FEEDING ECOLOGY OF MURRES (ALCIDAE: URIA SPP.)
       Sabir Bin Muzaffar

9:42  Break

10:00 – 12:00 Contributed Papers Disease Ecology – Disease Ecology I
       Session Chair: Jordan Mencher

10:00 83. HEALTH EVALUATION OF KELP GULLS (LARUS DOMINICANUS) AT THE BAY OF TALCAHUANO, CHILE
       Daniel González-Acuña

10:07 84. KEY PLAYERS IN HUMAN RABIES EXPOSURE AND THE ROLE OF STRIPED SKUNKS IN KANSAS
       Claudia Ganser

10:14 85. AN OVERVIEW AND UPDATE OF “HAIR-LOSS SYNDROME” CAUSED BY EXOTIC LICE IN WASHINGTON DEER
       Kristin Mansfield

10:25 86. SOCIETY, WILDLIFE DISEASE AND WILDLIFE CONSERVATION: OXYMORON OR EVOLUTIONARY SIBLINGS
       Milt Friend
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<tr>
<td>11:00</td>
<td>WDA Business Meeting (open to all registrants)</td>
<td>Semiahmoo Ballroom</td>
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<td>12:00</td>
<td>Lunch</td>
<td>Garden Terrace Pavilion under the Tent</td>
</tr>
<tr>
<td>1:00</td>
<td>Contributed Papers: Topics in Ungulate Disease Ecology</td>
<td>Semiahmoo Ballroom</td>
</tr>
<tr>
<td>1:00</td>
<td>87. A COMPARISON OF POTENTIAL PATHOGENS FROM SYMPATRIC BIGHORN SHEEP, DOMESTIC SHEEP AND MULE DEER DURING A BIGHORN SHEEP DIE-OFF IN WEST-CENTRAL MONTANA</td>
<td>Neil Anderson</td>
</tr>
<tr>
<td>1:15</td>
<td>88. WILDLIFE DISEASE IN THE AGE OF METAGENOMICS</td>
<td>Mary Poss</td>
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<tr>
<td>1:30</td>
<td>89. PATHOGENICITY OF EPIZOOTIC HEMORRHAGIC DISEASE VIRUS SEROTYPE 6 IN WHITE-TAILED DEER</td>
<td>Elizabeth Howerth</td>
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<td>1:45</td>
<td>90. WHITE-TAILED DEER CARCASS DECOMPOSITION AND POTENTIAL EXPOSURE OF SCAVENGERS TO CHRONIC WASTING DISEASE IN WISCONSIN</td>
<td>Christopher Janelle</td>
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<tr>
<td>2:00</td>
<td>91. SOCIALLY FACILITATED TRANSMISSION OF CHRONIC WASTING DISEASE AMONG FEMALE WHITE-TAILED DEER</td>
<td>Michael Samuel</td>
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<tr>
<td>2:15</td>
<td>92. BRUCELLOSIS IN WYOMING NON-FEEDGROUND ELK: CHALLENGING DOGMA</td>
<td>Hank Edwards</td>
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<tr>
<td>2:30</td>
<td>93. ADAPTIVE MANAGEMENT TO REDUCE BRUCELLOSIS TRANSMISSION RISK AMONG ELK ATTENDING SUPPLEMENTAL FEEDGROUNDS IN WYOMING</td>
<td>Brandon Scurlock</td>
</tr>
<tr>
<td>2:45</td>
<td>94. DETECTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX IN SWABS AND FECES FROM BCG-VACCINATED AND M. BOVIS-CHALLENGED WHITE-TAILED DEER AND THEIR ENVIRONMENT USING POLYMERASE CHAIN REACTION</td>
<td>Pauline Nol</td>
</tr>
<tr>
<td>2:52</td>
<td>95. A SERIES OF CRANIAL OSTEOCHONDROMAS IN FIVE FREE-RANGING WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS)</td>
<td>Kevin Keel</td>
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<tr>
<td>3:00</td>
<td>Break</td>
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### 3:30 – 5:00 Contributed Papers: Tools and Techniques I

**Session Chair: Rob Bildfell**

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<tr>
<td>3:30</td>
<td>96. ANALYSIS OF CARFENTANIL-XYL AZINE IMMobilization in Captive Elk by Bispectral Index</td>
<td>Terry Kreeger</td>
</tr>
<tr>
<td>4:00</td>
<td>98. Rift Valley Fever: An Exercise to Evaluate the State and Federal Response to a Hypothetical Introduction of the Disease into Florida</td>
<td>Paul Gibbs</td>
</tr>
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<td>4:15</td>
<td>99. Passive Surveillance as a Tool for Investigating Patterns of Disease in Wild Raccoons</td>
<td>Ian Barker</td>
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<td>4:30</td>
<td>100. The Role of the Redwood Chipmunk (<em>Tamias oregonensis</em>) in the Ecological Maintenance of <em>Anaplasma phagocytophilum</em></td>
<td>Nathan Nieto</td>
</tr>
<tr>
<td>4:45</td>
<td>101. We Have All of These Samples, Now What?</td>
<td>Laurie A. Baeten</td>
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</tbody>
</table>

**6:00 – 7:00 Pre-Banquet Mixer**  
**Pre-function Area**

**7:00 – 10:00 WDA Banquet and Awards**  
**Semiahmoo Ballroom**

**9:30**  
**Nightly Beach Bonfire**

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### FRIDAY August 7, 2009

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<td>7:00</td>
<td>Continental Breakfast</td>
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**8:00 – 8:30 Contributed Papers: Disease Ecology II**

**Session Chair: Felicia Nutter**

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<th>Time</th>
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<tr>
<td>8:00</td>
<td>102. Hypophosphatemia and Associated Rickets in Hand-Reared Moose (<em>Alces alces</em>) Calves in Alaska</td>
<td>Kimberlee Beckmen</td>
</tr>
<tr>
<td>8:15</td>
<td>103. White-Nose Syndrome in Bats: Threat Management and Conservation Parallels to Amphibian Chytridiomycosis</td>
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</table>
### 8:45-10:00 Contributed Papers: Avian Influenza

**Session Chair:** Thijs Kuiken

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<tr>
<td>8:30</td>
<td>104. FARM-SIDE RISK ASSESSMENT FOR AVIAN INFLUENZA VIRUS TRANSMISSION: EXPERIMENTAL INFECTION OF PERIDOMESTIC PASSERINES WITH LOW PATHOGENICITY AVIAN INFLUENZA VIRUS (LPAIV)</td>
<td>Nicole Nemeth</td>
</tr>
<tr>
<td>8:45</td>
<td>105. AVIAN INFLUENZA VIRUS PERSISTENCE IN FILTERED WATER FROM WATERFOWL HABITATS IN GEORGIA</td>
<td>Shamus P. Keeler</td>
</tr>
<tr>
<td>9:00</td>
<td>106. THE “HUMAN INFLUENZA RECEPTOR” NEU5ACA2,6GAL IS WIDELY EXPRESSED AMONG DIFFERENT TAXA OF WILD BIRDS</td>
<td>Elsa Jourdain</td>
</tr>
<tr>
<td>9:15</td>
<td>107. SHEDDING LIGHT ON LOW-PATHOGENIC AVIAN INFLUENZA VIRUS INFECTION OF MALLARDS: IMPACT OF VIRAL SHEDDING CHARACTERISTICS ON SURVEILLANCE AND RESEARCH</td>
<td>Kaci K. VanDalen</td>
</tr>
<tr>
<td>9:30</td>
<td>108. EVALUATION OF AN EPITOPE-BLOCKING ENZYME-LINKED IMMUNOSORBENT ASSAY FOR THE DETECTION OF ANTIBODIES TO INFLUENZA A VIRUS IN DOMESTIC AND WILD AVIAN AND MAMMALIAN SPECIES</td>
<td>Heather Sullivan</td>
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<td>9:45</td>
<td>109. SURVEILLANCE FOR AVIAN INFLUENZA IN WILD BIRDS IN RUSSIA, GREENLAND, AND MEXICO</td>
<td>John A. Baroch</td>
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<td>10:00</td>
<td><strong>Break</strong></td>
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### 10:30-11:45 Contributed Papers: Tools and Techniques II

**Session Chair:** Peregrine Wolff

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<td>110. HOST SELECTION BY CULEX PIPiens MOSQUITOES AND WEST NILE VIRUS AMPLIFICATION</td>
<td>Gabriel Hamer</td>
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<td>10:45</td>
<td>111. FIELD EVALUATION OF THE FLUORESCENCE POLARIZATION ASSAY FOR USE IN DIAGNOSING BRUCELLA ABORTUS INFECTIONS IN BISON IN THE GREATER YELLOWSTONE AREA</td>
<td>Brant Schumaker</td>
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<tr>
<td>Time</td>
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<tr>
<td>10:52</td>
<td>112. CYTOKINE GENE EXPRESSION FOLLOWING BCG VACCINATION AND <em>MYCOBACTERIUM BOVIS</em> CHALLENGE IN THE EURASIAN BADGER (<em>MELES MELES</em>)</td>
<td>Roland Ashford</td>
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<td>10:59</td>
<td>113. MEASURING METACARPAL CORTICAL BONE MASS IN FREE-RANGING BLACK BEARS (<em>URSUS AMERICANUS</em>) USING PORTABLE RADIOGRAPHY</td>
<td>Rita Seger</td>
</tr>
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<td>11:06</td>
<td>114. RESULTS OF WASHING OILED SEA OTTERS: OLIVE OIL AND OTHER PHENOMENA</td>
<td>David Jessup</td>
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<tr>
<td>11:30</td>
<td><strong>Closing Comments - Safe Travels!</strong></td>
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<td><strong>WILDLIFE – DOMESTIC ANIMAL - HUMAN INTERFACE</strong>&lt;br&gt;Chair: Dolores Gavier-Widén, Sweden</td>
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<td><strong>TOOLS AND TECHNIQUES I</strong>&lt;br&gt;Chair: Rob Bildfell, USA</td>
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<td><strong>AVIAN INFLUENZA</strong>&lt;br&gt;Chair: Thijs Kuiken, The Netherlands</td>
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<td>[104 – 109]</td>
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GENERAL SESSION POSTERS
Chair: Felicia Nutter, USA...............pg. 139–178..............................[P1 – 40]
## PRESENTATION SCHEDULE FOR POSTERS

### Student Poster Session
**Tuesday 5:30 – 7:00P**

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<td>Samantha E. Allen</td>
<td>[SP 1] Antimicrobial Resistance in Generic <em>Escherichia coli</em> isolated from wildlife living in rural, urban, and natural environments</td>
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<td>Amanda J. Cyr</td>
<td>[SP 2] Comparison of Nobuto Strips and Serum to Detect Exposure to Canine Distemper and Parvoviruses in Wisconsin Carnivores</td>
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<td>Pamela J. Ferro</td>
<td>[SP 3] Phylogenetic Analysis of the Nonstructural (NS) Gene of Avian Influenza Viruses Isolated from Hunter-Harvested Waterfowl, Texas Coast</td>
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<td>Amanda M. Fluegel</td>
<td>[SP 4] Quantification of Cytokine mRNA and Expression Patterns in Brucellosis Infected Elk</td>
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<td>Richard W. Gerhold</td>
<td>[SP 5] Trichomonosis Outbreak in Passerines in the Southeastern United States</td>
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<tr>
<td>Richard W. Gerhold</td>
<td>[SP 6] Identification, Distribution, and Cross-Species Transmission of <em>Eimeria</em> Spp. in Captive-Raised Game Birds in the United States</td>
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<td>Maëlle Gouix</td>
<td>[SP 7] Verminous Pneumonia in the Threatened St. Lawrence Estuary Beluga Population</td>
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<td>N. Jane Harms</td>
<td>[SP 8] Tree Swallows (<em>Tachycineta Bicolor</em>) on Reclaimed Wetlands in the Athabasca Oil Sands: An Indicator for Reclamation Success?</td>
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<td>Chelsea Himsworth</td>
<td>[SP 9] Poxvirus Infection in an American Red Squirrel (<em>Tamiasciurus Hudsonicus</em>) from Northwestern Canada</td>
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<td>Chelsea Himsworth</td>
<td>[SP 10] Pathology and Epidemiology of Phocid Herpesvirus-1 Infections in Wild and Rehabilitating Harbour Seals (<em>Phoca Vitulina</em>) in the Northeastern Pacific</td>
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Jeffrey M. Lorch  [SP12] A PCR METHOD FOR DETECTING THE WHITE-NOSE SYNDROME-ASSOCIATED GEOMYCES SP. FUNGUS ON THE SKIN OF BATS


Paul T. Oesterle  [SP 14] THE EFFECTS OF BLOOD ON AVIAN INFLUENZA VIRUS DETECTION BY RT-PCR

Alexandra Reid,  [SP 15] PLASMA PATTERN RECOGNITION RECEPTORS IN WALLEYE (SANDER VITREUS)

Mark G. Ruder  [SP 16] ASSOCIATION OF MYCOPLASMA COROGYPSI AND POLYARTHRITIS IN FREE-RANGING BLACK VULTURES (CORAGYPS ATRATUS) IN VIRGINIA

Brant A. Schumaker  [SP 17] A RISK ANALYSIS OF BRUCELLA TRANSMISSION AMONG BISON, ELK, AND CATTLE IN THE NORTHERN GREATER YELLOWSTONE AREA

Melanie L. Smith  [SP 18] BLOOD CHEMISTRY LEVELS OF FREE-RANGING AND CAPTIVE WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS) IN TEXAS

General Poster Session
Tuesday 10:00 – 10:30 & 3:00 – 3:30

Erik O. Ågren  [P 1] ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY (ARVC)-LIKE DISEASE IN A RED FOX (VULPES VULPES)

Timothy P. Algeo  [P 2] ASSESSING ORV BAiT UPTAKE BY RACCOONS WITH TETRACYCLINE BIOMARKERS: IS DEPOSITION EQUAL WITHIN AND BETWEEN TISSUE TYPES?

Tom Bailey  [P 3] OBSERVATIONS ON FOOT AND MOUTH DISEASE IN VACCINATED AND UNVACCINATED WILDLIFE IN THE UNITED ARAB EMIRATES

Jeremiah Bautista  [P 4] POSSIBLE BIOINDICATORS OF POLLUTION EXPOSURE IN PARALABRAX NEBULIFER FROM LONG BEACH HARBOR, SOUTHERN CALIFORNIA

Holly M. Brown  [P 5] IDENTIFICATION AND GENETIC CHARACTERIZATION OF CYTAUXZOON FELIS FROM BOBCATS (LYNX RUFUS) AND DOMESTIC CATS (FELIS CATUS)
Justin D. Brown  [P 6] TWO OUTBREAKS OF CANINE PARVOVIRAL ENTERITIS IN RACCOONS (PROCYON LOTOR) IN THE SOUTHEASTERN UNITED STATES

Ignasi Marco  [P 7] EXPERIMENTAL INFECTION IN LAMBS WITH A BORDER DISEASE VIRUS (BDV) ISOLATED FROM PYRENEAN CHAMOIS (RUPICAPRA PYRENAICA)

Amy Kuenzi  [P 8] WHEN IS ENOUGH SAMPLING ENOUGH? POPULATION DYNAMICS AND ZOONOTIC INFECTIOUS DISEASE: THE CASE OF DEER MICE (PEROMYSCUS MANICULATUS) AND SIN NOMBRE VIRUS

Kimberlee Beckmen  [P 9] CHEMISTRY REFERENCE RANGES IN A CAPTIVE HERD OF WOOD BISON (BISON BISON ATHABASCAE)

Mark Drew  [P 10] OCCURRENCE OF MYCOPLASMA ARGININI IN BIGHORN SHEEP (OVIS CANADENSIS) IN CENTRAL IDAHO


Rebecca Dunne  [P 13] SUCCESSFUL TREATMENT OF A CANADA GOOSE (BRANTA CANADENSIS) WITH PRESUMED CAPTURE MYOPATHY

Alan M. Fedynich  [P 14] ASSESSING LEAD SHOT INGESTION IN GREEN-WINGED TEAL AND NORTHERN SHOVELERS

Daniel González-Acuña  [P15] HELMINTHS AND ECTOPARASITES OF BLACK NECKED SWAN (CYGNUS MELANOCORYPHUS MOLINA, 1872) IN CHILE

Sonya Gowtage  [P 16] THE DEVELOPMENT OF A BAIT FOR THE DELIVERY OF AN ORAL BCG VACCINE FORMULATION AGAINST BOVINE TUBERCULOSIS (MYCOBACTERIUM BOVIS) TO WILD BADGERS (MELES MELES)

Kristin Mansfield  [P 17] SEVERE HOOF DEFORMITIES IN FREE-RANGING ELK IN WESTERN WASHINGTON

Kristen Holt  [P 18] UTILIZING REAL-TIME PCR TO DETECT BORRELLIA BURGDORFERI INFECTION IN IXODES PACIFICUS
Elsa Jourdain  [P 19] EXPERIMENTAL INFECTION OF MALLARDS \textit{(ANAS PLATYRHYNCHOS)} WITH LOW-PATHOGENIC INFLUENZA VIRUSES: SUCCESSIVE CHALLENGES WITH HOMOLOGOUS AND HETEROLOGOUS SUBTYPES

Gretchen Kaufman  [P 20] INTERDISCIPLINARY MASTER OF SCIENCE DEGREE PROGRAM IN CONSERVATION MEDICINE

M. Kevin Keel  [P 21] CHRONIC WASTING DISEASE IN AN ISOLATED OUTBREAK WITH LOW PREVALENCE: ASCENDING THE SLIPPERY SLOPES OF AN EPIDEMIC CURVE IN WEST VIRGINIA

Dyanna M. Lambourn  [P 22] IDENTIFICATION OF MULTIPLE SPECIES APICOMPLEXAN PROTOZOAN MENINGOEENCEPHALITIS IN HARBOR SEALS \textit{(PHOCA VITULINA)} OF THE PACIFIC NORTHWEST

Raphaela Stimmelmayr  [P 23] IN-WATER SURVEY OF INJURIES IN HAWKSBILL \textit{(ERETMOCHELYS IMBRICATA)} AND GREEN TURTLES \textit{(CHELONIA MYDAS)} IN THE MARINE ENVIRONMENT OF ST. KITTS, LESSER ANTILLES

Hae Rim Lee  [P 24] SURVEY OF AVIAN PARAMYXOVIRUS INFECTIONS IN WILD WATERFOWL IN KOREA

Kimberlee Beckmen  [P 25] CHARACTERIZATION OF TEMPORAL AND SPATIAL DISTRIBUTION OF VIRUSES IN MOOSE AND CARIBOU THROUGHOUT ALASKA

David R. Marks  [P 26] AN EMERGENCY RESPONSE TO THE DETECTION OF PSEUDORABIES IN MICHIGAN USING THE INCIDENT COMMAND SYSTEM (ICS)

Nicole Nemeth  [P 27] CLINICAL AND PATHOLOGICAL ASSESSMENT OF WEST NILE VIRUS INFECTION IN THE AMERICAN \textit{(CORVUS BRACHYRHYNCHOS)} AND FISH CROW \textit{(C. OSSIFRAGUS)}

Sophia Papageorgiou  [P 28] FIRST REPORT OF A SUITE OF TICK-BORNE INFECTIONS IDENTIFIED IN MONGOLIAN REINDEER \textit{(RANGIFER TARANDUS)}

Nader Pestehchian  [P 29] HELMINTH PARASITES OF ANATIDAE IN IRAN

Nader Pestehchian  [P 30] HELMINTH PARASITES OF STRAY DOGS FROM THE ISFAHAM REGION OF IRAN

Stephen Raverty  [P 31] ABDOMINAL TELEMETRY IMPLANT DISPLACEMENT AND LOSS OF A VANCOUVER ISLAND MARMOT \textit{(MARMOTA VANCOUVERERNSIS)}
Stephen Raverty  [P 32] PUTATIVE HERPESVIRAL ULCERATIVE ESOPHAGITIS IN A STRANDED YEARLING HARBOUR PORPOISE (*PHOCEONA PHOCEONA*) FROM BRITISH COLUMBIA, CANADA

Michael J. Yabsley  [P 33] INFECTION DYNAMICS OF TWO NORTH AMERICAN *TRYPANOSOMA CRUZI* RESERVOIRS (*PROCYN LOTOR* AND *DIDELPHIS VIRGINIANA*) WITH GENETICALLY DISTINCT ISOLATES OF THE PARASITE

Jeff Root  [P34] LONGITUDINAL ANTIBODY RESPONSES OF RACCOONS NATURALLY EXPOSED TO MULTIPLE SUB-TYPES OF INFLUENZA A VIRUS

Rita L. Seger  [P 35] CALCITRIOL IS PRODUCED DURING URSINE HIBERNATION DESPITE PROLONGED ANURIA

Heong-Wha Shin  [P 36] WATERBIRD MORTALITY FROM BOTULISM TYPE C IN NAMDONG WATER RESERVOIRS

Kristy Pabilonia  [P 37] CHARACTERIZATION OF UPLAND GAMEBIRD FACILITIES IN THE UNITED STATES: POTENTIAL FOR HUMAN AND WILD AND DOMESTIC BIRD INTERACTIONS

Marco Ignasi  [P 38] OUTBREAK OF SEPTICEMIC SALMONELLOSIS CAUSED BY *SALMONELLA HESSAREK* IN MIGRATING SONG THRUSHES (*TURDUS PHILOMELOS*)

Elizabeth A. Wheeler  [P 39] STAGES OF FETAL DEVELOPMENT IN CALIFORNIA SEA LIONS (*ZALOPHUS CALIFORNIANUS*)

Michael J. Yabsley  [P 40] DESCRIPTION OF NOVEL *BABESIA* SPECIES AND ASSOCIATED LESIONS FROM COMMON MURRES (*URIA AALGE*) FROM CALIFORNIA
1. KILLER FOAM: LARGE MARINE BIRD STRANDING EVENT DUE TO HARMFUL ALGAL BLOOM PRODUCING NOVEL PROTEIN SURFACTANT

David A. Jessup, Melissa Miller, Hannah Nevins, California Department of Fish and Game, MWVCRC, 1451 Shaffer Rd., Santa Cruz, CA 95060, USA; Raphael Kudela, Ocean Sciences Department, University of California-Santa Cruz, Santa Cruz, CA 95060, USA

Presenting author: Jessup, David

Summary: A novel type of harmful algal bloom (HAB), one that kills marine birds by producing a surfactant foam that destroys waterproofing, has been identified and characterized.

In November 2007, a series of beaching events involving more than 500 marine birds of various species occurred within Monterey Bay over approximately 3 weeks. This event was variously blamed on the aerial spraying of a pheromone product for light brown apple moth (LBAM), a hypothesized spill of non-petroleum oil, and/or a massive red tide event that occurred in Monterey Bay during the same time period. Affected birds presented with wet feathers and were weak and hypothermic, some had a linseed oil-like smell. Scant, slimy pale yellow-green fluid could be wiped off the feathers of affected birds on presentation, but it dried out with time. The birds beached in 3 distinct pulses that corresponded temporally with the presence of a large dinoflagellate bloom just offshore. Upon washing, rehydration, warming, and nutritional supplementation, many affected birds recovered, suggesting that the product was minimally toxic or nontoxic. Using GCMS, LCMS, UV spectroscopy, algal culture, pathology, feather exposure experiments other methods the event was ultimately traced to the dominant dinoflagellate in the red tide, _Akashiwo sanguinea_. During breakdown this organism elicited large quantities of a protein dimer of the same composition and molecular weight as protein recovered from feathers of affected birds, but was not present on unaffected birds. Wave action and agitation of the affected waters produced surface foam and scum that when spread on normal feathers, acted as an effective wetting agent. Although the protein was relatively easy to clean off the birds using modified oil spill procedures, the event occurred just following seasonal migration of many species from the arctic. It affected about 10% of northern fulmars (_Fulmarus glacialis_) arriving in Monterey Bay; of which approximately half died. Significant mortality in surf scoters (_Melanitta perspicillata_) and Clark’s (_Aechmorhopus clarkii_) and western grebe (_Aechmorhopus occidentalis_) added to large numbers of these species killed by the Cosco Busan oil spill which occurred 125 miles north in San Francisco Bay concurrently. _Akashiwo sanguinea_ blooms forming a proteinaceous material similar to that found in the 2007 event have been previously linked to a coral bleaching event. This is the first report of an ostensibly non-toxic, but harmful algal bloom (HAB) caused by a dinoflagellate surfactant protein impacting marine birds.

Acknowledgements: Staff and volunteers associated with Monterey SPCA, Monterey Bay Aquarium, University of California - Santa Cruz, Native Animal Rescue, the Oiled Wildlife Care Network, University of California-Davis: Wildlife Health Center, Monterey Bay Aquarium Research Institute and other agencies and organizations made this research and recovery effort possible.
2. SHIPWRECKS LEAD TO UNHEALTHY CORAL REEFS: A CASE STUDY
AT PALMYRA ATOLL NWR

Thierry M. Work, U. S. Geological Survey-National Wildlife Health Center, Honolulu Field Station, PO Box 50167, Honolulu, HI 96850, USA; Greta S. Aeby, University of Hawaii, Hawaii Institute of Marine Biology, PO Box 1346, Kaneohe, HI 96744, USA; James E. Maragos, U. S. Fish & Wildlife Service, Pacific Islands Refuges, PO Box 50167, Honolulu, HI 96850, USA

Presenting author: Work, Thierry

Summary: We documented the presence of an invasive cnidarian associated with a shipwreck at Palmyra Atoll that has the potential of wiping out a major portion of the reef in this important wildlife refuge.

Coral reefs can undergo relatively rapid changes in the dominant biota, a phenomenon referred to as phase shift. Various reasons have been proposed to explain this phenomenon; however, pinpointing the actual factors responsible can be problematic. In the course of doing coral disease surveys at Palmyra, we discovered an invasive cnidarian associated with a shipwreck. Systematic surveys were done to document the extent of the invasion and consisted of diver tows, underwater transects, quadrat counts, and sampling of corals for histopathology. We documented an invasive cnidarian (Rhodactis howesii) to be unambiguously associated with man-made structures at Palmyra. Currently, two square km of reef are occupied with an estimated total of 141,000,000 organisms. This is the first time that a phase shift in a coral reef has been unambiguously associated with man-made structures. If the invasion continues on its current course, the entire western shelf of Palmyra risks losing its coral biota. Options being considered by the USFWS to deal with this will be costly and labor-intensive thereby highlighting the importance of dealing with such issues earlier than later.
3. LANDSCAPE EPIDEMIOLOGY IN A CHANGING ENVIRONMENT: THE INFLUENCE OF LAND USE PATTERNS AND VIRAL PROPERTIES ON THE EMERGENCE OF RABIES

Samantha M. Wisely, Sarah Bowe, Division of Biology, Kansas State University, Manhattan, KS 66506, USA; Ali Sydney, Philip Schumm, Caterina Scoglio, Dept. of Electrical and Computer Engineering, Kansas State University, Manhattan, KS 66506, USA

Presenting author: Wisely, Samantha

Summary: In model simulations, land use practices and viral latency influenced the successful emergence and duration of rabies emergence on the landscape.

In the Great Plains, exurbanization, the migration of urban residents to rural environments, provides new habitat niches for zoonotic diseases. We used striped skunk (Mephitis mephitis) movement data, and previously published data on rabies etiology to parameterize and construct an individual-based, dynamic contact network. We predicted the spread of rabies by varying parameters in two ways: 1) the habitat configuration at the entry point of the disease into the ecosystem, 2) the mean and variance of the incubation period. We simulated spatial heterogeneity by varying host density across habitat types found on the Upper Kansas River watershed. Individuals were represented as nodes which were connected in a probabilistic manner based on proximity. We used a Susceptible, Exposed, Infected (SEI) model of transmission. We varied the duration and distribution of time individuals spent in the exposed category. The virus propagated faster and further in a matrix of forest and grassland than in agriculture and grassland. Although exurban habitat composed only a fraction of the available habitat, >90% was used by rabies to spread. Higher variability in incubation time increased persistence of the rabies virus on the landscape. This model provided insights into the mechanisms of epidemiology in rabies. Long incubation periods of even a few individuals allowed for maintenance on the landscape. Forest, exurban, and urban habitats provided disease highways along which rabies could spread. The increased exurbanization of the Great Plains is projected to increase woody habitats via fire suppression. The increase of forested habitats in the urban and exurban matrix is therefore forecasted to enhance the spread of zoonotic disease.
4. EMERGENCE OF TICK-BORNE DISEASE ASSOCIATED WITH BIODIVERSITY AND FOREST CHANGE IN THE WESTERN US

Janet E. Foley and Nathan Nieto, UC Davis, Vet Med & Epi, Davis CA 95616, USA; Patrick Foley, California State University Sacramento Biological Sciences, Sacramento CA 95819, USA

Presenting author: Foley, Janet

Summary: Emerging tick-borne disease is associated with high biodiversity in small mammal and vegetation communities and mature second-growth forest.

An important ecosystem service of intact forests is protection from emerging infectious diseases. The tick-transmitted disease granulocytic anaplasmosis overlaps in ecology with Lyme disease in the western US, and both occupy forest that is increasingly structured into a patchwork of old, newly modified, and maturing second-growth. We hypothesized that areas of second-growth succession would have an increase in tick and rodent abundance as community structure is reassembled, facilitating emergence of anaplasmosis. We evaluated Anaplasma phagocytophilum presence as a function of vegetation, tick, and rodent communities in four sites in California. Sampling was performed at four state parks with mature and peripheral redwood habitat in northern California. Within each park, twelve 50 m long transects were established and vegetation assessed by point intercept sampling on the forest floor, canopy, and at 1-3 m high. Two times per year, animals were trapped and tested. Analysis consisted of logistic regression to evaluate risk factors for their ability to account for Anaplasma risk and correspondence analysis to associate Anaplasma with particular vegetation and small mammals. Rodents were more exposed to infection if they were woodrats (Neotoma spp.) or chipmunks (Tamias spp.) (two reservoirs) or from northern parks. High-risk transects had high biodiversity in ticks, rodents, and vegetation, as well as intermediate-sized trees with a high mean and variance in diameter at breast height. Correspondence analysis of rodents, disease, and vegetation defined disease clusters with chipmunks and large redwoods at one park, but with woodrats and oaks at another. Thus the two most important “signals” accounting for enzootic and potentially emerging anaplasmosis were high biodiversity and mature second-growth forest.

Acknowledgements: We thank Niki Drazenovich, Elizabeth Holmes, Greta Wengert, and Edwin Saada for field and laboratory assistance. Personnel at each of the study sites, and the California State Parks provided invaluable access and logistical support. Financial support was provided by the UC Davis Center for Vectorborne Diseases and the Committee on Research.
5. THE ECOLOGY OF EMERGING DISEASES AMONG POPULATIONS OF WILD FISH

James Winton, US Geological Survey, Western Fisheries Research Center, 6505 NE 65th Street, Seattle, WA 98115, USA

Presenting author: Winton, James

Summary: This presentation will use examples of emerging diseases in populations of wild fish to highlight factors affecting the ecology of fish diseases.

Historically, most fish health research was directed towards identification, treatment or prevention of diseases of captive animals; however, recent studies in natural systems indicate that, in addition to being an important component of natural mortality, infectious and parasitic diseases can contribute to population oscillations, extinction of endangered species, reduced host fitness, increased susceptibility to predation and explosive losses following the introduction of exotic pathogens. This presentation will use several examples of endemic and emerging diseases in wild fish that have been associated with population-level effects in North America. These include: whirling disease in wild-spawning rainbow trout (Oncorhynchus mykiss) in the Rocky Mountain West, viral hemorrhagic septicemia in the North Pacific Ocean and Great Lakes, and ichthyophoniasis in adult Chinook salmon (Oncorhynchus tshawytscha) in the Yukon River. Disease is often ignored as a factor affecting wild populations of fish and wildlife because the effects are difficult to observe and quantify. As poikilotherms, fish are highly dependent on environmental conditions, especially temperature, to help maintain homeostasis and other critical physiological processes such as immune function that can affect disease progression. Increased recognition of fish diseases as a potential population-limiting factor is partly the result of the emergence of high profile pathogens. There is growing concern that increased global trade, habitat alterations and other anthropogenic stressors, including climate change, will affect the distribution or severity of fish diseases and contribute to population-scale losses in these important natural resources. The examples in this presentation serve to demonstrate the impacts of emerging diseases on wild fish populations and highlight factors affecting the ecology of fish diseases.

Acknowledgements: This work was funded by the US Geological Survey.
6. BAT WHITE-NOSE SYNDROME: AN EMERGING FUNGAL PATHOGEN?

David S. Blehert, Anne E. Ballmann, Brenda M. Berlowski-Zier, Jeffrey M. Lorch, and Carol U. Meteyer, USGS-National Wildlife Health Center, 6006 Schroeder Rd., Madison, WI 53711, USA

Presenting author: Blehert, David

Summary: A previously undescribed fungus, Geomyces sp., is associated with white-nose syndrome, an emergent disease linked with the estimated mortality of over 400,000 cave-hibernating bats of the northeastern and mid-Atlantic United States. White-nose syndrome (WNS) is a condition associated with an unprecedented bat mortality event in the northeastern and mid-Atlantic United States. Since the winter of 2006-2007, bat declines ranging from 80-97% have been documented at surveyed hibernacula. This presentation summarizes evidence indicating an association between WNS and a newly described fungus, Geomyces sp. Following necropsy, bat muzzle and wing skin samples were submitted for histologic and culture analyses. Histology sections were stained with PAS and fungal cultures (Sabouraud dextrose agar) were incubated at 7°C. Fungal isolates were identified by microscopy and by PCR amplification/sequencing of the rRNA gene internal transcribed spacer region using primers ITS4 and ITS5. Other techniques under development include fungus-specific PCR for screening environmental and tissue samples, and in situ hybridization for identification of fungal hyphae in histologic sections. Histopathological analyses demonstrated that 90% of necropsied bats (n=117) submitted from WNS-suspect sites exhibited a cutaneous fungal infection. Direct microscopy, culture, and PCR/sequencing analyses confirmed that the skin of WNS-affected bats was colonized by genetically identical isolates of a psychrophilic (cold-loving) fungus with a unique conidial morphology. There is a growing body of evidence supporting a strong association between WNS and cutaneous infection by a newly discovered psychrophilic fungus. The growth temperature requirements of the fungus are consistent with the core temperatures of hibernating cave-bat species throughout temperate regions of the world. Given the hundreds of thousands of hibernating bats found throughout the WNS-affected region, this condition represents an unprecedented threat to bats of the northeastern United States and beyond.
7. ONE HEALTH

T. Treadwell, CDC/CCID/NCZVED, 1600 Clifton Rd, NE, MS A-30, Atlanta, Georgia 30333, USA

Presenting author: Treadwell, Tracee

Summary: This presentation will describe the One Health program at the Centers for Disease Control and Prevention.

The interaction between animals, humans and the environment is very complex and requires a multi-disciplinary approach to research and investigation. This presentation will describe the reasons for this approach and how we are trying to accomplish this goal.
8. AN INFECTIOUS DISEASE MODEL FOR MOUNTAIN GORILLAS:
EPISTEMIC AVOIDANCE BY POPULATION DISPERSAL

Christopher A. Whittier, Felicia B. Nutter, Barrett D. Slenning, Michael K. Stoskopf, North Carolina State University College of Veterinary Medicine, Raleigh, NC 27606, USA; Philip L. F. Johnson, University of California, Berkeley, CA 94720, USA; Jamie O. Lloyd-Smith, University of California, Los Angeles, CA 90095, USA

Presenting author: Whittier, Christopher

Summary: An individual-based, stochastic, discrete time disease transmission model for mountain gorillas predicts that pathogen spread is limited by natural gorilla group behavior but is facilitated by human contact, leading to more severe outbreaks.

Infectious disease threats to mountain gorillas (Gorilla beringei beringei) are considered serious but poorly understood, and can be investigated using computer modeling. A model that captures the population structure, gorilla intergroup contact, and human-gorilla contact will help predict the spread and threat of infectious diseases introduced into the gorilla population. We developed an individual based, stochastic, discrete-time susceptible-infected-recovered (SIR) model that simulated pathogen spread in the Virunga mountain gorilla population. The model integrated gorilla group interaction and individual migration parameters, acute and chronic disease transmission and recovery probabilities, and different population structures and levels of human contact. Outbreak severity was characterized by cumulative percentage of the population infected from an average of 500 simulations. The model was tested by comparing results from: an actual versus a simulated outbreak; simplified versus actual population structure; infection initiated in different groups; and different levels of human contact. Outbreak outcome depended on overall population structure and the sizes of initially infected gorilla group and neighboring groups, but severe epidemics were rare in the absence of human contact. Incorporating even a small group of regular human visitors with limited contact led to more severe gorilla outbreaks. The rich mountain gorilla information database helped create an effectual pathogen transmission model. Naturally infrequent gorilla group interactions and migrations limit pathogen spread whereas regular human contacts facilitate pathogen spread among gorilla groups, thereby increasing outbreak levels. This model aids mountain gorilla conservation by increasing our understanding of factors that limit or facilitate pathogen spread in the population. It can inform important policy and management decisions for the mountain gorilla population.
9. FARM VISITATION BY WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS): IMPLICATIONS FOR MITIGATION OF BOVINE TUBERCULOSIS TRANSMISSION

Ryan S. Miller, APHIS, Veterinary Services, Centers for Epidemiology and Animal Health, 2150 Centre Ave, Fort Collins, Colorado, 80524 USA; Are R. Berentsen, Mike R. Dunbar, APHIS, Wildlife Services, National Wildlife Research Center, 4101 La Porte Ave, Fort Collins, Colorado, 80521 USA; Regina Misiewicz, APHIS, Wildlife Services, National Wildlife Research Center, 4101 La Porte Ave, Fort Collins, Colorado, 80521 USA

Presenting author: Miller, Ryan S.

Summary: White-tailed deer demonstrated distinct seasonal and diurnal trends in farm visitation which differed greatly between deer suggesting that mitigations to guard against transmission of bovine tuberculosis between cattle and deer should focus on individual animals that are most likely to visit farms at specific periods.

In 1994 and 2005 Mycobacterium bovis (bTB) was identified in free ranging white-tailed deer (Odocoileus virginianus) populations in Michigan and Minnesota. Currently, the contact rate (direct and indirect) between cattle and deer, rates of farm visitation by deer, and co-use foraging resources by cattle and deer are not well understood. To evaluate the extent to which deer and livestock share forage resources and to evaluate farm visitation by deer, 25 female white-tailed deer were captured and fitted with global positioning system collars adjacent to the bTB infected zone in Michigan’s Lower Peninsula. Collars recorded geographic locations every two hours for one year. In addition, data were collected on cattle farming practices, including cattle use areas, timing of cattle use and feeding and location of stored cattle feed. Deer location data were integrated with farm use data to determine the timing and frequency of farm visitation and resource use by deer. Results indicate 66% of farm visitation was conducted by 19% of deer. Visitation peaked June 1 accounting for 33% of visits. One-third of locations were in cattle use areas. Deer visited 54% of farms within their home range, primarily at night (64%) and commonly visited multiple farms in a day. These findings suggest that mitigation and control efforts to guard against potential transmission of bTB between cattle and deer should account for frequency and timing of deer visitation. Deer visitation of multiple farms may contribute to local area spread of bTB. Focusing mitigation efforts, lethal or non-lethal, on individual deer that are most likely to visit farms may reduce overall mitigation costs while maximizing reduction in potential bTB transmission to cattle and between farms.
10. THE ROLE OF BATS IN LYSSAVIRUS EVOLUTION AND EMERGENCE: RABIES IN FLAGSTAFF, ARIZONA

C. Rupprecht, I. Kuzmin, L. Orciari, M. Niezgoda, A. Velasco, P. Yager, J. Blanton, J. Ellison, CDC, Atlanta, GA, USA; E. Lawaczeck, C. Yu, Arizona Department of Health Services, Phoenix, AZ; S. Ferrat, Coconino County Animal Management, Flagstaff, AZ, USA; D. Bergman, K. Wennig, USDA, Wildlife Services, Phoenix, AZ, USA; D. Slate, USDA, Wildlife Services, Concord, NH, USA

Presenting author: Rupprecht, Charles

Summary: Identification of the emergence of a unique viral focus among skunks and foxes in a previously unaffected portion of northern Arizona suggests that a common bat rabies virus variant is responsible for novel host shifts and perpetuation of intra-specific transmission pathways at an unprecedented scale. Throughout the world, specific lyssaviruses circulate within a variety of mesocarnivores and multiple taxa of bats, typically along the lines of intraspecific transmission pathways. In the USA, bats, skunks, and foxes serve as major rabies reservoirs of different viral variants throughout major portions of the southwestern states, such as in Arizona. Historically, rabies was only detected among bats in northern Arizona, until 2001. During that year, rabies was diagnosed in striped skunks (Mephitis mephitis) in the city of Flagstaff, Coconino County. In response to these unusual index cases, additional rabies surveillance, viral characterization, and wildlife vaccination occurred over the next several years to try to delineate, describe, and limit the disease in this area. Health communications were targeted to local residents to provide basic education about rabies and to minimize public health repercussions. Animals suspected of rabies were captured and euthanized. Brain samples were collected and rabies virus antigens were detected by the fluorescent antibody test. Tissues from rabid animals were analyzed with panels of monoclonal antibodies to identify antigenic variants and amplicons generated by RT-PCR were sequenced. Murine neuroblastoma cells were used for rabies virus isolation from the salivary glands of rabid animals. A trap, vaccinate, and release (TVR) program was conducted in response to the apparent outbreak. The program was focused where rabid animals were found. Wild carnivores were live-trapped, vaccinated with an inactivated rabies virus vaccine, marked with ear tags, and released. In addition, baits laden with a vaccinia-rabies glycoprotein recombinant virus were distributed by hand in suitable habitats in an attempt to augment the TVR program. Rabies virus neutralizing antibodies were detected in the sera of recaptured animals using the rapid fluorescent focus inhibition test. Antigenic typing and genetic sequencing of samples obtained from rabid wild carnivores in Flagstaff resulted in characterization of a rabies virus variant associated with big brown bats (Eptesicus fuscus). Subsequent surveillance demonstrated a cyclic pattern of rabies occurrence, despite vaccination. For example, in 2001, 19 rabid skunks were diagnosed in the area, but none were reported in 2002-03. Thereafter, rabies reappeared with 5 rabid skunks and a rabid gray fox (Urocyon cinereoargenteus) in 2004, and a rabid skunk, rabid gray fox and rabid cat during 2005. No cases of this rabies virus variant were detected in Flagstaff during 2006-07, and vaccination was discontinued. Additional wildlife cases were diagnosed again in this locality between November 2008 and April 2009, including more than six rabid skunks and 17 gray foxes. Isolation of virus from the salivary glands of affected animals yielded concentrations similar to those observed from reservoirs in other long established enzootic localities. Rabies virus neutralizing antibodies were not detected readily from animals except those recaptured after parenteral vaccination. Analyses obtained to date implicate one common bat rabies virus variant as the
original source of a new infectious focus among several species of rabid carnivores in northern Arizona, despite wildlife management attempts at vaccination to control the outbreak. Explanations are only speculative as to how and why this specific nidus originated in this particular locality. Prior to recent development, this region of the state consisted primarily of montane coniferous forest, dominated by stands of ponderosa pine (Pinus ponderosa). Today, the Flagstaff area varies considerably, developed into a urban/suburban community of single family homes, condominiums, apartment complexes, a golf course, and shopping areas, dispersed among remnant patches of pine forest. Such alterations have created ideal edge habitats for highly adaptive wildlife populations, such as skunks and foxes. Introduction of an infectious agent to susceptible individuals, such as via consumption of rabid bats, may occur as single isolated dead end events, or develop into an epizootic with the potential for future enzootic maintenance. Enhanced epidemiological surveillance coupled with renewed wildlife immunization trials present novel opportunities for insights into pathogen emergence, adaptation, evolution, prevention, and control.
11. CHANGES IN FEEDING GARDEN BIRDS IN ENGLAND WITH WIDESPREAD SALMONELLA INFECTION IN OTHER SPECIES VIA ENVIRONMENTAL CONTAMINATION

J. Paul Duff, the Veterinary Laboratories Agency (VLA) Penrith, UK, CA11 9RR; Paul Holmes VLA Shrewsbury, UK; Christina Papadopoulous, VLA Weybridge, UK.

Presenting author: Duff, James Paul

Summary: Feeding wild birds in the garden has increased and changed significantly in the last 2 decades in the UK and resulted in an increased environmental contamination with bacterial pathogens, and now, clear evidence of a wide range of spill-over hosts.

There have been significant changes in the garden bird feeding industry in the UK in recent decades. The industry is currently estimated at more than $16.5 million (£25M) per year. We believe that despite advice this has led to greater environmental contamination with the 3 Salmonella typhimurium phage types associated with garden birds. Using national VLA (Veterinary Laboratory Agency) data, and standard bacteriology, garden bird adapted salmonellas were compared in garden passerine species, domesticated animals, pets and wild animals over an 8 year period. All domesticated animals had isolates and evidence of clinical disease of varying severity. We also compared data for the same phage types supplied by the Health Protection Agency in humans over this period. There appears to be widespread spatial and temporal infection with host adapted garden bird Salmonella phage types in England and Wales, in a wide range of species, including humans. There are obvious zoonotic risks associated. However we believe that, with some exceptions, clinical disease in humans is mild/rare. We question whether further increased environmental contamination will change the disease epidemiology, and ask how these changes could be prevented. As feeding of garden birds has changed to become a very common and popular hobby, there has been increased environmental contamination with bacterial pathogens. We show evidence of infection in a very wide range of species, including man. We ask how these changes may progress, because there are several significant influencing factors, including - the financial recession (reducing purchase of bird food and feeders), changes in the pathogen and host resistance, and the education initiatives aimed at the public using best garden practices.

Acknowledgements: Professor John Threfall, HPA England
12. POULTRY BRED IN OPEN RANGE AND WILD WATERFOWL: ARE THE LIAISONS DANGEROUS?


Presenting author: Artois, Marc

Summary: We present current results of several studies carried out to investigate the risks associated with avian influenza and wild birds for outdoor poultry production. The Ain "department" in France is famous for its typical production of poultry outdoors. Moreover the same region is an important area for wild birds wintering and nesting. In winter several dozen of thousand of wild waterfowl are hibernating there. Both populations are separated by physical barriers such as fences, and for centuries no sanitary hazard or no trouble has been recorded. Nevertheless the recent HPAI outbreaks in Europe showed that potentially HP influenza strains can outbreak locally from LP strains circulating among wild free living birds and free range poultry. The risks associated with the influenza virus transmission have been listed and described. We have focused on the probability of introduction of a virulent AIV strain, by direct or indirect contact between poultry and wild birds visiting the areas used by poultry during day time. Ornithological data have been collected by transect and point watching; a survey was carried out so as to ask farmers if they can recognise the larger birds that were observed on their farm. A semi quantitative risk analysis has been attempted to rank the bird species according to the probability they transmit the virus by direct or indirect route. Currently a list of birds present in the immediate vicinity of the areas frequented by poultry has been made for the spring and summer seasons. Winter and autumn data are pending. In addition to the list of the most frequent small (i.e. garden) bird species observed, a relatively robust list of large birds usually or exceptionally mentioned by the farmers was established. A preliminary ranking of bird species by probability of IA virus transmission was established based on a qualitative estimation of bird feeding behaviour/body mass and IA prevalence. Although the results are incomplete, they suggest that direct contact between source (reservoir) birds and poultry is negligible. Indirect contacts remain possible but limited to a range of potential “liaison” species for which the degree of infectious contact with source birds is still under investigation. A tentative list of at-risk species will be soon available for further examination of transmission behaviour and simulation modelling of virus transmission.

Acknowledgements: This study is supported by a grant of the French agriculture ministry to the Institut Technique de l’Aviculture (ITAVI)
13. NECROPSY FINDINGS IN PERIURBAN WILD RODENTS (*SCIURUS CAROLINENSIS, TAMIASCIURUS HUDSONICUS, EUTAMIAS STRIATUS, MARMOTA MONAX*) IN ONTARIO, 1976-2009

Douglas Campbell, Ian K. Barker, Claire Jardine, Canadian Cooperative Wildlife Health Centre, Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, N1G 2W1, Canada

Presenting author: Jardine, Claire

Summary: Trauma and infectious disease were the most common diagnoses in all four species, while poisoning also occurred commonly in the grey squirrel (*Sciurus carolinensis*).

Sciurid rodents are common in urban and suburban areas and interact with humans and domestic animals. The study uses diagnostic records to summarize the diseases and causes of death commonly determined in these animals (*Sciurus carolinensis, Tamiasciurus hudsonicus, Eutamias striatus, Marmota monax*), and any changes in the frequency of their occurrence over time. Case records of the Canadian Cooperative Wildlife Health Centre and the Ontario Veterinary College were searched for reports of incidents involving these species. Cases were summarized by primary diagnosis and other significant findings.

471 records in total were found. Trauma was diagnosed in 118. Infectious disease, including visceral larval migrans, West Nile virus, toxoplasmosis and poxvirus, was found in 163.

Poisonings, primarily with anticoagulant rodenticides, occurred in 47 cases. Important causes of death are related to interactions with humans and other animals, and include traumatic injuries, deliberate or accidental poisonings, and parasitic infections acquired through exposure to raccoon (*Procyon lotor*) and cat feces. No diseases were identified that might represent health hazards to humans or domestic animals.
14. CONSERVATION ARK: DEVELOPING WILDLIFE HEALTH MONITORING AND DISEASE SURVEILLANCE CAPABILITIES IN SOUTH AUSTRALIA

David J. McLelland, Sue Bigwood, Ian Smith, Lynley Johnson, David Schultz, Wendy Foster, Mark Lethbridge, and Wayne Boardman, Conservation Ark, Zoos South Australia, Frome Road, Adelaide, SA, 5000, Australia

Presenting author: McLelland, David

Summary: Conservation Ark is positioning Zoos South Australia to take an active lead in wildlife health monitoring and disease surveillance in South Australia.

In recent times there has been mounting awareness of the importance of the health of wildlife populations in the conservation of biodiversity, and to domestic animal, human, and ecosystem health. Monitoring the health of wildlife populations is being increasingly utilised as an indicator of the health of the ecosystems they inhabit.

In response to the biosecurity implications of emerging infectious diseases, and the significant role of wildlife in the epidemiology of many of these diseases, the Australian Wildlife Health Network was established by the Federal Department of Agriculture, Fisheries and Forestry to coordinate the reporting of wildlife disease incidents at a national level. However, responsibility for human and production animal health, domestically, rests with state governments. On the ground investigation of wildlife disease has thus far been similarly coordinated at the state level, though the relative involvement of governments, universities and zoological institutions varies from state to state.

Currently in South Australia (SA), the investigation and reporting of wildlife disease is gaining attention across government departments in response to the development of a biosecurity plan for SA. However, wildlife disease surveillance, investigation and research are not being conducted or coordinated to the level seen in several other states.

In 2008, Conservation Ark was established to formally represent, and to enable the expansion and development of, the conservation and research activities of Zoos SA. We believe Conservation Ark is well positioned to take an active lead in monitoring the health of regional wildlife populations, and work collaboratively with the SA government to improve the investigation and surveillance of wildlife diseases. This presentation will discuss how Conservation Ark is working to achieve these aims. We are interested in the experiences of other institutions involved in wildlife health monitoring and disease surveillance, especially those that have developed from a similar base. We hope this talk will engender such discussion.
15. EVIDENCE OF MORBILLIVIRUS INFECTIONS IN SEA OTTERS IN WASHINGTON STATE

Nancy J. Thomas, USGS-National Wildlife Health Center, Madison WI 53711, USA; Jeremiah T. Saliki, Athens Veterinary Diagnostic Laboratory, University of Georgia, Athens GA 30602, USA; Jay W. Davis, Deanna Lynch, US Fish and Wildlife Service, Western Washington Fish and Wildlife Office, Lacey WA 98503, USA; Ronald J. Jameson, USGS-Western Ecological Research Center (retired), Corvallis OR 97333, USA; Steven Jeffries, Washington Department of Fish and Wildlife, Lakewood WA 98498, USA; J.P. Dubey, USDA-Agricultural Research Service, Animal and Natural Resources Institute, Beltsville MD 20705, USA

Presenting author: Thomas, Nancy

Summary: Necropsy and serologic data indicate that sea otters along the coast of northwestern Washington have had fatal and non-fatal morbillivirus infections.

Marine morbillivirus outbreaks due to dolphin morbillivirus, porpoise morbillivirus, phocine distemper virus, and canine distemper virus have been recorded in cetaceans and pinnipeds, primarily in the north Atlantic and Mediterranean regions. A new report documents phocine distemper virus infections in Alaskan sea otters, and indicates that this virus has been introduced into the Pacific region since 2000 (Goldstein et al. 2009 June. Emerg Infect Dis.). Washington sea otters (Enhydra lutris kenyoni) found dead and in suitable post-mortem condition have been examined by necropsy since 1989. Microscopic lesions suggestive of morbilliviral infection were evaluated by immunohistochemistry using anti-canine distemper virus antibodies. Frozen tissues from suspicious cases were tested using a differential PCR technique to distinguish the four known marine morbilliviruses. In addition 30 live, clinically healthy sea otters were captured for health and contaminant screening in 2001-2002. Sera from these live-caught otters were tested using a serum neutralization technique for antibodies to the known marine morbilliviruses. Tissues from eight dead sea otters were positive by IHC or PCR for a canine distemper-like morbillivirus. At least one case has occurred each year since 2004. Furthermore, serum from 24/30 (80%) live sea otters contained antibodies against canine and phocine distemper viruses. Necropsy and serologic data indicate that sea otters along the coast of northwestern Washington have had fatal and non-fatal morbillivirus infections. Non-fatal exposure was very common in the animals examined between 2001 and 2002. Alaskan sea otters were reintroduced to the Washington coast in 1969, and the population has continued to increase in numbers and range since the late 1970s.
16. THE ROLE OF WILDLIFE COLLECTION AND CARE IN OIL SPILL RESPONSE: THE COSCO BUSAN CASE STUDY

Michael H. Ziccardi, J. Gregory Massey, Kirsten V. K. Gilardi, and Jonna A.K. Mazet, Wildlife Health Center, School of Veterinary Medicine, University of California, Davis, CA 95616, USA

Presenting author: Ziccardi, Michael

Summary: This presentation will detail oiled wildlife response activities (including rehabilitation, volunteer efforts and emergency response management) within the overall spill response structure using the 2007 Cosco Busan oil spill as an example.

The Oiled Wildlife Care Network was established in 1994 by the California Department of Fish and Game to ensure that oiled wildlife receive the best possible care by applying the highest caliber science, best medical therapies, and immediate access to the most advanced facilities. During response, the OWCN receives assistance from 25 member organizations, uses twelve regional facilities, helps to organize wildlife data and samples from both live and dead wildlife impacted during spills, and acts as a key information source for agencies and industry members involved in the response. Since 1997, the OWCN has become recognized as the world leader in oil spill response, rescue, and rehabilitation. An example of the multi-faceted impact of oiled wildlife care to overall spill response efforts was seen starting on November 7th when the container ship M/V Cosco Busan struck the San Francisco Bay Bridge. Significant challenges occurred during this response, including initial confusion over the volume of spilled oil, tremendous numbers of wildlife reports (and interest) from the public, and significant public and legislative scrutiny over response efforts. Ultimately, the OWCN captured 1,084 live birds, collected 1,854 dead birds, and successfully released 418 (39%). Subsequent to this spill, many local, state and federal investigations have been conducted to determine better ways of responding in the future. However, due to the construction of specifically-designed oiled wildlife facilities, extensive training of personnel and volunteers, pre-identification of required supplies and equipment, and development of standardized protocols, the success of the wildlife efforts in this spill were felt to be significantly better than what could be expected outside of California.

Acknowledgements: The authors thank staff of DFG-OSPR, and the staff and volunteers of the OWCN (and its member organizations) for their tremendous help during this spill.
17. PERFLUOROOCTANESULFONATE (PFOS) AND PERFLUOROOCTANE-SULFONYLAMIDE (PFOSA) IN BOTTLENOSE DOLPHINS (TURSIOPS TRUNCATUS): AN INVESTIGATION INTO TWO UNUSUALLY HIGH MORTALITY EPIZOOTICS.

Romona Haebler, Atlantic Ecology Division, National Health and Environmental Effects Research, Office of Research and Development, U.S. Environmental Protection Agency, Narragansett, RI, 02882, USA; Douglas Kuehl, Mid-Continent Ecology Division, National Health and Environmental Effects Research Laboratory, Office of Research and Development, U.S. Environmental Protection Agency, Duluth, MN, 55804, USA; Charles Potter, Museum of Natural History, Smithsonian Institution, Washington, D.C., 20562, USA; Garet Lahvis, Department of Behavioral Neuroscience, Oregon Health and Science University, Portland, OR, 97239, USA; Michael Donahue, Ronald Regal, Department of Mathematics and Statistics, University of Minnesota-Duluth, Duluth, MN, 55812, USA

Presenting author: Haebler, Romona

Summary: High levels of PFOS and PFOSA, two marine environmental contaminants, were detected in tissues of bottlenose dolphins (Tursiops truncatus) that died during two major unusual mortality events in 1987-88 and 1990 using electrospray ionization LC/MS, an analytical technique not yet available at the time of the mortalities. The implications of this work are that there are other potential environmental contaminants that may be causing harm to wildlife that we are able to detect at a given time.

Along the Atlantic coast of the United States during 1987 and 1988, bottlenose dolphins (Tursiops truncatus) suffered one of this country’s largest marine mammal mass mortality events. An estimated 50% of all near-shore bottlenose died during this short period. Two years later a second, although less dramatic, event occurred along the US coastline of the Gulf of Mexico. The cause of these mortalities is uncertain; however, morbillivirus infection seemed to have spread rapidly throughout the dolphins. Suppression of the animals’ immune system by high concentrations of chemical contaminants was suggested as a contributing factor. To investigate this hypothesis, we determined by GC/MS the concentration of many polychlorinated and polybrominated chemicals, such as PCBs, chlorinated pesticides, and brominated flame retardants, as well as mercury, determined by AA, in the affected animals. Development of electrospray ionization LC/MS allowed us to re-examine these same tissues (liver) for the presence of PFOS and a metabolic precursor PFOSA. Concentrations of PFOS in the affected bottlenose were found to be greater than, and statistically different from, those found in other species, and to other bottlenose dolphin populations not affected during the epizootics. PFOS concentrations were found to be as great as, or greater than, concentrations of PCBs, 13 chlorinated pesticides, and PBDPEs. PFOS concentrations were generally less than mercury residues. PFOS was found to be readily transferred in utero from mother to fetus. PFOS was found in 100% of the bottlenose dolphins analyzed. The concentrations found were some of the highest recorded for wildlife, including eagles, turtles, mink, polar bears, and other marine mammals. The 1987/88 bottlenose dolphins had higher mean PFOS concentrations, and were significantly different than a group of Atlantic coast common and whitesided dolphins collected during the same time period, but not experiencing the high frequency of mortality. PFOSA was found in 90% of the bottlenose dolphins analyzed. The concentrations of PFOSA were approximately ten times less than those for PFOS in each animal. Adult female PFOS concentrations generally decreased with age (length), but the decrease was not statistically significant. Fetus PFOS concentrations were higher than those of the mother for 2 of 3
fetus/mother pair. The mean PFOS concentration of three fetus samples was greater than those for the adult male, adult female, or immature bottlenose.
18. CULTIVATION OF A HERPESVIRUS THAT PROBABLY CAUSES 
BENIGN GENITAL PLAQUES IN BOTTLENOSE DOLPHINS (TURSIOPS 
TRUNCATUS)

Niels van Elk, Dolfinarium Harderwijk, Strandboulevard Oost 1, Harderwijk, 3841 AB, The Netherlands; 
Marco van de Bildt, Ton de Jong, Ab Osterhaus, Thijs Kuiken, Erasmus Medical Centre, Dr. 
Molewaterplein 50, Rotterdam, 3000 CA, The Netherlands

Presenting author: Kuiken, Thijs

Summary: We report the first cultivation of a herpesvirus that probably causes genital plaques in 
bottlenose dolphins.

Mucosal plaques occur on the genital mucosa of bottlenose dolphins (Tursiops truncatus) both 
in the wild and in captivity. Although herpesvirus has been detected in these lesions by 
polymerase chain reaction (PCR), the virus has not been cultivated, and the pathology and 
epidemiology of the infection are poorly described. We studied genital herpesvirus infection in a 
zoo collection of male (n = 21) and female (n = 15) dolphins by polymerase chain reaction, virus 
cultivation, DNA sequencing, phylogenetic analysis, and histopathology. Using the newly 
isolated virus, we also developed a direct ELISA for antibodies to this virus. Herpesvirus infection 
was significantly associated with mucosal plaques on penis (3 of 21) or vulva (4 of 15). Penile 
plaques showed epithelial hyperplasia and contained herpesvirus. Herpesvirus was cultivated 
and identified as a gammaherpesvirus. Seropositivity in adults was higher in juveniles. 
Seroconversion occurred at onset of sexual behavior. Together, we here report the first 
successful cultivation from bottlenose dolphins of a herpesvirus that probably causes benign 
genital plaques and is likely transmitted by sexual contact.
19. DISEASES AND WILDLIFE TRANSLOCATIONS: ENDANGERED LAYSAN DUCKS AS AN EXAMPLE

Thierry M. Work, U. S. Geological Survey, National Wildlife Health Center, Honolulu Field Station, PO Box 50167, Honolulu, HI 96850, USA; John H. Klavitter, U. S. Fish & Wildlife Service, Midway Atoll National Wildlife Refuge, PO Box 50167, Honolulu, HI 96850, USA; Michelle Reynolds, U. S. Geological Survey, Pacific Islands Ecosystem Science Center, P.O. Box 44, Hawaii National Park, HI 96718, USA; David Blehert, U. S. Geological Survey, National Wildlife Health Center, 6006 Schroeder Rd., Madison, WI 53711, USA

Presenting author: Work, Thierry

Summary: Endangered Laysan ducks that were translocated from Laysan to Midway Atoll suffered catastrophic mortality due to botulism type C thereby highlighting the importance of implementing habitat management prior to translocating wildlife.

Endangered Laysan ducks *Anas laysanensis* are only found on Laysan Island. In 2004 and 2005, 42 ducks were translocated from Laysan to Midway to establish a new population. In anticipation of the translocation, new wetlands were created on Midway to enhance duck populations. In 2008, there was a catastrophic mortality of Laysan ducks on Midway. Based on clinical signs, botulism was suspected, and management measures (carcass collection) were implemented. Regrettably, response to the outbreak was stymied by the remoteness of the refuge, the logistics of the situation and inability to manage water sources. Over 180 ducks (ca. 40-50% of the Midway population) were killed by botulism type C. Ominously, Laysan ducks on Midway are infected with proventricular nematodes, a major historical cause of death in ducks on Laysan. Because of this event, USFWS recognizes that Midway Atoll NWR must be managed, in part, as a wetland refuge and not just a seabird refuge. Future translocation of ducks to other islands will require comprehensive wetland management plans. Developing the ability to control water on existing wetlands on Midway will not only help abate future botulism events but should also mitigate effects of proventricular nematodes.
20. IMPACT OF RANAVIRUS IN FINFISH IN THE MURRAY-DARLING BASIN RIVER SYSTEM OF AUSTRALIA

Richard J. Whittington, Joy Becker, Alison Tweedie, Anneke Rimmer, Zita Ritchie, Martin Asmus and Dean Gilligan; OIE Reference Laboratory for EHN virus, Faculty of Veterinary Science, The University of Sydney, Camden, NSW 2570, Australia and New South Wales Department of Primary Industries, Australia

Presenting author: Whittington, Richard

Summary: Despite opportunity for spread of ranavirus since 1986 with alien fish carrier hosts across thousands of kilometers of rivers - which may have contributed to the decline of native finfish populations - preliminary findings suggest low prevalence of ranavirus outside of the range of the original outbreaks.

The ranavirus EHNV (Family Iridoviridae) emerged in 1986 in Australia, devastating redfin perch (Perca fluviatilis) populations. Subsequently, related viruses emerged in amphibians including salamanders in North America. Ranaviruses are not host specific and may be responsible for species declines. Determining their geographic distribution, host range and virulence is required to inform conservation management. Random geographic coordinate sampling of all catchments in the Murray-Darling Basin of Australia, an area of 1 million square kilometers, is being undertaken progressively to obtain samples from selected finfish species so as to detect EHNV infection at a prevalence of <10% with 95% confidence, using virus isolation (lethal sampling) and/or serology (non-lethal sampling), depending on species and conservation status.

Specific immunological reagents are being developed and a standard bath challenge model is being used to determine susceptibility of key species to EHNV. Outbreaks of EHNV remain confined to the original region in southeastern Australia, despite opportunity for infection to spread and disease to occur elsewhere in susceptible hosts such as redfin perch. Thus far there is no evidence of spread of EHNV to other compartments of the Murray-Darling Basin or to other free-living species. Redfin perch is an indicator species for occurrence of clinical EHNV infection in a catchment, with the most recent outbreak being in 2008, more than 20 years after the first appearance of the disease. Although other species appear to be susceptible experimentally, it is difficult to show an association between EHNV and species abundance, given other factors that negatively impact finfish populations such as drought and habitat disturbance. Although the survey is ongoing, reasons for the apparent restricted distribution of EHNV will be discussed.

Acknowledgements: This study is funded by the Murray-Darling Basin Authority and the University of Sydney.
21. EMACIATION/MALNUTRITION SYNDROME IN STRANDED HARBOR SEAL PUPS FROM SAN JUAN COUNTY, WASHINGTON


Presenting author: Gaydos, Joseph K.

Summary: Approximately 50% of stranded harbor seal pups stranding in San Juan County present with emaciation/malnutrition. The cause is unknown, but could be due to limited prey availability for pregnant females or high levels of human disturbance separating critical bonding between females and pups.

Pacific harbor seals (Phoca vitulina richardsi) are the most abundant marine mammal in the inland marine waters of Washington and British Columbia. In San Juan County, Washington annual aerial surveys are used to estimate the harbor seal population, which is currently estimated to be approximately 5,000 animals. The population is thought to have been at carrying capacity since 2000. Approximately 50 harbor seals strand annually in San Juan County and complete necropsies are performed on carcasses in suitable condition. Between 2002 and 2008, complete necropsies were performed on 68 stranded harbor seal pups. Of the necropsied animals, emaciation/malnutrition syndrome was believed to be the primary cause of death in 38% (n=26) with some degree of interannual variation in prevalence. Emaciation/malnutrition was believed to be a contributing factor in an additional 12% of cases diagnosed with omphalitis or omphalophlebitis (n=4), herpes virus associated adrenal adenitis (n=2), and bronchopneumonia (n=2). As an age-class, harbor seal pups are over-represented in documented harbor seal mortality in San Juan County, comprising 71% of strandings. It is not unusual for some wildlife populations to experience high neonatal mortality. The cause of emaciation / malnutrition syndrome seen in 50% of stranded harbor seal pups is unknown, but could be due to limited prey availability for pregnant females or high levels of human disturbance separating critical bonding between females and pups.

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22. FEATHER-LOSS DISORDER IN CHICKS OF TWO SPHENISCUS PENGUIN SPECIES

Olivia J. Kane, Jeffrey R. Smith, P. Dee Boersma, Department of Biology, University of Washington, Box 351800, Seattle, WA 98195, USA; Nola J. Parsons, Venessa Strauss, Southern African Foundation for the Conservation of Coastal Birds, PO Box 11116, Bloubergrant, 7443, South Africa; Cecilia Villanueva, Centro Nacional Patagónico CONICET, Blvd Brown 2825 Puerto Madryn 9120, Chubut, Argentina

Presenting author: Kane, Olivia

Summary: A new feather-loss disorder, first reported in African penguin chicks in 2006 and in Magellanic penguin chicks in 2007, reduced growth and likely survival.

Feather-loss is uncommon in birds and rarely reported in the wild. We report the first observations of feather-loss in South Africa and Argentina in two species of Spheniscus penguins. Feather-loss was first seen in African (Spheniscus demersus) in 2006 and Magellanic (S. magellanicus) penguins in 2007. In 2006 (7%) and in 2007 (20%) African chicks lost feathers after admittance to SANCCOB. In 2007, we found 10 featherless Magellanic chicks in Argentina. The featherless chick was smaller than down-covered chicks. In 2008, we found featherless penguin chicks in the wild in South Africa and Argentina. Neither the cause nor the impact of a penguin feather-loss disorder, first observed in a South African rehabilitation center in 2006 (African penguins) and in Argentine colonies in 2007 (Magellanic penguins), is known but it appears to be contagious as it is more common in the rehabilitation center than in the wild. The disorder is costly, reducing growth and delaying completion of the juvenile molt. Featherless chicks are smaller and survival of affected penguins is likely reduced.

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23. CRYPTOCOCCOSIS IN OREGON WILDLIFE

Rob J. Bildfell, Beth A. Valentine; Oregon State University Veterinary Diagnostic Laboratory, College of Veterinary Medicine, Corvallis, OR 97331, USA; Peregrine L. Wolff, Oregon Department of Fish and Wildlife, Corvallis, OR 97331, USA; Jim M. Rice, Marine Mammal Institute, Oregon State University, Newport, OR 97365, USA; Edmond J. Brynes III, Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, North Carolina 27710, USA

Presenting author: Bildfell, Rob

Summary: Cryptococcus species have been demonstrated in necropsy materials from porpoises (two) and elk (three) collected in Oregon during the past three years. Both isolates obtained were of C. gattii, a species considered invasive to the Pacific Northwest and of public health interest.

Cryptococcus gattii has been reported as an important cause of disease in both humans and animals on Vancouver Island and more recently in Washington and Oregon. Documenting the spread of this fungus and the species affected are important from a public health aspect and may prove useful in attempts to manage affected sylvatic species. More precise identification of subpopulations of infected wildlife may even help elucidate the microhabitats preferred by C. gattii. Routine diagnostic investigations of mortalities/diseased wild mammals submitted to the Oregon State University Veterinary Diagnostic Laboratory during the past three years were reviewed to determine if cryptococcosis had been diagnosed. Case histories including clinicopathologic findings and various ancillary tests were reviewed and geographic locations noted. Five cases affecting both aquatic (two porpoises) and terrestrial (three elk (Cervus elaphus)) wild mammals were identified in western Oregon, involving several counties. Only 2 cases were successfully cultured but both yielded VGII variants of C. gattii: VGIIa for a harbor porpoise (Phocoena phocoena) and VGIIb for a Roosevelt's elk (C. elaphus roosevelti). Multiple organ systems were generally involved and in the case of the elk, generalized debilitation was noted. These cases document the presence of both the major and minor variants of the Vancouver Island C. gattii outbreak within wild species in Oregon. Involvement of porpoises has been previously documented (Brynes et al. 2009 JID,199:1-6) but no case of C. gattii in free-ranging elk has been reported. It is unclear whether these mammals are acting as vectors to spread of the fungus. Biologists, hunters and fishermen should be aware of the potential for exposure to the agent although it should be noted that the yeast form found in tissues is not thought to be highly infectious. Affected elk were in very poor body condition but there are insufficient data to determine whether this is a cause or effect of the fungus. Body systems targeted were generally similar to other species; respiratory and central nervous systems.

Acknowledgements: Thanks to ODFW biologists and volunteers of the Marine Mammal Institute of OSU for their excellent assistance and to Peggy Dearing for microbiologic expertise. Partial financial support from NIH/NIAID R01 grant AI39115 to Joseph Heitman.
24. CHRONIC LYMPHOCYTIC LEUKEMIA IN A CAPTIVE FEMALE NORTHERN SEA OTTER (ENHYDRA LUTRIS KENYONI)

**Martin Haulena**, Vancouver Aquarium, PO Box 3232, Vancouver, BC, V6B 3X8, Canada; **Stephen Raverty**, Animal Health Center, 1767 Angus Campbell Road, Abbotsford, BC, V3G 2M3, Canada; **Kendal E. Harr** #10 1595 Clivedon Avenue, Annacis Island, Delta, BC, V3M 6M2, Canada

**Presenting author**: Haulena, Martin

**Summary**: This is the first case report of chronic lymphocytic leukemia diagnosed ante-mortem in a northern sea otter (*Enhydra lutris kenyoni*) stranded and recovered coincident with the Exxon Valdez oil spill.

As part of the recovery effort with the Exxon Valdez oil spill, some sea otters (*Enhydra lutris kenyoni*) were initially triaged in Alaska and then allocated to aquaria throughout North America. Long term clinical and pathologic follow up of these animals has been inconsistent. To establish possible sequelae of oil exposure in sea otters, we present the following case. A 21-year-old, 23 kg female sea otter that originally stranded as a juvenile during the Exxon Valdez oil spill in 1989, had been maintained at the Vancouver Aquarium with minimal health problems until she presented with a sudden onset of head tilt and lethargy in 2008. Diagnostic modalities employed in this case included complete blood count, serum chemistry, radiography, magnetic resonance imaging, bone marrow biopsy, and histopathology. MRI of the brain was consistent with an otitis media. Hematology identified a neutropenia and lymphocytosis, consistent with leukemia. A diagnosis of chronic lymphocytic leukemia was confirmed by a bone marrow biopsy, cytology and histopathology. Necropsy disclosed generalized lymphadenopathy and emaciation and histopathology confirmed lymphocytic leukemia. This report describes the clinical and pathologic diagnosis of leukemia in an otter that survived the Exxon Valdez oil spill. Chronic lymphocytic leukemia in other species is due to acquired injury to lymphocytic DNA versus an inherited defect. Exposure to benzene and other hydrocarbons has been associated with the development of a number of pathologic processes, including leukemia in humans. Although no direct link to previous exposure to petroleum products can be made in the current report, this study does highlight the need for long-term surveillance of marine populations that have been exposed to oil spills.

**Acknowledgements**: The authors wish to thank veterinary technicians Chelsea DeColle and Danielle McLaughlin and the marine mammal care staff at the Vancouver Aquarium including Brian Sheehan, Julie Gorman, and the rest of that talented team. We would also like to thank Canada West Veterinary Specialists and Critical Care Hospital including Drs. Marina Ivancic, Mike Higgins, and Vincent Defalque.
25. UNUSUAL SOUTHERN RIGHT WHALE MORTALITY EVENTS AT PENINSULA VALDES, ARGENTINA

M. M. Uhart, Southern Right Whale Health Monitoring Program, Argentina; Global Health Program, Wildlife Conservation Society, Chubut, Argentina; V. Rowntree, Southern Right Whale Monitoring Program, Argentina; Whale Conservation Institute, University of Utah, Salt Lake City, UT USA; A. Chirife and N. Mohamed, Southern Right Whale Health Monitoring Program, Argentina; L. M. Pozzi, Southern Right Whale Health Monitoring Program, Argentina; CONICET, Chubut, Argentina; M. Franco, Cuerpo de GuardaFaunas, Subsecretaría de Turismo, Chubut, Argentina; Denise McAloose, Global Health Program, Wildlife Conservation Society, Bronx, NY USA; M. Sironi, Southern Right Whale Health Monitoring Program, Argentina; Instituto de Conservación de Ballenas, Buenos Aires, Argentina

Presenting author: Uhart, Marcela

Summary: Unusually high mortalities of Southern Right Whales at Peninsula Valdes, Argentina, in 2007 and 2008 are considered the most extreme mortality events ever observed in any baleen whale.

Peninsula Valdés (PV) in Argentina is the major nursery ground for the southwest Atlantic Southern Right Whale (SRW, *Eubalaena australis*) population. Probably due to the topography and currents of the Peninsula’s large bays, most of the whales that die become stranded on the beaches, allowing for reasonably accurate mortality estimates. Systematic efforts to evaluate SRW health through post-mortem examinations began in 2003. Since 2003, 292 SRW deaths have been recorded, with peaks in 2005, 2007 and 2008. Ninety percent of beached whales were calves and most of them females. In 2007 and 2008, 83 and 98 whales respectively, died and stranded at PV, in what are considered the most extreme mortality events ever observed in any baleen whale. We discuss environmental conditions prior to and during the events and report results from analyses of whale tissues and water samples collected in the gulfs where the whales died. Necropsies provided no evidence for cause of death in either year. Investigation of marine mammal unusual mortality events (UME) is challenging and complex, and critical information is often times missed as onset is not readily recognized. The immediate cause of death, predisposing factors, and population effects of UME have only been identified for a small percentage of investigated cases. With an annual population growth rate near 7% for the period 1971-2000, the PV SRW might have the capacity to overcome years of high calf mortality. Conversely, events of this nature could drive their sister species in the northern hemisphere towards extinction.

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26. HARMFUL ALGAL BLOOMS (HAB) IN THE ST. LAWRENCE ESTUARY (SLE): IMPLICATIONS FOR SPECIES AT RISK

Lena N. Measures, Michel Starr, Michael Scarratt, Sonia Michaud, Maurice Lamontagne Institute, Fisheries and Oceans Canada, P.O. Box 1000, 850 Route de la Mer, Mont-Joli, QC, G5H 3Z4, Canada; Stéphane Lair, Centre québécois sur la santé des animaux sauvages / Canadian Cooperative Wildlife Health Centre, Faculté de médecine vétérinaire, Université de Montréal, P.O. Box 5000, 3200 Rue Sicotte, St. Hyacinthe, QC, J2S 7C6, Canada; Robert Michaud, Groupe de Recherche et d’Éducation sur les Mammifères Marins, P.O. Box 223, 108, de la cale sèche, Tadoussac, QC, G0T 2A0, Canada; Pierre Bélanger, St. Lawrence National Institute of Ecotoxicology, 5040 Montana, Montreal, QC H2J 3C3, Canada; Andrew Wotherspoon, Michael Quilliam, National Research Council of Canada, Institute for Marine Biosciences, 1411 Oxford Street, Halifax, NS, B3H 3Z1, Canada

Presenting author: Measures, Lena

Summary: Harmful algal blooms (HAB) in the St. Lawrence Estuary (SLE) may threaten the long term recovery of the threatened SLE beluga population. A multi-species mortality event associated with an intense harmful algal bloom (HAB) in the St. Lawrence Estuary (SLE) in August 2008 resulted in death of invertebrates and vertebrates including the threatened SLE beluga. We hypothesize that exposure to saxitoxins may threaten the recovery of this species at risk.

During an intense algal bloom of Alexandrium tamarense in the SLE in August 2008, carcasses of invertebrates, fish, birds, seals and whales were observed ashore or drifting. Various carcasses including SLE beluga (Delphinapterus leucas) were examined at necropsy to determine cause of death and their tissues tested for saxitoxin and its analogues (STXs) using ELISA and HPLC. Stranded SLE beluga have been examined at necropsy since 1983 to determine cause of death. Other stranded marine mammals have been sampled for various research projects since 1996. Marine mammals stranded prior to 2008 were also tested for STXs. STXs were detected in the liver, kidneys, faeces and/or stomach of seals and SLE beluga during the 2008 HAB. No significant disease was observed during complete necropsies of 31 marine mammals. Traces of STXs were detected in the liver of SLE beluga, and other whales stranded prior to 2008. This is the first well-documented case of multi-species mortalities of marine fauna linked to a PSP-producing algal bloom. Such extreme HAB events may have little effect on marine populations including the threatened SLE beluga in the long term as long as the frequency or intensity of HABs does not increase. The role of chronic sub-lethal exposure to STXs over many years may be significant, particularly to species at risk, but requires further study.
27. KILLER WHALES AT RISK: CAN WE SUSTAIN THESE CHARISMATIC CREATURES IN THE FACE OF CONSERVATION THREATS?

Peter S. Ross, Research Scientist, Institute of Ocean Sciences, Fisheries and Oceans Canada, 9860 West Saanich Rd., P.O. Box 6000 Sidney, BC, V8L 4B2 Canada. TEL. 1.250.363.6806  FAX 1.250.363.6807
http://www-sci.pac.dfo-mpo.gc.ca/osap/people/ross/ross_e.htm

Presenting author: Ross, Peter

Summary: The killer whale (*Orcinus Orca*) populations of the NE Pacific Ocean face a daunting set of threats, including noise and disturbance, diminished abundance of prey, and exceptionally high levels of toxic chemicals. Research in British Columbia and Washington State has shed light on the nature of these threats, using minimally invasive biopsy techniques, novel field studies, and newly developed laboratory methods to measure health. However, it is the acquisition of knowledge on the individual identities of these killer whales that provides the ultimate basis for a biological and ecological understanding of the nature of the threats at the population level. Each and every resident killer whale is known to researchers, by age, by sex, by family association, and by feeding type. By combining multiple lines of evidence, scientists have painted a bleak picture about the future of these animals. The long lives, high trophic level, and very large habitat needs of killer whales render them exceptionally vulnerable to anthropogenic activities. At one killer whale per 100,000 humans in the trans-boundary region of southern BC and Washington State, these killer whales are special!
28. INVASION ECOLOGY OF BLACKLEGGED TICKS AND LYME DISEASE IN THE MIDWESTERN UNITED STATES

Sarah A. Hamer, Department of Fisheries and Wildlife, Michigan State University, 13 Natural Resources Building, East Lansing, MI 48824, USA; Graham J. Hickling, Department of Forestry, Wildlife, and Fisheries, University of Tennessee, 248 Ellington Place, Knoxville, TN, USA; Edward D. Walker, Department of Microbiology and Molecular Genetics, Michigan State University, 6154 Biomedical Physical Sciences Building, East Lansing, MI 48824, USA; Jean I. Tsao, Department of Fisheries and Wildlife and Department of Large Animal Clinical Sciences, Michigan State University, East Lansing, MI 48824, USA

Presenting author: Hamer, Sarah

Summary: Wildlife sentinels and genetic investigations have elucidated an active invasion of blacklegged ticks and the Lyme disease pathogen into Michigan, thus providing an early warning to human and veterinary medical communities to have an increased awareness for tick-associated illness throughout the state.

In response to recent findings of blacklegged ticks (Ixodes scapularis) in Lower Michigan, we hypothesized an invasion of the Lyme disease system was occurring, and that assessment of the genetic diversity of the Lyme disease pathogen, Borrelia burgdorferi, would be useful in tracking the route and mechanisms of invasion from endemic foci. A five-year field investigation was initiated to study the process of invasion. This included sampling ticks off vegetation, live-trapped small and medium mammals, wild birds, hunter-harvested white-tailed deer (Odocoileus virginianus), and pet dogs (Hamer, 2009, Am J Vet Res 70:49-56) to capture the dynamic invasion front. Sampling occurred at eight sites along broad transects throughout the presumed invasion zone. Ticks of all species and tissue samples from wildlife were tested for infection through amplification of an internally transcribed spacer region from the rRNA operon of B. burgdorferi, which subsequently provided the template for strain identification through DNA sequencing and phylogenetic analyses. An active invasion of blacklegged ticks was demonstrated most clearly by increasing rates of infestation of white-footed mice over space and time. B. burgdorferi was detected in wildlife outside the blacklegged tick invasion zone, suggesting cryptic pathogen maintenance. Pathogen genetic diversity was greatest where blacklegged ticks have been established longest.

Using a comprehensive approach, we sampled wildlife, tick, and pathogen communities to describe an active invasion of blacklegged ticks. Detection of emerging Lyme disease risk during the invasion process allows early management interventions to reduce human and animal disease. Invasion dynamics are complex, as invading blacklegged ticks are encountering wildlife already infected with the Lyme disease pathogen. Phylogenetic analyses of pathogen strains from zones of invasion and cryptic transmission highlight the ecological mechanisms facilitating invasion.

Acknowledgements: We thank Michelle Rosen and Jennifer Sidge for their assistance in the field and laboratory, and Michigan Department of Natural Resources and Kellogg Biological Station for site access.
29. MANIPULATIVE EXPERIMENTS EXPLORING TRANSMISSION OF A ZOONOTIC PATHOGEN IN ITS HOST POPULATION

Karoun H. Bagamian, Population Biology, Ecology and Evolution Program, Emory University, Atlanta, GA 30329, USA; James N. Mills, Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, GA 30329, USA; Richard J. Douglass, Dept of Biology, Montana Tech, Butte, MT 59701, USA

Presenting author: Bagamian, Karoun H.

Summary: Manipulative experiments in outdoor, natural enclosures can be used to study the transmission dynamics of hantaviruses in their natural host populations. Previous investigations of zoonotic pathogens in reservoir host populations have yielded conflicting data regarding the effects of infection on host health and the relationship between host population density and infection prevalence. We tested these questions by running manipulative field experiments using the deer mouse (Peromyscus maniculatus)-Sin Nombre hantavirus (SNV) host-parasite system. We constructed six 0.10 hectare enclosures in Butte, Montana. One infected (“infective”) and a predetermined number of uninfected (“susceptible”) wild adult male deer mice were released into each enclosure to create “high” or “low” density populations. During the field season, we collected descriptive data and biweekly (2007) and weekly (2008) blood, saliva, and urine samples from the experimental mice. We determined presence of SNV IgG antibody and antibody titers in blood samples using enzyme immunoassays. We tested for the presence of SNV RNA (as a surrogate measure of viremia) in blood samples using a nested RT-PCR. There was a seasonal trend in the incidence of transmission events, significant differences between the two density treatments on certain physiological variables, and no differences in weight gain between the density treatments or infected and uninfected mice. Individual deer mice have a highly variable immunological response to natural SNV infection. We are the first group to successfully run field experiments that follow SNV transmission in deer mice under controlled conditions. Our preliminary results provide further insight into the effect of density on the transmission of a zoonotic pathogen in a host population and the effects of density and infection on reservoir host health. Our methodologies might be used in similar host-pathogen systems and to address other important questions in the field of wildlife disease ecology.

Acknowledgements: My advisors, my field assistants, and the staff and undergraduates of Montana Tech provided me with endless support. The NIH, CDC, and Emory University provided funding for this endeavor.
30. SEASONALITY AND SEX STRUCTURE IN THE EPIDEMIOLOGY OF SIN NOMBRE VIRUS IN DEER MICE (*P. MANICULATUS*)

**Sean M. Laverty**, Department of Mathematics, 155 South 1400 East, University of Utah, Salt Lake City, UT, 84112-0090, USA; **Frederick R. Adler**, Department of Mathematics, 155 South 1400 East University of Utah, Salt Lake City, UT, 84112-0090 and Department of Biology, 257 South 1400 East, University of Utah, Salt Lake City, UT, 84112-0090, USA

**Presenting author:** Laverty, Sean

**Summary:** We explore the interactions between population sex structure and seasonal variability in host demography and epidemiology to understand the low prevalence of Sin Nombre virus in deer mice.

The importance of seasonality has long been known in many human diseases and has become an important topic in wildlife diseases. In particular, seasonal changes in host immunity, physiology, and behavior could play important roles in regulating transmission and maintaining the low prevalence of SNV in deer mice (*Peromyscus maniculatus*). Deer mice were live-captured from 19 sites in the Great Basin Desert of central Utah during the spring and fall of each year from 2002-2008. Animals were weighed, sexed, and individually tagged for identification. Blood samples were taken to test for SNV exposure with ELISA. The Cormack-Jolly-Seber model was used to estimate capture and apparent survival probabilities. These estimates were used to parameterize differential equation models describing SNV dynamics in deer mice. Samples from simulation results were compared to field data to evaluate the behavior of the models. Preliminary results indicate that males and larger or scarred individuals are more likely to be seropositive at the time of initial capture. Individuals initially captured during the spring season were more likely to be seropositive than those captured during the fall season. We will address seasonality and its interaction with other factors that promote seropositivity. Previous analysis by Adler et al., 2008 (Am Nat, 172(6): 855-867) showed that higher prevalence in males could be attributed to higher susceptibility or encounter rates. Additionally, the observed sex-ratio bias towards males at low population density was at least partially explained by differential survivorship. Knowledge of whether or not these heterogeneities between the sexes are maintained across seasons would certainly strengthen our understanding of the host-virus interactions and provide explanations for field data.

**Acknowledgements:** SML thanks M. Denise Dearing for the opportunity to work with a fascinating system.
31. IMMUNOHISTOLOGICAL EVALUATION OF DEVIL FACIAL TUMOUR DISEASE AND IDENTIFICATION OF A BIOMARKER FOR DISEASE DIAGNOSIS

C. Tovar, C. Blizzard, A. Kreiss and G. Woods, Menzies Research Institute, Private Bag 29, Hobart, TASMANIA, 7001, Australia

Presenting author: Tovar, Cesar

Summary: This study confirms the neuroectodermal origin of the Devil Facial Tumour Disease cells and presents new sensitive and specific markers that will greatly facilitate the diagnosis of the disease in histological samples.

Devil Facial Tumour Disease (DFTD) is a unique infectious cancer that is threatening the survival of the Tasmanian devil (Sarcophilus harrisii), a species endemic to Tasmania. This research aims to examine the histological nature of the tumour and to identify specific tumour antigens that can be used for the development of diagnostic tools. Indirect immunofluorescence techniques on DFTD cultured cells and immunohistochemistry on tumour biopsies were used to study the histological nature of DFTD. DFTD tumour cells were positive for a range of neural markers. Notably, the cells expressed Nestin, a class VI intermediate filament protein, which has been described as a specific marker of stem cells. This study supports the concept that DFTD cells are derived from neural crest stem cells. We also propose that Nestin, in combination with other biomarkers, could be useful for the diagnosis of DFTD. The improvement of the diagnosis of DFTD and the finding that over expressed proteins in the tumour can be recognised with specific markers open new opportunities for the understanding and management of this intriguing disease.

Acknowledgements: We would like to thank the collaboration of the Neurorepair Group of Menzies Research Institute, Dr. Eric Guiler, Tasmanian Devil Research Grant and Save the Tasmanian Devil Program.
32. MOLECULAR EPIDEMIOLOGY OF RABIES IN THE CENTRAL GREAT PLAINS: DO HOST ECOLOGY AND LANDSCAPE INFLUENCE VIRAL EMERGENCE?

Heather D. Barton, Samantha M. Wisely, Kansas State University Division of Biology, 116 Ackert Hall, Manhattan KS, 66506, USA; Rolan Davis, Kansas State University College of Veterinary Medicine, 101 Trotter Hall, Manhattan, KS, 66056, USA

Presenting author: Barton, Heather

Summary: Rabies strains interact differently with landscape features, and may require strain-specific management strategies.

The Central Great Plains contains two unique striped skunk (Mephitis mephitis) rabies strains, North Central and South Central rabies. For effective management, we need to understand the interactions among rabies virus and ecological factors. We investigated virus epidemiology, skunk population dynamics, and rabies movement across the landscape to understand these interactions. Brain tissues were sampled from 86 rabies-positive striped skunks from Oklahoma, Kansas, Nebraska, South Dakota, and North Dakota from 2003-2008. Rabies RNA and skunk DNA were isolated from each sample. Sequence data were used for rabies analyses and microsatellite data for skunk analyses. We estimated basic diversity statistics, and dN/dS for both strains. AMOVAs and SAMOVAs were conducted for both strains to assess barriers to rabies spread. We determined effective population size for skunks within strain ranges, and conducted population structure analyses to determine the presence of skunk sub-populations. We also determined number of effective migrants among Midwest skunks. Results indicate that the North Central strain was more diverse than the South Central strain, and appears to be under less purifying selection. Additionally, striped skunks in the Central Great Plains are panmictic. Landscape analyses indicate that rivers are not barriers to striped skunk dispersal, but do impede spread of rabies. By studying three different factors influencing infection with rabies, we gain better insight into the rabies system as a whole, which can aid in more effective management procedures. A key finding is that despite the presence of a panmictic host population, North Central and South Central rabies strains behave differently across the landscape. The unique strain characteristics suggest that different disease management strategies may be necessary to control North Central and South Central rabies.
33. EFFECT OF AGE ON SHEDDING OF AVIAN INFLUENZA VIRUS IN MALLARDS (ANAS PLATYRHYNCHOS)

Taiana P. Costa and Elizabeth W. Howerth, Department of Pathology, College of Veterinary Medicine, The University of Georgia, 501 DW Brooks Drive, Athens, GA, 30602, USA; Justin D. Brown and David E. Stallknecht, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, 589 DW Brooks Drive, Athens, GA, 30602, USA

Presenting author: Costa, Taiana P.

Summary: Although Mallards (Anas platyrhynchos) from different age groups become infected and shed low pathogenic avian influenza (LPAI) viruses, age at time of infection affects the extent of viral shedding and consequently may impact transmission of LPAI viruses within the wild bird reservoir system.

Little is known about potential effects of age at infection on extent of shedding associated of LPAI virus in wild birds. Such information is needed to fully evaluate experimental infection and field surveillance data often derived from birds of varying ages. Mallards (Anas platyrhynchos) were divided into five age classes: 2 weeks, and 1, 2, 3, and 4 months. For each age class, 15 Mallards were evenly divided between two viral treatments and one negative control group. Treatment groups were inoculated via choanal cleft with 0.1 ml of media containing an infectious titer of 106 EID50 of one of two LPAI viruses: A/Mallard/MN/355779/00 (H5N2) and A/Mallard/MN/199106/99 (H3N8). Virus isolation and rRT-PCR were performed on oropharyngeal (OP) and cloacal swabs. Serum samples were tested using the AGID and blocking ELISA tests. The one month old group had the highest number of virus isolations from cloaca and the lowest Ct values. The average Ct values from OP swabs were consistently higher than values from cloacal swabs supporting replication of the viruses in the gastrointestinal tract. Incomplete seroconversion was observed in the two week old birds. The results of this study indicate that although age does not affect susceptibility to infection with LPAI viruses, it does influence the extent of viral shedding. The higher prevalence of infection observed in juvenile ducks under field situations has generally been attributed to acquisition of population immunity to these viruses. It is possible that the maturation of the immune system also may affect these differences in prevalence, along with additional factors related to host behavior and biology.

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34. AVIAN INFLUENZA INFECTION DYNAMICS AMONG SHOREBIRD HOSTS AT THE DELAWARE BAY SPRING MIGRATION STOPOVER SITE

Angela M. Maxted, M. Page Luttrell, Virginia Goekjian, and David E. Stallknecht, Southeastern Cooperative Wildlife Disease Study, The University of Georgia, 589 D.W. Brooks Drive, Athens, GA, 30602, USA

Presenting author: Maxted, Angela

Summary: While our current and prior research has demonstrated that ruddy turnstones (Arenaria interpres) are capable of amplifying avian influenza viruses (AIV) over short time spans and within local areas, the infection dynamics observed in this study suggest that shorebirds are not large scale maintenance hosts for AIV.

Thorough understanding of AIV epizootiology in shorebirds is necessary to determine this group’s ability to maintain AIV in nature. Our objective was to examine temporal interactions between AIVs and their shorebird hosts during spring migratory stopover at Delaware Bay, with a particular focus on disease dynamics within ruddy turnstones (Arenaria interpres). During three spring migration stopovers (2006-2008), shorebirds were captured with cannon nets by New Jersey and Delaware state personnel for a long-term population study. Cloacal samples were collected with sterile cotton swabs and placed in 2ml of brain-heart infusion transport media containing antibiotics. AI viruses were isolated in embryonated chicken eggs according to established protocol. Blood samples (<1% of an individual’s body mass) were collected by jugular venipuncture. Serum samples were tested for antibodies against AIV internal proteins using agar gel immunodiffusion. Statistical analyses, including regression model fitting, were performed using program JMP. Fitted time series plots of AIV prevalence and seroprevalence in ruddy turnstones over the course of the stopover revealed patterns typical of an epizootic. Peak AIV prevalence (8.0-22.7%) occurred between 22-25 May with 80% population seroconversion by 29 May. AIV prevalence in sanderlings was positively correlated with prevalence in ruddy turnstones. Although ruddy turnstones at Delaware Bay appear to be competent hosts for AIV infection, the marked epizootic prevalence and seroconversion patterns observed indicate that nearly all infected birds acquire infection locally and recover before resuming northward migration. However, lack of persistent antibodies in ruddy turnstones may allow recurrent AIV infection. Rare infections in sympatric shorebird species may be due to relatively higher population immunity upon arrival, and likely result from virus spillover events.

Acknowledgements: We thank USDA-ARS for funding this project, and Mandy Dey, Kevin Kalasz, and Larry Niles for capture of and permissions to sample shorebirds in New Jersey and Delaware.
35. EVALUATION OF CANADA GEESE *(BRANTA CANADENSIS)* AS SENTINELS FOR DETECTING LOCAL TRANSMISSION OF AVIAN INFLUENZA VIRUSES

Whitney Kistler, Michael J. Yabsley, Southeastern Cooperative Wildlife Disease Study, The University of Georgia, Athens, GA, 30602, USA; Daniel B. Warnell, School of Forestry and Natural Resources, The University of Georgia, Athens, GA, USA; David E. Stallknecht, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA, USA; Thomas J. Deliberto, Kyle Van Why, Paul C. Wolf, Darren L. Bruning, James C. Cumbee, Randall M. Mickley, Carl W. Betsill, United States Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services, National Wildlife Disease Program, Fort Collins, CO, USA

Presenting author: Kistler, Whitney

Summary: Using serological testing, Canada geese were shown to be effective sentinels for detection of local transmission of avian influenza virus.

Little is known about local transmission and maintenance of avian influenza (Al) viruses. Canada geese (*Branta canadensis*) were tested as sentinels because they have a near ubiquitous distribution, are easy to sample, and frequent areas where other AIV hosts are present. To evaluate Canada geese as sentinels for avian influenza viruses, 953 serum samples were collected from nine states (GA, MA, MN, MS, NC, NJ, PA, WA, and WV). Sample collection took place during the summer of 2008. Agar gel immunodiffusion (AGID) and a commercial blocking ELISA (bELISA) tests were used to detect antibodies to Al viruses. After initial serological testing, positive samples and a subset of negative samples will be serotyped using a virus neutralization assay. Highest antibody prevalence rates were detected in Massachusetts (21.1% AGID, 31.6% bELISA), Minnesota (9.6%, 22.9%), and Pennsylvania (5.3%, 25%). Few positives were detected in Mississippi (0%, 0.9%), North Carolina (0.9%, 0.9%) and West Virginia (0%, 7.3%). Overall, significantly more geese were positive by bELISA (113 (11.9%) compared with AGID (30 (3.1%)). These results indicate that the bELISA assay is more sensitive than the AGID assay. Additionally, a higher prevalence was detected at sites in northern states as compared with sites in southern states. These data are in agreement with virus isolation data from ducks which indicate viral shedding is highest in northern wintering states. Furthermore, the results indicate high levels of exposure in geese and we believe that they can be effectively utilized as sentinels for regional and local transmission of Al viruses.

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36. INVESTIGATION OF AN OUTBREAK OF BOVINE TUBERCULOSIS IN THE HOOK LAKE WOOD BISON RECOVERY PROJECT HERD

Chelsea G. Himsworth, Department of Veterinary Pathology, Western College of Veterinary Medicine, 52 Campus Drive, Saskatoon, SN, S7N 5B4 Canada; Brett T. Elkin and John S. Nishi, Wildlife Division, Government of the Northwest Territories Environmental and Natural Resources, 5102 50th AVE, Yellowknife, NWT, X1A 3S8, Canada; Aleksija S. Neimanis, Department of Pathology and Wildlife Diseases, National Veterinary Institute, SE 751 89 Uppsala, Sweden; Claude Turcotte and Om Surujballi, Canadian Food Inspection Agency, Mycobacterial Diseases Center of Expertise, Ottawa Laboratory Fallowfield, 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada; Konstantin P. Lyashchenko, Chembio Diagnostic Systems, Inc., 3661 Horseblock Road, Medford, NY, 11763, USA; Fredrick A. Leighton, Canadian Cooperative Wildlife Health Center, Department of Veterinary Pathology, Western College of Veterinary Medicine, 52 Campus Drive, University of Saskatchewan, SK, Saskatchewan, S7N 5B4, Canada

Presenting author: Himsworth, Chelsea

Summary: This study highlights difficulties associated with salvaging tuberculosis-free animals from endemically infected herds, including the possibility of undetected Mycobacterium bovis infection and the inconsistent performance of ante-mortem tuberculosis diagnostic tests.

The Hook Lake Wood Bison Recovery Project was initiated to create a tuberculosis-free captive bison (Bison bison) breeding herd using calves captured from infected wild herds. Nine years into the project, bovine tuberculosis (bTB) was detected and the herd was destroyed. This study investigated bTB epidemiology and test performance in this herd. Herd management records and both ante-mortem and post-mortem bTB test data were analysed. Qualitative methods were used to determine the most likely source of infection. Quantitative methods were used to assess the ante-mortem performance of the caudal fold test (CFT), Fluorescent Polarization Assay (FPA), Multiantigen Print Immunoassay (MAPIA), and Rapid test (RT) through comparison to post-mortem culture and histopathology results. The most likely source of bTB in this herd was a wild-caught founder animal with chronic bTB omphalophlebitis. Ante-mortem tuberculosis test performance was inconsistent during the project, and although the MAPIA appeared to have superior diagnostic sensitivity, some infected bison escaped detection by all ante-mortem tests. While the sensitivity of ante-mortem bTB testing in bison can be optimized through use of multiple diagnostic tests in parallel, and by inclusion of tests that utilize multiple antigens, there remains a significant potential for infected animals to escape detection and be misidentified as bTB-free for many years.
37. SEX–SPECIFIC CONTACT RATES: POTENTIAL ROUTES OF DISEASE TRANSMISSION IN ELK (CERVUS ELAPHUS)

Eric Vander Wal, Philip D. McLoughlin, Francois Messier, Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK, S7N 5E2, Canada; Doug Bergeson, Parks Canada, 118 Wasagaming Drive, Wasagaming, MB, R0J 2H0, USA; Paul C. Paquet, Faculty of Environmental Design, University of Calgary, 2500 University Drive NW, Calgary, AB, T2N 1N4, Canada

Presenting author: Vander Wal, Eric

Summary: Unequal contact rates across seasons and among sex combinations of elk (Cervus elaphus) dyads imply separate routes of bTb (Mycobacterium bovis) transmission.

Contact rate is one of the most fundamental variables for understanding disease transmission among individuals. It is, however, very difficult to obtain biologically realistic estimates that are relevant to the pathogen or consequent disease of concern. Bovine tuberculosis (bTb; Mycobacterium bovis) is one such pathogen of concern to wildlife. Elk (Cervus elaphus) are thought to be the primary reservoir species for bTb in the Riding Mountain National Park (MB, CAN) region. Ongoing monitoring suggests that adult female and male elk have similar bTb prevalence. Logically, several hypotheses follow: one suggests homogeneous transmission of bTb among elk (i.e., equal contacts between female–female, female–male, and male–male). We fitted female and male elk with SirTrack proximity collars in 2007–2009. Contacts consisted of events where two collared animals were ≤1 m apart. We recorded data on contact time and duration. We compared seasonal contact rates among sex combination dyads. We observed limited inter–sex contacts and differences between female–female and male–male contact rates. Female–female contacts occurred more frequently than male–male and female–male contacts. The understanding of bTb disease ecology (e.g., intraspecific transmission and contact rates) in social ungulate populations, particularly elk, is limited. The implication of heterogeneous inter–sex contact rates is that sex–specific routes of bTb transmission might occur within the population, consequently affecting the approach for management or eradication of the disease.

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38. BRUCELLOSIS IN BARREN-GROUND CARIBOU ON SOUTHAMPTON ISLAND, NUNAVUT

N. Jane Harms, University of Saskatchewan, Western College of Veterinary Medicine, Department of Veterinary Pathology, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada; Mitch Campbell, Government of Nunavut, Department of Environment, PO Box 120, Arviat, Nunavut X0C 0E0, Canada; Brett T. Elkin, Government of the Northwest Territories, Department of Environment and Natural Resources, 600, 5102-50th Avenue, Yellowknife, NWT, X1A 3S8, Canada; Klaus Neilsen: Canadian Food Inspection Agency, Ottawa Laboratory (Fallowfield; OLF), 3851 Fallowfield Rd. PO Box 11300, Ottawa, ON, K2H 8P9, Canada; Frederick A. Leighton and Aleksija S. Neimanis, University of Saskatchewan, Western College of Veterinary Medicine, Department of Veterinary Pathology, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada

Presenting author: Harms, N. Jane

Summary: Rangiferine brucellosis may result in severe reproductive tract lesions in both male and female caribou. Brucellosis likely affects the reproductive performance of individual animals and may have a negative effect on the overall reproductive success of the herd.

Rangiferine brucellosis, caused by Brucella suis biovar 4, is present in barren-ground caribou (Rangifer tarandus) herds across North America. Only recently has evidence of brucellosis been found in caribou on Southampton Island, Nunavut, and the population is in decline. This study was undertaken to assess brucellosis as a factor in the low reproductive success of the herd. The testes and epididymi from 20 male caribou and the uteri (n=20), and both uteri and placentae (n=16) from female caribou from Southampton Island were collected, examined for gross and histologic lesions, and tested for evidence of B. suis using AMOS-PCR. Sera from the examined caribou were tested for evidence of exposure to Brucella spp. using the fluorescence polarization assay and the competitive ELISA. Multiple tissues from 15 fetuses were also examined histologically. Nearly all male caribou with gross lesions had histologic lesions and all were AMOS-PCR positive for B. suis. Though no gross or histologic lesions were noted in the reproductive tract of pregnant females, 7 of 16 were positive for B. suis on AMOS-PCR. Histologic lesions were noted in uteri of 4 of 20 of the non-pregnant females, and 12 of 20 were AMOS-PCR positive. Brucella suis is present in the reproductive tracts of caribou on Southampton Island, and is a cause of pathologic lesions that range in distribution and severity. All male caribou with gross lesions were positive on AMOS-PCR, but females with no lesions were also positive, and 1 of 4 females with histologic lesions were negative. Rangiferine brucellosis may be a factor in the declining reproductive success of the herd and poses a zoonotic risk to humans who contact infected animals.

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39. THE ELK BRUCELLOSIS TEST-AND-SLAUGHTER PROGRAM: DOES IT WORK?

Laura L. Meadows, Todd E. Cornish, University of Wyoming, Department of Veterinary Sciences, 1174 Snowy Range Road, Laramie, WY 82070, USA; Matthew J. Kauffman, University of Wyoming, Department of Zoology and Physiology, 1000 E. University, Biological Science Building Room 419, Laramie, WY 82071, USA; Timothy J. Robinson, University of Wyoming, Department of Statistics, 1000 E. University, Dept. 3332, Laramie, WY 82071, USA; William H. Edwards, Cynthia Tate, Wyoming Game and Fish Department, 1147 Snowy Range Road, Laramie, WY, 82070, USA; Terry J. Kreeger, Wyoming Game and Fish Department, 2362 Highway 34, Wheatland, WY 82201, USA

Presenting author: Meadows, Laura

Summary: The Wyoming Game and Fish Department has successfully decreased brucellosis seroprevalence in feedground elk following implementation of a 5-year test-and-slaughter pilot program.

In an attempt to reduce inter- and intraspecific transmission of brucellosis, the Wyoming Game and Fish Department implemented a five-year pilot test-and-slaughter program in 2006. The pilot program is focused on the Muddy Creek feedground with the primary objective to achieve a statistically significant reduction in brucellosis seroprevalence. In the winters of 2006-2009, elk (Cervus elaphus) were captured in a corral trap on Muddy Creek feedground in western Wyoming. Serum collected from adult (>= 1.5 year old) females was tested for antibodies to B. abortus using standard serum assays (card, standard plate, rivanol and complement fixation tests and the fluorescence polarization assay). A competitive ELISA was used to identify Brucella strain-19 vaccine titers. Seropositive elk were slaughtered and tissues collected for bacterial culture. isolates were identified as B. abortus by biochemical and molecular tests. Two incisors were collected for cementum annuli analysis to estimate age of each seropositive elk. To date, 1021 elk have been tested for exposure to B. abortus with 163 found to be seropositive and shipped to slaughter. From 2006 to 2009, annual seroprevalence on the Muddy Creek feedground was 36.71%, 16.46%, 12.66% and 7.0%, respectively. The average decline was 9.18% per year. We have demonstrated a decline in brucellosis seroprevalence each year of the project suggesting that test-and-slaughter may be an effective tool to reduce the risk of brucellosis transmission, but final statistical analyses are underway. The results of our analyses will assist laboratory technicians to more accurately identify elk that have an active Brucella infection and provide vital information to help determine if the program should be expanded beyond the pilot stage.

Acknowledgements: Thanks to all of the wardens, biologists, technicians, graduate students and externs who helped with trapping and sample collection. Special thanks to the crew in the WGFD Wildlife Disease Lab.
40. CHARACTERIZATION OF MALIGNANT CATARRHAL FEVER VIRUSES IN TENNESSEE CERVID POPULATIONS UTILIZING REAL-TIME POLYMERASE CHAIN REACTION

Robin L. Cissell, Stephen Kania, Robert Donnell, University of Tennessee, College of Veterinary Medicine Department of Pathobiology, 2407 River Drive, Knoxville, TN 37996, USA

Presenting author: Cissell, Robin

Summary: Malignant Catarrhal Fever viruses (MCFVs) infect livestock and wildlife and may cause disease or death. We are performing real-time PCR on blood and/or lymph node samples from white-tailed deer and other cervids to determine which of these viruses may have been transmitted from or may be transmitted to domestic livestock.

Malignant Catarrhal Fever viruses infect livestock and wildlife and may cause disease or death. We believe domestic MCFV carriers interact with cervids spreading MCFVs into the population, and white-tailed deer (Odocoileus virginianus) associated-MCFV is endemic in white-tailed deer populations. We intend to estimate the prevalence of MCFVs in Tennessee cervid populations. Convenience samples including blood, lymph nodes, liver and/or spleen were obtained from cervids harvested in the 2006-2008 hunting seasons, University of Tennessee necropsy services, and local mixed species farms. DNA was extracted from all tissue and/or blood samples using the DNeasy Tissue Kit (Qaigen, Valencia, CA). Real time PCR primers and probe to detect Ovine Herpesvirus-2 (OvHV-2), MCFV-WTD and Caprine Herpesvirus-2 (CpHV-2) were developed based upon gene information for each virus published on GenBank, accession numbers AY839756, AF387516 and AF283477 respectively. All samples will be analyzed for presence of these three MCFVs utilizing the StepOne® unit (Applied Biosystems). To date MCFV-WTD positive samples were detected in 4 cervids of 278 tested, giving an estimated prevalence of 1.4%. Thus far, none of 230 cervids were positive for CpHV-2 DNA. OvHV-2 DNA screening will be performed. DNA extractions and screening of additional samples for MCFV viral DNA is ongoing. Seroprevalence of MCFV antibody has been investigated previously in cervid species, but the most commonly utilized technique (competitive inhibition ELISA) does not allow characterization of the specific MCFV to which the animal has been exposed. Development of real-time PCR to specifically identify the MCFV infecting cervids will help identify the source of disease in the population. Characterization of MCFV prevalence may also identify a source of morbidity and mortality in cervid populations not previously investigated.

Acknowledgements: DNA from an MCFV-WTD positive deer and CpHV-2 infected deer was provided by Dr. Hong Li of the USDA-ARS for use as controls. Kate Carpenter provided assistance in the laboratory.
41. APPLICATION OF SPATIAL GENETIC ANALYSES TO REVEAL CORRELATIONS BETWEEN WHITE-TAILED DEER DISPERSAL AND CHRONIC WASTING DISEASE SPREAD IN WISCONSIN

Stacie J. Robinson, Michael D. Samuel, University of Wisconsin, Madison, WI, 53706, USA; Julie A. Blanchong, Iowa State University, Ames, IA, 50011, USA; Kim T. Scribner, Michigan State University, East Lansing, MI, 48824, USA; Julie A. Langenberg, Wisconsin Dept. of Natural Resources, Madison, 2801 Progress Road, WI, 53707, USA; Daniel A. Grear, Penn State University, University Park, PA 16802, USA

Presenting author: Robinson, Stacie J.

Summary: We present genetic patterns of white-tailed deer (Odocoileus virginianus) dispersal as related to CWD spread around two core infected areas in Wisconsin. Comparison of these patterns suggests variation in deer movement and disease spread in different landscapes.

Chronic wasting disease (CWD) in Wisconsin is concentrated in two foci, disease sparks radiating from each. It is suspected that deer (Odocoileus virginianus) dispersing from CWD-affected areas into naïve populations contribute to CWD spread. To understand the pattern and risk of CWD spread we investigated gene flow patterns of deer surrounding disease foci. We used a landscape genetic approach to correlate patterns of genetic dispersal to geographic disease patterns around the western and eastern CWD cores in southern Wisconsin. We used measures of genetic autocorrelation to define the extent genetic neighborhoods in each area. We also used spatial autocorrelation to describe the clustering of CWD prevalence around each core area. We then used linear regression to determine the strength of association between the patterns of genetic neighborhoods and CWD prevalence. We found marked differences in genetic neighborhoods of the western versus eastern core areas. Dispersal was more localized in the heavily forested west, while gene flow ranged farther in the east with more fragmented habitat. The degree to which genetic dispersal predicted CWD spread also differed between west and east. Spatial patterns of CWD prevalence differed in western and eastern areas. They also related differently to deer dispersal, indicating that diverse factors may be contributing to spread of disease around each core area. By examining environmental differences between the western and eastern landscapes we will be able to better determine the underlying drivers shaping patterns of CWD spread. Future risk assessment and management of disease will rely on understanding of these localized processes.
42. INFLUENCE OF BIOTIC AND ABIOTIC FACTORS ON MARINE MAMMAL STRANDINGS IN THE SAINT-LAWRENCE ESTUARY AND GULF OF ST. LAWRENCE (1994 TO 2008)

Marie-Hélène Truchon, Maurice-Lamontagne Institute, 850 de la Mer, Mont-Joli, QC, G5H 3Z4, Canada; Institut des Sciences de la Mer, 310 allée des Ursulines, Rimouski, QC, G5L 3A1, Canada; Lena Measures, Maurice-Lamontagne Institute, 850 de la Mer, Mont-Joli, QC, G5H 3Z4, Canada; Jean-Claude Brêthes, Institut des Sciences de la Mer, 310 allée des Ursulines, Rimouski, QC, G5L 3A1, Canada

Presenting author: Truchon, Marie-Hélène

Summary: This study of biotic and abiotic factors in the St. Lawrence Estuary (SLE) and Gulf of St. Lawrence (GSL) with respect to marine mammal stranding events demonstrates the value of stranding data as indicators of oceanographic and environmental changes including events such as toxic algal blooms, and helps in monitoring trends in marine mammal populations.

Marine mammal strandings have occurred annually over many decades within the St. Lawrence ecosystem. No studies have analyzed rigorously temporal stranding patterns with respect to environmental influences. To better understand environmental mechanisms driving temporal variations of marine mammals strandings, we systematically analysed stranding records from 1994 to 2008. Numbers of stranding events were used as the sampling unit for analysis excluding drifting carcasses, cases involving human activities and non-verifiable cases. Temporal patterns were analysed by ANOVA and Kruskal-Wallis tests. Biotic and abiotic factors associated with variations in strandings were performed using a multivariate redundancy analysis (RDA) and multiple regression models using R, version 2.8.1. We observed an increase in strandings over time (p<0.001; R2adj.=0.65 ) with a strong seasonal pattern for all species. Number of strandings was higher in summer than other seasons. Annual variations in numbers of summer strandings were principally explained by krill abundance and species-specific abiotic factors such as sea surface temperature. Results indicate that resource availability could be a driving factor influencing stranding events with other factors (i.e. sea surface temperature, volume of cold intermediate water layer) having an indirect influence on productivity. In 2008 strandings observed during late summer were associated with an *Alexandrium tamarense* toxic algal bloom. Biotic and abiotic factors affect marine mammals in the St. Lawrence ecosystem and stranding data have proved useful in monitoring some effects of oceanographic changes.
43. PREVALENCE OF POTENTIALLY PATHOGENIC BACTERIA IN THE FECES OF STRANDED AND WILD HARBOR SEALS (PHOCA VITULINA) IN CENTRAL CALIFORNIA

Denise J. Greig, Frances M.D. Gulland, Elizabeth A. Wheeler, The Marine Mammal Center, 2000 Bunker Road, Sausalito, CA 94965, USA; Spencer Jang, William R. Pritchard Veterinary Medical Teaching Hospital, School of Veterinary Medicine, University of California, Davis, Davis, CA 95616, USA; Ailsa J. Hall, Sea Mammal Research Unit, Scottish Oceans Institute, University of St Andrews, St Andrews KY16 8LB, UK

Presenting author: Greig, Denise

Summary: This study demonstrates that harbor seals are exposed to and can spread fecal zoonotic bacteria especially Vibrio parahemolyticus, in coastal waters.

As the coastal human population grows, there is concern about bacteria flowing from land to sea and affecting the marine ecosystem and human health. Harbor seals (Phoca vitulina) inhabit this land/sea interface, can be infected with zoonotic bacteria, and may play a role in the dynamics of coastal bacteria. Our objective was to compare the prevalence of fecal bacteria between stranded, sick harbor seals and apparently healthy wild harbor seals from different locations. Fecal swabs were collected from sick, injured and orphaned seals (n=135) along the central California coast on admission to rehabilitation and from wild harbor seals in San Francisco (SF, n=38) and Tomales (TB, n=61) bays. Fecal swabs were cultured for Escherichia coli O157, Clostridium perfringens, Vibrio spp., Campylobacter spp., and Salmonella spp. Binomial tests (R version 2.7.2) were used to detect differences in prevalence between stranded and wild caught harbor seals. Clostridium perfringens was more prevalent among stranded (57%) than wild seals (41%, p=0.019). Vibrio spp. were more prevalent among wild (24%) than stranded seals (12%, p=0.021). Vibrio parahemolyticus was detected in SF (42%) but not TB. Small numbers of Vibrio cholerae were detected from SF (2.6%) and stranded (5.9%) seals. E. coli O157 is rare in marine mammals and was not detected in this study. The high prevalences of Clostridium perfringens likely represent normal enteric flora. Campylobacter spp. and Salmonella spp. prevalences were low (<15%), with no differences between wild and stranded seals. These bacteria were not associated with overt disease. This study demonstrates that seals are exposed to and can spread fecal zoonotic bacteria, especially V. parahemolyticus, in coastal waters.
44. THE PHYSICAL EFFECTS OF CHEMICALLY AND PHYSICALLY DISPERSED OIL ON WILDLIFE

Rebecca S. Duerr, Animal Science Department, University of California, Davis, One Shields Ave, Davis, CA 95616, USA; Michael H. Ziccardi, J. Gregory Massey, Oiled Wildlife Care Network, Wildlife Health Center, School of Veterinary Medicine, University of California, Davis, One Shields Ave, Davis, CA 95616, USA; Yvonne Addassi, Office of Spill Prevention and Response, California Department of Fish and Game, 1700 K St, Sacramento, CA 95814, USA

Presenting author: Duerr, Rebecca

Summary: At the concentrations measured in this study, Corexit 9500 may impact the waterproofing characteristics of feathers through alterations in the geometry of feather microstructures and an increase in deposition of crystalline particulate material.

Oil spill dispersants have pre-approval for use under certain circumstances, due to presumed benefit to surface-dwelling animals. This study models the effects of an animal swimming through a plume of dispersed oil to identify physical changes to feathers or hair associated with exposure to varying concentrations of oil and dispersant. Test solutions were generated using CROSERF procedures (NRC, 2005. Oil Spill Dispersants: Efficacy and Effects, pg 200-1). Common murre (Uria aalge) feathers and sea otter (Enhydra lutris) pelt swatches were randomly assigned to 10 exposure solutions: Plain Instant Ocean (IO), IO and oil x 3 concentrations, IO and dispersant x 3 concentrations, and IO with oil and dispersant x 3 concentrations. Light microscopy, SEM, and x-ray mapping were utilized to examine exposed tissues. Exposed feathers were geometrically evaluated. A blinded observer scored images for changes. TPH measures were obtained for unexposed feathers and fur, exposure solutions, and feathers and fur exposed to each solution. Common murre feathers exposed to solutions containing Corexit 9500, with or without the addition of Prudhoe Bay crude oil, showed geometric alterations in microstructural spacing and increased amounts of crystalline particulate material as compared to feathers exposed to plain seawater or mechanically dispersed oil. No significant changes were seen in exposed otter pelt. This preliminary study attempts to address the dearth of information regarding the effects of dispersants on birds and mammals at risk of oil exposure. We found that exposure to dispersants may adversely affect waterproofing by altering the geometry of feather structures and increasing the amount of crystalline particulate material on exposed feathers. Further studies are needed to provide response agencies with more complete information involving risks and benefits of dispersant use after oil spill events.

Acknowledgements: This study was supported by the California Department of Fish and Game's Office of Spill Prevention and Response Scientific Study and Evaluation Program.
45. BREVETOXIN INDUCED MORBIDITY AND MORTALITY IN STRANDED SEA TURTLES AND SEA BIRDS IN FLORIDA

Deborah Fauquier, Charles Manire, Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, FL 34236, USA; Leanne Flewelling, Jan Landsberg, Fish and Wildlife Research Institute, 100 Eighth Ave. SE, St. Petersburg, FL 33701, USA; Martha Keller, Pelican Man’s Bird Sanctuary, 1708 Ken Thompson Parkway, Sarasota, FL 34236, USA; Christine Kreuder, Wildlife Health Center, UC Davis, One Shields Ave, Davis, CA, USA

Presenting author: Fauquier, Deborah

Summary: The majority of the sea birds and sea turtles sampled during the 2005 and 2006 red tide events were positive for brevetoxin, indicating that brevetoxin intoxication may play a larger role in the morbidity and mortality of sea birds and sea turtles off the west coast of Florida than previously recognized.

On Florida’s west coast, the most prevalent harmful algal bloom involves the red tide organism, Karenia brevis, a dinoflagellate that produces brevetoxins. This study investigated the extent that brevetoxin intoxication contributed to morbidity and mortality in stranded sea turtles and sea birds along the central west coast of Florida. Stranded sea turtles and sea birds were recovered and brought into rehabilitation or necropsied at two rehabilitation centers from 2005 through 2007. Blood or fecal samples, (including serial blood or fecal samples from a select number of live animals), were collected from animals on admission. Dead animals were necropsied and tissues collected for histopathology. Tissues collected for brevetoxin analysis included bile, feces, kidney, liver, lung, and stomach contents. A competitive ELISA to detect brevetoxins (PbTX) was performed according to Naar et al. (2002) on tissues and plasma, and a direct ELISA was performed according to Maucher et al. (2007) on whole blood. Two red tide events occurred: January-October 2005 and August-December 2006. Sea birds and sea turtles stranding during these events had clinical signs of brevetoxicosis including disorientation, paralysis, and seizures. Brevetoxicosis appeared to contribute to stranding in 69% (n=94) of sea birds and 94% (n=54) of sea turtles. The majority of stranded sea birds and sea turtles in 2005-2007 were positive for brevetoxin in blood, feces or at least one tissue at necropsy. Brevetoxin intoxication may play a greater role in regulating populations by negatively impacting individual health and decreasing survival. Sea birds cleared the toxin in 5-10 days and sea turtles cleared the toxin in 30-50 days. Treatment should focus on ways to increase excretion of the toxin in animals undergoing rehabilitation.

Acknowledgements: We thank the staff and volunteers of Mote Marine Laboratory, Pelican Man’s Bird Sanctuary, and the Florida Sea Turtle Stranding Network. This project was supported by Morris Animal Foundation and an EPA Star Fellowship.
46. THE ECOLOGY OF ASPERGILLOSIS IN SEA BIRDS: BRIDGING THE GAP BETWEEN ENVIRONMENT AND DISEASE VIA MICROSATELLITE ANALYSIS

Julia D. Burco, J. Gregory Massey, and Michael H. Ziccardi, Wildlife Health Center, School of Veterinary Medicine, University of California, One Shields Ave., Davis, CA 95616, USA; Barbara A. Byrne, Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California, One Shields Ave., Davis, CA 95616, USA; Kízee A. Etienne and Arummozhi Balajee, Mycotic Disease Branch, Center for Disease Control and Prevention, 1600 Clifton Rd., Atlanta, Georgia, 30333, USA

Presenting author: Burco, Julia

Summary: Higher environmental loads of Aspergillus fumigatus in rehabilitation centers, as well as evidence of closely related genotypes between clinical cases and the local rehabilitation environment, suggest that sea birds often acquire and develop disease while in captivity. Therefore, management actions should target a reduction of Aspergillus fumigatus in microenvironments to which birds are exposed during the rehabilitation process.

Aspergillosis remains a major contributor to sea bird mortality during oil spill responses and while undergoing rehabilitation. Until recently, it has largely been unknown how local environmental load plays a role in development of disease, and whether diseased birds acquire Aspergillus spp. from their natural environments or while undergoing rehabilitation. Air, water, and surface sampling were performed in three sea bird rehabilitation facilities and six natural sea bird loafing areas along the northern California coast. Aspergillus fumigatus isolates from these environmental samples (n=51), as well as clinical samples from sea birds undergoing rehabilitation at a large aquatic bird rehabilitation between Feb. 2006 and Feb. 2008 (n=34), were banked and subsequently genotyped using microsatellite analysis. A combination six STRAf (deValk, 2005, J Clin Microbiol 43:4112-20) and BD (Bart-Delabesse, 1998, J Clin Microbiol 36:2413-8) primers were used to amplify different loci and create a dendrogram. Aspergillus spp. and A. fumigatus air fungal load was found to be significantly higher in the rehabilitation centers when compared to natural sea bird environments (p<.05). Although genetic diversity of A. fumigatus was high (82 distinct isolates), there were close genetic clusters between local rehabilitation and clinical samples.

A higher rehabilitation center environmental load of A. fumigatus, as well as evidence of closely related genotypes between clinical and the local rehabilitation environment, suggest that sea birds often acquire and develop disease in captivity. Various outdoor microenvironments in the rehabilitation environment also appear to have higher Aspergillus spp. loads locally, which could be useful information in developing management recommendations.

Acknowledgements: Funding for this research was provided by the Oiled Wildlife Care Network. Special thanks to staff of the Farallon National Marine Sanctuary, International Bird Rescue Research Center, and UC Davis Wildlife Health Center.
47. EVIDENCE OF LEAD EXPOSURE IN A FREE-RANGING POPULATION OF KEA (NESTOR NOTABILIS)

Jennifer M. McLelland*, Brett D. Gartrell, Wendi D. Roe, New Zealand Wildlife Health Centre, Institute of Veterinary and Biomedical Sciences, Massey University, New Zealand; Clio Reid, School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington, New Zealand; Kate Mclnnes, Department of Conservation, 18-32 Manners St, Wellington, New Zealand
*current address, 86A Ashley St, Torrensville, SA, 5031, Australia

Presenting author: McLelland, Jennifer

Summary: This study found that lead exposure was ubiquitous across the study population and may be an important factor in kea morbidity and mortality, as a result lead abatement in areas frequented by kea is being considered.

Kea (Nestor notabilis) are threatened high-country parrots endemic to New Zealand. Their foraging behavior and inquisitive nature frequently leads to foreign substance ingestion. This study examined lead exposure by surveying blood lead concentrations in a population of wild kea by reviewing pathology database archives and analyzing lead concentrations in archived tissue samples. Between April 2006 and November 2007, 38 kea of various ages visiting the Aoraki/Mt Cook Village and national park in the South Island of New Zealand were captured, examined and blood collected. Blood was analysed for lead content using a portable blood lead analyser (LeadCare®, ESA Inc, Chelmsford, Massachusetts, 01824, USA). Blood for hematology and biochemsistry was submitted to a commercial laboratory. A retrospective analysis of wild kea pathology and archived samples was also carried out. Necropsy reports were reviewed and fresh frozen and formalin-fixed liver and kidney were analysed for lead. All birds sampled had detectable blood-lead concentrations ranging from 0.028 mg/L to 3.43 mg/L (mean = 0.428 mg/L ± 0.581). Elevated tissue-lead with Ziehl-Neelson positive intra-nuclear inclusion bodies in the renal tubular epithelial cells was found in 7 of 15 kea necropsied. Other pathological findings were not consistent between birds. This study has demonstrated a severe anthropogenic health problem affecting the sample population. Lead on buildings and rubbish is a threat to kea. The potential effects of lead on intelligence and learning ability (Burger & Gochfeld, 2005, Neurotox, 26:615-624; Needleman, 2004. Ann. Rev. Med, 55:209-222) as well as other body systems may be detrimental to the survival of the species. Our study examines a single population and further work to investigate the exposure to lead of different age groups of kea at this and other locations is underway.

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48. BUILDING A BRIDGE BETWEEN SCIENCE AND SOCIETY: THE IMPLICATIONS OF SPENT LEAD FROM AMMUNITION

Patrick T. Redig, Luis Cruz-Martinez, The Raptor Center, College of Veterinary Medicine, University of Minnesota, 1920 Fitch Avenue, St. Paul, MN 55108, USA; Donald R. Smith, PhD., Department of Environmental Toxicology, University California Santa Cruz, 1156 High Street, University of California, Santa Cruz, California 95064, USA

Presenting author: Cruz-Martinez, Luis

Summary: To present science-based evidence that links spent lead from ammunition used for deer hunting as a major source of exposure and intoxication for bald eagles and to illustrate the potential risks for humans consuming game shot with lead-based ammunition.

The prevalence of lead poisoning in bald eagles (Haliaeetus leucocephalus) admitted at The Raptor Center has remained constant despite the banning of lead shot for waterfowl hunting. Our hypothesis is that spent lead from ammunition present in deer (Odocoileus spp.) carcasses and gut piles represent an important source of lead exposure for eagles. Our sample size consisted of 300 lead poisoned bald eagles admitted at The Raptor Center from 1996 to 2008. The medical records of these birds were analyzed for four epidemiological parameters: 1) seasonal prevalence and relationship with deer hunting season onset in Minnesota, Wisconsin and Iowa; 2) correlation of the animal recovery location with deer hunting zones; 3) lead isotope ratio analysis of metal fragments recovered from the gastrointestinal tract of lead-poisoned bald eagles and of whole blood; and 4) comparison of kidney copper concentrations from lead-exposed vs. non-exposed eagles. We established a significant seasonal and geographical association (p<0.01) between deer season and deer hunting zones with the incidence of eagle poisoning. The lead isotope ratio analysis from blood and fragment samples was within the isotope ratio from ammunition samples. Kidney copper concentrations were significantly higher in lead-exposed eagles (p=0.002). Our results strongly support the hypothesis that spent lead from ammunition represents a source of lead exposure for eagles. These results are in accordance with a significant body of scientific study linking spent lead from ammunition with the poisoning of wildlife species worldwide. This linkage prompted the discovery of lead fragments in venison in 2007. This finding has raised concerns about human exposure to lead from the consumption of venison and other hunted game meat.
49. CYLICOSPIRURA SPECIES (NEMATODA: SPIOERCIDAE) AND STOMACH NODULES IN COUGARS (PUMA CONCOLOR) AND BOBCATS (LYNX RUFUS) IN OREGON

Jayde A. Ferguson, Oregon State University, Department of Microbiology, 220 Nash Hall, Corvallis, OR, USA; Karen Woodberry, Tufts University Cummings School of Veterinary Medicine, 200 Westboro Rd., N. Grafton, MA, USA; Colin M. Gillin, State Veterinarian, Oregon Department of Fish and Wildlife, 7118 Vandenberg Ave., Corvallis, OR, USA; DeWayne H. Jackson, Research Project Leader, Oregon Department of Fish and Wildlife, Roseburg, OR, USA; Justin Sanders, Whitney Madigan, Oregon State University, Department of Microbiology, 220 Nash Hall, Corvallis, OR, USA; Robert J. Bildfell, Oregon State University, College of Veterinary Medicine, 146 Magruder Hall, Corvallis, OR; Michael L. Kent, Oregon State University, Department of Microbiology, 220 Nash Hall, Corvallis, OR, USA

Presenting author: Ferguson, Jayde

Summary: We characterized nodular stomach worms infecting cougars by morphological and molecular analyses and showed support that severe infections are associated with cougars killed for safety concerns.

Oregon cougars (Puma concolor) are regularly euthanized because they threaten safety of domestic animals and humans. Previous necropsies indicated these cats had prominent stomach nodules. Cylicospirura felineus and C. subaequalis are two nodular-forming nematodes that infect North American felids but historically have not been detected in Oregon felids. Some biologists hypothesize these infections are linked to aberrant behavioral changes. Stomachs and proximal duodena of 160 cougars and 17 bobcats (Lynx rufus) collected from 1999-2007 were examined for Cylicospirura spp. Worms were identified by comparing teeth morphology. Histology (H&E or Mason’s trichrome) was also performed. We statistically compared worm burden between cougars killed due to aberrant behavior to those killed by hunters or for other reasons. Cylicospirura spp. from eight cougars and eight bobcats were used to compare mtDNA (cox1 gene) sequences by standard methods using the primer set NTF–NTR as described Casiraghi et al. (Parasitology, 2001). Phylogenetic trees were generated by three methods: Neighbor-Joining, Maximum Likelihood, and Bayesian Inference.

Cougars had 73.1% prevalence, 38 worms/ cougar mean intensity, and 82.5% nodules prevalence. Cougars killed for safety concerns had a significantly higher worm burden than cougars killed for other reasons. Bobcats had fewer nodules and worms. Both tooth structure and sequence comparisons indicated that the worms from the two host species were different. The majority of stomach nodules in Oregon wild felids were caused by Cylicospirura spp. We found no significant difference between eastern and western cougars, but cougars with aberrant behavior had a significantly higher worm burden than those apparently healthy. Interestingly, there was roughly the same number of problematic cougars in both areas of the state. This study supports the hypothesis that the abundant worm infections may impact cougars and be associated with aberrant behavior.

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50. SURVEY AND MOLECULAR SEQUENCING OF SARCOCYSTIS SPP. FROM SKELETAL MUSCLE OF FREE-RANGING FISHERS FROM PENNSYLVANIA

Richard W. Gerhold, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia Athens, GA 30602 and Department of Poultry Sciences, The University of Georgia, Athens, GA 30602, USA; Michael J. Yabsley, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602 and Warnell School of Forestry and Natural Resources, The University of Georgia, Athens, GA 30602, USA; Jennifer C. Wester and Jeff L. Larkin, Department of Biology, Indiana University of Pennsylvania, Indiana, Pennsylvania, 15705, USA

Presenting author: Gerhold, Richard

Summary: Nucleotide sequencing of the fisher Sarcocystis spp. disclosed a 98.3-99.1% identity to an Anser albifrons Sarcocystis sp. isolate from GenBank indicating that these sarcocysts likely represent a previously undescribed species.

In 2002, meningoencephalitis caused by Sarcocystis neurona was diagnosed in a fisher (Martes pennanti) from Garrett County Maryland. To determine the prevalence of Sarcocystis spp. in fishers and if fishers are potential intermediate hosts for S. neurona from this geographical region, Sarcocystis PCR was performed on 30 fishers collected from Pennsylvania. DNA was extracted from 0.5 g skeletal muscle from 30 road-killed fishers collected as part of research project in Central and Western Pennsylvania. The 18S small subunit rRNA gene of Sarcocystis spp. was amplified by PCR from the extracted DNA using primers 18S9L and 18S1H. Nucleotide sequencing was performed on a subset of these amplicons and resultant sequences were analyzed. Twenty-seven (90%) of the fishers were positive for Sarcocystis spp. from DNA extracted from the skeletal muscle. Nucleotide sequencing was performed on a subset of the amplicons and compared to available sequences in GenBank. All fisher sequences shared a 98.3-99.1% nucleotide identity to Sarcocystis sp. cyst type 1 Anser albifrons. It is likely that these sarcocysts found in the fishers represent a previously undescribed Sarcocystis spp. Further surveys and molecular analysis will be performed on fisher samples from the region.
51. NICHE PARTITIONING AND SEASONALITY OF TICKS IN FREE-RANGING AFRICAN BUFFALO (SYNCERCUS CAFFER)

Kadie Anderson, Anna Jolles, College of Veterinary Medicine, Oregon State University, Corvallis, OR 97331, USA; Vanessa Ezenwa, Department of Biological Sciences, University of Montana, Missoula, MT 59812, USA

Presenting author: Anderson, Kadie

Summary: Seasonal distribution and abundance patterns of ticks among free-ranging African buffalo were investigated with the goal of understanding the epidemiology of tick-related disease and morbidity in this wildlife host.

Ticks affect wildlife and livestock directly and via transmission of important microparasitic diseases. We studied tick infestation patterns on African buffalo (Syncerus caffer), asking (i) what tick species occur, and how do they interact?; (ii) how do tick burdens and distribution vary seasonally?; and (iii) what host factors affect tick burdens? We sampled 143 adult female African buffalo for ticks, 84 in July 2008, and 59 in October 2008. For all hosts, we collected data on age, body condition, lactation and pregnancy. We collected ticks at random from the three most infested body areas, the axilla, inguinal and perianal regions. Using digital photographs, adult and nymphal ticks were counted in the same body areas. Interactions among tick species were assessed by quantifying attachment site preferences and correlating body burdens with each species. We used general linear models to explore the effects of host characteristics and season on tick infestation. Two tick species were abundant on buffalo, Amblyomma hebraeum and Rhipicephalus evertsi. They differed in attachment sites, and their abundances per host were unrelated. Tick burdens increased from July to October; in July, animals in better condition had lower tick burdens. Pregnant and older animals had more ticks. Differences in attachment site suggest niche partitioning between tick species on buffalo. Consistent with this, lack of a negative correlation between Amblyomma and Rhipicephalus burdens may indicate avoidance of competition. Higher tick burdens following the dry season suggest reduced host resistance under resource limitation. Older and pregnant animals appear more susceptible to ticks. The association between poor body condition and higher tick burdens could be driven by condition-dependent susceptibility or effects of tick infestation on health.
52. THE ROLE OF NATURAL ANTIBIOTICS IN IMMUNOLOGICAL PROTECTION OF ALTRICIAL YOUNG OF THE AUSTRALIAN PLATYPUS (ORNITHORHYNCHUS ANATINUS)

Camilla M. Whittington, University of Sydney, Faculty of Veterinary Science, Lab 311 RMC Gunn Building B19, Camperdown, NSW 2006 Australia; Katherine Belov, University of Sydney, Faculty of Veterinary Science, Lab 311, RMC Gunn Building B19, Camperdown, NSW 2006 Australia; Julie A. Sharp, University of Melbourne, Department of Zoology, University of Melbourne, VIC 3010 Australia; Anthony Papenfuss, The Walter and Eliza Hall Institute of Medical Research, WEHI Bioinformatics Division, Parkville, VIC 3052 Australia

Presenting author: Whittington, Camilla

Summary: Platypus hatchlings emerge from their eggs at a very early stage with an undeveloped immune system, but we have found that protection of these young from infection is not conferred by the production of natural antibiotics in the mother’s milk, as has been previously assumed.

Hatchlings of the oviparous platypus (Ornithorhynchus anatinus) emerge at an early stage in development compared to eutherian mammals, and so lack a developed immune system. Hatchlings are presumed to be exposed to pathogens in the nesting burrow, yet avoid infection. Based on findings in other mammals, it was previously assumed that the production of natural antibiotics and immunoglobulins in milk confers protection on monotreme young. Using the recently sequenced platypus genome, we searched for the sequences of genes coding for antimicrobial peptides called cathelicidins and defensins. Primers were designed and optimised to assess expression of these genes in a range of different tissues, including milk cells, using reverse transcription polymerase chain reactions. This study provides the first assessment of the tissue expression patterns of these antimicrobial peptides in a monotreme. We found no evidence of expression of cathelicidins or defensins in platypus milk, suggesting that the platypus relies on an alternative mode of innate immunological protection for its altricial young. This finding was unexpected, because the milk of marsupials, which are also born at an altricial stage, contains these natural antibiotics, as does eutherian milk. We suggest several alternative mechanisms for the immunological protection of platypus young. This research provides insight into the basic biology of a unique but poorly studied animal, and paves the way for further research into the health and diseases of the platypus, particularly those affecting young animals.

Acknowledgements: We thank Erin Noonan and Tom Grant for provision of milk and tissue samples. CW is supported by a Fulbright Scholarship and an Australian Postgraduate Award.
53. MICROSATellite MARKERS DEVELOPED FOR THE STUDY OF LEPROSy IN Nine-BANDED ARMADillos

L. Chinchilla, A. Woodard, M. Welch, C. Brooks. Mississippi State University, 295 Lee Blvd., Harned Hall 114, Mississippi State, MS 39762, USA

Presenting author: Chinchilla, Leah

Summary: We present evidence that genes orthologous to those that provide human immunity to leprosy may influence the geographic structure of the disease in nine-banded armadillo populations.

Ecological and evolutionary forces driving host and pathogen interactions can induce geographic variation in the basic reproduction number (Ro) for the parasite and thus the pattern of infection. The interaction between leprosy and nine-banded armadillos (Dasypus novemcinctus) provides an opportunity to examine the factors contributing to the variation in Ro between populations.

Functional loci were determined based on a literature search identifying genes associated with human immune response to leprosy. The sequences for these genes were then BLASTed against the armadillo genome to locate homologous genes. Microsatellites in close proximity to these armadillo genes were located and primers for these and several anonymous microsatellites were developed. Fragment analysis using these amplified regions allowed us to calculate Gst, a measure of the heterozygosity of subpopulations as compared to the total population, for each locus. Two statistical tests were used to assess any differences of Gst between functional and anonymous loci. The Mann-Whitney U test revealed that Gst values for functional loci were significantly higher than Gst values for anonymous loci. A modified Lewontin-Krakauer test allowing for a priori hypotheses involving loci under selection showed that variance in Gst was also higher for functional loci than for anonymous loci.

Our results suggest that local adaptation may influence the geographic distribution of leprosy in armadillo populations. However, the genes used to provide preliminary results are involved in a generalized immune response, thus other pathogens may be exerting selective pressures on these loci. Further examination of genes involved in response specifically to leprosy as well as the inclusion of larger sample sizes will be instrumental in fully understanding the genetic component of the distribution of leprosy.

Acknowledgements: Many thanks go to Dr. William Loughry and Dr. Richard Truman for lending efforts and expertise to the project.
54. THE POTENTIAL ROLE OF COLLARED PECCARIES IN THE TRANSMISSION OF INFLUENZA A VIRUSES

Paul T. Oesterle, National Wildlife Research Center (USDA/APHIS/WS), 4101 Laporte Avenue, Fort Collins, CO 80521, USA; Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, CO 80523, USA; J. Jeffrey Root, National Wildlife Research Center (USDA/APHIS/WS), 4101 Laporte Avenue, Fort Collins, CO 80521, USA; Kathryn P. Huyvaert, Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, CO 80523, USA; Alan B. Franklin, National Wildlife Research Center (USDA/APHIS/WS), 4101 Laporte Avenue, Fort Collins, CO 80521, USA

Presenting author: Oesterle, Paul

Summary: Collared peccaries and feral swine belong to the same suborder, have overlapping ranges, share similar habitats, and are susceptible to many of the same diseases. We suggest that, similar to swine, peccaries are important in the ecology and evolution of influenza A viruses (FLUAV).

Influenza A viruses represent a serious threat to poultry and human health. Waterfowl are the natural reservoir, but FLUAV have become established in several mammalian species. Swine are considered a mixing vessel for FLUAV. In this study we will determine if peccaries (Pecari tajacu) are also capable of performing this function. Respiratory tissues, blood, and nasal swabs were collected from hunter-killed peccaries in Texas. Sera were tested by bELISA for the presence of anti-FLUAV antibodies, and antibody subtype(s) will be identified by hemagglutination inhibition (HI) tests. Nasal swabs were tested by reverse transcription polymerase chain reaction (RT-PCR) for the presence of FLUAV RNA, and the tissues were preserved and will be assessed for the presence of receptors to human and avian virus types. Many results are pending, including receptor identification and subtyping; however, thus far one peccary tested antibody positive by bELISA for FLUAV. No nasal swabs tested positive for FLUAV RNA. Peccaries are common throughout much of the southwestern United States, Mexico, and Central America. Swine are believed to facilitate genetic shift of FLUAV, and peccaries may serve a similar role in FLUAV ecology. Here, we present evidence that free-ranging peccaries are exposed to FLUAV. The clinical effects of FLUAV on peccaries remain unknown, but this species may be capable of trafficking FLUAV across international borders and throughout its extensive range.

Acknowledgements: We would like to thank Janine Romines and Michael Bodenchuk for sample collection and Tyler Campbell for advice on peccaries. Without their help, this project would not have begun.
55. CONSUMPTION OF BAITS CONTAINING RACCOONPOX-BASED PLAGUE VACCINES PROTECTS PRAIRIE DOGS AGAINST PLAGUE INFECTION

Tonie E. Rocke, Nicola Pussini, Judy Williamson, USGS National Wildlife Health Center, 6006 Schroeder Rd., Madison, WI 53711, USA; Jorge E. Osorio, University of Wisconsin, School of Veterinary Medicine, 1655 Linden Dr., Madison, WI 53706, USA

Presenting author: Rocke, Tonie

Summary: Vaccination of prairie dogs against plague via consumption of vaccine-laden baits improved their survival against lethal challenge with Y. pestis, demonstrating the feasibility of oral vaccination as a tool to reduce plague outbreaks.

Prairie dogs (Cynomys spp.) are highly susceptible to plague (Yersinia pestis) and, along with other rodents, they are considered a significant reservoir of the disease for other wildlife, domestic animals, and humans. We developed and tested oral vaccines to improve prairie dog survival upon plague exposure and reduce outbreaks. Using recombinant raccoon pox (RCN) as a vaccine vector for plague antigens (F1 and V), vaccine-laden baits were offered for voluntary consumption several times to a group of 16 black-tailed prairie dogs (C. ludovicianus). For comparison, another group of prairie dogs (n=12) was injected subcutaneously (two times) with F1-V fusion protein (40 µg), a vaccine demonstrated to induce immunity to plague in mice and other mammals. Control animals received baits containing RCN without the inserted antigen (n=8) or injected diluent (n=7). Antibody titers to plague antigens increased significantly (P < 0.05) in vaccinated groups compared to controls, although titers were higher (P < 0.0001) in the F1-V injected group compared to oral vaccines. Upon challenge with 70,000 cfu Y. pestis, oral vaccines survived at a higher rate than the F1-V injected group (P = 0.025) and much higher (P < 0.0001) than the control group. These results demonstrate that oral vaccination of prairie dogs using RCN-based plague vaccines provides significant protection against plague challenge at dosages that simulate simultaneous delivery of the plague bacterium by numerous (3-10) flea bites. Reduction of plague outbreaks in prairie dogs through oral vaccination in targeted locations would minimize the risk of disease transfer to other animals, particularly the endangered black-footed ferret (Mustela nigripes) which relies exclusively on prairie dogs for food and habitat.
56. **SALMONELLA IN RACCOONS (PROCYON LOTOR) IN ONTARIO, CANADA**

Claire Jardine, Department of Pathobiology, University of Guelph, Guelph, Ontario, N1G 2W1, Canada; Richard J. Reid-Smith, Departments of Pathobiology and Population Medicine University of Guelph, Guelph, Ontario, N1G 2W1, and Laboratory for Foodborne Zoonoses, Public Health Agency of Canada, Guelph, Ontario, N1G 3W4, Canada; Nicol Janecko and Scott McEwen, Department of Population Medicine, University of Guelph, Guelph, Ontario, N1G 2W1, Canada

**Presenting author:** Jardine, Claire

**Summary:** Although the prevalence of *Salmonella* is high in raccoons in Ontario, raccoons do not appear to be persistently colonized by the same strain suggesting regular reinfection from dietary or environmental sources.

Little is known about the role raccoons (*Procyon lotor*) play as maintenance hosts of *Salmonella*. The purpose of this study was to determine the prevalence, serotypes, and antimicrobial resistance of *Salmonella* found in raccoons in Ontario, and to determine if raccoons are potential maintenance hosts of *Salmonella* in the environment. In 2007, we conducted a cross sectional survey of *Salmonella* in raccoons living on two sites: an urban residential area, and a rural area. We also conducted a longitudinal study at a third site, on the grounds of the Toronto Zoo. Animals were live-trapped and anesthetized prior to fecal sample collection, and then released. For the longitudinal study, samples were collected from live-trapped animals once monthly from June to October, 2007. Samples were cultured for *Salmonella* and tested for resistance to 15 antimicrobials. *Salmonella* was isolated from 45% of 182 samples. There were 16 serotypes; the most frequent was *S. typhimurium*. Five isolates were resistant to one or more antimicrobials; two had extended-spectrum cephalosporin resistance. Only one of 11 animals captured in four consecutive trapping sessions had the same *Salmonella* serotype on two consecutive samples. The high prevalence of *Salmonella*, including several multi-drug resistant isolates, found in raccoons living in close proximity to humans in this study is a potential cause for public health concern. The results of the longitudinal analysis suggest that although raccoons may play a role in disseminating *Salmonella* into the environment, they are not likely persistently colonized with the same strain, but require reinfection from dietary or environmental sources.

**Acknowledgements:** The authors thank the Ontario Ministry of Natural Resources and Toronto Zoo for assistance with trapping.
57. A NETWORK MODEL OF DISEASE RISK ALONG A GRADIENT IN RESERVOIR HOST BIODIVERSITY

Christopher P. Brooks, Department of Biological Sciences, 114 Harned Hall, P.O. Box GY, Mississippi State University, Mississippi State, MS 39762, USA; Haimeng Zhang, Department of Mathematics and Statistics, Mississippi State University, Mississippi State, MS 39762, USA

Presenting author: Brooks, Christopher

Summary: The way human risk of infection changes with changing biodiversity is governed by heterogeneity in the regional species pool and any bias between the way communities are changed and hosts’ capacity to acquire and pass on infection.

Community structure is heterogeneous at a variety of spatial and temporal scales, and this variation has been shown to influence the risk of zoonotic disease. Current theoretical models are intractable when considering more than a few species. We develop a network model of interactions to quantify the diversity-disease risk relationship. This graph-based approach allows us to use matrix products to calculate risk to humans as the entomological inoculation rate (EIR) – the number of potentially infectious bites/host.

Decreasing vector species richness in the community always decreased EIR. Removal of vectors having the highest biting rate caused a more rapid initial decline than other scenarios. Removal of hosts caused a change in risk proportional to the difference in mean host capacity in the community before and after alteration. The overarching result is that when host competence co-varies with the likelihood of being lost or added to the community, the shifts in disease risk can range over several orders of magnitude. Our results have two important implications: first, that the role that biodiversity plays in disease risk is likely to be pathogen and landscape specific. Second, this work confirms the potential value of zooprophylaxis.
58. HISTOPATHOLOGICAL AND EPIZOOTIOLOGICAL INVESTIGATIONS ON IDIOPATHIC CARDIOMYOPATHY IN FREE-RANGING EURASIAN LYNX (LYNX LYNX) FROM SWITZERLAND

Marie-Pierre Ryser-Degiorgis, Nadia Robert, Centre for Fish and Wildlife Health (FIWI), Institute for Animal Pathology, Vetsuisse Faculty, University of Bern, Postfach 8466, CH-3001 Bern, Switzerland

Presenting author: Ryser-Degiorgis, Marie-Pierre

Summary: Marked histological cardiac lesions and heart murmurs occur at an increased prevalence in reintroduced Eurasian lynx of all age groups in the Swiss Alps, and although the significance of these findings is unclear, further investigations regarding possible etiologies are required to determine the need for management measures.

Myocard fibrosis (MF) and arteriosclerosis of the coronary arteries (AS) are common in Swiss lynx (LYNX LYNX). Some healthy animals present a heart murmur, and fatal heart failures occasionally occur. This study aims to assess the prevalence and severity of cardiac findings in the lynx population, and to identify associated risk factors. Necropsy reports of 97 Swiss lynx found dead or shot in the Jura Mountains or in the Alps from 1988 to 2008, and formalin-fixed heart samples of 79 of them were available. All slides were stained with van Gieson and examined by light microscopy in a blind study, using a scoring system for MF and AS. As controls, samples from 38 hunted lynx from Sweden were processed and analysed in the same manner. From 2001 to 2008, 20 lynx caught in the frame of biological studies were submitted to a routine clinical examination including basic heart auscultation. Overall prevalence of histological lesions was close to 70% in both countries. Prevalence of moderate and severe lesions was highest in the Alps (34.5%), and lowest in Sweden (9.7%). Four lynx (20%) presented a heart murmur. Histological lesions, murmurs and fatalities most commonly affected adult males from the Alps. The results suggest that mild MF and AS are common in Eurasian lynx. They also indicate a higher prevalence of abnormal cardiac findings in the inbred Swiss alpine population. A clear relationship between histological lesions and heart murmurs has not been established so far, and the etiology of these findings is unknown. Among others, a genetic origin has to be considered. This hypothesis needs to be assessed to define whether management measures are required.

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59. EPIDEMIOLOGY OF HPAI IN WILD BIRDS IN MONGOLIA

Martin Gilbert, Damien O. Joly, William B. Karesh, Wildlife Conservation Society, 2300 Southern Boulevard, Bronx, NY 10460, USA; Justin D. Brown, David E. Stallknecht, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Erica Spackman, David E. Swayne, U.S. Department of Agriculture, Agricultural Research Service, Southeast Poultry Research Laboratory, Athens, GA 30605, USA; Carol Cardona, University of California, Davis, CA 95616, USA

Presenting author: Joly, Damien

Summary: Based on bird counts and avian influenza sampling in Mongolia, we demonstrate that wild birds are capable of moving highly pathogenic avian influenza long distances, but found no evidence the virus became endemic in wild birds.

Since its emergence in 1997 and subsequent re-emergence in 2003, a highly pathogenic strain of avian influenza (HPAI) virus (AIV) subtype H5N1 has affected humans, domestic poultry, and wildlife across Eurasia and Africa. Prior to 2005, outbreaks in wild birds were sporadic and thought to relate to spillover from infected domestic poultry. The situation changed dramatically in April 2005, with the onset of an outbreak of HPAI H5N1 in wild migratory water birds at Qinghai Lake in northern China. We conducted sampling in Mongolia to test the hypotheses that a) wild birds could move HPAI H5N1 long distances, and b) HPAI H5N1 can become endemic in wild bird populations. Mongolia was ideal as there are very few domestic poultry in that region, thus the presence of HPAI could only be explained by introduction by migratory birds during their migration. Birds were captured using species appropriate methods. Tracheal, cloacal and/or oropharyngeal swabs were collected and stored in viral transport media. Faecal samples were collected opportunistically from single species congregations. Samples were frozen in the field using liquid nitrogen either immediately post collection or within six hours. Total RNA was extracted with a procedure optimized for cloacal swab samples. The RNA was screened for AIV by real-time RT-PCR (rRT-PCR) using the USDA standard. All rRT-PCR positive samples were processed for virus isolation in embryonated chicken eggs and were tested for H5 subtype virus by the USDA H5 rRT-PCR test. Over a four year study period (2005-2008), faecal, oropharyngeal, and cloacal samples were obtained from 6,038 live birds of 59 species across 44 geographically isolated sites. In 2005, a die-off of birds (n = 116, nine species) was reported at Erhel Lake, and during a subsequent investigation we were able to isolate HPAI H5N1 from one of four carcasses suitable for necropsy (a whooper swan (Cygnus cygnus)). In addition the Mongolian government reported isolates from three whooper swans and one bar-headed goose (Anser indicus). No further isolates of HPAI H5N1 were detected. The isolation of H5N1 in wild birds in an area where there are no domestic birds, strongly suggests that at least one species of migratory bird is able to carry the virus over long distances and introduce it to new waterfowl populations. We note that this species is as yet unidentified. Aside from two isolations of HPAI H5N1 by the Mongolian government in the spring of 2006, there was no further evidence the presence of the virus in Mongolian wild birds, suggesting that the virus did not become endemic in the Eurasian flyway.

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authors and do not necessarily reflect the views of the U.S. Agency for International Development, the Centers for Disease Control and Prevention or Wildlife Conservation Society.
60. IMMUNISATION OF TASMANIAN DEVILS AGAINST DEVIL FACIAL TUMOUR DISEASE TUMOUR CELLS

Alexandre Kreiss, Gregory M. Woods, Menzies Research Institute, University of Tasmania, Private Bag 29, Hobart, Tasmania 7001, Australia

Presenting author: Kreiss, Alexandre

Summary: Tasmanian devils (Sarcophilus harrisii) immunised against devil facial tumour disease (DFTD) tumour cells showed weak or no immune response against the disease, although one animal appeared to be protected against a first challenge with live tumour cells.

Tasmanian devils (Sarcophilus harrisii) are facing extinction by a newly recognised tumour disease, devil facial tumour disease (DFTD), which is transmitted as a cell allograft across the MHC barriers. Multiple measures are required to preclude the extinction of this iconic marsupial, including research on prevention methods, such as immunisation. Three captive healthy Tasmanian devils were immunised with X-irradiated DFTD tumour cells in the presence of an adjuvant. Immunisations were carried out at different time points and serum samples were collected prior to and at regular intervals after immunisations. Anti-DFTD antibodies were assayed in a flow cytometry experiment to determine whether an immune response against the disease had been evoked. To test the efficacy of the immunisation, the three Tasmanian devils were challenged with live DFTD tumour cells, injected in the subcutaneous tissue of the cheek and/or gingival sub mucosa. Two Tasmanian devils did not show anti-DFTD antibodies against DFTD tumour cells and developed DFTD tumours several weeks after challenge. One Tasmanian devil had a weak antibody response and did not develop DFTD tumours after a first challenge, but succumbed to the disease after being challenged a second time several months later. Protection against DFTD was induced in one immunised Tasmanian devil, but not in two others. To test for long term immunity, this ‘immune’ animal was challenged a second time several months after the last immunisation, which resulted in tumour development. This suggests that it is possible to induce immunity against DFTD, but it is likely to be only short term. We propose that differences in MHC genes might provide some devils with the ability to respond against DFTD.

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61. INVESTIGATION OF WILD AND FERAL CARNIVORES AS RESERVOIRS OF ALEUTIAN DISEASE VIRUS

Mark L. Drew, Idaho Department of Fish and Game, 16569 S. 10th Ave, Caldwell, Idaho 83607, USA; Scott Stopak, USDA Wildlife Services, 9158 W. Blackeagle, Boise, Idaho 83709, USA

Presenting author: Drew, Mark

Summary: Wild and feral carnivores were trapped and tested for Aleutian Disease (AD), however the serological tests used could not discriminate between AD, Canine Parvovirus and Feline Panleukopenia virus.

A number of mustelids, including short-tailed weasel (Mustela erminea), fishers (Martes pennanti), marten (Martes americana), and river otters (Lontra canadensis) can be infected with Aleutian Disease (AD) and serological evidence for infection in striped skunk (Mephitis mephitis), raccoons (Procyon lotor), wild American mink (Mustela vison), and red fox (Vulpes vulpes) has been detected (Mañas et al. 2003). Furthermore, a role for American raccoons in the transmission of virus has been suggested (Oie et al. 1996) and viral DNA sequences have been identified in American raccoons and striped skunks (Oie et al. 1996). This study was conducted to determine if wild and feral carnivores trapped around mink ranches had evidence of exposure to AD and to help develop best management practices that would minimize the risk of incursion of these animals into ranched mink facilities.

Wild and feral carnivores were trapped in leghold or box traps at mink ranches with (n=2) and without (n=2) known AD activity. All captured animals were euthanized by gunshot and sampled. Samples collected included blood, feces and tissues from various organs. Blood was placed into sterile glass tubes, centrifuged and sera decanted and frozen. Feces were collected from the rectum and frozen. Tissue samples including the heart, lung, liver, spleen, kidney and intestine were collected and placed in 10% buffered formalin.

Sera and feces were submitted for testing to a variety of laboratories. Initial screening for AD exposure was done using the Counter Electrophoresis test (CEP) at the Blue Cross Animal Hospital, Burley, ID and confirmatory testing using the Lateral Flow test (LF) was done at MVC Mink Services, Medford, WI. Sera were tested for antibodies to Canine Parvovirus (CP) and Feline Panleukopenia (FPL) using an immunofluorescent assay at the Washington Animal Disease Diagnostic Laboratory, Pullman, WA. Feces were tested for the presence of AD virus using PCR at the Wisconsin Veterinary Diagnostic Laboratory, Madison, WI.

A total of 19 feral cats, five skunks and one mink were trapped and sampled from the four mink ranches. Of these, one feral cat, four skunks and one mink were positive for AD exposure using the CEP. All animals were negative for AD exposure using the LF.

Testing for exposure to other paroviruses indicated that 15/19 and 14/15 feral cats were positive for CP and FPL, respectively. No skunks or mink were positive for CP or FPL.

The presence of AD virus was not detected in any of the cats, skunks or mink using the PCR on feces.

The origin of AD is unknown, nor is the natural host. Wildlife, especially wild mink, are generally considered to be the origin of the virus as well as a potential reservoir of AD for ranched mink. Wild carnivores have been found with antibodies to AD using the CEP in many locations. Serological evidence of exposure to AD has been found in striped skunks, raccoons and red fox (Ingram and Cho 1974), river otters (Wells et al. 1989) and wild and feral mink in Europe (Fournier-Chambrillion et al. 204, Mañas et al. 2003, Yamaguchi and McDonald 2001). Viral DNA
sequences similar to AD virus have been identified in American raccoons and striped skunks (Oie et al. 1996). Domestic skunks have been shown to have exposure to an AD like virus (Pennick et al. 2007). In addition, domestic ferrets are susceptible to AD, although the virus seems to be a ferret adapted strain (Welchman et al. 1993).

The CEP test was developed to help mink farmers detect AD exposed animals and institute control measures. It has a high specificity and sensitivity in mink, but its utility in other carnivore species is unknown. Despite this, the CEP is use commonly by mink ranchers and researchers to determine AD exposure in wild and feral carnivores. Numerous mink ranch experts claim that the CEP is very specific and sensitive in all species, but confirmatory data are lacking.

The LF test uses the same antigen as the CEP, and the test has a high sensitivity and sensitivity in mink. The application of the LF to other carnivores has not been previously reported. Generally, positive LF test results are confirmed by a viral protein test.

The PCR for AD is very specific and should be able to be used in all species. The lack of PCR positive results indicates that AD virus was not present in the fecal samples tested. The negative results do not rule out the presence of AD in these animals, as the shedding rate of AD virus, at least in domestic mink, is relatively low and more virus is shed in urine than in feces.

The high prevalence of antibodies to CP and FPL in the feral cats indicates that these animals are exposed to and possibly infected with these viruses. The one feral cat with a positive CEP test is likely a cross reaction with these other parvoviruses. Based on these results, it does not appear that feral cats or wild skunks are of concern as a wildlife reservoir for AD in ranched mink in Idaho. The single wild mink that did test positive on the CEP likely was exposed, but the importance of wild mink to transmission of AD to ranched mink is unknown at this time.

Further investigation of wild mink and skunks around mink farms is needed to clarify the risk of AD transmission to ranched mink.
62. EBOLA IN GREAT APES IN NORTHERN CONGO: AN UPDATE FROM THE FIELD

Kenneth N. Cameron, Alain U. Ondzie, Patricia E. Reed, Global Health Program, Wildlife Conservation Society, 2300 Southern Boulevard, Bronx, NY 10460, USA; David B. Morgan, Congo Program, Wildlife Conservation Society, B.P. 14537, Brazzaville, Republic of Congo; Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, 2001 N. Clark Street, Chicago, IL 60614, USA; Crickette M. Sanz, Department of Anthropology, Washington University, 1 Brookings Drive, Saint Louis, Missouri 63130, USA; Department of Primatology, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, 04103 Leipzig, Germany

Presenting author: Cameron, Kenneth

Summary: Despite speculation that Ebola Hemorrhagic Fever is decimating apes in the Odzala region of the Republic of Congo, intensive surveillance in the region has not identified further outbreaks since the last confirmed EHF outbreak in 2005.

Ebola hemorrhagic fever (EHF) has exhibited up to 95% mortality in western lowland gorillas (Gorilla gorilla gorilla) and central chimpanzees (Pan troglodytes troglodytes). Although EHF itself is not expected to cause extinction of these species, it may render them critically vulnerable to other key threats, such as hunting pressure and habitat alteration. In the Republic of Congo (ROC) the Wildlife Conservation Society Global Health Program is conducting ecological and carcass surveillance, carcass sampling, Ebola and ancillary diagnostics; conducting transmission dynamics studies; establishing in-country diagnostic capacity; implementing a human health early warning system and outreach education; and investigating the potential use of vaccination to protect ape populations against EHF. Carcass surveillance is the primary mode of identifying EHF outbreaks in wildlife. Surveillance methods include forest surveys, covering approximately 4,000 km², and a hunter-based carcass reporting system, covering nearly 40,000 km² of forest habitat in remote areas considered at high risk of EHF outbreaks. The last confirmed EHF outbreak in ROC occurred in Odzala-Kokoua National Park in 2005. Since then, 10 ape carcasses have been confirmed in ROC. Nine of these were reported from a single locality in early 2007. No carcasses have tested positive for Ebolavirus, including a carcass from the 2007 event. Tissue from a great ape carcass associated with the 2007 mortality event tested negative for Ebolavirus. To date, no EHF outbreaks have been established. Despite intensive surveillance, relatively few ape carcasses have been found since the 2005 outbreak. With the exception of the 2007 event, carcass numbers in the region appear to reflect normal background mortality. Despite speculation to the contrary, no EHF outbreaks have been detected in the region since 2005.

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63. EXCHANGE OF GASTRO-INTESTINAL HELMINTH SPECIES AMONG FOUR SPECIES OF KANGAROOS AND WALLABIES IN WESTERN VICTORIA, AUSTRALIA

M. Aussavy, E. Bernardin, Ecole Nationale Vétérinaire, Toulouse, France; A. Corrigan, Parks Victoria, Halls Gap, Victoria, Australia; I. Beveridge, University of Melbourne, Veterinary Clinical Centre, Werribee, Victoria, Australia

Presenting author: Beveridge, Ian

Summary: Grey kangaroos shared most of their helminth species, whereas wallabies shared far fewer species; only one specie was identified as a common pathogen likely to infect re-introduced rock-wallabies.

Exchange of gastrointestinal parasites among grey kangaroos (Macropus fuliginosus and M. giganteus), red-necked wallabies (Macropus rufogriseus) and swamp wallabies (Wallabia bicolor) was examined in an area of western Victoria, Australia, in which the four species are sympatric. The study was opportunistic but was undertaken as brush-tailed rock wallabies (Petrogale penicillata) were being reintroduced to the area and potential disease threats to the reintroduction were being investigated. Forty-five macropods were examined, comprising 15 M. giganteus, eight M. fuliginosus, 12 M. rufogriseus and 10 W. bicolor. Five species of anoplocephalid cestodes, 56 species of strongylid nematodes and two species of oxyurid nematodes were recovered. Of the 25 species found in grey kangaroos, 22 (88%) were shared between the two species. By comparison, of the 22 species found in red-necked wallabies, only 3 (14%) were shared and these were with swamp wallabies. Likewise, of the 20 species found in swamp wallabies, 3 (15%) were shared with red-necked wallabies. Of the commonly shared species, only one, Globocephaloides trifidospicularis, has been identified as a primary pathogen. The results are discussed against the current reintroduction of the brush-tailed rock wallaby, Petrogale penicillata, to the area and the possibilities of transmission of parasites to a newly re-introduced host.
64. ARE PYRENEAN CHAMOIS INFECTED WITH BORDER DISEASE
VIRUS PERSISTENTLY INFECTED ANIMALS?

Servei d'Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain; R. Rosell. Centre de Recerca en Sanitat Animal (CReSA), UAB-IRTA, Campus de la Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain and Departament d'Agricultura, Alimentació i Acció Rural, Generalitat de Catalunya, Barcelona, Spain

Presenting author: Marco, Ignasi

Summary: Pyrenean chamois with the disease associated to a Border Disease Virus may not be persistently infected animals.

Severe outbreaks of disease associated with Border Disease Virus (BDV) infection have decimated Pyrenean chamois (Rupicapra pyrenaica) populations in the Central Pyrenees (NE Spain) since 2001. It is not known whether diseased chamois are persistently infected (PI) animals or not. We studied 105 chamois with the disease associated to BDV infection. One animal (chamois-1) survived 1 month and blood samples were taken five times. Another two chamois (chamois-2 and chamois-3) survived for four and seven days, respectively, and blood samples were taken two times. The rest of chamois were sampled only at one time. RT-PCR was used to detect BDV in spleen. Seroconversion was analyzed by a commercial ELISA and virus neutralization test (VNT) using six pestivirus strains: BVDV-1, BVDV-2, BDV Spain 97, BDV Moredun, BDV 137/4 and BDV chamois. In chamois-1, 2 and 3, RT-PCR results were positive and ELISA negative at all time points. The rest were RT-PCR positive except two animals. Only four of these RT-PCR positive chamois were ELISA positive. On VNT, one animal was negative, one positive (1:20 titre for Spain-97 strain) and two could not be analyzed. Confirmation of PI status requires identification of virus in two separate samples with a minimum of 21 days. We verified it in only one chamois, because diseased chamois do not survive for long when captured. Altogether it indicates that diseased chamois could be PI animals. However, the high mortality recorded (as much as 86%) and the low seroprevalence before the outbreak of the disease, indicate that it is very unlikely that these chamois were PI animals.

Acknowledgements: We thank the rangers and staff of the National Hunting Reserves for capture of diseased chamois. This study was funded by the Direcció del Medi Natural del Department de Medi Ambient de la Generalitat de Catalunya and by grant CGL2006-11518/BOS from the Spanish government.
65. WILDLIFE DISEASES OF CONCERN IN CHINA

Hongxuan He, National Research Center for Wildlife Born Diseases, Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China; Tel:+86-10-64807118; E-mail: hehx@ioz.ac.cn

Presenting author: He, Hongxuan

Summary: This paper reviews the major wildlife diseases in China.

Wildlife species can play a role in disease transmission or serve as reservoirs. Understanding wildlife disease ecology is critical for reducing risks posed to domestic animals and human health. Wildlife diseases also are important with respect to animal welfare and maintaining biodiversity. China is rich in wildlife diversity. Highly Pathogenic H5N1 Avian Influenza virus has been recognized for over a decade with enormous impacts across Asia, Africa and Europe. Severe Acute Respiratory Syndrome was one of the most serious public health crises in China. Newcastle Disease spreads rapidly among birds living in close proximity. Brucellosis has been reported in 25 of 32 Chinese provinces with some endemic areas remaining. Plague is one of the oldest identifiable diseases. Dengue virus is transmitted through the bite of the mosquito and is currently considered the most common arthropod-borne disease in the world. Epidemic hemorrhagic fever cases have recently been increasing near Tianjin City. Foot-and-mouth disease appeared in the eastern provinces of Shandong and Jiangsu during 2005, subsequently spreading to suburban Beijing, to the northern province of Hebei and to northwestern autonomous region Xinjiang Uyghur. Rabies has become a primary concern occurring in 23 of Chinese provinces. Chlamydophila psittaci is a lethal intracellular bacterial species. Peste des petits ruminants (PPR), which is also known as goat plague, is a disease of increasing importance in China wherever small ruminants form an important component of agricultural food production.
66. LEAD OBJECTS INGESTED BY COMMON LOONS IN NEW ENGLAND

Mark A. Pokras, Center for Conservation Medicine, Cummings School of Veterinary Medicine, Tufts University, 200 Westboro Rd., N. Grafton, MA, USA. Tel: 508-839-7918. Fax: 508-839-7930. Email: mark.pokras@tufts.edu

Presenting author: Pokras, Mark

Summary: Ingestion of lead fishing gear has been found to cause significant mortality in common loons on lakes in New England.

Lead poisoning from ingested fishing gear has regularly been reported in a variety of avian species including the common loon (Gavia immer), mute swan (Cygnus color), trumpeter swan (Cygnus buccinator) and sandhill crane (Grus canadensis). Evidence gathered from necropsies conducted at the Wildlife Clinic at Tufts Cummings School of Veterinary medicine suggests that ingestion of lead weights is the number one killer of breeding adult common loons in New England. The current study quantifies the size, mass, and types of lead fishing gear ingested by common loons. Between 1987 and 2000, 522 common loon carcasses were collected from the six New England states and submitted to the Tufts Wildlife Clinic for necropsy. Ingested lead objects were visually classified into the following six categories: Sinkers, Jighead, Split Shot, Ammunition, Other, and Unknown (original use could not be determined because of wear, fragmentation or deformation). The recovered objects were weighed to the nearest 0.1 g, and length and width measured to the nearest 0.05 mm. Objects were then tested for lead using a commercial, buffered rhodizonate dye swab test. Toxicological analyses of loon livers were also performed. Of 222 lead objects, sinkers were most common (48%), followed by jigheads, split shot, and ammunition (19%, 12%, and 11%). The largest weighed 25 g, but most weighed < 10 g. Most were < 25.4 mm long. All loons ingesting lead objects had liver lead levels consistent with lead poisoning. Given what we know about the toxicity of lead to loons, humans, and many other species, efforts should be made to utilize non-toxic alternatives and minimize the introduction of lead into the environment. Barring the complete elimination of lead for sporting uses, a clear understanding of the types of gear that pose the greatest threat to loons and other wildlife will allow us to formulate rational policies to protect and manage these species.

Acknowledgements: Thanks to Mr. Rawson Wood, Ms. C. Perry, and Drs. J. McIntyre, P. Spitzer, J. C. Franson, R. Poppenga and R. Haebler, and the veterinary students and volunteers who helped over the years.
67. HEAVY METALS AND ORGANIC CONTAMINANTS: SILENT KILLERS OF MIGRATORY WATERFOWL IN LATIN AMERICA

A. Alonso Aguirre, Conservation Medicine Program, Wildlife Trust, 460 West 34th Street, 17th Floor, New York, NY 10001, USA

Presenting author: Aguirre, Alonso

Summary: Management on an international basis is needed to effectively combat disease problems in migratory birds.

The North American Waterfowl Management Plan was signed by Canada, Mexico and the United States with the purpose of restoring depleted waterfowl populations and to conserve vital wetland habitat. This plan states that "factors affecting carrying capacity of migration and wintering areas should be examined to acquire information needed to enhance habitat and control waterfowl losses due to disease, lead poisoning, and other contaminants", and that participation of the three countries is needed to manage and solve problems related to this internationally shared resource. Botulism, avian cholera, and lead poisoning are the major diseases that affect waterfowl. When infectious agents are involved, disease carriers in the population can serve to move the problem from one area to another following a time sequence and a flyway pattern. Therefore, what happens in Canada is often of consequence to waterfowl in the United States, and what happens there is often of consequence to waterfowl wintering in Mexico. The contrary is also true. It is known that 1/2 to 2/3 of the annual life cycle of waterfowl is spent in stopover and wintering areas. This period is critical in terms of survival because it is here that waterfowl experience the greatest resource scarcity, intraspecific competition, and density related mortality. These conditions are increased by loss and alteration of wetlands and deepwater habitats diminishing the ability of waterfowl to occupy stable, mature environments on a long-term basis. These characteristics prevail on the wintering grounds and stopover areas where management of more birds with less habitat must be accomplished. Disease is a direct expression of ecological imbalance, habitat conditions, and management, being a barometer that reflects the health condition of the resource. It is difficult to assess the actual loss of waterfowl attributable to lead poisoning. One indicator of the lead problem is the percent of waterfowl found with ingested lead. Lead is the only shot used and more lead poisoning cases are very likely to occur because conditions allowing shot availability to waterfowl are present in these wetlands. These conditions are the intensity of shooting, firmness of the soil substrate, siltation rates, depth of water, and wave action. It is also important to consider mortality of waterfowl while migrating to the wintering grounds due to lead acquired in the stopover areas. Environmental factors causing stress, such as crippling, food scarcity, migration, parasitism, or severe infection may increase mortality due to lead poisoning. Lead is stored in the bones along with calcium ions, and is likely to be released during these stressed situations when calcium is needed and mobilized. The efforts spent in habitat preservation, investigating diseases and environmental pollutants, and biological investigations on migratory waterfowl by Canada and the United States should be expanded to the wintering grounds in Mexico and other Latin American countries, to help understand what is happening to the resource in these areas. Reasons for the decline of some populations of waterfowl are largely unknown. Diseases and pollution of the environment by toxic chemicals may be contributing directly or indirectly to these declines.
68. SOURCES OF LEAD AND RECOMMENDATIONS TO REDUCE EXPOSURES IN WASHINGTON STATE

HOLLY G. DAVIES, Washington State Department of Ecology, PO Box 47600, Olympia, WA 98504-760, USA

Presenting author: Davies, Holly

Summary: Lead exposure in Washington is harmful, widespread, and has no single solution. The Lead Chemical Action Plan (CAP) is part of Ecology’s strategy to reduce threats from persistent, bioaccumulative, and toxic chemicals (PBTs). The goal of the PBT Rule is to reduce and phase-out PBT uses, releases, and exposures in Washington for both people and the environment. Lead was chosen for the third CAP because of its widespread distribution, how much is known on its uses and health effects, and the many known opportunities to reduce its use and impact. Lead-based paint is the largest single source of elevated blood lead levels for children in the US. Everyone has some exposure to lead, and harmful effects can occur from relatively common everyday sources. There is no known safe level of lead for children. Data on the health effects of lead, the prevalence in Washington, its uses, current laws and regulations, and economic costs were gathered from state and federal agencies, industry, environmental groups, and the published literature. Information on lead and options to reduce or phase out the uses, releases and exposures was discussed with an advisory committee of 17 representatives of business, health, environmental and local government organizations. Options were evaluated on economic and social impacts, environmental and human health benefits associated with implementing the action, feasibility, and the availability and effectiveness of safer alternatives. We estimated the amount of lead used and released from all sources in Washington. About sixty percent of homes in Washington were built before the federal ban on lead-based paint in 1978, and about half of those were built before 1960, when lead in paint was more common and found at higher concentrations. The largest current use of lead is in automotive batteries, most of which are recycled. Other large uses of lead include ammunition, fishing weights, and wheel weights. Lead is released from industrial sources, especially from large users of energy. Many people in Washington think that the risk of lead exposure has been eliminated by banning its use in most new paint and gasoline and they are very resistant to change. Wheel weights are an example of a product where industry is willing to switch to safer alternatives. Because harmful lead exposure is relatively common and comes from many sources, an effective program to reduce exposure requires the use of several different approaches including public education, increased blood lead testing, continued environmental testing, removal of existing exposure sources, and preventing new sources of exposure. We present a series of initial actions that address the worst sources of exposures along with options for further actions in the future as needed.
69. EFFECTS OF ENVIRONMENTAL METHYLMERCURY EXPOSURE ON REPRODUCTION IN WHITE IBISES (*EUDOCIMUS ALBUS*)

Nilmini Jayasena and Peter C. Frederick, Department of Wildlife Ecology and Conservation, University of Florida, 110 Newins-Ziegler Hall, Gainesville, FL-32611, USA

Presenting author: Jayasena, Nilmini

Summary: Chronic exposure to environmentally relevant doses of methylmercury was shown to affect pairing behaviour and cause endocrine disruption in White Ibises, with potential to cause effects at the population level.

Methylmercury is a global environmental contaminant, mostly known for its neurotoxic effects. However, there is increasing evidence that it has adverse effects on reproduction and could also act as an endocrine disruptor. We hypothesise that exposure to methylmercury could cause reproductive effects in wading birds that affect population level parameters. We took an experimental approach to look for evidence of reproductive impairment at environmentally relevant doses in the White Ibis (*Eudocimus albus*), a species known to be chronically exposed in the Florida Everglades. Wild-caught birds were exposed via diet, from 90 days to 3 years of age, at levels of 0.0001 (control), 0.01, 0.03 and 0.3 ppm (wet weight) methylmercury. The birds were kept in a large free-flight aviary in groups of 40 birds each, and were free to reproduce within treatment groups. Reproductive behaviour was observed in three breeding seasons. Faecal samples were collected for analysis of steroid hormone metabolites. The most obvious effect was on pairing behaviour. We observed homosexual nesting in males in all groups, but with significantly higher homosexual nesting in the dosed groups. There was a significant effect of treatment on faecal estradiol, with males in the high dose group, and homosexual males having elevated levels. This study indicates that chronic exposure to methylmercury at environmentally realistic doses has the ability to cause reproductive impairment leading to population level effects. Further, we found evidence of endocrine disruption, which may affect pairing behaviour, though mechanisms are not well understood at present. While other studies have found correlative evidence of reproductive impairment in birds at low levels, this was the first experimental study in avians to look for effects at such low levels.

Acknowledgements:
70. THE EFFECT OF BRODIFACOUM ON JAPANESE QUAIL (COTURNIX JAPONICA) COAGULATION: A MODEL FOR ASSESSMENT OF EXPOSURE IN WILD BIRDS

Kristin H. Webster, Tony D. Williams, Simon Fraser University, Burnaby, BC V5A 1S6; Kendal E. Harr, Idexx Laboratories Inc., #10 Cliveden Ave, Annacis Island, Delta, BC, V3M 6M2, Canada; Courtney A. Albert and John E. Elliott, Science and Technology Branch, Environment Canada, Delta, BC, V4K 3N2, Canada

Presenting author: Harr, Kendal

Summary: Prothrombin time and activated clotting time have proven to be reliable methods of assessment of brodifacoum exposure in quail and will therefore likely be useful in the assessment of rodenticide intoxication in owls, seabirds, and other impacted populations. Brodifacoum is an effective tool for controlling rodent populations. Numerous avian deaths have occurred due to secondary brodifacoum intoxication. Rodent-consuming birds, such as owls and raptors, in which the rodenticide may bioaccumulate are greatly impacted. As a second-generation, long-acting anticoagulant, brodifacoum disrupts hepatic production of vitamin K-dependant clotting factors, necessary for a functional extrinsic coagulation pathway. The extrinsic or amplification pathway is critical for avian hemostasis and is most commonly measured by the prothrombin time (PT) assay. PT was performed using chicken-origin thromboplastin. This study measured the PT, activated clotting time (ACT), hemoglobin, polychromatophil and reticulocyte levels in Japanese quail (Coturnix japonica) exposed to 0, 0.8, 1.6, 2.5, and 3.4 mg brodifacoum per kg body weight at 1, 3, 5 and 7 days post-exposure. ACT and PT in normal and corn oil control quail ranged from 48-170 and 11-15 seconds respectively. ACT and PT were prolonged in samples from quail gavaged at any dosage on day one with generally increased prolongation over time at days 3 and 5. Fifty-fold prolongation was documented at the higher brodifacoum dosages and correlated to petechial hemorrhages found at necropsy [CMG]. Prothrombin time and activated clotting time have proven to be reliable methods of assessment of brodifacoum exposure in quail and will therefore likely be useful in the assessment of rodenticide intoxication in owls, seabirds, and other impacted populations. Though species-specific assay development is required, rodenticide evaluation may be accomplished in a similar manner as domestic mammalian species.

Acknowledgements: We would like to acknowledge Kim Cheng and Darren E. Bennett for technical assistance with the quail handling and husbandry.
71. BIOCHEMISTRY RESULTS OF BLOOD SAMPLES OF ORYX AND GAZELLES SHOW INCREASING CARDIAC AND LIVER PROFILE ENZYMES

Saud Anagariyya, National Wildlife Research Center, PO Box 1086, Taif, Saudi Arabia

**Presenting author:** Anagariyya, Saud

**Summary:** Biochemistry results of blood samples of oryx and gazelles in both sexes showed increasing of cardiac and liver profile enzymes that can affect the liver functions and resulted anaemia.

The heavy mortality of Rheem (Sand) gazelles (*Gazella subgutturosa marica*) from 1998 to 2007 was related to very unfavourable environmental conditions, i.e. drought. The excessive ambient temperature during summer, scarcity and poor quality of food by lack of rain may be a major cause for the death of most adult oryx and gazelles followed by a dehydration and hyperthermia. Ongoing serological (oryx=16) and biochemical (oryx = 4; gazelle=4) screening carried out in summer on captured wild-born individuals confirms the absence of detrimental infectious diseases in the ungulate herds of Mahazat as-Sayd Protected Area.

In areas with sporadic unpredictable rains like Mahazat as-Sayd, food consumption is highly variable and is strongly correlated to rainfalls. As in all dry areas, food consumed by oryx and gazelles contains a high percentage of cellulose and lignin.

Biochemistry results of blood samples of oryx and gazelles in both sexes showed increasing of cardiac and liver profile enzymes that can affect the liver functions and resulted anaemia.

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72. INTOXICATION OF NONTARGET WILDLIFE WITH RODENTICIDES IN NORTHWESTERN KANSAS

Mark G. Ruder, John A. Bryan, II, and M. Kevin Keel, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, Georgia, 30602, USA; Robert H. Poppenga, California Animal Health and Food Safety Laboratory, School of Veterinary Medicine, University of California, Davis, California, 95616, USA; Matt Bain, Kansas Department of Wildlife and Parks, Colby, KS, 67701, USA; Jim Pitman, Kansas Department of Wildlife and Parks, Emporia, KS, 66801, USA

Presenting author: Ruder, Mark

Summary: Several widely available rodenticide compounds commonly utilized in black-tailed prairie dog control efforts were implicated in recent mortality events involving multiple avian and mammalian wildlife species in northwestern Kansas.

The perception of prairie dogs both as a nuisance species and a keystone species presents a management challenge. Multiple toxicants, including anticoagulant rodenticides and zinc phosphide, are widely used in northwestern Kansas for controlling black-tailed prairie dog (Cynomys ludovicianus) populations. The extent of nontarget and secondary poisoning of wildlife is currently unknown and warrants further investigation. During January and February of 2009, approximately 45 wild turkeys (Meleagris gallopavo), one raccoon (Procyon lotor), and an American badger (Taxidea taxus) were found dead in multiple locations in Logan County, Kansas. Department of Wildlife and Parks personnel submitted six turkeys, one raccoon, and one badger to the Southeastern Cooperative Wildlife Disease Study (Athens, GA, USA) for post-mortem examination. Anticoagulant rodenticide assays were performed on liver samples from all individuals and on crop contents of all turkeys. Assays to detect phosphene gas (indicative of zinc or aluminum phosphide toxicosis) were performed on the liver and crop contents of all turkeys. All carcasses contained hemorrhagic lesions consistent with vascular insult or a coagulopathy. Chlorophacinone was detected in the liver of the American badger and raccoon, while brodifacoum, and bromadiolone also were present in the raccoon. Phosphene gas was detected in the crop contents of all wild turkeys, consistent with zinc phosphide poisoning, and the crop contents of one turkey contained chlorophacinone, indicating exposure. These mortality events document nontarget intoxication of multiple species, including suspected secondary chlorophacinone poisoning of a mustelid. These events may be related to black-tailed prairie dog control, which is mandatory in Logan County. The potential risk to black-footed ferrets (Mustela nigripes) and other carnivores should be considered when wildlife, livestock, and land managers are selecting prairie dog control methods. Risks to carnivores may include secondary poisoning or a decrease in prey base.
73. THE EPIDEMIOLOGY OF PASSERINE SALMONELLOSIS DURING THE 2009 EPIZOOTIC AND A CONCURRENT PINE SISKIN INCURSION

S. M. Hernandez-Divers, K. Keel, A. Cartoceti, J. Brown, R. Gerhold, and M. Ruder, Warnell School of Forestry and Natural Resources (Hernandez-Divers) and the Southeastern Cooperative Wildlife Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; J. Mauer, Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA 30602, USA; S. Sanchez, Athens Diagnostic Laboratory, College of Veterinary Medicine, University of Georgia, Athens, GA 30602, USA

Presenting author: Hernandez-Divers, S.M.

Summary: This presentation will discuss the relationship of Salmonella typhimurium phage types among avian host species, to human peanut butter-associated cases during the 2009 epizootic, and the theories behind these relationships, which may lead to further understanding of the ecology of Salmonella in passerines.

Avian salmonellosis is a common disease caused by Salmonella enterica serovar Typhimurium. During 2009, an unusual number of birds with salmonellosis were presented to SCWDS. Our objectives were to determine the genetic relationship between avian and human peanut butter-associated Salmonella cases, and between Salmonella types, avian host and geographic location. Organs of birds with salmonellosis were cultured. The clonal nature of the Salmonella isolates was investigated using repetitive interspersed PCR (REP-PCR) and pulse field gel electrophoresis (PFGE). Bacterial Barcodes was used for REP-PCR. Briefly, REP-PCR selectively amplifies distinct genomic regions, amplicons are then size fractionated through a gel matrix to yield fingerprint patterns resembling "bar codes" functioning like a signature for bacterial strains. Agarose-embedded bacterial genomic DNA was digested with 10 units of Smal. DNA fragments were separated by PFGE using the CHEF DR-II apparatus. The PGFE patterns of human salmonellosis cases were obtained through PulseNet. The avian isolates belonged to Salmonella typhymurium Group B. The avian phage types were not related to the human cases. The bird isolates are very closely related. There are two clones that only differ by two bands by PFGE. REP-PCR is more discriminatory and shows the same pattern as PFGE. Backyard bird feeding is a billion-dollar industry that can fuel disease emergence and transmission. This year’s epizootic received national attention due in part to human Salmonella cases. Few studies investigate the ecology of this important pathogen. Understanding the clonal relationship of Salmonella isolates and their relationship to host specificity will help determine patterns of mortality observed in epizootics and whether Salmonella isolates from wild birds could pose a threat to domestic animal or human health.

Acknowledgements: We would like to thank Paula Bartlett, Amy McKinney, Ashley Phillips and Franchesca Broders for their technical assistance in the bacteriology laboratory.
74. EPIDEMIOLOGY OF DUCK PLAGUE VIRUS IN WILD WATERFOWL

M. Kevin Keel, David Stallknecht, Ginger Goekjian and John R. Fischer, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, Georgia 30602, USA; David Cob, North Carolina Wildlife Resources Commission, 512 North Salisbury Street, Raleigh, North Carolina 27604, USA

Presenting author: Keel, Kevin

Summary: Surveillance of wild and peridomestic waterfowl for duck plague virus revealed a low carrier rate among wild waterfowl and the prevalence was highest among Northern Pintails (Anas acuta) suggesting certain species of wild ducks may be a significant reservoir of the virus.

The epizootiology of duck plague virus (DPV) infection in waterfowl, whether captive, feral or wild is poorly understood. Epornitics have occurred in captive waterfowl or semi-wild ducks in park-like settings and many have concluded that such ducks may be the source of infection for wild waterfowl. We used a nested PCR specific for duck plague virus to test samples of cloacal swabs and trigeminal ganglia from semi-wild waterfowl (e.g. park ducks), introduced non-migratory waterfowl (e.g. resident mallards), waterfowl released for shooting and natural populations of truly “wild” waterfowl. The nearly 2000 samples represented 22 species of truly “wild” waterfowl, non-migratory mallards (Anas platyrhynchos) either released for hunting or established in the wild, domestic mallards and mallard-hybrids and Muscovy ducks (Cairina moschata). It was assumed detection of viral DNA in trigeminal ganglia but not cloacal swabs would indicate latent infection whereas PCR-positive cloacal swabs would indicate active shedding of the virus. Latently infected birds were identified among 9 species; northern pintails (Anas acuta) had the highest prevalence (8.8%). Cloacal shedding was rarely detected (2/1818). Few captive-reared released mallards were available for testing but one of the eleven was latently infected. No latently infected park ducks were identified. The results indicate wild birds may serve as a reservoir for duck plague virus. Northern pintails, a species reportedly resistant to the virus, had the highest rate of latent infections. However, low rates of infection were identified in other waterfowl from varied families. One latently infected captive-reared released mallard was identified suggesting that these birds also could serve as a source of virus for naïve waterfowl. No latently infected feral ducks were identified from parks.
75. DISCOVERY OF CAECIDOTEA RACOVITZAI (ISOPODA) AS A SECOND INTERMEDIATE HOST FOR THE EXOTIC DIGENEAN TREMATODE LEYOGONIMUS POLYOON AND ITS RELATIONSHIP TO MORTALITY IN AMERICAN COOTS (FULICA AMERICANA)

Patricia J. Zellmer, Todd C. Huspeni, University of Wisconsin-Stevens Point, Biology Dept. TNR Bldg, 800 Reserve St., Stevens Point, WI 54481, USA; Kay Brockman-Mederas, Wisconsin Dept. of Natural Resources, 647 Lakeland Rd, Shawano, WI 54166 , USA

Presenting author: Zellmer, Patricia

Summary: We report on the discovery of the isopod Caecidotea racovitzai as a natural second intermediate host for the digenean parasite Leyogonimus polyoon, an exotic helminth responsible for the death of thousands of American coots within the Mississippi Flyway, and the implications for parasite transmission.

Since 1998, American coot (Fulica americana) mortality at Shawano Lake, WI, from Leyogonimus polyoon exceeds 31,500 birds. Limited distribution of the first intermediate host, Bithynia tentaculata, may have restricted the parasite's distribution until recently. We identify the isopod Caecidotea racovitzai as second intermediate host, and evaluate intermediate host demographics for disease. Invertebrates collected every six weeks from May through October, 2008, at Shawano Lake were identified and evaluated for presence of Leyogonimus polyoon metacercariae, the infective stage for coots. Caecidotea racovitzai was identified as the sole second intermediate host of L. polyoon. Metacercariae were removed and excysted to verify identity of L. polyoon. Isopod density, infection prevalence, and intensity were determined with dredge samples collected every six weeks. We examined the data for patterns in isopod population structure, metacercarial intensity, and the relationship of these factors to parasite transmission. Isopod density and prevalence of infection varied significantly among collections. Average prevalence was 14.1% across collections. While intensity of infection ranged from 1 to 80 metacercariae, average intensity ranged from 2.71 (May) to 6.82 (September) per infected isopod. Infection intensities observed in individual coots, coupled with massive die-off counts, necessarily requires that Leyogonimus polyoon utilizes an abundant or abundantly infected second intermediate host. Likelihood of coot mortality caused by high intensity infections is affected by the spatial and temporal overlap of coots, infected Bithynia tentaculata, and isopods, and thus this risk is spatially local and temporally focal.

Acknowledgements: Special thanks to Wisconsin DNR staff, ten years of student research assistants, valued colleagues in UWSP Biology Department, especially Sol Sepsenwol and Steve Taft, Rebecca Cole (USGS), and Corenna Kerstner-Wood.
76. ECOLOGICAL CORRELATES OF BUGGY CREEK VIRUS INFECTION IN HOUSE SPARROW NESTLINGS

Valerie A. O'Brien and Charles R. Brown, University of Tulsa, 800 S. Tucker Drive, Tulsa, Oklahoma, 74104, USA

Presenting author: O'Brien, Valerie A.

Summary: Using a comprehensive, field-based, ecological approach, we identified the factors most likely associated with the transmission and occurrence of an alphavirus responsible for an epizootic in introduced house sparrow nestlings, which will enable us to more accurately predict infection or recognize emergence.

Identifying ecological factors involved in arbovirus infection in vertebrates can be important in monitoring epizootics. Buggy Creek virus (BCRV) is an arbovirus transmitted by the ectoparasitic swallow bug, which parasitizes cliff swallows (Petrochelidon pyrrhonota) and introduced house sparrows (Passer domesticus). Cliff swallows are relatively unaffected by BCRV, but house sparrow nestlings reared in swallow nests are often infected and may suffer infection-related mortality. We examined ecological correlates potentially associated with BCRV infection and mortality in house sparrow nestlings. Blood samples were collected from 4–17 day old house sparrow nestlings in the summers of 2006-2008 using standard field-based protocols. Ecological data were recorded at the individual, nest, and colony level in 2007. Blood samples were screened for BCRV using RT-PCR and plaque assay. Results were analyzed to determine ecological factors related to infection and mortality. Possible predictors of nest success (≥ 1 nestling reaching age 12 days) were modeled using multiple logistic regression. Spatial characteristics associated with house sparrow nests were most important in BCRV prevalence, while BCRV infection in vectors and site occupancy by cliff swallows in the prior year were not associated with infection. BCRV infection and brood size at sampling were strong predictors of nest failure. Results will help us predict likely foci and strength of BCRV infection in house sparrow colonies, more efficiently monitor the BCRV epizootic, and recognize when and where changes may be occurring that could promote virus evolution and emergence. The influences driving and shaping enzootic and epizootic arboviral transmission can be complex and highly interactive. These results demonstrate the value in adopting a comprehensive, ecologically-oriented approach to the study of arbovirus transmission dynamics.
77. VOLATILE COMPONENTS OF UROPYGIAL SECRETIONS IN THE GRAY CATBIRD (DUMETELLA CAROLINENSIS)

Rebecca J. Whelan, Department of Chemistry and Biochemistry, Oberlin College, Oberlin OH 44074, USA; Tera C. Levin, Department of Chemistry and Biochemistry, Oberlin College, Oberlin OH 44074 and Department of Biology, Oberlin College, Oberlin OH 44074, USA, Current address: Department of Molecular and Cell Biology, Univ. of California, Berkeley, Berkeley, CA 94720, USA; Jennifer C. Owen, Department of Fisheries and Wildlife, Michigan State Univ., East Lansing, MI 48824 and Department of Large Animal Clinical Sciences, Michigan State Univ., East Lansing, MI 48824, USA; Mary C. Garvin, Department of Biology, Oberlin College, Oberlin OH 44074, USA

Presenting author: Garvin, Mary

Summary: We detected five carboxylic acids, ethanoic (acetic), propanoic (propionic), 2-methylpropanoic (isobutyric), butanoic (butyric), and 3-methylbutanoic (isovaleric) in the uropygial secretions of gray catbirds; the signal strength for none of the volatiles varied with exogenous testosterone or migratory disposition.

The uropygial gland of birds produces secretions that are important in maintaining the health and structural integrity of feathers. Volatile components of gland secretions are particularly interesting because of their potential importance in olfactory communication within and across species. We identified the volatile compounds of the uropygial gland of gray catbirds (Dumetella carolinensis) and tested the hypothesis that gland secretions would vary with exogenous hormones or migratory disposition. We used solid-phase microextraction headspace sampling followed by gas chromatography-mass spectrometry to detect and identify volatiles in uropygial secretions of captive gray catbirds. Birds were treated with exogenous hormones via subdermal implants and migratory disposition was induced through manipulation of photoperiod. We detected the following carboxylic acids, listed in order of abundance: ethanoic (acetic), propanoic (propionic), 2-methylpropanoic (isobutyric), butanoic (butyric), and 3-methylbutanoic (isovaleric). Signal strength did not vary for any compound as a result of treatment with exogenous testosterone or migratory disposition. We found no effect of migration or exogenous hormones on the presence of these volatile components in the uropygial fluids, despite reports in other bird species that gland secretions vary seasonally (Reneerkens et al., 2008; Douglas et al., 2008) in response to changes in the annual cycle, such as breeding and migration and associated changes in diet (Sandilands et al., 2004). The uniform diet and environmental conditions provided for captive birds in our laboratory experiment could account for this result.
78. LYMPHOPROLIFERATIVE DISEASE VIRUS IN A WILD TURKEY IN SOUTHERN ARKANSAS

Andrew N. Cartoceti, Andrew B. Allison, and M. Kevin Keel, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, Georgia, 30602, USA

Presenting author: Cartoceti, Andrew

Summary: Lymphoproliferative disease virus (LPDV), a retrovirus responsible for a rare neoplastic disease in domestic turkeys, was confirmed for the first time in a wild turkey in the United States.

Virus-induced lymphoproliferative neoplasms are an economically important group of diseases in domestic poultry that are caused by a herpesvirus and three groups of retroviruses. In contrast, these neoplasms are only a sporadic cause of mortality in wild upland game species and, to date, only one retrovirus (reticuloendotheliosis virus) has been confirmed as an etiologic agent. In January of 2009, a wild turkey (Meleagris gallopavo) was found recumbent and disoriented with profuse diarrhea in Columbia County, Arkansas. The bird expired just prior to collection and Arkansas Game and Fish Commission personnel submitted the carcass to the Southeastern Cooperative Wildlife Disease Study (Athens, GA, USA) for post-mortem examination. Virus isolation was performed on samples of the lung and spleen and aerobic culture was performed on samples of the liver and spleen. Grossly, the spleen was markedly enlarged with fine white speckling in the parenchyma. The liver was enlarged with multiple, 1- to 8-mm diameter, pale yellow foci on the surface. The wall proximal small intestine was diffusely thickened. Histologically, dense infiltrates of neoplastic leukocytes were present in multiple organs, including the intestine, liver, kidney, spleen and pancreas. Lymphoproliferative disease virus (LPDV) was isolated from lung tissue. LPDV has previously been reported as a sporadic cause of neoplasia in domestic turkeys in Israel and the United Kingdom. This is the first report of LPDV in a wild turkey, the first instance of this virus in the United States, and the first time that LPDV has been isolated in cell culture. There is limited understanding of LPDV and other virus-induced neoplasms in wild birds; however, these viruses may have important implications for game and endangered species management and domestic poultry operations.

Acknowledgements: We thank Susan Gregory of the Arkansas Game and Fish Commission for the submission of this case.
79. REOVIRUS-ASSOCIATED NECROTIZING ENTERITIS IN AMERICAN CROWS

Carol Meteyer, Doug Docherty, Hon Ip, Nathan Ramsay, USGS National Wildlife Health Center, 6006 Schroeder Rd, Madison WI 53575, USA; Emi Saito, USGS National Wildlife Health Center, 6006 Schroeder Rd, Madison WI 53575; Current Address: USDA, APHIS, VS, Centers for Epidemiology and Animal Health, 2150 Centre Ave., Building B, Fort Collins, CO 80526, USA; J. Lindsay Oaks; Washington Animal Disease Diagnostic Laboratory, Box 647034, Washington State University, Pullman, WA 99164-7034, USA

Presenting author: Meteyer, Carol

Summary: A novel Orthoreovirus is associated with fatal necrotizing enteritis in American crows and has been diagnosed in 14 States, from New York to the state of Washington; crow mortality associated with this syndrome has recurred annually in some states since it was first diagnosed at the National Wildlife Health Center during the winter of 2001-2002.

Fatal enteritis in American crows (Corvus brachyrhynchos) associated with reovirus was first detected during surveillance for West Nile virus in 2002. A focused diagnostic investigation was subsequently conducted on American crows dying from hemorrhagic enteritis to determine factors that contribute to this syndrome in crows. American crows that were submitted to the National Wildlife Health Center for West Nile virus surveillance from Washington state during September 2003 were necropsied using a uniform protocol. Virus isolation in Vero cells was performed on intestine, spleen and kidney. Intestine was cultured for aerobic and anaerobic bacteria, for Salmonella using XLT agar, and submitted for parasitology evaluation. Multiple tissues including intestine, spleen, and liver were examined for histopathology. Necrotizing enteritis and splenic necrosis were present in 10/20 crows and a novel orthoreovirus was isolated from all ten. Of these 10 crows, liver necrosis was present in four, Escherichia coli was isolated from seven, Clostridium perfringens positive for alpha toxin from three, Clostridium sordelli from one, and intestinal coccidia from two. The significance of this reovirus in the fatal necrotizing enteritis in American crows has yet to be established. Pathogenicity studies are ongoing to determine the relative importance of the multiple potential pathogens identified in these birds. The population significance of this syndrome compounded by the continued mortality in corvids due to West Nile virus is also unknown.
80. PATHOGENS OF GREATER SAGE-GROUSE (CENTROCERCUS UROPHASIANUS)

Cheryl A. Mandich, University of Wyoming, PO Box 51587, Casper WY 82605-1587, USA; Robert S. Seville, University of Wyoming, 125 College Dr, Casper WY 82601, USA

Presenting author: Mandich, Cheryl

Summary: A survey is being conducted of pathogens that may result in critical fitness consequences for Greater Sage-grouse.

Greater sage-grouse (Centrocercus urophasianus) have decreased in number over the past 50 years and are a candidate for federal protection. To identify potential pathogens that may impact individuals and populations, a survey is being conducted on greater sage-grouse in central Wyoming. Deceased birds are tested for West Nile virus. Fecal samples were collected at roosting locations of birds being collared, stored in potassium dichromate (K2Cr2O7) and processed following procedures of Duszinkski et al. (2008). Slides were prepared using blood collected via toe nail clipping and stained using Giemsa (Pritchard and Kruse, 1982). Birds were examined for ectoparasites by dust-ruffling (Walter and Clayton, 1997) using pyrethrin, a natural bio-degradable insecticide produced from chrysanthemums, which causes ectoparasites to drop from the bird. Deceased birds were submitted to the Wyoming State Veterinary Laboratory for analysis. Ectoparasites (lice and mites) and fecal parasites (Eimeria spp.) were not detected in any of the sage-grouse samples. Blood parasites (Haemoproteus spp. and Plasmodium spp.) were found in approximately 25% of samples examined. One female tested positive for West Nile virus.

Parasites have the potential to contribute to species decline (McCallum and Dobson, 1995) and West Nile virus may reduce survival rates of greater sage-grouse (Naugle et al., 2004). Limited research has been conducted on sage-grouse parasites in Wyoming since the mid-1900s (Patterson, 1952). With the potential for being listed under the Endangered Species Act and subjected to increasing habitat loss, this survey to identify potential pathogens that may impact stressed individuals will provide base-line data.

Acknowledgements: Bureau of Land Management, Wyoming Game & Fish Department, University of Wyoming Graduate School, Bates Hole/Shirley Basin Local Sage-grouse Working Group, National Institutes of Health (#P20 RR016474)
81. URBANIZATION EFFECTS ON PARASITIC INFECTIONS IN SONG BIRDS

Carin K. Williams, Vanessa O. Ezenwa, Creagh W. Breuner, University of Montana, Missoula, MT 59812, USA

Presenting author: Williams, Carin

Summary: Urban song sparrows appear to be under less pressure from gastrointestinal parasite infections than rural song sparrows suggesting that they may be able to decrease investment in immunity.

Urbanization, a major threat to biodiversity, is increasing across the globe. Few studies have considered the impact of urbanization on parasite infections in wildlife. I tested the hypothesis that urbanization leads to changes in parasite prevalence and infection intensity in songbirds. I will explore several mechanisms causing the differences. I trapped songbirds in mist nets at two urban and two rural sites in Missoula, MT in 2008. I sexed, weighed, and measured each individual, collected blood samples to test for immune function, and avian malaria infection, and collected a fecal sample to test for helminth infection. To determine malaria infection, I stained blood smears with a Giemsa stain and examined the slides under an oil immersion. I performed fecal egg counts using fecal smears and fecal floats and identified the eggs to the nearest taxon possible. At each site, I performed point counts to determine avian diversity and density. Avian diversity was lower at the urban sites, while density was not significantly different. Malaria infection was not present in any of the birds examined. I identified three taxa of gastrointestinal parasites: nematodes, tapeworms, and coccidians. Infection prevalence was similar between sites, but intensities were greater in rural songbirds. Parasites can cause significant damage to their hosts. Infection may play a role in population declines associated with urbanization. My results suggest that for gastrointestinal parasites this is not the case. But why is infection intensity lower in urban birds? Exposure rates may be lower due to differences in avian diversity, an inhospitable environment for free-living gastrointestinal parasites, or higher host resistance due to increased food availability or stronger immune system investment.
82. RANGE EXPANSION OF ALCATAENIA LONGICERVICA (EUCESTODA: DILEPIDIDAE) COMPLEMENT CHANGES IN THE FEEDING ECOLOGY OF MURRES (ALCIDAE: URIA SPP.)

Sabir B. Muzaffar, Department of Biology, College of Science, United Arab Emirates University, PO Box 17551, Al Ain, United Arab Emirates

Presenting author: Muzaffar, Sabir

Summary: Range expansion of the North Pacific tapeworm, Alcataenia longicervica, into the Northwest Atlantic, reflects long term changes in the ecology of murres (Alcidae: Uria spp.).

Seabirds are prominent components of the marine environment and their parasites offer an insight into seabird ecology. Parasites also provide information on historical biogeography of hosts and thus may reveal broad changes in the marine ecosystem. I assessed the helminths of two murre species (Uria spp.) to determine parasite species composition and assess changes since the 1960s in their parasite fauna in the Northwest Atlantic marine environment. One hundred Common (U. aalge) and Thick-billed Murres (U. lomvia) were collected from breeding colonies along the coasts of Labrador, Newfoundland and Greenland as well as from the Newfoundland murre hunt (non-breeding). Each bird was frozen and their gastrointestinal tracts were dissected to collect and preserve helminths following standard techniques. A total of 623 helminths representing Digenea, Eucestoda, Nematoda and Acanthocephala were recorded. Parasite species composition was different compared to the 1960s and over 85% of the specimens were tapeworms (mostly Alcataenia). High prevalence (26.3%) and mean intensity (14.6) were recorded for A. longicervica, a Pacific species recorded recently from Newfoundland. Tapeworm species composition in murres was different compared to earlier studies from the Northwest Atlantic and Alcataenia spp. were dominant. Periodic mixing of populations of Thysanoessa species, the euphausiid intermediate host of Alcataenia, likely triggered the range expansion of A. longicervica from Pacific to the Northwest Atlantic. Thus, profound changes in the Northwest Atlantic are reflected in the helminth species composition.

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83. HEALTH EVALUATION OF KELP GULLS (LARUS DOMINICANUS) AT THE BAY OF TALCAHUANO, CHILE

Daniel González-Acuña, Universidad de Concepción, Facultad de Medicina Veterinaria, Casilla 537, Chillán, Chile; Fabiola Cerda, Universidad del Bio Bio, Facultad de Ciencias de la Salud y alimentos, Andrés Bello S/n Chillán, Chile; Juana López, René Ortega, Corvalán Felipe, Universidad de Concepción, Facultad de Medicina Veterinaria, Casilla 537, Chillán, Chile; Christian Mathieu, Andrés Servicio Agrícola y Ganadero, SAG Lo Aguirre, Santiago, Chile

Presenting author: González-Acuña, Daniel

Summary: Different samples (Hematology, Serum, PCR, parasites, bacterial cultures) from 90 Kelp Gulls were collected in the Bay of Talcahuano, Chile and analyzed during 2007 and 2008. The Gulls were positive to different parasites and infectious disease, some of them were zoonotic diseases.

Gulls have been identified as carriers of bacteria, viruses and parasites. The marked increase in Chile in the last years of the Kelp Gull (Larus dominicanus) and its carrion feeding habits, led us to suspect that this Gull is a carrier of pathogenic disease, some of which could be of public health significance. To corroborate this hypothesis, we made different analyses in stool samples and tissue. For the detection of bacteria, fecal and intestinal samples were analyzed with the commercial UltraCleanTM fecal Kit. Oric primers for Salmonella and IS 9000 for M. avium sp. paratuberculosis were used. The detection of these bacteria was done by real time SYBR green PCR on the LightCycler® 2.0.

For viral detection traquean stools were analysed for influenza, Nile Virus and Newcastle with the commercial kit MagMAXTM-96 Al/ND.

The parasites were isolated with the traditional techniques and identified following the taxonomic key for identification.

We detected 29% positive to Salmonella enteritidis, and 24.5% seropositive to Newcastle (titres between 1/20 and 1/320).

We detected 11 taxa of helminths, three of Phthiraptera and one of mites. Seven of these parasites are new reports for the Chilean diversity.

Two major infectious diseases of public health importance were reported, Salmonella enteritidis, which showed a higher presence in summer and fall and Newcastle which presented a 24.5 % positivity with titres between 1/20 and 1/320. Seven of the 15 reported parasites represent new records for Chile. Three of the helminths may have public health implications.

Acknowledgements: This work was founded by Fondecyt Nº1070464 project.
84. KEY PLAYERS IN HUMAN RABIES EXPOSURE AND THE ROLE OF STRIPED SKUNKS IN KANSAS

Claudia Ganser, Heather D. Barton, Samantha M. Wisely, Division of Biology, Kansas State University, Manhattan, KS, USA; Susan Moore, Cathleen Hanlon, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA

Presenting author: Ganser, Claudia


Public health is enhanced when the risks of disease exposure are reviewed and quantified. For rabies virus, contact with wildlife or infected domestic animals is a risk factor for human exposure. Pathways of human exposure can be decreased if the most probable routes of exposure to rabies are examined. We reviewed 16,945 cases submitted for rabies testing at the Kansas State School of Veterinary Medicine from 1998-2008. We standardized data on exposure, creating categories of positive exposure, possible exposure, and no exposure. Using the 1,142 positive cases, we determined which species were the primary causes of human exposure and which wildlife species and companion animals are most frequently exposed or infected by striped skunks (Mephitis mephitis), the reservoir host. Striped skunks accounted for 44.54 ± 14.67 (mean ± S.D), 7.72 ± 3.90 and 4.27 ± 2.49 of the dog, cat and human exposures respectively. Secondary human exposure resulted from contact with 7.82 ± 2.86 cats, 4.27 ± 2.49 striped skunks, 2.36 ± 1.91 cows and 1.82 ± 0.98 bats. Companion animals live at the human-wildlife interface and frequently lead to human rabies exposure. Dog vaccination has reduced human rabies cases, and enforcement of cat vaccination would decrease exposure further. Exposure was frequently a result of human interference of domestic animal-wildlife interactions as well as improper carcass disposal techniques. Another source of human exposure was contact with infected livestock, resulting from unawareness of rabies symptoms and treatment without safety precautions such as gloves.

Acknowledgements: KSU Conservation Genetic and Molecular Ecology Laboratory, Kansas State University Rabies Diagnostic Laboratory, Kansas State University
85. AN OVERVIEW AND UPDATE OF “HAIR-LOSS SYNDROME” CAUSED BY EXOTIC LICE IN WASHINGTON DEER

Kristin G. Mansfield, Washington Department of Fish and Wildlife, 2315 N. Discovery Place, Spokane Valley, WA 99216, USA; Jeffrey A. Bernatowicz, Washington Department of Fish and Wildlife, 1701 South 24th Ave., Yakima, WA 98902, USA; P. Briggs Hall, 3017 Lake Langlois Rd. NE, Carnation, WA 98014, USA; James W. Mertins, U.S. Department of Agriculture, Animal and Plant Health Inspection Service, Veterinary Services, National Veterinary Services Laboratories, 1800 Dayton Ave., Ames, IA 50010, USA; Ella L. Rowan, Washington Department of Fish and Wildlife, 2315 N. Discovery Place, Spokane Valley, WA 99216, USA; William Moore, Washington Department of Fish and Wildlife, 1701 South 24th Ave., Yakima, WA 98902, USA; Jack A. Mortenson, U.S. Department of Agriculture, Veterinary Services, 530 Center St. NE, Suite 335, Salem, OR 97301, USA

Presenting author: Mansfield, Kristin

Summary: An update on "Hair-loss Syndrome" in black-tailed deer is presented, along with information on a similar condition in mule deer caused by exotic lice.

“Hair-loss syndrome” (HLS) in black-tailed deer (Odocoileus hemionus columbianus) was first described in Washington in 1996, and is caused by heavy infestations with an Old World species of louse Damalinia (Cervicola) sp. Affected deer develop a hypersensitivity reaction, leading to excessive grooming and eventual loss of hair. The geographical distribution of HLS has expanded since 1996, and is now endemic in black-tailed deer west of the Cascades from the Canadian border to northern California. Despite mortalities attributed to HLS, and the opinions of some wildlife managers that HLS has contributed to localized declines in black-tailed deer, studies conducted to date have not demonstrated significant population impacts on black-tailed deer. In 2003, the Washington Department of Fish and Wildlife (WDFW) began receiving reports of a condition resembling HLS in deer east of the Cascades, at the black-tailed deer - mule deer (Odocoileus hemionus hemionus) intergrade zone in the south central part of the state. Lice were collected from deer and identified as Bovicola tibialis, the chewing louse of fallow deer (Dama dama). In 2006, WDFW received numerous reports of dead deer (particularly fawns) with hair loss in south central Washington, and these carcasses were heavily infested with Bovicola tibialis. The number and geographical distribution of reports of HLS in eastern Washington deer have increased steadily over the past 6 years, with reports now extending to the Idaho and Canadian borders. Deer surveys and harvest data suggest mule deer populations in some affected counties have declined by about 50% since 2004. It is unknown if Bovicola tibialis infestations are the sole reason for the decline, but they are suspected to be a factor.
86. SOCIETY, WILDLIFE DISEASE AND WILDLIFE CONSERVATION: OXYMORON OR EVOLUTIONARY SIBLINGS?

Milton Friend, Emeritus Scientist, National Wildlife Health Centre, USGS Madison WI 53711, USA

Presenting author: Friend, Milt

Summary: At first flush, wildlife disease and wildlife conservation may be seen as contradictory or incongruous terms as the first typically evokes thoughts of illness and death while the latter promotes thoughts of protection and sustainability. Nevertheless, it is also reasonable to consider both terms as intractable offsprings from their human parent-society. I suggest that the evolution of human society is a major factor driving the types and magnitude of wildlife losses from disease as well as viewpoints that dictate the context for wildlife conservation along the continuum of recorded history. This presentation pursues these relations for the insights they may provide in guiding our efforts in addressing wildlife disease for the benefit of free-ranging wildlife populations and human society alike.
87. A COMPARISON OF POTENTIAL PATHOGENS FROM SYMPATRIC BIGHORN SHEEP, DOMESTIC SHEEP AND MULE DEER DURING A BIGHORN SHEEP DIE-OFF IN WEST-CENTRAL MONTANA

Neil Anderson, Deborah L. McCauley, Montana Fish, Wildlife and Parks, 1400 South 19th Avenue, Bozemen, MT 59718, USA; Fred Jakubowski, Thomas Carlsten, Montana Fish, Wildlife and Parks, 56 Manor Drive, Townsend, MT 59644, USA; Jenny L. Sika, Montana Fish, Wildlife and Parks, 930 Custer Avenue West, Helena, MT 59620, USA; Jennifer Ramsey, Montana Fish, Wildlife and Parks, 1400 South 19th Avenue, Bozemen, MT 59718, USA

Presenting author: Anderson, Neil

Summary: Comparison of test results from bighorn sheep, domestic sheep and mule deer collected during a bighorn sheep die-off suggest that domestic sheep shared potential pathogens with free-ranging bighorns dying from pneumonia.

Bighorn sheep (Ovis canadensis) were introduced into the Elkhorn Mountains of west-central Montana in the mid 1990s. The population increased in number to approximately 250 animals until the winter of 2007-08 when about 84% of the population died from a pneumonia related epizootic. Domestic sheep and mule deer (Odocoileus hemionus) occupying the same range as the bighorn sheep were tested to determine if they shared potential pathogens that may have played a role in the bighorn sheep die-off. Samples from 29 bighorn sheep succumbing to pneumonia were collected in an effort to determine the causative agents associated with the die-off. Lung tissue was collected from 29 carcasses and blood samples were collected from 12 individuals demonstrating clinical symptoms of pneumonia. Tissues were submitted for testing to determine the pathogens associated with the die-off. Blood, pharyngeal swabs and fecal samples were collected from 25 domestic sheep within bighorn sheep range and tested to determine if they shared pathogens. Tissues, blood and fecal samples were also collected from 12 sympatric mule deer and tested for potential pathogens. Fecal samples were also collected from elk (Cervus elaphus), mule deer and domestic goats within the area to evaluate parasite loads. Test results from all species examined were compared to determine the potential role, if any, they may have played in the bighorn sheep die-off. Pasteurella spp., Moraxella ovis and Mycoplasma ovipneumonia were isolated from lung tissue of dead bighorns and pharyngeal swabs collected from domestic sheep occupying similar range during the epizootic. Both the bighorn sheep and domestic sheep shared similar gastro-intestinal parasites including Nematodirus spp. and Eimeria spp. Testing tissues and fecal samples from sympatric mule deer suggested no shared bacterial pathogens and limited shared gastrointestinal parasites. Domestic goats and mule deer had similar species of parasites as bighorn sheep but at low prevalence. The findings of this investigation indicates that domestic sheep had many potential pathogens in common with bighorn sheep dying from pneumonia and may have played a role in the observed epizootic even though direct contact could not be confirmed. We suggest that maintaining spatial and temporal separation of domestic and bighorn sheep is vital to preserving bighorn sheep populations.

Acknowledgements: We would like to acknowledge the Montana Department of Livestock Diagnostic Laboratory, the Washington Animal Disease Diagnostic Laboratory (WADDL), the Caine Veterinary Teaching Hospital (Caine), Floyd Seesee, Tom Besser and Frances Cassirer for their contributions to this project.
88. WILDLIFE DISEASE IN THE AGE OF METAGENOMICS

Mary Poss, Stephan Schuster, Nicola Wittekindt, Penn State University, University Park, PA 16802, USA; Paul Chafee Cross, Northern Rocky Mountain Science Center, USGS, PO Box 173492, 229 AJM Johnson Hall, Bozeman, MT 59717-4392, USA

Presenting author: Poss, Mary

Summary: We describe novel microorganisms identified by a metagenomic analysis, which was conducted to identify the endemic microbial population in healthy mule deer and elk tissue samples.

Organisms responsible for endemic infections in many wildlife species are unknown because wildlife infections often go undiagnosed unless mortality is high. Understanding the community of microorganisms in a species is becoming increasingly important because both genetic changes in an endemic microbe or cross-species transfers can lead to serious disease. We used 454 Life Sciences high throughput sequencing technology and developed advanced computational methods to detect the microbial populations that are present in tissues from healthy mule deer (Odocoileus hemionus) and elk (Cervus elaphus). Target organisms were independently verified by traditional methods. We identified novel retroviruses and a previously described poxvirus in both mule deer and elk samples. Multiple bacterial species, including several Mycoplasma species were detected. Our libraries were made from RNA suggesting that all organisms were replicating. Our data demonstrate several new bacterial and viral organisms that appear to be endemic in wild ungulate species. These methods have application to understand seasonal and geographic variation in microbial populations in wildlife species.

Acknowledgements: This work was funded in part by a grant from USGS.
89. PATHOGENICITY OF EPIZOOTIC HEMORRHAGIC DISEASE VIRUS SEROTYPE 6 IN WHITE-TAILED DEER

E.W. Howerth, Department of Pathology, College of Veterinary Medicine, The University of Georgia, Athens, Georgia 30602, USA; A. J. Allison, D. G. Mead, D.E. Stallknecht, Department of Population Health and Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, Georgia 30602, USA

Presenting author: Howerth, Elizabeth

Summary: This study confirms that epizootic hemorrhagic disease virus serotype 6, which is newly introduced in the US, causes disease in white-tailed deer.

Epizootic hemorrhagic disease virus (EHDV) serotype 6 is new to the US. It has been isolated from white-tailed deer (Odocoileus virginianus) (WTD) in multiple states and years, but its potential to cause disease in wildlife is uncertain. The purpose of this study was to demonstrate that this serotype can cause disease in WTD. Five deer were inoculated with EHD virus serotype 6 via subcutaneous and intradermal inoculation. Blood was collected on postinoculation day (PID) 0, 3, 5, 7, 10, and 18 for viral isolation and titer, serology, a complete blood count, and coagulation assays (APTT and PT). At death or euthanasia animals were necropsied and tissues collected for virus isolation and histopathology. All became infected, morbidity was 100%, and one died PID 4. Clinical signs included erythema, head tremors, laminitis, and coagulation failure. Peak viremia coincided with peak fever. Two animals killed on PID 12 and two killed PID 18 had hemorrhage in tissues. Histopathology was consistent with EHD; all had encephalitis. This study confirms that EHDV serotype 6 causes disease in WTD. How widespread this new EHDV serotype will become and its impact on WTD is yet to be determined.
90. WHITE-TAILED DEER CARCASS DECOMPOSITION AND POTENTIAL EXPOSURE OF SCAVENGERS TO CHRONIC WASTING DISEASE IN WISCONSIN

C. Jennelle, C. Nolden, E. Berkley, Department of Forest and Wildlife Ecology, University of Wisconsin, 1630 Linden Drive, Madison, WI 53706, USA; M. Samuel, U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, University of Wisconsin, 1630 Linden Drive, Madison, WI 53706, USA; D. Keane, D. Barr, Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin, Madison, WI 53706, USA; C. Johnson, J. Vanderloo, J. Aiken, Department of Animal Health and Biomedical Sciences, University of Wisconsin, 1655 Linden Drive, Madison, WI 53706, USA

Presenting author: Jennelle, Christopher

Summary: We found no evidence of TSE transmission to scavengers of deer carcasses in Wisconsin, but potential exposure to CWD laden carcasses may be heightened during winter months when carcass materials persist longer.

Chronic wasting disease (CWD) is an infectious transmissible spongiform encephalopathy (TSE) afflicting cervids. We addressed the potential role of white-tailed deer (Odocoileus virginianus) carcasses as sources of CWD material to vertebrate scavengers in Wisconsin. We estimated deer carcass decomposition rates, characterized vertebrate scavenger communities, quantified relative activity of scavengers to determine CWD exposure risk, and tested representative scavengers for TSE. We placed 40 disease-free deer carcasses and nine gut piles in the CWD-affected area of Wisconsin from September to April in 2003 through 2005. We used remotely operated cameras to identify visitors and scavengers at deer carcasses and determine relative activity. We used Kaplan-Meier survival analysis and a generalized linear mixed model to determine the rate and driving factors of carcass removal (decomposition) from the environment. We tested 812 representative mammalian scavengers, collected in the CWD-affected area of Wisconsin, for TSE infection using the IDEXX HerdChek enzyme-linked immunosorbent assay (ELISA). We recorded 42 mammalian and avian species at deer carcasses. Prominent scavengers included crows (Corvus brachyrhynchos), raccoons (Procyon lotor), and opossums (Didelphis virginiana). Carcasses persisted for 18 to 101 days, while gut piles lasted for three days. Scavenger activity and higher temperatures were associated with greater rates of carcass removal. Four mammals tested positive using ELISA, but were negative with Western blot. Infected deer carcasses serve as a potential environmental source of CWD prions to a wide variety of mammalian and avian scavengers. Our results show that many species of birds and mammals could consume infectious prions from deer that die from CWD. Further research is needed to determine the susceptibility of scavenging mammals to CWD and the role of vertebrates in the maintenance and spread of CWD, and should be considered in the dynamics of other disease systems.

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91. Socially Facilitated Transmission of Chronic Wasting Disease Among Female White-Tailed Deer

Daniel A. Grear, Michael D. Samuel, University of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53706, USA; Kim T. Scribner, Byron V. Weckworth, Michigan State University; Julie A. Langenberg, Wisconsin Department of Natural Resources, 2801 Progress Road, Madison, WI 53716, USA

Presenting author: Samuel, Michael

Summary: Direct deer-to-deer transmission of CWD between closely related female deer may be an important route of CWD transmission and disease spread in free-ranging populations.

Little is known about the routes of chronic wasting disease (CWD) transmission among free-ranging cervids. We evaluated the hypothesis that CWD transmission is socially facilitated among adult female white-tailed deer (Odocoileus virginianus). Our analysis used spatial location and genetic relatedness for 1,387 female deer and spatial location of 1,321 adult male deer harvested during 2002-2004 CWD control efforts in Wisconsin. We found the spatial genetic structure of female deer to be more organized than random at distances of < 3.2 km. The pattern of spatial relatedness based on matrilineally-inherited mtDNA was 50 fold higher than bi-parentally inherited microsatellite DNA. These results suggest spatial overlap of females from different social groups, and high rates of male dispersal and breeding across female groups. The probability of CWD infection in adult females was only slightly affected by the number of spatially proximate (< 3.2 km) infected unrelated females. In contrast, probability of infection increased 30-50 fold when a closely related (full-sibling, mother-offspring) female was infected.
92. BRUCELLOSIS IN WYOMING NON-FEEDGROUND ELK: CHALLENGING DOGMA

William Edwards, Doug McWhirter, Terry Kreeger, and Brandon Scurlock, Wyoming Game and Fish Department, 1174 Snowy Range Road, Laramie, WY 82070, USA; Arthur Middleton, University of Wyoming, Coop Fish and Wildlife Research Unit, Dept 3166, 1000 E. University Ave, Laramie, WY 82071, USA

Presenting author: Edwards, Hank

Summary: Recent research has documented the establishment of brucellosis in elk populations not associated with supplemental winter feedgrounds; this finding significantly complicates efforts to eradicate this disease from elk of the Greater Yellowstone Area.

Brucellosis is enzootic in elk (Cervus elaphus) and bison (Bison bison) of the Greater Yellowstone Area, comprising the last reservoir of Brucella abortus in the United States. Brucellosis appears to be maintained by elk utilizing winter feedgrounds, because historically the incidence of brucellosis is low (2-3%) in herd units surrounding but not utilizing feedgrounds. Blood sample kits were sent to elk hunters requesting they collect blood from their harvested animal and complete a data sheet. Samples were returned to the Wyoming Game and Fish Department’s Wildlife Disease Laboratory, processed and tested for brucellosis using the card test, standard plate test, rivanol, fluorescent polarization assay, and complement fixation. A competitive ELISA was used to identify Brucella strain-19 vaccine titers. Serological profiles were categorized using the USDA’S Brucellosis Eradication Uniform Methods and Rules, with the exception that all suspect reactions were considered positive.

Additional monitoring included collection of any aborted fetuses or associated tissues for culture. Over 7,300 free-ranging elk samples were analyzed. Historically, seroprevalence levels averaged 2-3% in non-feedground elk, while those associated with feedgrounds ranged from 9-50%. From 2006-2008, seroprevalence levels rose to 10.2% in northwestern elk herd units. Brucella abortus was cultured from an aborted elk fetus from the northwestern herd units. Conventional dogma has been that without feedgrounds, brucellosis would be unable to maintain itself in elk populations not utilizing feedgrounds. The three year rise in seroprevalence of the northwestern herd units suggests that brucellosis has become established in elk populations not reliant on feedgrounds. This finding presents considerable disease management complications for state and federal wildlife managers working toward brucellosis eradication. Solutions for controlling this disease must go beyond feedground closure if eradication is to be achieved.

Acknowledgements: The authors would like to sincerely thank cooperating elk hunters, numerous field personnel as well as Jessica Jennings and Stacy Dauwalter of the Wildlife Disease Laboratory.
93. ADAPTIVE MANAGEMENT TO REDUCE BRUCELLOSIS
TRANSMISSION RISK AMONG ELK ATTENDING SUPPLEMENTAL
FEEDGROUNDS IN WYOMING

Brandon M. Scurlock, Eric Maichak, Jared Rogerson, Wyoming Game and Fish Dept., Pinedale, Wyoming 82941, USA; John Henningsen, Wyoming Game and Fish Dept., Jackson, Wyoming 82901; Paul Cross, US Geological Survey, Bozeman, Montana 93457, USA

Presenting author: Scurlock, Brandon

Summary: Findings of intensive brucellosis research on elk utilizing supplemental winter feed grounds in Wyoming were applied to develop the 'Target Feedground Project', an adaptive strategy incorporating feeding management manipulations to reduce risk of brucellosis transmission among elk.

Brucellosis in wildlife comprises the last nidus of Brucella abortus in the US. Wyoming feeds elk (Cervus elaphus) to maintain separation of elk and cattle, reducing disease transmission risk. However, feeding elk concomitantly perpetuates brucellosis in elk. Management strategies to reduce brucellosis in elk are needed to lower interspecific disease transmission risk. Research of brucellosis in feedground elk was conducted during 2006-2008. Major results indicated that 1) 75% of transmission events (elk-fetus contacts) on feedgrounds occurred on feedlines, 2) brucellosis seroprevalence in elk attending feedgrounds is positively correlated with mean feeding end-date, and 3) elk density during calving season may increase with number of days spent on supplemental feed. Findings from this research lead to the development of the Target Feedground Project, an adaptive strategy incorporating feeding management manipulations to reduce risk of brucellosis transmission among elk on 8 'Target Feedgrounds' in western Wyoming. Elk-fetus contacts were reduced 66-75% utilizing Low-Density feeding compared to traditional feeding. Manipulating end-feeding dates through systematic reductions in rations resulted in terminating feeding 21 days earlier than long-term means in 2008 and 2009. Brucellosis prevalence surveillance is ongoing. Continued success of the Project should result in a sustainable reduction of brucellosis in elk and associated decreased risk to cattle, lower elk feeding costs, and continued operation of feedgrounds to minimize elk-cattle commingling, elk damage, and sustain elk numbers that meet public expectation. However, the Project is not suitable for all 23 feedgrounds, brucellosis will not be eliminated in elk, and elk on Target Feedgrounds remain susceptible to new diseases that may arise.

Acknowledgements: Kate Belinda, Hank Edwards- Wyoming Game and Fish Department Wyoming Wildlife/Livestock Disease Partnership (funding entity)
94. DETECTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX IN SWABS AND FECES FROM BCG-VACCINATED AND M. BOVIS-CHALLENGED WHITE-TAILED DEER AND THEIR ENVIRONMENT USING POLYMERASE CHAIN REACTION

P. Nol, J. Rhyian, USDA-APHIS-VS National Wildlife Research Center, 4101 LaPorte Ave., Fort Collins, CO, 80521, USA; J. Triantis, L. Linke, M. D. Salman, Animal Population Health Institute, Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO, 80526, USA

Presenting author: Nol, Pauline

Summary: We developed molecular methods to detect Mycobacterium tuberculosis complex (Mtbc) in cervid feces, oropharyngeal swabs, and in soil, feed, and hay, in order to monitor shedding of Mtbc by white-tailed deer in experimental and wild settings.

By developing molecular techniques that detect Mycobacterium tuberculosis complex (MtbC) in feces, oropharyngeal swabs, and environmental samples we expected to be able to detect shedding of MtbC in BCG-vaccinated white-tailed deer (Odocoileus virginianus) and M. bovis-infected deer and determine differences in shedding rates between vaccinated/M. bovis-infected deer and nonvaccinated/M. bovis-infected deer. We developed techniques for extracting mycobacterial DNA from cervid feces, nasal and pharyngeal swabs, from soil, feed pellets, and hay. We used a PCR assay that targets the IS6110 regions of M. tuberculosis complex. Analytical sensitivity was measured to determine the best technique to optimize on the detection. We applied these techniques to samples collected from white-tailed deer that were orally or parenterally vaccinated with M. bovis BCG and experimentally infected with virulent M. bovis. Our techniques were able to detect MtbC at a range of 3-50 cells per gram of feces/environmental sample or per swab. Minimal detection of MtbC occurred after vaccination and challenge in both vaccinates and nonvaccinates. Soil and feed samples, but not hay samples, tested positive for MtbC after vaccination. We developed sensitive and specific molecular tools to monitor white-tailed deer and their environment for shedding of M. bovis and BCG. Application of these techniques to BCG-vaccinated and M. bovis-challenged white-tailed deer produced results that indicated that deer shed M. bovis and BCG only intermittently at 1-3 months after vaccination and 1-4 months after M. bovis challenge. Our techniques and data will aid future research in vaccination and management of bovine tuberculosis in deer.

Acknowledgements: We thank the students in the Salman Lab for their assistance in the laboratory and we thank the NADC Animal Care Staff for caring for and assisting with the deer.
95. A SERIES OF CRANIAL OSTEochondromAS IN FIVE FREE-RANGING WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS)

M. Kevin Keel, John Bryan, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, Georgia 30602, USA; Keith G. Thompson, Pathobiology Section, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Tennant Drive, Palmerston North, New Zealand; Samantha E.J. Gibbs, Division of Migratory Bird Management, U.S. Fish and Wildlife Service, 4401 North Fairfax Drive, Arlington, VA 22203, USA

Presenting author: Keel, Kevin

Summary: We present a case series of five wild white-tailed deer with osteochondromas, a neoplasm rarely reported in white-tailed deer and not diagnosed at the Southeastern Cooperative Wildlife Disease Study until 2002.

Other than cutaneous fibromas, neoplasia is uncommon in wild white-tailed deer. Boney tumors seem to be among the least common type. Rare reports of cranial tumors in deer have variably described them as osteomas or osteochondromas. We received five such tumors and all were determined to be consistent with osteochondromas. Between November, 2003 and February, 2009, the Southeastern Cooperative Wildlife Disease Study received the heads of five white-tailed deer (Odocoileus virginianus) with prominent hard masses involving the skull. The deer were from Georgia, Mississippi, Missouri, South Carolina and West Virginia. The heads were radiographed and the masses were sectioned using a band saw. The hard, boney masses were decalcified using a formic acid solution prior to sectioning for histology. Five-micrometer thick sections were stained by Hematoxylin & Eosin and examined microscopically to characterize the neoplasm. Each deer had a single, large, immovable mass, from 6 x 6 x 9 cm to 17 x 24 x 14 cm, typically protruding from the flat bones of the skull. The common finding of endochondral ossification beneath an expanding cap of disorganized hyaline cartilage confirmed the diagnosis of osteochondroma. The tumors most closely resembled a syndrome of osteochondromatosis described in cats. The potential outcome of the neoplasms in these deer is uncertain. They were progressive and variably invaded the nasal cavities but only one had evidence of malignant transformation. In two cases, individuals observed the deer at multiple times and noticed an increase in size of the mass. The deer were typically in good nutritional condition in spite of the heavy proliferation of bone.

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ANALYSIS OF CARFENTANIL-XYL AZINE IMMOBILIZATION IN CAPTIVE ELK BY BISPECTRAL INDEX

Terry Kreeger, Cynthia Tate, Matthew Huizenga, Cole Hansen, Wyoming Game and Fish Department, 2362 Highway 34, Wheatland, WY 82201, USA; Khursheed Mama, Department of Clinical Sciences, Colorado State University, Fort Collins, CO 80523-1620, USA

Presenting author: Kreeger, Terry

Summary: Analysis by bispectral index determined that carfentanil-xylazine does not induce general anesthesia in elk.

The bispectral index (BIS) is a continuous single variable representing a weighted sum of electroencephalogram (EEG) subparameters. The BIS provides a single datum point that can be statistically analyzed to evaluate depth of anesthesia. We used BIS to determine if carfentanil-xylazine should be considered a general anesthetic in elk (Cervus elaphus). Six captive, adult female elk in southeastern Wyoming were used in this study. The minimum alveolar concentration (MAC) for isoflurane was determined for each elk using tail clamp as the noxious stimulus. The BIS, electrocardiogram, non-invasive blood pressure, pulse oximetry, rectal temperature, and arterial blood gases were also measured. The BIS value (mean ± SD) associated with MAC was considered the reference indicator of general anesthesia. Several weeks later, the same elk were given carfentanil (0.01 mg/kg) and xylazine (0.1 mg/kg) and data as before were recorded upon induction and 10, 20, and 30 minutes thereafter. The MAC for isoflurane was 1.5 ± 0.1% (mean ± SE) with an associated BIS value of 49.9 ± 2.6. The BIS for carfentanil-xylazine was 71.9 ± 2.0 (P = 0.0001). The BIS values in elk given isoflurane were consistent with those for general anesthesia in humans (45-65), thus corroborating the use of BIS in elk. The BIS value for carfentanil-xylazine was in the range of sedation in humans (65-85). These data along with empirical observations suggest that while heavy sedation (immobilization/chemical restraint) is likely in elk given carfentanil-xylazine, they are not anesthetized.

Acknowledgements: We acknowledge the contributions of R.B. Heath for the development of the gas delivery device for elk.
97. EVALUATION OF A COMMERCIAL BELISA SEROLOGIC ASSAY FOR AVIAN INFLUENZA VIRUS DETECTION IN WILD BIRDS

Justin Brown, Page Luttrell, Roy Berghaus, Whitney Kistler, Shamus Keeler, Taiana Costa, Michael Yabsley, and David Stallknecht, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; David Swayne, United States Department of Agriculture, Agricultural Research Service, Southeast Poultry Research Laboratory, Athens, GA, USA; Kathy Velek, IDEXX Laboratories, One IDEXX Drive, Westbrook, ME, USA; Marcy Uhart, Hebe Ferreyra, Martin Gilbert, William Karesh, Damien Joly, Wildlife Conservation Society, Bronx, NY, USA; Jeffrey Hall, United States Geological Survey, National Wildlife Health Center, Madison, WI 53711, USA

Presenting author: Brown, Justin

Summary: The IDEXX blocking ELISA was a more sensitive serologic test than the AGID for detecting antibodies to type A influenza viruses in wild birds after experimental and natural infection.

Currently, avian influenza (AI) virus surveillance in wild birds relies predominately on virus isolation. A sensitive and specific test to detect AI virus antibodies would complement existing surveillance strategies and has the potential to provide a cost efficient and rapid approach to identify wild bird species involved in AI epidemiology. To evaluate the efficacy of a commercial blocking ELISA (bELISA) and the agar gel immunodiffusion (AGID) tests for detection of antibodies to AI virus in wild birds, we tested 281 serum samples from various wild avian species experimentally infected with AI viruses. Included in these samples were 178 samples from birds with confirmed AI infections (122 with low pathogenic avian influenza viruses and 56 with highly pathogenic avian influenza viruses) and 103 samples from uninfected, negative control birds. Additionally, we tested 2,747 field serum samples collected from 65 wild bird species representing 8 orders with the AGID and the bELISA tests. Based on the experimental samples, the sensitivities of the bELISA and AGID assays were 0.820 and 0.674, respectively. Both tests had an estimated specificity of 1.00. Consistent with the experimental findings, the sensitivity of the bELISA on field samples was greater or equal to the AGID sensitivity for all species.

The results of this study indicate that the bELISA is a more sensitive serologic test than the AGID for detecting prior AI infection in wild birds. The results discussed herein will provide real field examples to demonstrate the potential utility of the bELISA for AI surveillance in wild birds.

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98. RIFT VALLEY FEVER: AN EXERCISE TO EVALUATE THE STATE AND FEDERAL RESPONSE TO AN HYPOTHETICAL INTRODUCTION OF THE DISEASE INTO FLORIDA

Paul Gibbs, Stasia Bembene, Tineke Kramer and Jocelyn Mullins, College of Veterinary Medicine, University of Florida, Gainesville, FL 32608, USA; Greg Christy and Thomas Holt, Division of Animal Industry, Florida Department of Agriculture and Consumer Services, Nathan Mayo Building, 407 South Calhoun Street, Tallahassee, FL 32399, USA

Presenting author: Gibbs, Paul

Summary: An exercise on Rift Valley Fever (RVF), designed to test interagency collaboration between those responsible for animal (including wildlife) and human health, illustrated that RVF posed a significant threat to wildlife in Florida and further that infection of ruminant wildlife would make control and eradication of the disease exceedingly difficult.

Rift Valley fever (RVF) is a zoonotic viral disease endemic to Africa. US mosquitoes can transmit the virus. If introduced to the USA, RVF could have a greater impact than West Nile virus on the animal and human populations. An exercise was held November 2008 to test Florida’s preparedness. In partnership with the State’s Emergency Operations Center, a 3 day, multi-agency (State and Federal) exercise, was organized to test Florida’s response to a simulated outbreak of RVF. The outbreak was characterized by an initial recognition of increased calf mortality followed by mild to severe human cases in other parts of the state. The outbreaks occurred in the late fall, were of limited extent, and “died out”. While under the scenario RVF did not become established in any wildlife populations in Florida, incidents were incorporated into the scenario that involved wildlife. From observation during the exercise and through a subsequent questionnaire, the 100 plus participants found the exercise realistic, but challenging. Since little is known of the susceptibility of US wildlife species to RVF virus, the wildlife specialists found it was difficult to speculate on the epidemiology of RVF in wildlife. This exercise can be considered an example for future multi-agency exercises dealing with a vector-borne disease with a) a zoonotic component and b) involving ruminant wildlife. The exercise highlighted a) that RVF might be very difficult to control and b) the need for more information on the susceptibility of North American wildlife species to Rift Valley fever virus.
99. PASSIVE SURVEILLANCE AS A TOOL FOR INVESTIGATING PATTERNS OF DISEASE IN WILD RACCOONS

Lonnie S. Pyne, Dept. of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, N1G 2W1, Canada; David L. Pear, Dept. of Population Medicine and Canadian Cooperative Wildlife Health Centre, Ontario/Nunavut Region, Canada; G. Douglas Campbell, Canadian Cooperative Wildlife Health Centre, Ontario/Nunavut Region, Canada; Ian K. Barker, Canadian Cooperative Wildlife Health Centre, Ontario/Nunavut Region and Dept. of Pathobiology; Ontario Veterinary College, University of Guelph, Guelph, ON, N1G 2W1, Canada

Presenting author: Barker, Ian

Summary: Data acquired during passive surveillance for disease in wildlife proved promising as a tool for investigating the patterns of canine distemper in raccoons in Ontario.

The Canadian Cooperative Wildlife Health Centre (CCWHC) maintains a passive or scanning surveillance database, recording submissions of wildlife for disease investigation. The utility of such data as a surveillance tool for the investigation of patterns of disease was examined using canine distemper in raccoons (Procyon lotor). Raccoon submissions to the Ontario/Nunavut Region, CCWHC, from the province of Ontario over the 5-year period 2001-2006 were examined for the presence of spatial, temporal and spatio-temporal clusters of canine distemper (CD) using spatial scan statistics in SaTScanTM. Raccoon submissions were geo-referenced, and designated as CD ‘cases’ or as non-CD ‘controls’. Using a Bernoulli (case vs. control) model, temporal scans were done on individual years and the entire study period. Using the space-time permutation model, space-time scans were done on individual years and the entire study period. Temporal scans detected a statistically significant cluster from mid-August to the end of October 2002. The spatial scan detected a cluster surrounding the Greater Toronto Area (GTA) when individual years were scanned in 2001 and 2005. The space-time scan detected clusters near Toronto in 2001, 2002, 2005, and 2006. The time of each temporal and space-time cluster coincided with the mating season or the period when young raccoons disperse. These periods of movement are known to coincide with increases in cases of CD. The consistent finding of space and/or space-time clusters near the GTA may reflect the high density of raccoons in this environment, but the lack of raccoon submissions from certain regions in Ontario should be considered when interpreting these results.
100. THE ROLE OF THE REDWOOD CHIPMUNK (TAMIAS OCHROGENYS) IN THE ECOLOGICAL MAINTENANCE OF ANAPLASMA PHAGOCYTOPHILUM

Nathan C. Nieto, Janet E. Foley, School of Veterinary Medicine, Department of Medicine and Epidemiology, University of California, Davis, California, 95616, USA

Presenting author: Nieto, Nathan

Summary: The redwood chipmunk (Tamia ochrogenys) is experimentally reservoir competent for Anaplasma phagocytophilum and frequently infected in nature.

Granulocytic anaplasmosis is an emerging tick-transmitted disease that persists in rodent-Ixodes ricinus complex tick cycles across the Holarctic. We wished to determine the reservoir of Anaplasma phagocytophilum in the western United States. Redwood chipmunks (Tamia ochrogenys) were live trapped, marked, examined for ectoparasites, and bled to test for infection and exposure to A. phagocytophilum. All ticks were placed in vials containing 70% ethanol. Whole blood was placed in EDTA tubes. Ticks were keyed out to species. DNA from both ticks and whole blood was extracted using a kit (Qiagen). Taqman PCR was used to identify infection. IFA was used to identify exposure to A. phagocytophilum. To conduct reservoir competence experiments, chipmunks were brought into the lab and experimentally infected with A. phagocytophilum and infection was monitored for 4 months. Unexposed I. pacificus ticks that had fed on infected chipmunks were fed on naive mice following the molt. Redwood chipmunks are common in habitats where A. phagocytophilum is common, have high PCR- and seroprevalence, and are infested with a diversity of Ixodes spp. ticks. Experimental infection of seven wild-caught redwood chipmunks induced chronic waxing and waning rickettsemia. Xenodiagnosis of chipmunks successfully infected pools of I. pacificus larvae. We show that chipmunks are reservoir-competent for GA and are important for maintaining infection in nature, thus contributing to risk of infection in humans, domestic animals, and wildlife.

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101. WE HAVE ALL OF THESE SAMPLES, NOW WHAT?

Laurie A. Baeten, Colleen Duncan, Kristy Pabilonia, Veterinary Diagnostic Laboratory, Colorado State University, 300 W Drake Road, Fort Collins, CO 80523, USA

Presenting author: Baeten, Laurie

Summary: A review of current diagnostic techniques and how best to utilize them when testing samples collected from wildlife species.

Diseases of free-ranging animals are increasingly being identified as threats to various populations as well as crossing over to humans and domestic livestock. As such, there has been an increase in the demands for disease diagnosis in wildlife species. As most diagnostic assays have been designed for use in domestic animals and humans, their application in alternate species is sometimes questionable. In an attempt to obtain the most accurate and reliable data a solid understanding of each diagnostic assay is required, including sensitivity, specificity and any limitations of the test methods in question. The objective of this presentation is to provide a review of current diagnostic techniques available for molecular, virological, bacteriological and serological methods. Included in the review will be a discussion on how to choose which testing methods are most appropriate for wildlife samples as well as highlighting those methods that may be useful for ante-mortem surveillance vs. post-mortem disease investigation.
102. HYPOPHOSPHATEMIA AND ASSOCIATED RICKETS IN HAND-REARED MOOSE (ALCES ALCES) CALVES IN ALASKA

Kimberlee B. Beckmen, Alaska Department of Fish and Game, Division of Wildlife Conservation, 1300 College Road, Fairbanks, AK 99701, USA; Kathy A. Burek, Alaska Veterinary Pathology Services, 23834 The Clearing Dr, Eagle River, AK 99577, USA

Presenting author: Beckmen, Kimberlee

Summary: Five bottle-reared moose calves died at 32-53 days of age from hypophosphatemia with multiple fractures of long bones and ribs, “rachitic rosyary”, and enlarged metaphyses.

Three orphan and two captive-born moose (Alces alces) calves at a research facility were euthanized at 32-53 days of age with multiple pathologic fractures. One additional orphan calf survived. The facility had previously successfully bottle-raised calves with a similar husbandry regime. Ante-mortem blood and serum samples were evaluated for complete blood cell counts and clinical chemistries. Complete necropsy and histopathological examinations were completed on all fatalities and two normal free-ranging calves were collected for comparison examinations. Ante-mortem serum and post-mortem selected tissues were analyzed for trace element concentrations along with milk formula, available forage and water supplies. Previously collected tissues and serum analysis from similarly aged free-ranging calves was utilized in the comparisons. Gross necropsy findings included multiple fractures of long bones and ribs, “rachitic rosyary”, and enlarged metaphyses. Histopathologic findings were consistent with “rickets” osteomalacia and osteopenia. The animals also had degenerative myopathy and myositis. Serum albumin, calcium and phosphorus were low and Ca:P ratio (corrected for low albumin) was elevated. Pathologic fractures, histopathologic bone maturation defects and clinical signs were consistent with a rickets-type disease. Low serum phosphorus and elevated Ca:P ratio confirmed a primary phosphorus deficiency. Insufficient serum was available to determine vitamin D status. Blood selenium and serum iron were significantly low and arrested growth lines in some animals suggested a protein deficiency. Multiple perturbations of essential trace elements and possibly low dietary protein were hypothesized as causes for the lesions seen.

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103. WHITE-NOSE SYNDROME IN BATS: THREAT MANAGEMENT AND CONSERVATION PARALLELS TO AMPHIBIAN CHYTRIDIOMYCOSIS

Alison H. Robbins, MS, DVM, 65 Arrowhead Road, Concord, MA 01742, USA; Bryan Windmiller, MS, PhD, Hyla Ecological Services, 65 Arrowhead Road, Concord, MA 01742, USA

Presenting author: Robbins, Alison

Summary: White-nose syndrome has a number of close epidemiologic parallels to amphibian chytridiomycosis: captive breeding and the selection for disease resistant individuals may be the best short term conservation strategy to prevent extinctions and to recover decimated populations.

White-nose syndrome (WNS) is a recently identified and rapidly spreading epizootic of cave-hibernating bats in the northeastern United States. This syndrome is characterized by observable fungal growth around the nose and the wing membranes of hibernating bats, emaciation, abnormal behavior, and mortality rates that often exceed 95%. Since its discovery in 2007, the syndrome has spread to hibernacula in eight northeastern states, and if its spread continues, it may threaten the extinction of federally listed species and the extirpation of common species in large areas of their range. Though much is still unknown, there are a number of close parallels to amphibian chytridiomycosis (Bd), a fungal epizootic that has caused the extinction of more than 100 frog species in recent decades. Both WNS and Bd are likely to have resulted from the introduction of a novel fungal pathogen (Geomyces sp. is suspect causative agent in WNS), the epizootics affect multiple host species, both are associated with population-wide mortality rates that may reach 100%, both infected frogs and bats can be readily rehabilitated at the individual level, in both cases mortality is seasonal and affected by the temperature tolerances of the fungal pathogen, and in both cases the fungal pathogen can probably persist as a saprobe independent of the host species and thus avoid selection pressure against complete elimination of host populations. Despite a decade of research on the disease ecology and epidemiology of chytridiomycosis since it was identified in 1998, it has thus far been impossible to either stop the spread of the disease on contiguous land masses or to eliminate the fungus from the environment. Instead, the most promising management practices for chytridiomycosis (captive breeding of threatened species or populations and attempts to breed disease-resistant individuals) may offer hope for bat populations threatened by WNS, especially if applied early in the WNS epizootic.
104. FARM-SIDE RISK ASSESSMENT FOR AVIAN INFLUENZA VIRUS TRANSMISSION: EXPERIMENTAL INFECTION OF PERIDOMESTIC PASSERINES WITH LOW PATHOGENICITY AVIAN INFLUENZA VIRUS (LPAIV)

Nicole M. Nemeth, Theodore D. Anderson, Nicholas O. Thomas, and Alexis R. Freifeld, National Wildlife Research Center, USDA/APHIS/WS, 4101 Laporte Ave., Fort Collins, CO 80521, USA

Presenting author: Nemeth, Nicole

Summary: Passerines demonstrated low levels of oral Low Pathogenicity Avian Influenza Virus (LPAIV) shedding that did not result in cage mate transmission, providing evidence that these birds are not likely to play a significant role in natural transmission cycles.

LPAIV poses a threat to agriculture, including poultry and game bird farms; however, the dynamics and possible sources of farm-to-farm transmission are not completely understood. We examined the potential role of free-ranging passerines in the spread of AIV. European starlings (Sturnus vulgaris) and house sparrows (Passer domesticus) were inoculated (n=18 of each) with low pathogenicity (LP) AIV (H3N8, isolated from free-ranging waterfowl) via oculonasal/oral routes, while an equal number of non-inoculated birds were co-housed with inoculates. Four weeks post-inoculation, birds underwent homologous challenge. Oral and cloacal swabs were collected from 1-14 days post-inoculation (DPI) and post-challenge, and swabs were tested by quantitative RT-PCR. Birds were bled weekly for four weeks post-inoculation and two weeks post-challenge, and sera were tested by bELISA and/or hemagglutination inhibition. Respiratory and gastrointestinal tissues were tested by RT-PCR from a subset of birds from 3-5 DPI. Most inoculated individuals (9/18 sparrows, 18/18 starlings) had evidence of low-level oral LPAIV shedding, usually of 3-4 days duration, while no cloacal shedding was detected. No cage mate transmission was detected and most inoculated birds seroconverted by 14 DPI (16/18 sparrows, 15/18 starlings). Challenge and tissue tropism results are pending. House sparrows and European starlings are abundant, widespread passerines that commonly reside on farms and share food and water sources with captive bird flocks. These species appear susceptible to LPAIV infection and therefore may be useful in serosurveillance. However, they are unlikely to play a role in transmission. Responses may vary among avian species and LPAIV subtypes, and additional experimental studies would provide further insight into the role of passerines in AIV ecology.

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105. AVIAN INFLUENZA VIRUS PERSISTENCE IN FILTERED WATER FROM WATERFOWL HABITATS IN GEORGIA

Shamus P. Keeler and Dave Stallknecht, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, 589 D. W. Brooks Street, Athens, GA 30602, USA

Presenting author: Keeler, Shamus P.

Summary: Water was collected from waterfowl habitats in Georgia and used to determine whether abiotic factors beyond pH, salinity, and temperature affect avian influenza virus persistence in aquatic environments.

Avian influenza virus (AIV) is known to persist within aquatic environments under certain conditions. Previous work has focused on pH, salinity, and temperature within distilled water. The objective of this project is to determine if temperature, salinity, and pH are the overriding abiotic factors affecting AIV persistence in natural water. Water samples were collected from fifteen waterfowl habitats distributed across the state of Georgia. The water was filtered using 0.22 μm filters to remove a majority of the organic material within the samples. The pH and salinity were determined for each sample after filtration. The duration of persistence within each water sample was determined for two wild-bird origin influenza viruses at 10°C, 17°C, and 28°C. The results were compared to determine the effect of pH, salinity, and temperature on viral persistence in natural water. As the temperature increased viral persistence decreased in all 15 water samples. Viral persistence was low within water samples with pH and salinities that were outside the previously determined ideal ranges. A large variation was observed in viral persistence within pH ranges of 6.8-7.6 and salinities of 30ppm to 130ppm. The relationship between temperature and AIV persistence in natural water was consistent with previous observations in distilled water. The large variation observed in viral persistence in water samples with pH (7.2-8.4) and salinities (>25,000ppm) within the previously determined ideal ranges indicates that other abiotic factors affect AIV persistence within aquatic environments. These results contribute to our understanding of the ecology of AIV and may help in identifying habitats with an increased likelihood of persistence.
106. THE “HUMAN INFLUENZA RECEPTOR” NEU5ACALPHA2,6GAL IS WIDELY EXPRESSED AMONG DIFFERENT TAXA OF WILD BIRDS

P. Ellström, E. Jourdain, O. Gunnarsson, J. Waldenström, B. Olsen, Kalmar University, Kalmar SE-391 82, Sweden

Presenting author: Jourdain, Elsa

Summary: Histochemistry with Sambucus nigra agglutinin, a lectin that specifically recognizes alpha2,6-linked sialic acids, revealed that the tracheas of nine wild bird species express alpha2,6-linked sialic acid residues, which are usually considered as “human influenza receptors”.

Human influenza A isolates use Neu5Ac(alpha2,6Gal)GalNAc, an alpha2,6-linked sialic acid (SA), to bind epithelial cells, whereas avian isolates usually have tropism for alpha2,3-linked SAs. Because little is known on the expression of alpha2,6-linked SAs in birds, we studied their expression on the tracheal epithelium of nine wild bird species. Tracheas were collected from birds recently dead from physical injury and kept frozen at -80°C. Each bird was thawed and the trachea dissected before fixation with 4% paraformaldehyde and TBS sucrose. Tracheas were embedded in OCT compound (Tissue Tech) and frozen in iso-pentane on dry ice. Sections were stained with Sambucus nigra agglutinin (SNA), a lectin that specifically binds alpha2,6-linked SAs. Lectin binding was revealed using the DIG-glycan differentiation kit (Roche Applied Science) and Vulcan Fast Red (Biocare Medical). Tracheas from three birds of each species were studied. Pretreatment of some tracheas with neuraminidase from Artrobacter ureafaeceus guarantied binding specificity. We found that alpha2,6-linked SAs were expressed on the tracheal epithelium of all species included in the study. Staining was abolished by pre-treatment with neuraminidase, showing that SNA binding was specific for SAs. Our results show that alpha2,6-linked SAs, often considered as “human influenza receptors”, are expressed in the trachea of several bird species and suggest that tracheal infection by human influenza isolates might occur in birds. Further studies are needed to determine whether influenza A viruses with tropism for Neu5Ac(alpha2,6Gal)GalNAc are indeed able to replicate in wild bird tracheas. Such studies are important to assess the role of birds as potential mixing vessels for influenza A viruses.

Acknowledgements: We thank Charlotte Bergström and her colleagues from Kalmar County Hospital, Sweden.
107. SHEDDING LIGHT ON LOW-PATHOGENIC AVIAN INFLUENZA VIRUS INFECTION OF MALLARDS: IMPACT OF VIRAL SHEDDING CHARACTERISTICS ON SURVEILLANCE AND RESEARCH

Kaci K. VanDalen, Heather J. Sullivan, Nicole L. Mooers, Alan B. Franklin, Susan A. Shriner, United States Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services, National Wildlife Research Center, 4101 Laporte Ave, Fort Collins, CO 80521, USA

Presenting author: VanDalen, Kaci

Summary: Shedding characteristics of mallards infected with Low-Pathogenic Avian Influenza (LPAI) suggest environmental sampling (feces and water) may be the best strategies for detecting LPAI in an area.

Influenza A viruses have been isolated from a wide range of wild avian species. Wild mallards (Anas platyrhynchos) are considered one of the primary reservoir species for these viruses. Understanding virus transmission and shedding characteristics of mallards is therefore critical when designing influenza A virus surveillance strategies in avian species. We orally inoculated three-month and six-month old mallards with LPAI virus subtypes H4N6 and H3N8 to investigate virus shedding characteristics. We collected cloacal and oral-pharyngeal swabs from each duck as well as fresh feces and water samples from each pen. We then exposed an additional eight mallards to the water tanks used by the experimentally infected mallards and collected swabs and water samples. All samples were tested using real time RT-PCR. All orally inoculated mallards and naive mallards exposed to LPAI contaminated water shed virus and produced an antibody response. On average, fecal samples had significantly higher viral loads and were detectable for two days longer than oral-pharyngeal or cloacal samples. Viral loads were significantly higher for older ducks compared to juveniles. These results indicate that wild birds can transmit LPAI though a common water source and that focusing surveillance efforts on fecal and/or water samples may improve the likelihood of detecting avian influenza viruses in the environment. In addition, differences in shedding characteristics between mature and juvenile mallards indicate that prevalence estimates may be skewed if bird age is unknown. Preliminary results also indicated that co-infection with more than one LPAI subtype could affect shedding characteristics.
108. EVALUATION OF AN EPITOPE-BLOCKING ENZYME-LINKED IMMUNOSORBENT ASSAY FOR THE DETECTION OF ANTIBODIES TO INFLUENZA A VIRUS IN DOMESTIC AND WILD AVIAN AND MAMMALIAN SPECIES

Heather J. Sullivan, Kaci VanDalen, Kevin T. Bentler, Alan B. Franklin, and J. Jeffrey Root, United States Department of Agriculture, Wildlife Services, National Wildlife Research Center, Fort Collins, Colorado, 80521, USA; Bradley J. Blitvich, Department of Veterinary Microbiology and Preventive Medicine, Iowa State University, Ames, Iowa 50011, USA

Presenting author: Sullivan, Heather

Summary: The epitope-blocking enzyme-linked immunosorbent (bELISA) assay reported herein provides a rapid, reliable, and inexpensive technique for surveillance of influenza A virus exposure in taxonomically diverse vertebrate species.

Recently, the Asian strain of highly pathogenic avian influenza H5N1 has attracted world-wide attention because it has been responsible for significant mortality in many domestic and wild species, surveillance studies have been initiated to monitor the activity and spread of select influenza A virus subtypes. The objective of this study was to develop a bELISA using commercially available reagents that would provide research and diagnostic laboratories a rapid and inexpensive method to screen large numbers of serum samples from both domestic and wild animals for antibodies to influenza A virus. Direct ELISAs were performed to ensure that the commercial monoclonal antibody and nucleoprotein antigen could sufficiently bind and produce an enzymatic reaction measureable by a spectrophotometer. For the bELISA, these reagents were then independently optimized using well-characterized serum samples from experimentally infected and mock infected waterfowl. A total of 251 serum samples from experimentally infected vertebrates and 745 serum samples collected in serosurveys belonging to 12 species (eight orders, 12 families) were used to evaluate the bELISA. The platform we used was similar to a previously published bELISA used for West Nile virus surveillance by Blitvich et al.(2003, J. Clin. Micro, 41: 1041-1047). We used logistic regression to compare detection rates of antibodies to influenza A virus in sera from experimentally challenged raccoons (Procyon lotor) and mallards (Anas platyrhynchos) (both negative control and infected animals) using the bELISA and AGID assay. For the 251 serum samples evaluated from the experimental inoculations, the concordance between the AGID assay and bELISA was 82.1%(95% CI = 77.3, 86.8). Based on odds ratios, the bELISA was 2.5 (95% CI = 1.6, 3.8) times more likely than the AGID assay to detect antibodies to influenza A virus in the experimentally challenged animals. The AGID assay has been the traditional 'gold standard' when dealing with a large number of serum samples for antibodies to influenza A virus during surveillance studies but due to limitations it may not be ideal for use with all species. We have developed a sensitive, inexpensive, objective, species-independent bELISA platform that can be performed in most laboratories and can screen for a variety of influenza A virus-specific subtypes. For these reasons this diagnostic assay is ideal for large scale serological studies in multiple domestic and wild mammalian and avian species.

Acknowledgements: We are indebted to T. Anderson (National Wildlife Research Center (NWRC)) for logistical assistance and the Texas Wildlife Services (WS), Pennsylvania WS for assistance with sample collection. We also thank the many public and private land stewards that allowed us to access to their lands for trapping. In addition, we thank R. A. Bowen (Colorado
State University) and C. Driscoll (Maryland Department of Natural Resources) for providing sera for evaluation.
109. SURVEILLANCE FOR AVIAN INFLUENZA IN WILD BIRDS IN RUSSIA, GREENLAND AND MEXICO

John A. Baroch, Thomas J. Deliberto, National Wildlife Disease Program, Wildlife Services, APHIS/USDA, 4101 LaPorte Ave., Fort Collins, CO 80521, USA; A. Alonso Aguirre, Wildlife Trust, 460 West 34th Street, 17th Floor, New York, NY 10001-2320, USA; Vasilii V. Baranyuk, Wrangel Island Nature Reserve, 35-40 Lomonosovsky Prospect, Moscow, Russia, 119192; Ole R. Therkildsen, Department of Wildlife Ecology and Biodiversity, National Environmental Research Institute, Kalo, Grenavej 14, DK-8410 Ronde, Denmark; Alexander Rodriguez-Palaci, Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster, OH 44691, USA

Presenting author: Baroch, John

Summary: Cooperative initiatives by the USDA National Wildlife Disease Program (NWDP) have established surveillance for avian influenza and other avian diseases in strategically important areas used by migratory birds entering the United States, and have built a foundation for future cooperation.

Russia, Greenland and Mexico possess important breeding and wintering areas for migratory water birds and provide a potential link for the movement of HPAI H5N1 to the U.S. Surveillance in these areas can only be accomplished by cooperation among multiple organizations and requires technical and political support. Greenland, Mexico, and Wrangel Island in Russia are strategically important areas that present unique logistical and technical challenges to conducting wildlife disease surveillance. The NWDP has built cooperative relationships with national, international, government, NGO, and university partners to deploy qualified scientists and provide technical and logistical support to field survey teams. These efforts have generated new data on avian influenza and other avian pathogens, including Newcastle Disease Virus and Clostridium difficile, as well as new information on water bird distribution and movements, and have developed valuable collaborative relationships and logistical support systems. The spread of HPAI H5N1 has illustrated the importance of cooperative surveillance of transboundary zoonotic diseases in wildlife. Three examples of successful international collaboration are surveillance of wild birds in Russia, Greenland, and Mexico. These projects demonstrate additional benefits to our knowledge of other wildlife diseases and wildlife ecology, and should facilitate effective responses to future zoonotic disease issues.
110. HOST SELECTION BY CULEX PIPIENS MOSQUITOES AND WEST NILE VIRUS AMPLIFICATION

Gabriel L. Hamer, Department of Pathobiological Sciences, University of Wisconsin, Madison, WI 53706, USA; Daniel B. Hayes, Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI 48824, USA; Tony L. Goldberg, Department of Pathobiological Sciences, University of Wisconsin, Madison, WI 53706, USA; Uriel D. Kitron, Department of Environmental Studies, Emory University, Atlanta, GA 30322, USA; Jeffrey D. Brawn, Department of Natural Resources and Environmental Sciences, Program in Ecology, Evolution, and Conservation Biology, University of Illinois, Champaign, IL 61820, USA; Marilyn O. Ruiz, Department of Pathobiology, University of Illinois, Champaign, IL 61820, USA; Scott R. Loss, Conservation Biology Graduate Program, University of Minnesota, St. Paul, MN 55108, USA; Edward D. Walker, Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824, USA.

Presenting author: Hamer, Gabriel

Summary: We identified the avian host selection of Culex pipiens, the primary vector of West Nile virus (WNV) in Chicago, Illinois, and determined the most important avian hosts for WNV amplification, which included American robin, blue jay, and house finch. Recent field studies have suggested that the dynamics of West Nile virus (WNV) transmission are influenced strongly by a few key super spreader bird species that function both as primary blood hosts of the vector mosquitoes (in particular Culex pipiens) and as reservoir-competent virus hosts. To confirm this pattern, we performed a mosquito blood meal analysis integrating host-feeding patterns of Cx. pipiens, the principal vector of WNV in the eastern United States north of the latitude 36°N and other mosquito species with robust measures of host availability, to determine host selection in a WNV-endemic area of suburban Chicago, Illinois, during 2005–2007. Measures of host abundance and competence and Cx. pipiens feeding preference were combined to estimate the amplification fractions, a measure of the contribution to transmission, for the different bird species. Cx. pipiens fed predominantly on birds (83%) and mammals (19%). American robins (Turdus migratorius) were marginally overused and several species were underused on the basis of relative abundance, including the common grackle (Quiscalus quiscula) and house sparrow (Passer domesticus). The most important avian hosts included American robin (35%), blue jay (Cyanocitta cristata) (17%) and house finch (Carpodacus mexicanus) (15%). We identified a genetic basis for the inclination for mammal feeding in the Culex pipiens complex mosquitoes in Chicago IL. These individuals with higher rates of mammal feeding (Cx. pipiens molestus) provide a mechanism for bridge vector transmission from birds to humans. Our predictions were that approximately 66% of WNV-infectious Cx. pipiens became infected from feeding on just a few species of birds, including American robin, blue jay, and house finch.

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111. FIELD EVALUATION OF THE FLUORESCENCE POLARIZATION ASSAY FOR USE IN DIAGNOSING BRUCELLA ABORTUS INFECTIONS IN BISON IN THE GREATER YELLOWSTONE AREA

Brant A. Schumaker, Ian A. Gardner, University of California, Davis, One Shields Ave., Davis, CA 95616, USA; Barbara A. Corso, USDA-APHIS-VS, Centers for Epidemiology and Animal Health, 555 South Howes Street, Suite 200, Fort Collins, CO 80521, USA; Jack C. Rhyian, USDA-APHIS-VS, National Wildlife Research Center, 4101 Laporte Avenue, Fort Collins, CO 80521, USA; L. Michael Philo, USDA-APHIS-VS, Western Region, 9439 Owl Way, Bozeman, MT 59718, USA; Mo D. Salman, Colorado State University, Fort Collins, CO 80523, USA

Presenting author: Schumaker, Brant

Summary: The fluorescence polarization assay proved to be a very sensitive test with reduced specificity in a disease-endemic population of bison in the Greater Yellowstone Area and illustrates the importance of test evaluation in the appropriate target population.

The purpose of this project was to determine the accuracy of the fluorescence polarization assay (FPA) for the screening of Brucella abortus infection in bison (Bison bison). No reliable ante-mortem gold standard exists. The sensitivity and specificity of diagnostic tests is critical for appropriate agricultural and wildlife brucellosis management. Samples were taken from two different herds; the brucellosis-infected herd in Yellowstone National Park and brucellosis-free privately-owned bison from western Montana. Serum samples were taken from all animals ante-mortem for serology and organ samples were taken on necropsy for culture. Ten different serologic tests were performed. Test performance characteristics were calculated. A Bayesian analysis was used to fit estimates of sensitivity, specificity, and prevalence in the absence of a gold standard for diagnosis of Brucella. A decision-tree analysis was also performed, looking at the optimal battery of diagnostic tests to be used for accurate classification of disease status.

While none of the animals in the disease-free herd tested positive by FPA analysis, the FPA showed limitations compared to other tests in the infected herd. Statistically significant differences were not shown between tests nor for targeted versus full tissue sampling for bacterial culture. The FPA proved to be a very sensitive test with similar challenges to other tests with respect to specificity in a disease-endemic population. This study illustrates the importance of test evaluation in the appropriate target population, as opposed to using strictly known disease-positive and negative animals. Further discussion will focus on the challenges posed when no gold standard is available for negative animals. The relationship between age class and test/disease status will also be discussed.
112. CYTOKINE GENE EXPRESSION FOLLOWING BCG VACCINATION AND MYCOBACTERIUM BOVIS CHALLENGE IN THE EURASIAN BADGER (MELES MELES)

R. Ashford, S. Lesellier, S. Palmer, S. Gowtage, D. Davè, D. Dalley, R.G. Hewinson and M. Chambers, Veterinary Laboratories Agency, Woodham Lane, Addlestone, Surrey, KT15 3NB, UK; B. Catchpole, Department of Pathology and Infectious Diseases, Royal Veterinary College, Hawkshead Lane, North Mymms, Hatfield, Hertfordshire, AL9 7TA, UK

Presenting author: Ashford, Roland

Summary: Measurement of cytokine mRNA following administration of BCG, and subsequent challenge with Mycobacterium bovis, revealed cell-mediated immune responses associated with vaccination and disease progression in Eurasian badgers.

The immunological response to intra-muscular BCG vaccination against bovine tuberculosis is poorly characterized in the Eurasian badger (Meles meles). In part, this is due to a lack of immunological reagents for this species. The application of semi-quantitative RT-PCR for the measurement of cytokine mRNA represents a valuable approach with which to investigate cell-mediated immune responses. Captive badgers were given intra-muscular BCG vaccine then challenged subsequently with virulent M. bovis. A group of control animals received no vaccine. Blood samples were collected fortnightly during the course of the study, from which peripheral blood mononuclear cells (PBMCs) were isolated. Vaccine efficacy was assessed on the basis of pathology post-mortem.

Isolated PBMCs were stimulated overnight with a range of specific antigens. RNA was extracted from stimulated cells and reverse transcribed, prior to amplification of cytokine mRNA using real-time PCR. Six cytokines (interferon-gamma, interleukin-2, interleukin-4, interleukin-6, interleukin-10 and tumour necrosis factor-alpha) were quantified.

Vaccination with BCG provided protection against M. bovis challenge, as demonstrated by reduced pathology post-mortem. Measurement of cytokine mRNA by semi-quantitative RT-PCR revealed immunological responses to both vaccination and disease progression. We have demonstrated that the measurement of cytokine mRNA by RT-PCR can reveal immunological responses associated with BCG vaccination and tuberculosis in the badger. In the UK, the badger is a wildlife reservoir of bovine tuberculosis, and hence a source of infection in cattle. One potential strategy to reduce the incidence of tuberculosis (alongside a range of control measures) is the vaccination of badgers with BCG. Information regarding fundamental immunological responses to disease is beneficial to the development of vaccination strategies.
113. MEASURING METACARPAL CORTICAL BONE MASS IN FREE-RANGING BLACK BEARS (URUS AMERICANUS) USING PORTABLE RADIOGRAPHY

Rita L. Seger and Robert C. Causey, Department of Animal and Veterinary Sciences, William A. Halteman, Department of Mathematics and Statistics, and Frederick A. Servello, Department of Wildlife Ecology, University of Maine, Orono, Maine, USA; Randal A. Cross and Walter J. Jakubas, Maine Department of Inland Fisheries and Wildlife (DIFW), Bangor, Maine, USA; Richard M. Seger, Spectrum Medical Group, Bangor, Maine, USA. Author contact: rita.seger@umit.maine.edu

Presenting author: Seger, Rita L.

Summary: A portable x-ray unit was used to obtain forepaw radiographs of free-ranging black bears in a study of ursine bone mass that compared active and hibernating bears.

A study of skeletal mechanotransduction compared bone mass (BM) between free-ranging black bears (Urus americanus) that were active or hibernating (Seger, 2009 Univ Maine). Effects on BMD of age, sex, body condition and lactation status were assessed. Forepaw radiographs were obtained during 2005-2007 from trapped bears mid-May through June, hunter-killed bears during September, and radio-collared, hibernating bears mid-January through March. This was accomplished using a portable x-ray unit (XR200, Golden Engineering, Centerville, Indiana) and radiographic film cassettes with high resolution intensifying screens. Metacarpal index was determined by digital x-ray radiogrammetry (Sectra Imtec, AB, Linkoping, Sweden), and values for second, third and fourth metacarpals were averaged as a measure of cortical BM. Ages were known or determined by cementum annuli. Body condition index (BCI) was measured by the method of Cattet et al., 2002 (Can J Zool, 80:1156-1161). Radiographs were obtained on 167 female bears and 78 male bears. BM varied with age and sex, and not with body condition or lactation status. Analysis was restricted to females. Age-adjusted BM was greater in autumn than in winter in younger bears, and there was no significant difference in older bears. The XR200 is recommended as an exceptionally portable x-ray unit that produced high quality radiographs and performed well under a variety of field conditions. Digital x-ray radiogrammetry provided a useful measure of BM that proved sufficiently precise to elucidate effects of several factors relevant to bone metabolism. Unloading-induced bone loss would be expected to affect bears of all ages, so the radiographic findings indicate that unloading-induced bone loss may not occur during ursine hibernation.

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114. RESULTS OF WASHING OILED SEA OTTERS: OLIVE OIL AND OTHER PHENOMENA

David A. Jessup, Sharon Toy-Choutka, Francesca Batac, Ben Weitzman, California Department of Fish and Game, MWVCR, 1451 Shaffer Rd., Santa Cruz, CA 95060, USA; Michael J. Murray, Monterey Bay Aquarium, 886 Cannery Row, Monterey, CA 93940, USA; David Casper, Robin Duncan, Laura Yeates, Long Marine Laboratory, University of California-Santa Cruz, Santa Cruz, CA 95060, USA

Presenting author: Jessup, David

Summary: Methods used to wash sea otters have been improved such that coat recovery times can be more than cut in half, stress reduced, costs reduced and outcomes improved.

Three years of research on the physiology of washing sea otters (Enhydra lutris) revealed that some simple changes in materials and methods of washing oiled sea otters, primarily the liberal use of warm soft water for rinsing and for recovery pools, could reduce time required for the hair coat to recover water repellency by 50% or more. This research was inspired by published Canadian work on the anatomy of river otter (Lontra canadensis) fur, observations on electron micrographs of sea otter pelts washed by traditional methods that showed residual salt and soap scum adhering to underhairs, and observed improvement in recovery rates of marine birds bathed in warm fresh water. In the first phase of the study, researchers standardized variables such as detergent concentration, washing and rinsing time, water temperature, room temperature, and drying time and temperature, all of which influence core body temperature, recovery of coat insulation, and normal behaviors during and immediately after washing. The best results came from washing an anesthetized otter for 30 minutes with a 2.5 to 4 percent concentration of dish washing liquid, rinsing it for an hour in fresh, soft water (four grains of hardness per gallon) warmed to 80 or 90 degrees F, toweling off surface water, and drying the animal for 10 minutes with a high-volume warm-air dryer. Phase two focused on the best recovery medium to use after washing. Researchers used the method described above to wash two well-acclimated male sea otters and then released them into four different types of water: ambient seawater (roughly 44 degrees F) warm seawater (about 60 F), ambient soft fresh water (about 45 F), and warm soft fresh water (62 F). Rest periods between trials varied from two to six months. The ambient sea water trial was repeated towards the end of the project to test whether the otters may have learned behaviors during the progression of trials that would help them more quickly regain waterproofing, but researchers identified no such adaptive behaviors. A third phase of trials involved simulating exposure to oil during washing and recovery. Researchers first dipped anesthetized otters in an agitated mixture of canola oil and sea water. They massaged this mix into the fur to mimic the effects of grooming. They then washed the animals the same way as in previous trials and released them into warm (62 F) softened fresh water. These oiled otters recovered just as fast (in about two days) as the unoiled otters subjected only to washing. Thus oiling the otters (albeit with non-toxic oils) did not slow the time it took the animals to regain normal waterproofing of their coats, an encouraging result.

Bathing in either warm or cold soft water reduced the time research otters needed to recover control of thermal retention qualities of their hair coat to about two days, as opposed to 7-8 days if they bathed in either warm or cold sea water. Reduced recovery time had a profound effect on metabolic rate as measured by core body temperature and food consumption/weight loss. Subsequent trials showed these same improvements still held when sea otters were dipped in canola oil sea water mixtures before washing. In February of 2009 a badly tarred subadult
female sea otter was washed using slight modifications of the procedures used in the research trials and her recovery was rapid and complete. Liberal use of olive oil allowed softening and removal of her tar and after being nicknamed Olive Oil she developed a national and international following on Facebook. This method of communication proved to be an excellent public outreach and education tool in this case. Although various threats remain to recovery of listed populations of both northern and southern sea otters, improvements in washing methods suggest that considerably better results could be expected should we have another Exxon Valdez type oil spill.

Acknowledgements: The staff of the UC Santa Cruz Marine Mammal Physiology Research Project under the leadership of Dr. Terrie Williams and the cooperation of many organizations of the Sea Otter Alliance are deeply appreciated.
SP 1. ANTIMICROBIAL RESISTANCE IN GENERIC *ESCHERICHIA COLI*
ISOLATED FROM WILDLIFE LIVING IN RURAL, URBAN, AND NATURAL ENVIRONMENTS

**Samantha E. Allen,** University of Guelph Department of Pathobiology, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; **Richard J. Reid-Smith,** University of Guelph, Department of Population Medicine & Laboratory for Foodborne Zoonoses, Public Health Agency of Canada, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; **Nicol Janecko,** University of Guelph, Department of Population Medicine, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; **Patrick Boerlin,** University of Guelph, Department of Pathobiology & Laboratory for Foodborne Zoonoses, Public Health Agency of Canada, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; **Claire Jardine,** University of Guelph, Department of Pathobiology, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada

**Presenting author:** Allen, Samantha

**Summary:** Wildlife may have a role as a reservoir of antimicrobial resistant bacteria, and as indicators of the spread of anthropogenic antimicrobial resistance in the environment.

The objective of this study is to compare the prevalence and patterns of antimicrobial resistance in *generic Escherichia coli* isolated from wildlife living in farm, urban (residential and landfill sites), and natural (conservation areas) environments. Samples were collected from 308 small mammals (rodents and insectivores) trapped at seven farms (n = 71), four conservation areas (n = 51), ten residential areas (n = 153) and nine landfill sites (n = 33) from May to October, 2008. *E. coli* was recovered from fecal pellets collected from 163 (54%) animals, and up to three isolates of *E. coli* per animal were evaluated for resistance to 15 antimicrobials using broth microdilution. Resistance was detected in *E. coli* from 26/52 (50%) animals trapped at farm sites, in 4/69 (6%) animals trapped at residential sites, and in 1/20 (5%) animals trapped at landfill sites. No resistance was detected in isolates from 22 animals trapped at four conservation sites. These preliminary results appear to support a possible association between proximity to antimicrobial use in humans and domestic animals, and the occurrence of antimicrobial resistance bacteria in wildlife. Wildlife may have a role as a reservoir of antimicrobial resistant bacteria, and as indicators of the spread of anthropogenic antimicrobial resistance in the environment.
SP 2. COMPARISON OF NOBUTO STRIPS AND SERUM TO DETECT EXPOSURE TO CANINE DISTEMPER AND PARVOVIRUSES IN WISCONSIN CARNIVORES

Amanda J. Cyr, Shelli A. Dubay, College of Natural Resources, University of Wisconsin Stevens Point, 2100 Main Street, Stevens Point, WI 54481, USA; Julia Langenberg, Department of Natural Resources, 2801 Progress Road, Madison, WI 53716, USA

Presenting author: Cyr, Amanda

Summary: The purpose was to determine exposure of raccoons and coyotes to canine distemper and parvoviruses and to evaluate the efficacy of using Nobuto strips for distemper and parvovirus serosurveillance.

Our project purpose is to determine if Nobuto strips are an effective tool for distemper and parvovirus serosurveillance in Wisconsin carnivores. Whole blood collection is difficult and requires specific handling and storage protocols. Blood samples dried on Nobuto strips, small filter paper, are cost-efficient and easy to store and collect. Wisconsin Trappers Association members collected paired blood samples, a whole blood and a Nobuto strip sample, from harvested coyotes (Canis latrans) and raccoons (Procyon lotor) during the 2008-2009 trapping season. We processed whole blood samples in the laboratory by extracting serum via centrifugation. Nobuto strips were eluted in 1.0ml phosphate buffered saline for one hour. Resulting sera and Nobuto solutions were sent to Michigan State University for antibody determination. A titer ≥ 1:25 was evidence of exposure for parvoviruses and a titer ≥ 1:16 was evidence of exposure to canine distemper. Paired blood samples were collected from 59 coyotes and 72 raccoons. Preliminary results show that Nobuto strip samples agreed with serum results between 43 percent and 72 percent, depending on species and disease. Determining the efficacy of Nobuto strips in disease surveillance is beneficial in facilitating blood collections from wildlife in the field. In order to use Nobuto strips in wildlife disease surveillance, antibody results must be comparable to that of whole blood serum. We will discuss the implications of using Nobuto strips for serosurveillance in wildlife.
SP 3. PHYLOGENETIC ANALYSIS OF THE NONSTRUCTURAL (NS) GENE OF AVIAN INFLUENZA VIRUSES ISOLATED FROM HUNTER-HARVESTED WATERFOWL, TEXAS COAST

Pamela J. Ferro, Markus J. Peterson, Blanca Lupiani, Texas A&M University, College Station, TX 77845, USA; C. Todd Davis, Ruben O. Donis, Division of Viral and Rickettsial Diseases, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA; Todd Merendino, Ducks Unlimited, Texas Gulf Coast, Bay City, TX 77414, USA; Matt Nelson, Texas Parks and Wildlife, Bay City, TX 77414, USA

Presenting author: Ferro, Pam

Summary: Data presented here demonstrate the co-circulation of avian influenza NS1 alleles A and B on waterfowl wintering grounds.

The non-structural protein 1 (NS1) of influenza viruses is known to play an important role in virus virulence and two different gene pools (alleles A and B) exist among influenza viruses. Most non-avian origin isolates belong to allele A, while avian isolates belong to both groups. In this study we evaluated the diversity of the NS1 gene among influenza viruses isolated from wild waterfowl on their wintering grounds. Various influenza subtypes and isolates from Blue-winged Teal (Anas discors), Green-winged Teal (Anas crecca), Northern Shoveler (Anas clypeata), and Mottled Duck (Anas fulvigula) were included. The NS1 gene was amplified by RT-PCR and PCR products were directly sequenced using controlled termination of replication (BigDye Terminator kit; Applied Biosystems) and an ABI Prism 3130XL Genetic Analyzer (Applied Biosystems). A subset of published sequences was selected from GenBank where initial alignments were performed within the Avian Influenza Resources (MUSCLE) and further aligned utilizing MacClade 4 (Version 4.08, Sinauer Associates). Phylogenetic analyses were performed using maximum likelihood (GARLI and RAxML), maximum parsimony (PAUP), and Bayesian (MrBayes) methods. Each NS1 gene consisted of 690 nucleotides, no insertions or deletions were detected. Two distinct gene pools corresponding to the A and B alleles were identified with approximately 98% homology within and 71% between alleles. No relationships were noticed between hemagglutinin or neuraminidase subtype or waterfowl species and NS1 alleles. Our data support previous reports indicating the co-circulation of allele A and B in nature, as well as demonstrate co-circulation within waterfowl populations on wintering grounds. Data collected as part of this ongoing project provide valuable information pertaining to AIV present on the Texas Coast, a previously understudied waterfowl wintering ground. These data are part of the CSREES AICAP “Prevention and Control of Avian Influenza in the US”.

Acknowledgements: We deeply appreciate the waterfowl hunters of the Texas mid-coast and thank all of those who have participated in sample collections over the years.
SP 4. QUANTIFICATION OF CYTOKINE MRNA AND EXPRESSION PATTERNS IN BRUCELLOSIS INFECTED ELK

Amanda M. Fluegel, Jake E. Lowry, E. Lee Belden, and Gerard P. Andrews, Dept. of Veterinary Sciences, University of Wyoming, 1174 Snowy Range Road, Laramie, WY 82070, USA; William H. Edwards and Terry J. Kreeger, Veterinary Services, Wyoming Game and Fish Department, 1174 Snowy Range Road, Laramie, WY 82070, USA

Presenting author: Fluegel, Amanda

Summary: Cytokine mRNA expression patterns of brucellosis infected elk will provide insight into the immune response of elk to the bacterium and provide information to enhance protective immunity through vaccination.

Brucellosis, caused by Brucella abortus, is endemic in the Greater Yellowstone Area of Idaho, Montana, and Wyoming. The disease affects wild elk (Cervus elaphus) and bison (Bison bison) and domestic cattle. Previous studies have suggested that currently available brucellosis vaccines induce poor or no protection in elk (C. e. nelsoni). In this study mRNA expression was quantified by real-time reverse transcription-polymerase chain reaction (RT-PCR) to analyze cytokine profiles of elk in response to Brucella abortus. This RT-PCR measures expression of several important elk cytokines including interleukin (IL)-2, IL-4, IL-10, IL12-p40, IFN-gamma, TNF-alpha, and enzyme-inducible (i)NOS. Blood was collected from captive elk vaccinated with B. abortus S19 and feedground elk for RNA extraction and isolation of peripheral blood mononuclear cells (PBMCs). RT-PCR methodology was used to monitor induction of cytokine genes on in vitro antigenic stimulation of PBMCs using in vivo-induced (IVI) gene products, previously identified in our laboratory. Preliminary results suggest a down regulation of IL-2 and iNOS mRNA expression by malate dehydrogenase (an IVI gene) in S19 vaccinated elk. Furthermore, IL-10 levels were upregulated by malate dehydragenase in stimulated PBMCs of naïve elk. The expression of particular cytokines can allow differentiation of immune responses elicited to pathogens and indicate mechanisms of microbial pathogenesis. Species-specific reagents for cervine cytokines are lacking, therefore detection of cytokine mRNA provides an alternative approach to functional assays for detection of cytokines. Evaluation of IVI gene products using cytokine based analysis may suggest potential uses for these antigens as Brucella-specific diagnostic targets and may reveal elk specific immune responses to B. abortus.
SP 5. TRICHOMONOSIS OUTBREAK IN PASSERINES IN THE SOUTHEASTERN UNITED STATES

Richard W. Gerhold, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Department of Poultry Sciences, The University of Georgia, Athens, GA 30602, USA; M. Kevin Keel and Andrew N. Cartoceti, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Robert B. Beckstead, Department of Poultry Sciences, The University of Georgia, Athens, GA 30602, USA

Presenting author: Gerhold, Richard

Summary: Trichomonosis should be included in the differential diagnosis list of passerine mortality and morbidity events, especially when the events are associated with artificial feeders and waters.

Trichomonosis was diagnosed in several passerines, from multiple southeastern states during the winter and spring of 2009. The birds were submitted as salmonellosis suspects and several birds were dually infected with *Salmonella* spp. and *Trichomonas gallinae*. Numerous passerines were submitted to the Southeastern Cooperative Wildlife Disease Study (SCWDS) during the winter and spring of 2009 as salmonellosis suspects. Gross and microscopic examinations in some birds revealed lesions consistent with protozoal infection. Trichomonosis was diagnosed by a combination of histopathology in conjunction with PCR or culture. Trichomonosis was diagnosed by PCR or culture in at least 12 of the submitted passerines from multiple southeastern States. Several birds were dually infected with *Salmonella* spp. and *Trichomonas gallinae*. Careful examination of passerines submitted for post-mortem examination should be conducted to determine if mortality or morbidity is due to trichomonosis. Contaminated bird feeders and waters are likely sources of infection, thus it is not surprising that some birds are dually infected with *Salmonella* spp. and *Trichomonas gallinae*. Further research is needed to determine what impact trichomonosis can have in passerine populations.
**SP 6. IDENTIFICATION, DISTRIBUTION, AND CROSS SPECIES TRANSMISSION OF EIMERIA SPP. IN CAPTIVE-RAISED GAME BIRDS IN THE UNITED STATES**

Richard W. Gerhold, A. Lorraine Fuller, Lori A. Lollis, Robert B. Beckstead, and Larry R. McDougald, University of Georgia, Athens, GA 30602, USA

**Presenting author:** Gerhold, Richard

**Summary:** Our aim is to identify the various Eimeria species infecting captive reared game birds and determine the geographical distribution, host specificity, and pathogenicity of the coccidia. Coccidiosis caused by various Eimeria species is a major disease of captive-reared game birds released annually for hunting purposes. However, the Eimeria species infecting captive-reared game birds as well as the geographical distribution, host specificity, and pathogenicity of the coccidia parasites are incompletely known. Fecal, intestinal, or litter samples from captive reared Northern bobwhite (Colinus virginianus), Ring-necked pheasant (Phasianus colchicus), and Chukar (Alectoris chukar) were collected from numerous facilities from various locations throughout the United States. Coccidia containing samples were propagated and the oocysts were morphologically examined. Pure cultures are being propagated and PCR primers will be designed to distinguish the various Eimeria species. PCR testing with Eimeria species-specific primers will be conducted on the collected samples to determine geographical distribution of the various Eimeria species. Additionally, the host specificity of the Eimeria species will be determined by experimental infection of several gallinaceous species. To date, twenty-six Northern bobwhite, twenty Ring-necked pheasant, and thirteen Chukar Eimeria-positive samples have been collected from eight states. By PCR and sequence analysis, Northern bobwhites, Ring-necked pheasants, and Chukars contain at least four, five, and four Eimeria species, respectively. Geographical distribution and host specificity results are pending. Although coccidiosis is as a major disease of captive-reared game birds, there has been little research conducted. We have identified numerous Eimeria species within three captive game bird species by both classical and molecular parasitology methods. Comparison of the geographical distribution of the Eimeria species from captive-reared and free-ranging birds can aid in identifying factors associated with parasite distribution. Experimental cross transmission infections will be useful to determine the potential for disease in aberrant species.
SP 7. VERMINOUS PNEUMONIA IN THE THREATENED ST. LAWRENCE ESTUARY BELUGA POPULATION

M. Gouix, Faculté de médecine vétérinaire, Université de Montréal, 3200 Rue Sicotte, St-Hyacinthe, QC, J2S 2M2, Canada; L. Measures, Institut Maurice-Lamontagne, Ministère des Pêches et Océans, 850 Route de la Mer, Mont-Joli, QC, G5H 3Z4, Canada; S. Lair, Faculté de médecine vétérinaire, Université de Montréal, 3200 Rue Sicotte, St-Hyacinthe, QC, J2S 2M2, Canada

Presenting author: Gouix, Maëlle

Summary: Lungworms (Halocercus monoceris and Stenurus arctomarinus) are frequently associated with mortalities of juvenile beluga from the St. Lawrence Estuary (SLE) and thus may play a role in the failure of this population to recover.

Although lungworms are commonly found in stranded SLE belugas (Delphinapterus leucas), the dynamics between these parasites and their hosts are unknown. Therefore the objective of our project is to determine the prevalence, intensity and possible effect on the SLE population. We hypothesized that lungworm infections contribute to mortalities of juvenile animals. Since 1983, necropsies were performed on 175 stranded SLE beluga. These included histopathological examination of 18 systematic lung sections per animal. For 25 of those carcasses, lungs were frozen and later thawed for parasitological analyses. The tracheal, bronchial and bronchiolar lumens were examined for lungworms, then each lung was sliced systematically from cranial to caudal poles every 5 mm. Slices were rinsed in mammalian saline and worms recovered using a 250 µm sieve. Worms were fixed and cleared in hot 10% glycerine alcohol, then identified by species, sex and stage and counted using a microscope. Severe verminous pneumonia was observed in 15% of beluga at necropsy, and in 56% of dead juvenile beluga. Stenurus arctomarinus and Halocercus monoceris were found in 44% and 88% of cases, respectively. Intensities ranged from 2 to 17 for S. arctomarinus and up to 6990 for H. monoceris. S. arctomarinus and H. monoceris are present in almost all stranded beluga. Juveniles are more severely affected than adult beluga or unweaned calves. This age-biased aggregation of lungworms could limit the recovery of this population by affecting recruitment. Further studies analyzing the correlation between parasite intensity and severity of pneumonia, together with body condition indices, should provide comprehensive results that will help to better understand the role of lungworms in the health of SLE beluga.
SP 8. TREE SWALLOWS (TACHYCINETA BICOLOR) ON RECLAIMED WETLANDS IN THE ATHABASCA OIL SANDS: AN INDICATOR FOR RECLAMATION SUCCESS?

N. Jane Harms, University of Saskatchewan, Western College of Veterinary Medicine, Department of Veterinary Pathology, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada; Graham D. Fairhurst and Gary R. Bortolott, University of Saskatchewan, Department of Biology, 112 Science Place, Saskatoon, SK, S7N 5E2, Canada; Judit E. G. Smits, University of Saskatchewan, Western College of Veterinary Medicine, Department of Veterinary Pathology, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada

Presenting author: Harms, N. Jane

Summary: While variation occurs in the body condition, immune function and corticosterone levels of nestling tree swallows on oil sands reclaimed wetlands, current wetland reclamation techniques can support healthy populations of tree swallows under ideal weather conditions, and swallows appear relatively resilient to effects of contaminant exposure.

Companies developing the Athabasca oil sands are engaged in wetland reclamation. Tree swallows (Tachycineta bicolor) may serve as environmental sentinels of reclamation success or failure. We evaluated several health indicators in swallows nesting near reclaimed wetlands to examine the ability of these wetlands to support viable swallow populations. From May to July 2008, reproductive performance of 40 breeding pairs of tree swallows was measured on three reclaimed wetlands containing oil sands process affected material (OSPM) on Suncor Energy Inc. and Syncrude Canada Ltd. oil sands leases. Growth and survival of tree swallow nestlings were assessed. A subset of nestlings from each study site was examined for i) feather corticosterone levels using a newly developed technique, ii) adaptive T-cell mediated immune function, and iii) innate immune function using a whole blood chemiluminescence assay. Nestlings on an OSPM-affected wetland were in good body condition and mounted stronger delayed type hypersensitivity responses compared to reference nestlings. Corticosterone levels were higher in male nestlings on one OSPM-affected wetland compared to the reference wetland. Association between body condition of 12-day-old nestlings and feather corticosterone was dependent on sex of the nestling. Under the ideal weather conditions that pertained during this study, current wetland reclamation techniques can support healthy populations of tree swallows on the Athabasca oil sands. OSPM-affected wetlands had no negative effect on innate or adaptive immune function, or on body condition of neonatal birds.
SP 9. POXVIRUS INFECTION IN AN AMERICAN RED SQUIRREL (TAMIASCIURUS HUDSONICUS) FROM NORTHWESTERN CANADA

Chelsea G. Himsworth, Department of Veterinary Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, S7N 5B4, Canada; Kristyna M. Musil, Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, S7N 5B4, Canada; Lorraine Bryan, Canadian Cooperative Wildlife Health Center, University of Saskatchewan, Saskatoon, SK, S7N 5B4, Canada; Janet E. Hill, Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, S7N 5B4, Canada

Presenting author: Himsworth, Chelsea

Summary: This report describes a novel poxvirus-associated disease in a North American red squirrel from Yukon Territory, Canada.

Currently, there are two poxviruses known to cause disease in squirrels (genus Sciurus): squirrel fibroma virus (SFV) and squirrelpox virus (SQPV). The objective of this report is to describe the gross and microscopic pathology in a red squirrel (Tamiasciurus hudsonicus) suffering from a poxvirus-associated disease, and to identify the etiological agent. This analysis included necropsy, gross examination, histopathology, electron microscopy, and polymerase chain (PCR) reaction for SFV and SQPV. Pathology was limited to the skin and consisted of a proliferative and exudative dermatitis with intracytoplasmic epithelial inclusions, which, on electron microscopy, were observed to contain poxvirions. PCR on affected skin failed to identify either SFV or SQPV, although a novel poxvirus-associated sequence was amplified. Although the observed pathology was most similar to that described in cases of SQPV infection, PCR results suggest that the virus identified in this case is a novel poxvirus of North American red squirrels. To our knowledge, this is also the first report of poxvirus-associated disease in Canadian squirrels outside of Ontario.
SP 10. PATHOLOGY AND EPIDEMIOLOGY OF PHOCID HERPESVIRUS-1 INFECTIONS IN WILD AND REHABILITATING HARBOUR SEALS (PHOCA VITULINA) IN THE NORTHEASTERN PACIFIC

C. G. Himsworth, Department of Veterinary Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, S7N 5B4, Canada; M. Haulena, Vancouver Aquarium, PO Box 3232, Vancouver, BC, V6B 3X8, Canada; D. Lambourn, Washington Department of Fish and Wildlife, Marine Mammal Investigations, 7801 Phillips Rd. SW, Lakewood, WA, 98498 USA; J. Gaydos, The SeaDoc Society, UC Davis Wildlife Health Center, 942 Deer Harbor Road, Eastsound, WA, 98245 USA; J. Huggins, J. Calambokidis, Cascadia Research, 218 1/2 W 4th Ave., Olympia, WA, 98501 USA; J. Ford, Pacific Biologic Station, Fisheries and Oceans Canada, 3190 Hammond Bay Road, Nanaimo, BC, V9T 6N7, Canada; P. Ross, Institute of Ocean Sciences (Fisheries and Oceans Canada), 9860 West Saanich Rd, Sidney BC, V8L 4B2, Canada; S. Raverty, Animal Health Center, 1767 Angus Campbell Road, Abbotsford, BC, V3G 2M3, Canada

Presenting author: Himsworth, Chelsea

Summary: This is the first study to focus on the epidemiology and pathology associated with PHV-1 infection in harbour seals in the Northeastern Pacific.

Phocid herpesvirus-1 (PHV-1) infection was first recognized in Pacific harbour seals (Phoca vitulina) in California in the 1990s, and was identified in the Northeastern Pacific in 2000. The objective of this study was to retrospectively describe the epidemiology and pathology associated with PHV-1 in British Columbia, Canada and Washington, USA. Pathology reports for all harbour seals submitted to the Animal Health Laboratory (AHL), Abbotsford, British Columbia, from January 2000 to December 2008 were reviewed. The post-mortem examination performed on these animals included necropsy, histopathology, culture, and PCR for PHV-1. When available, pre-submission records, including geographic origin or site of stranding, and date of death or recovery of beach caste carcasses were also reviewed. Seventy PHV-1-positive seals were identified, all of which were neonates or juveniles submitted between July and October both from the wild and from rehabilitation facilities. PHV-1 associated lesions included adrenal and hepatic necrosis with intranuclear inclusions, although the majority of the animals presented with other pre-existing or supervening diseases. It appears that the epidemiology and pathology associated with PHV-1 infection in harbour seals from the Northeastern Pacific is similar to that reported in California. Exposure is likely widespread within the wild and in rehabilitation facilities, with morbidity and mortality occurring primarily in young seals and being due to PVH-1 alone or in concert with other disease processes.
SP 11. TRANSFER AND EFFECT OF MATERNAL ANTI-*PLASMODIUM* ANTIBODIES IN HAWAI‘I ‘AMAKIHI (*HEMIGNATHUS VIRENS VIRENS*)

Bobby Hsu and Patrick J. Hart, University of Hawaii at Hilo, 200 W.Kawili St., Hilo, HI. 96720, USA; J. Gregory Massey, UC Davis School of Veterinary Medicine, One Shields Ave., Davis, CA 95616, USA

Presenting author: Hsu, Bobby

Summary: Passive transfer of anti-*Plasmodium* antibodies to the eggs occurred in Hawai‘i ‘amakihi. However, patterns in immunological response of neonatal birds were not dictated solely by maternal antibodies.

If passive maternal-natal transfer of anti-*Plasmodium* antibodies occurs in Hawai‘i ‘amakihi (*Hemignathus virens virens*), the presence of maternal antibodies should be detectable in ‘amakihi eggs, and the short term effects of maternal antibodies should be observable in wild populations living at low elevations where avian malaria (*Plasmodium relictum*) is prevalent. We investigated data collected from wild ‘amakihi and captive canaries (*Serinus canaria*) as a laboratory model. First, using an Enzyme-Linked ImmunoSorbent Assay, we analyzed the plasma and eggs of breeding female ‘amakihi from a combination of low and high elevation sites on the Island of Hawai‘i for anti-*Plasmodium* antibodies. Second, we quantified anti-*Plasmodium* antibody levels in canary eggs from infected hens and plasma of offspring from both the infected and the uninfected hens. We quantified parasitemia in both groups by examining thin blood smears. Third, using data from the Biocomplexity of Avian Diseases project, we examined the seasonal relationship between anti-*Plasmodium* antibody level and parasitemia in infected hatch-year ‘amakihi with a multiple regression model. Analyses showed significantly higher anti-*Plasmodium* antibody levels in ‘amakihi eggs at low elevation. Canary hatchlings showed similar patterns of antibody response to infection, but the hatchlings from uninfected hens had a higher mean parasitemia that fluctuated more than the hatchlings from infected hens. Hatch-year ‘amakihi at low elevation exhibited a suppressed immunological response during earlier months of the year.

Passive transfer of anti-*Plasmodium* antibody to the eggs occurred in Hawai‘i ‘amakihi at our low elevation study site. Differences in infection levels of canary hatchlings indicated an advantage of maternal exposure to pathogen. We could not pinpoint the cause for the seasonal differences in hatch-year ‘amakihi with the limited information available from our three studies. A combination of effects from serological response in neonatal birds and maternal antibodies most likely influenced the patterns of immunological response in hatch-year ‘amakihi.

Acknowledgements: We thank Dr. Carter T. Atkinson for providing technical support, lab equipment, guidance on the data analysis, and sharing his knowledge on parasitology and immunology throughout this research project.
SP12. A PCR METHOD FOR DETECTING THE WHITE-NOSE SYNDROME-ASSOCIATED GEOMYCES SP. FUNGUS ON THE SKIN OF BATS

Jeffrey M. Lorch, USGS - National Wildlife Health Center, 6006 Schroeder Rd, Madison, WI 53711, USA; University of Wisconsin-Madison - Molecular and Environmental Toxicology Center, 1300 University Avenue, 1530 MSC, Madison, WI 53706, USA; Carol U. Meteyer, USGS - National Wildlife Health Center, 6006 Schroeder Rd, Madison, WI 53711, USA; Brenda M. Berlowski-Zier, USGS - National Wildlife Health Center, 6006 Schroeder Rd, Madison, WI 53711, USA; David S. Blehert, USGS - National Wildlife Health Center, 6006 Schroeder Rd, Madison, WI 53711, USA

Presenting author: Lorch, Jeffrey M.

Summary: A PCR method was developed to rapidly, selectively, and accurately detect the white-nose syndrome-associated Geomyces sp. fungus on bat wing tissue.

Skin infection by Geomyces sp. is a clinical indication of bat white-nose syndrome (WNS). Formerly, time-consuming fungal culture and/or histologic examination of bat skin were necessary to confirm infection. We developed a PCR test to specifically detect the WNS-associated fungus directly from bat wing skin in less than one day. Bat carcasses were obtained from hibernacula within and outside of the WNS-affected region. A 4 mm x 4 mm piece of wing tissue was excised from each animal for genomic DNA extraction/PCR analysis, and additional wing skin from each animal was used for companion histology and culture analyses. PCR was conducted using primers specific for the Geomyces sp. rRNA gene internal transcribed spacer region. Generation of a 586 nucleotide band indicated that Geomyces sp. DNA was present. PCR, histology, and culture results from each bat were compared to determine the efficacy of the method. Samples testing positive for Geomyces sp. infection by culture or histology (n=22) also tested positive by PCR 95% of the time. Due to competition by faster-growing microbes, culture can yield false-negative results. PCR had the capability to identify Geomyces sp. DNA in the absence of positive culture results. WNS was formerly diagnosed using culture and/or histological techniques. However, those methods are time-consuming, require specialized skills, and have the potential to yield false negative results. We developed an accurate PCR-based test for detection of Geomyces sp. with a significantly faster turn-around time than the previous methods. This technique will be useful in delivering results promptly to field personnel and wildlife managers, for expanded WNS-surveillance efforts, and for environmental surveys.
SP 13. VALIDATION AND APPLICATION OF HAIR CORTISOL CONCENTRATION AS A NON-INVASIVE BIOMARKER OF LONG-TERM STRESS IN FREE-RANGING GRIZZLY BEARS

Bryan J. Macbeth, Western College of Veterinary Medicine, Department of Veterinary Biomedical Sciences, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada; Marc R.L. Cattet, Canadian Co-operative Wildlife Health Centre, Department of Veterinary Pathology, Western College of Veterinary Medicine, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada; Gordon B. Stenhouse, Foothills Research Institute and Alberta Sustainable Resource Development, 1176 Switzer Drive, Hinton, AB, T7V 1X6, Canada; David M. Janz, Western College of Veterinary Medicine, Department of Veterinary Biomedical Sciences and Toxicology Centre, 52 Campus Drive, Saskatoon, SK, S7N 5B4, Canada

Presenting author: Macbeth, Bryan

Summary: We have developed, validated and applied a non-invasive technique to measure hair cortisol concentration in free-ranging grizzly bears which will further our understanding of linkages between landscape change, long-term stress, individual health and population performance in this species, and may be broadly applicable to similar studies in any mammal.

Human-caused environmental change negatively affects the sustainability of many wildlife populations. In Alberta, grizzly bears (Ursus arctos) occupy one of the most heavily populated and exploited landscapes across the species distributional range. Long-term physiological stress in individuals is proposed to be the predominant mechanism linking environmental change with impaired wildlife population health. Hair cortisol concentration has recently been validated as a biomarker of long-term stress in non-human primates. We have developed and validated an ELISA-based technique to measure hair cortisol in free-ranging grizzly bears. Hair collected by non-invasive DNA snagging methods is washed to remove external contamination then dried and ground to a fine powder. Twenty-five mg samples of powdered hair are extracted for 24 hours with methanol. Supernatant from extracted samples is dried under nitrogen gas at 38 °C, reconstituted in phosphate buffer (12 hours at 40°C) and analyzed with a commercially available ELISA kit. The technique is precise and accurate in ≥ 5 mg of hair. Cortisol varies with hair type, body region, colour and along the hair shaft. It is not influenced by environmental exposure (15+ days) or storage (>1 year). Hair cortisol (range 0.66-43.33 pg/mg) has been measured in >150 grizzly bears. Ongoing statistical analysis involves correlation of hair cortisol with life history traits (age, sex and reproductive classes) and tissue-based measures of long-term stress and individual health collected from the same animals. Hair cortisol will also be examined in the context of anthropogenic landscape change occurring in five populations of Alberta grizzly bears. Prudent use and limitations of this technique will be discussed. With minor species-specific modification, this technique should be broadly applicable to any mammal.
SP 14. THE EFFECTS OF BLOOD ON AVIAN INFLUENZA VIRUS DETECTION BY RT-PCR

Paul Oesterle, Kaci VanDalen, Alexis R. Freifeld, Nicholas O. Thomas, Theodore D. Anderson, National Wildlife Research Center (USDA/APHIS/WS), 4101 Laporte Avenue, Fort Collins, CO 80521, USA; Michael J. Bodenchuk, Bruce R. Leland, Wildlife Services (USDA/APHIS), Texas State Office, 3700 Fredericksburg Rd, Suite 140, San Antonio, TX 78211, USA; Robert G. McLean, Alan B. Franklin, National Wildlife Research Center (USDA/APHIS/WS), 4101 Laporte Avenue, Fort Collins, CO 80521, USA

Presenting author: Oesterle, Paul

Summary: Blood components are often considered inhibitors of reverse transcription polymerase chain reaction (RT-PCR); however, low concentrations of avian influenza virus (AIV) can still be detected by RT-PCR, even in the presence of high concentrations of blood in samples such as nasal swabs.

A relatively inexpensive method for AIV surveillance is sample collection from hunter-killed animals. However hunting-induced trauma often leads to blood-contamination of common sample types, such as nasal swabs in feral swine. In this study, we examined and quantified the effects of blood on the detection of AIV by RT-PCR. To mimic sampling conditions of hunter-killed animals, five blood concentrations (0 – 80% of the sample) and four different AIV doses (0 – 10E4 EID50) comprised 20 treatments. Each treatment was divided into five aliquots. Dacron swabs were placed into each aliquot and then transferred into cryovials with viral transport media. Each swab was tested in quadruplicate by RT-PCR along with negative and positive controls. The results were analyzed as a mixed model with repeated measures (dependant variable: virus detected, fixed variables: blood and virus concentrations, clot formation) and Akaike’s Information Criteria was used for model selection. Blood in swab samples caused a significant decline in the amount of AIV detected by RT-PCR. In addition, clotting of plasma exacerbated the decline in viral detection. However, despite these inhibitory factors, we still detected AIV on swabs from all treatment groups. Surveillance of wild animals for AIV can be labor intensive and costly; a less expensive alternative is sampling of hunter-killed animals. The disadvantage of using these animals is that hunting-induced trauma often results in widespread blood contamination throughout the carcass. This study illustrates that although blood components inhibit RT-PCR, AIV RNA detection is still possible even at low concentrations. Blood may bias the quantification, but does not to appear to bias detection of AIV.
SP 15. PLASMA PATTERN RECOGNITION RECEPTORS IN WALLEYE 
(SANDER VITREUS)

Alexandra Reid, John S. Lumsden, Department of Pathobiology, University of Guelph, 50 Stone Rd, Guelph, ON, N1G 2W1, Canada

Presenting author: Reid, Alexandra

Summary: Proteins of the innate immune system may be mediators of numerous systemic infections in walleye and rainbow trout in Ontario.

Walleye (Sander vitreus) are an economically important wild food fish that will have soluble plasma pattern recognition receptors that bind systemic pathogens and may mediate resistance to disease. Walleye and rainbow trout (Oncorhynchus mykiss) are bled and plasma collected. Modified bacterial binding assays and a novel viral assay are used to identify innate immune system proteins and analysed using 1D SDS PAGE and an indirect ELISA to identify potential soluble PRRs. Targeted proteins will be sequenced and physiochemical properties will be characterised. Further studies will identify functional properties of these proteins in innate immunity to circulating pathogens. Several innate immune system proteins are identified and sequenced, including several previously unidentified fish proteins that require calcium for binding to pathogens. Bacterial target is poorly recognised compared to other microbial targets. The functional significance of innate immune system proteins in walleye is interpreted in the context of relevance to host/pathogen interaction, particularly in the unexplored area of lectin/viral interaction. This project will have relevance to our understanding of innate immunity and perhaps management of disease in wild fish stocks in Ontario.

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SP 16. ASSOCIATION OF MYCOPLASMA COROGYPSI AND POLYARTHRITIS IN FREE-RANGING BLACK VULTURES (COROGYPS ATRATUS) IN VIRGINIA

Mark G. Ruder and M. Kevin Keel, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Sanford H. Feldman, Center for Comparative Medicine, University of Virginia, Charlottesville, VA 22908, USA; David L. McRuer and Elizabeth F. Daut, Wildlife Center of Virginia, Waynesboro, VA 22980, USA; Arno Wünschmann, Department of Veterinary Population Medicine, Veterinary Diagnostic Laboratory, College of Veterinary Medicine, University of Minnesota, St. Paul, MN 55108, USA

Presenting author: Ruder, Mark

Summary: Three free-ranging black vultures from Virginia, USA were diagnosed with polyarthritis between 2007 and 2009. Mycoplasma corogypsi was isolated and/or detected via PCR from affected joints in the absence of other detectable infectious organisms. We suggest an association between M. corogypsi and polyarthritis in black vultures.

Infectious polyarthritis of wild birds has been infrequently reported, although it is well known in the poultry industry. Mycoplasma spp. have been identified in association with polyarthritis in multiple mammalian and domestic avian species but not in wild birds. Although anecdotal reports of polyarthritic black vultures (Coragyps atratus) are not uncommon, no cause has been determined. Our findings suggest that M. corogypsi is a potential cause. Between October of 2007 and February of 2009, three black vultures were submitted to the Wildlife Center of Virginia (WCV; Waynesboro, VA, USA) with a history of being unable to fly. Physical examination, radiographs, and aseptic arthrocentesis were performed at WCV prior to euthanasia. Post-mortem examination was either performed at WCV or the carcass was sent to the Southeastern Cooperative Wildlife Disease Study (Athens, GA, USA). Mycoplasmal culture and/or PCR, as well as aerobic, anaerobic, and fungal cultures were performed on the joint fluid of each bird. Multiple tissues were processed for virus isolation in two of the three birds. All three birds were in poor nutritional condition and two or more joints had severe, erosive, fibrinoheterophilic arthritis with involvement of adjacent bone. Mycoplasma corogypsi was identified in affected joints of one bird by PCR and was isolated from the joints of two other birds. No additional bacteria, fungi, or viruses were detected in any case. Mycoplasma corogypsi was previously isolated from a black vulture with a footpad abscess in Alabama, USA and from the trachea of several species of falcon in the United Arab Emirates. It is not known if this bacterium is a primary or opportunistic pathogen of black vultures. Future research efforts should attempt to fulfill Koch’s postulates and investigate the geographic distribution and impact of this disease process in black vulture populations. In addition, knowledge of the host range will help identify any potential risk posed to sympatric Falconiformes that are threatened or endangered.

Acknowledgements: We thank Dr. Jonathan Sleeman for submission of these cases and Drs. Charles Hofacre and Naola Ferguson-Noel for laboratory assistance.
SP 17. A RISK ANALYSIS OF BRUCELLA TRANSMISSION AMONG BISON, ELK, AND CATTLE IN THE NORTHERN GREATER YELLOWSTONE AREA

Brant A. Schumaker, Tim E. Carpenter, University of California, Davis, One Shields Ave., Davis, CA 95616, USA; P.J. White, Rick Wallen, John Treanor, National Park Service, P.O. Box 168, Yellowstone National Park, WY 82190, USA; Rebecca Frey, USDA-APHIS-VS, PO. Box 1165, Emigrant, MT 59027, USA

Presenting author: Schumaker, Brant

Summary: This analysis will lead to a greater understanding of the relative risk of Brucella transmission across the northern Greater Yellowstone Area landscape.

Bison (Bison bison) and elk (Cervus elaphus) in the greater Yellowstone area (GYA) persist as the last reservoir of brucellosis (Brucella abortus) in the United States. The purpose of this study was to provide the risk estimates of Brucella transmission to cattle grazing in the northern Greater Yellowstone Area. This research focuses on northern GYA wildlife as ecologically and epidemiologically distinct subpopulations of elk and bison. A risk model was developed using home range kernel overlap as a proxy for spatio-temporal contact. We used historic and current demographic, seroprevalence, culture prevalence, and spatio-temporal distribution data as parameters in the model. Expert opinion was also used to smooth our parameter estimates. Model development will be built upon an already existing individual-based vaccination model (IBVM) developed by the National Park Service. This research is ongoing but results will be available in time to present at the meeting. This model will lead to a greater understanding of the relative risk of Brucella transmission across the northern Greater Yellowstone Area landscape. In addition, it may serve as a template for models of other diseases. This project fits into the National Brucellosis Elimination Zone concept of regionalization of the GYA put forward by USDA-APHIS. It may be expanded to include the entire GYA in an effort to inform policy makers of appropriate boundaries for regionalization.
SP 18. BLOOD CHEMISTRY LEVELS OF FREE-RANGING AND CAPTIVE WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS) IN TEXAS

Melanie L. Smith, Donald S. Davis, Texas A&M University, 4467 TAMU, College Station, Texas 77844-4467, USA

Presenting author: Smith, Melanie

Summary: To establish a normal range for the comprehensive metabolic panel (chemistry panel) for WTD in Texas taking into consideration age, gender, county of collection, season, capture method, and status based on captive or free-ranging.

The white-tailed deer (WTD) (Odocoileus virginianus) industry currently contributes over $650 million to the Texas economy (Anderson 14). To improve diagnostics there is a need to establish a normal blood biochemistry range taking into account differences in age, gender, county of collection, season, capture method, and status based on captive or free-ranging. Blood samples were collected from 384 WTD taken between October 2008 - April 2009 from 13 different counties throughout Texas. Blood samples were obtained from deer restrained by one of the following six methods: physical restraint, anesthetized using physical restraint method of drug administration, anesthetized using dart gun method of drug administration, drop-netted, net-gunned, or hunter harvested. Blood was collected using a 16 gauge, 2.58 cm needle by jugular venipuncture with syringes of varying sizes. Blood was then transferred to a Vacutainer that was refrigerated until processed by the Texas Veterinary Medical Diagnostic Laboratory (TVMDL). Samples will continue to be collected through October 2009, totaling close to 650 animals sampled.

Blood samples have been collected and processed, however analysis results have not yet been completed. Results will determine normal ranges of blood biochemistry and any differences that exist between the following: age groups fawns (<12 months), yearlings (≥12 months - <24 months) and adults (≥24 months), gender, location based on region (North, South, East, West), season (Spring, Summer, Fall and Winter), status (captive or free-ranging) and capture method (physical restraint, anesthetized using physical restraint method of drug administration, anesthetized using dart gun method of drug administration, drop-netted, net-gunned, or hunter harvested). Once normal ranges have been obtained, TVMDL will utilize these ranges for diagnostic purposes in WTD.

Acknowledgements: This project could not be possible without the support generated by the Texas Deer Association, my graduate committee and everyone who allowed samples to be collected from legally obtained white-tailed deer.
P 1. ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY (ARVC)-LIKE DISEASE IN A RED FOX (*Vulpes vulpes*)

**Erik O. Ågren**, Department of Pathology and Wildlife Diseases, National Veterinary Institute, SE 751 89 Uppsala, Sweden.

**Presenting author**: Ågren, Erik O.

**Summary**: The first case of arrhythmogenic right ventricular cardiomyopathy (ARVC)-like disease in free-ranging red fox is presented.

Arrhythmogenic right ventricular cardiomyopathy (ARVC) is a frequent cause of sudden death in humans. In animals, similar cardiac changes have been seen in dogs, especially boxers, and in domestic cats. This case, a free-ranging red fox (*Vulpes vulpes*), can be the first report of ARVC-like disease in a wildlife species. A red fox was shot in a hunt in February 2008 on the island of Sydkoster on the west coast of Sweden. The carcass was submitted to the National Veterinary Institute as part of a survey of internal parasites in Swedish red fox. A wildlife pathologist examined the carcasses and internal organs routinely, noting pathologic changes and visible parasites, during sampling. The fox was an adult female with dental attrition. The central parts of the right ventricle free wall was markedly thin over an oval, approximately 2x3 cm, area. Microscopically, there was varyingly marked to complete loss of myocytes in this area, replaced with fibro-adipose tissue containing scattered remnant degenerating myofibers. Heart pathology is rarely described in wildlife. The gross and microscopic findings in the heart are consistent with ARVC-like disease as described both in humans and in domestic animals. The fox in this case was an older animal in normal body condition that had been pregnant the previous year. In conclusion, this case of ARVC-like disease in red fox, had not apparently affected the animal to any greater extent, at the time of death.
P 2. ASSESSING ORV BAIT UPTAKE BY RACCOONS WITH TETRACYCLINE BIOMARKERS: IS DEPOSITION EQUAL WITHIN AND BETWEEN TISSUE TYPES?


Presenting author: Algeo, Timothy

Summary: We provide preliminary findings on tetracycline as a biomarker in oral rabies vaccination.

Rabies control with oral rabies vaccination (ORV) depends upon achieving sufficient vaccination rates to reduce disease incidence to below maintenance levels. Consequently, valid bait uptake assessments are critical. Tetracycline has historically been used for ageing and assessing bait uptake. We provide preliminary findings from assessing tetracycline deposition patterns in raccoons (*Procyon lotor*). We compared left and right first (PM1), and second (PM2) premolar, and canine teeth and mandibular bone tissue from raccoons from an ORV treatment area to determine whether the selection of one side versus the other for sampling for tetracycline biomarkers was important. We also compared PM1, PM2, and canine teeth and bone tissues to each other to determine whether tissue types provided similar tetracycline marking results. Tetracycline deposition was similar between left and right PM1 (P=0.265), PM2 (P=0.134) and canine (P=0.405) raccoon teeth, but differed between mandibular bones (P=0.0433). Raccoon PM1 were less frequently marked than were PM2 (P=<0.0001) and canine (P=<0.0001) teeth. Although PM1 were less frequently marked than were other tooth types, the relative ease of extraction of PM1 over PM2 teeth and the impracticality of canine tooth extraction from anesthetized animals for humane and other reasons indicates that the preferential use of PM1 teeth for bait uptake assessments from anesthetized raccoons be continued. However, we also suggest that the limitations of marking in PM1 be taken into consideration during bait uptake assessment efforts.
P 3. OBSERVATIONS ON FOOT AND MOUTH DISEASE IN VACCINATED AND UNVACCINATED WILDLIFE IN THE UNITED ARAB EMIRATES

Tom Bailey, The Dubai Falcon Hospital, P.O. Box 23919, Dubai, UAE; Declan O’Donovan, Wadi al Safa Wildlife Centre, P.O. Box 27875, Dubai, UAE; Joerg Kinne, Ulrich Wernery, Central Veterinary Research Laboratory, P.O. Box 597, Dubai, UAE

Presenting author: Bailey, Tom

Summary: Our paper compares and summarizes the features of two outbreaks of foot-and-mouth disease (FMD) in one unvaccinated collection and a second vaccinated collection of wild ungulates in the United Arab Emirates (UAE) and highlights the importance of vaccination protocols to protects wildlife in a region where infectious viral diseases, including FMD, are endemic.

Foot-and-mouth disease is a contagious but usually nonlethal disease of ruminants. The virus is endemic in domestic livestock populations in the Middle East, but is rarely reported in wildlife. We present observations on two outbreaks of FMD in one unvaccinated and a second vaccinated collection of wild ungulates in the UAE. Site 1 (unvaccinated) was a collection of dorcas gazelles (Gazella dorcas) (~100) and sika deer (Cervus nippon) (~25). Site 2 (vaccinated) was a collection comprising blackbuck (Antilope cervicapra) (~80), sand gazelle (Gazella subgutturosa marica) (~20), Arabian oryx (Oryx leucoryx) (~45), mountain gazelle (Gazella gazella) (~8), impala (Aepyceros melampus) (~48) and spekes gazelle (Gazella spekei) (~36) where most animals had been vaccinated annually against FMD since 2006. Affected animals were euthanased and submitted to the Central Veterinary Research Laboratory (CVRL, Dubai) for investigation. Necropsy and virology was conducted at the CVRL. Viral isolates were sent to the World Reference Laboratory at the Institute for Animal Health (UK) for characterization. The majority of gazelles and deer were severely lame and approximately 50-60% of the gazelles died at site 1 over a 6 wk period. Most free-ranging blackbuck were lame and FMD was confirmed in one euthanised blackbuck female and four dead juvenile animals at site 2. Oral and cardiac lesions were observed and FMD virus type O was isolated. The virus was closely related to FMD strains from India (Ind-2001) and Iran (Irn-2001). Except for a study by Kilgallon et al (2008) the immunological response to any FMD vaccine has not been established in exotic ungulates. The authors concluded that a single dose of FMD vaccine may not elicit a sufficient antibody response in Arabian oryx to confer lasting protection. Our observations indicate that, although the animals at site 2 were only vaccinated annually, they were afforded good protection when exposed to the same FMD strain that caused high mortality in unvaccinated gazelle at site 1.

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P 4. POSSIBLE BIOINDICATORS OF POLLUTION EXPOSURE IN PARALABRAX NEBULIFER FROM LONG BEACH HARBOR, SOUTHERN CALIFORNIA

Jeremiah Bautista and Cheryl Hogue, California State University, Northridge, Department of Biology, 18111 Nordhoff St., Northridge, CA 91330-8303, USA

Presenting author: Bautista, Jeremiah

Summary: Parasites of barred sand bass show patterns in prevalence and abundance that appear to be related to quality of the host’s habitat.

The barred sand bass (Paralabrax nebulifer) is an important coastal species that is host to over 14 taxa of parasites. Diversity and abundance of macroparasites of this fish were compared between the inner areas of Long Beach Harbor and offshore waters. Parasites as potential bioindicators of water quality were assessed. A total of 60 barred sand bass were sampled from two sites, the inner harbor and offshore waters of Long Beach, California. Fish were collected from October 2007 to September 2008 using hook and line, and standard length and weight were recorded. Parasites found were processed using standard parasitological techniques and identified. Histological changes in liver tissue was embedded in paraffin, sectioned at 5 um using a microtone, stained, and examined using a microscope. The most common parasite taxa infecting sand bass were Anisakis sp, Lacistorhynchus dollfusi, and copepods. Anisakis sp. was the only parasite that exhibited a higher prevalence (88%) outside the harbor compared to the inside (60%). Higher mean intensities of L. dollfusi were seen in hosts from outside the harbor.

Long Beach Harbor is an economically important port and habitat for a diversity of animals including the barred sand bass. Contaminant effects on this fish have previously been studied but parasite data is lacking. Parasites can be sensitive to changes in water quality and thus inform us about ecosystem health. Both prevalence and mean intensity of some common endoparasites of barred sand bass declined in fish inhabiting more polluted areas of the inner harbor.

Acknowledgements: This research was funded by the National Institute of Health MBRS Rise Program, grant no. GM063787.
P 5. IDENTIFICATION AND GENETIC CHARACTERIZATION OF CYTAUXZOOIN FELIS FROM BOBCATS (LYNX RUFUS) AND DOMESTIC CATS (FELIS CATUS)

Holly M. Brown, Department of Pathology, and David S. Peterson, Department of Infectious Diseases, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Kenneth S. Latimer, Covance Laboratories, Inc., 9200 Leesburg Pike, Vienna, VA 22182, USA

Presenting author: Brown, Holly

Summary: Utilizing the ribosomal internal transcribed spacer region 1 sequence as a marker to assess genotype variability, we identified multiple genetically distinct variants of C. felis within bobcat (Lynx rufus) and domestic cat (Felis catus) hosts.

Bobcats (Lynx rufus) are known reservoir hosts of Cytauxzoon felis while infection in domestic cats is generally fatal. Cats surviving infection, however, may serve as additional reservoirs. We hypothesized that there are genetically distinct variants of C. felis in bobcats and domestic cats, representing strains that have adapted to different feline hosts. We utilized real-time PCR analysis to test for C. felis infection in splenic tissue samples from 133 bobcats and blood samples from 96 asymptomatic, high-risk domestic cats. We designed a highly specific assay using a primer pair and fluorescent-labeled linear probe targeting a portion of the C. felis ribosomal 18S region that is poorly conserved among related piroplasms. Using standard PCR analysis, we then amplified and sequenced the C. felis ribosomal internal transcribed spacer region 1 (ITS1) from all C. felis-positive samples. C. felis ITS1 sequence data were aligned and analyzed to detect unique parasite genotypes within each host species. Real-time PCR analysis identified C. felis in 34/133 (25.6%) bobcats and 29/96 (30.2%) asymptomatic, high-risk domestic cats. Standard PCR amplifying C. felis ITS1 from positive samples and subsequent sequence alignment allowed for the identification of multiple genetically distinct C. felis variants within bobcat and domestic cat hosts. Real-time PCR detection of C. felis infection in wild bobcats and asymptomatic, high-risk domestic cats provides prevalence data for the parasite infection among these feline populations. Identification of unique C. felis genotypes suggests that there are different parasite strains, some of which may have adapted to and are now maintained in different feline hosts. A better understanding of the epidemiology of C. felis infection will enhance our ability to control this emerging feline infectious disease.

Acknowledgements: The authors thank Drs. J. Mitchell Lockhart and James O. Britt for their efforts in sample collection and submission. Funding for this project was provided by the Morris Animal Foundation.
P 6. TWO OUTBREAKS OF CANINE PARVOVIRAL ENTERITIS IN RACCOONS (PROCYON LOTOR) IN THE SOUTHEASTERN UNITED STATES

Justin D. Brown, Andrew Allison, Mark G. Ruder, John A. Bryan, and M. Kevin Keel, Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Belinda Burwell, Blue Ridge Wildlife Center, Millwood, VA, USA

Presenting author: Brown, Justin

Summary: Novel genetic variants of canine parvovirus were isolated from two raccoon (Procyon lotor) mortality events in the southeastern United States.

Existing experimental and field data suggest that raccoons are clinically susceptible to infection with feline panleukopenia virus, raccoon (Procyon lotor) parvovirus, and mink enteritis virus, but resistant to canine parvovirus (CPV) infection. Recently mortality associated with CPV infection, however, has been detected in raccoons in two geographically distinct locations in the Southeastern United States. Over a period of five days in September 2007, eight juvenile raccoons died during an outbreak of parvoviral enteritis at a rehabilitation center in Clarke County, VA, with one additional juvenile wild raccoon found dead on the premises. From October to December 2008, multiple juvenile raccoons were reportedly found dead at or near a rehabilitation center in Glynn County, GA, nine of which had been released several days earlier. Whole carcasses or tissues from 12 raccoons (8 VA, 4 GA) were submitted to the Southeastern Cooperative Wildlife Disease Study (Athens, GA, USA) for post-mortem examination, including virus isolation, histopathology, and immunohistochemistry. All raccoons examined had severe enteritis associated with viral antigen detected by immunohistochemistry in epithelial and inflammatory cells. CPV-2 was isolated from the feces/intestines of all VA and three GA raccoons. Sequencing of the CPV coding region from a representative isolate from each outbreak indicated that the viruses were novel genotypes and genetically distinct from one another. The mortality events described herein represent the first report of natural CPV infection and associated disease in raccoons. The impact that these novel CPV strains will have on wild or domestic animal health are not known; however, the detection of CPV infection in wild and released rehabilitated raccoons highlights the potential for viral spill-over and introduction into free-ranging animal populations. Further studies are ongoing to characterize these CPV strains antigenically and biologically.

Acknowledgements: We thank Dr. Jan Rossiter and Mr. Mark Heth for submission of the Georgia raccoon cases. We thank Dr. Jeremy Saliki and Mr. Charles Hong for their laboratory assistance.
P 7. EXPERIMENTAL INFECTION IN LAMBS WITH A BORDER DISEASE VIRUS (BDV) ISOLATED FROM PYRENEAN CHAMOIS (RUPICAPRA PYRENAICA)

O. Cabezón, R. Velarde, S. Lavín, I. Marco, Servei d’Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain; R. Rosell, Centre de Recerca en Sanitat Animal (CReSA), UAB-IRTA, Campus de la Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain. Departament d’Agricultura, Alimentació i Acció Rural, Generalitat de Catalunya, Barcelona, Spain; J. Segalés, Centre de Recerca en Sanitat Animal (CReSA), UAB-IRTA, Campus de la Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain.

Presenting author: Marco, Ignasi

Summary: The Border Disease Virus isolated from diseased Pyrenean chamois in NE Spain is infectious in experimentally infected sheep. Border disease (BD) is a congenital infection of sheep caused by Border Disease Virus (BDV) (Fam. Flaviviridae) that courses with reproductive disease. Since 2001, several outbreaks of disease associated to BDV infection have been detected in Pyrenean chamois (Rupicapra pyrenaica). This work describes the pathogenesis of this BDV in experimentally infected sheep. Eleven lambs were inoculated with 107 TCID50 of a BDV isolated from a diseased chamois (GenBank accession number AM905923). Five animals were kept as controls. Whole blood was collected at 2, 4, 7, 10, 14, 17, 21 and 28 days post-inoculation (pi). Necropsies were performed on days 7, 14, 21 and 28 pi and routine histopathological studies were performed. Reverse transcription-polymerase chain reaction (RT-PCR) was used to detect BDV in sera and tissue samples. Seroconversion was analysed by a commercial ELISA and virus neutralization test (VNT) using the homologous virus. No clinical signs or histopathological lesions were observed in any lamb. BDV was not detected in sera by RT-PCR. Sera of most lambs were positive to ELISA. All inoculated lambs had a strong neutralising antibody response detected from day 14 pi and reaching maximum antibody titres at day 28 pi. The present results are consistent with acute BD in domestic ruminants. Although we cannot detect the virus in sera samples, seroconversion of all experimentally infected lambs demonstrated that a BDV isolate from chamois is infectious in domestic sheep. These results have to be considered in future potential BDV control in communal alpine pasturing sheep flocks, in areas where chamois are infected with this BDV.
P 8. WHEN IS ENOUGH SAMPLING ENOUGH? POPULATION DYNAMICS AND ZOO NOTIC INFECTIONOUS DISEASE: THE CASE OF DEER MICE (PEROMYSCUS MANICULATUS) AND SIN NOMBRE VIRUS

Scott Carver, Amy Kuenzi, Richard Douglass, Department of Biology, Montana Tech of the University of Montana, 1300 Park St. Butte, MT 59701, USA; James N. Mills, Timothy Flietstra, Division of Viral and Rickettsial Diseases, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA

Presenting author: Kuenzi, Amy

Summary: Findings in this study may be applicable to sampling strategies for hosts and their pathogens, and be helpful to ecologists, wildlife biologists and public health officials dealing with emerging infectious diseases.

Field biologists face decisions about the optimization of sampling strategies which minimize the effort-to-benefit ratio. In general, “more sampling effort”, where possible, is considered better. Few studies however, examine the question: “how does a reduction in sampling frequency influence what we are trying to detect?” We use a longitudinal study of deer mouse (Peromyscus maniculatus) populations and prevalence of antibody to Sin Nombre virus (Bunyaviridae: Hantavirus) to assess how a reduction in sampling frequency influences the ability to document population demography of deer mice and dynamics of SNV infection. Data were collected monthly at three trapping grids near Cascade, Montana. We examined how sampling bi-monthly, quarterly, semi-annually and annually were related to the mean and variance of deer mouse abundance and dynamics of SNV. We also examined how this reduction in sampling frequency influenced detection of annual extremes in deer mice and SNV antibody (highs and lows). Reduced sampling frequency underestimated mean deer mouse abundance and progressively overestimated the mean number of deer mice with antibody and the mean antibody prevalence. Reduced sampling frequency also resulted in detecting fewer annual extremes of deer mouse abundance and infection. Our study indicates that mean deer mouse population abundance over time can be followed with reasonable accuracy while sampling less frequently than monthly. Sampling effort necessary to capture temporal dynamics of SNV infection however, differ from effort necessary to capture demographic patterns in deer mouse abundance. Findings in this study may be more widely applicable to sampling strategies for other hosts and their pathogens, and be helpful to health officials dealing with emerging infectious diseases.
P 9. CHEMISTRY REFERENCE RANGES IN A CAPTIVE HERD OF WOOD BISON (BISON BISON ATHABASCÆ)

Stephanie G. Crawford, Alaska Department of Fish & Game, Division of Wildlife Conservation, 1300 College Road, Fairbanks, AK 99701, USA; Leigh E. Strehlow, Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, AK 99775, USA; Kimberlee B. Beckmen, Alaska Department of Fish & Game, Division of Wildlife Conservation, 1300 College Road, Fairbanks, AK 99701, USA

Presenting author: Beckmen, Kimberlee

Summary: Serum chemistry reference ranges which varied by age, gender and season, were established for a captive herd of wood bison.

During a two-year long-quarantine and disease testing period, a herd of approximately 80 wood bison (Bison bison athabascae) will be subjected to periodic clinical health assessments. However, normal serum chemistry reference ranges necessary to evaluate the health status of individuals have not been established in free-ranging or captive wood bison. Samples were collected from clinically normal captive bison in southcentral Alaska during November 2008 (n=27) and March 2009 (n=30). Chemistry values were obtained on previously frozen sera using the HESKA Dri-Chem Veterinary Chemistry Analyzer: alanine aminotransferase, albumin, alkaline phosphatase, urea nitrogen, calcium, creatinine, creatine phosphokinase, globulin, gamma-glutamyl transferase, glucose, phosphorus, total bilirubin, total protein, and cholesterol. Reference ranges by age class adult (>3 yrs), subadult (< 3 yrs or >1 yr) and calves (<1 yr) were calculated as the mean ± two standard deviations. The results were compared by One-Way ANOVA (PopTools 3.0 in MS Excel) with at p<0.05. Significant differences were detected between genders for alanine aminotransferase, albumin, calcium, creatinine, glucose, gamma-glutamyl transferase, and total protein. Significant differences were also present among age classes for alkaline phosphatase, calcium, cholesterol, creatinine, creatine phosphokinase, globulin, phosphorous, total bilirubin, and total protein. Seasonally, all animals experience a significant decrease in cholesterol and BUN, while animals less than three years of age have significant increases in total bilirubin and phosphorus between November and March. There were significant differences based on age, gender, and season of collection. This study established clinically relevant reference ranges for normal captive wood bison.

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P 10. OCCURRENCE OF MYCOPLASMA ARGININI IN BIGHORN SHEEP (OVIS CANADENSIS) IN CENTRAL IDAHO

Mark Drew, Idaho Department of Fish and Game, Wildlife Health Laboratory, Caldwell, ID, USA; Glen Weiser, University of Idaho Caine Veterinary Teaching Center, Caldwell, ID, USA

Presenting author: Drew, Mark

Summary: Mycoplasma arginini was detected by serology and culture in a 15/31 bighorn sheep sampled in 2008 and 2009 in central Idaho, implying the presence of the organism and the potential for this agent to be involved in the respiratory disease complex in these herds.

A variety of pathogens, both primary and secondary, that are associated with disease in bighorn sheep (BHS) (Ovis canadensis) are known and documented. The majority of the pathogens found in BHS populations in others states and provinces have been found over time and across geographical areas in BHS in Idaho. Disease investigations and surveillance have been conducted in Idaho for many years in most of the accessible populations in the state. As part of an on-going assessment of BHS health status, BHS along the main Salmon River in central Idaho were captured and sampled. The sampling was conducted to determine background exposure to and presence of various pathogens.

BHS were captured using several methods. The majority of sheep were darted from the ground using Carfentanil (3 mg) and Xylazine (50-100 mg) in 1 cc darts and a Pneudart projector. Sheep were also captured using a helicopter and a drive net or a net gun. Once captured, sheep were restrained and positioned to allow for physical examination, application of radio collars and ear tags, and collection of biological samples. Samples collected included oropharyngeal swabs, blood, nasal swabs, and feces. Oropharyngeal swabs and nasal swabs were placed into Port-a-cul tubes or Amies media and refrigerated until submission to the Caine Veterinary Teaching Laboratory (CVTC), Caldwell, ID. Blood was collected by jugular venipuncture and placed in sterile glass tubes, allowed to clot, centrifuged and the serum decanted. Serum was submitted to the Idaho Animal Health Laboratory, Boise, ID and WADDL. Standard laboratory procedures were used for testing the samples for pathogens. Oropharyngeal and nasal swabs were streaked on blood agar plates and incubated in 5% CO2 for 48 hours. Specific isolates were identified using methods of Jaworski et al. 1993. A total of 11 and 20 BHS were captured and sampled in 2008 and 2009, respectively. Of these, 9/10 and 19/20 had serological titers to Mycoplasma spp. in 2008 and 2009, respectively. Mycoplasma arginini was isolated from 6/11 and 9/20 BHS in 2008 and 2009, respectively. One BHS in 2009 had a mixed isolation of M. arginini and M. ovipneumonia. The presence of Mycoplasma spp. was not unexpected in this herd, especially given the close proximity to Hells Canyon and the possibility of BHS moving between the two metapopulations. Mycoplasma ovipneumonia has been documented as a cause of lamb mortality in Hells Canyon (Besser et al. 2008). The prevalence of antibodies to Mycoplasma is similar between years, but the titer level is generally higher in 2009 than 2008. The low isolation rate of Mycoplasma arginini in 2008 likely reflects poor sample handling rather than the absence of the organism. The higher titers may indicate circulation of the organism within the metapopulation and may indicate a potential problem in lamb survival in summer of 2009. The presence of a new pathogen in BHS in Idaho is both of interest and concern. The lack of M. arginini in BHS from Hells Canyon and the lack of M. ovipneumoniae from central Idaho is curious and not easily explained. Additional data from lambs born in 2009 and possibly mortalities, would help to determine the importance of this finding.
P 11. ANALYSIS OF CAUSES OF MARINE MAMMAL STRANDINGS IN MARYLAND, 1990-2008

Cindy P. Driscoll, Tricia Kimmel, Jamie Schofield, Tamara O’Connell, Mike Neafsey, Maryland Department of Natural Resources Fish & Wildlife Health Program, 904 South Morris Street, Oxford, MD 21654, USA

Presenting author: Driscoll, Cindy

Summary: Causes of marine mammal strandings in Maryland have been attributed to boat strikes, fisheries entanglement, human interaction, infectious disease, and a variety of other causes. Implications of these findings relate to natural resources managment of protected species, fisheries and education about all natural resources.

The MD DNR has conducted marine mammal stranding response since 1990. While a variety of species have been documented, causes of death have been determined for relatively few cases due to advanced stages of decomposition. However, a complete necropsy is performed on each carcass regardless of condition code. Samples are collected and processed for diagnostic determination on appropriate carcasses. Stranding records from 1990-2008 were examined and analyzed. The parameters reported include species, age, condition code, geographic location, time of year, and cause of death.

Species were divided into odontocetes and mysticetes, and age was reported as calf, subadult, or adult. All were reported by month of stranding. Condition code was documented for four stages of decomposition based on the Smithsonian scale. Geographic location was divided between state coastal waters and the Maryland portion of the Chesapeake Bay. Cause of death was separated into categories including infectious disease, boat strike, fisheries entanglement, other known causes, and unknown causes. The most common species encountered in MD are the bottlenose dolphin (Tursiops truncatus) and the humpback whale (Megaptera novaengliae). More animals strand in summer months, in coastal waters and are a condition code three. More subadult or adult marine mammals strand in Maryland than calves. The majority of cases are of undetermined cause of death due to advancing decomposition and thus limited diagnostics. This analysis is important for fisheries management as well as protected species considerations. State representatives are asked to participate on fisheries take reduction teams with federal agencies to address entanglement reductions. Fishermen are a valued resource for states with fishing seasons, net mesh sizes and practices regulated to allow them to continue their livelihood and also to conserve protected marine mammals. This effort is the beginning of our attempt to analyze marine mammal stranding data for the benefit of both.

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P 12. RESULTS OF MARYLAND INTERAGENCY MONITORING FOR WEST NILE VIRUS, 1999-2008

Cindy P. Driscoll, Mike Neafsey, Maryland Department of Natural Resources, Cooperative Oxford Laboratory, 904 South Morris Street, Oxford, MD 21654, USA; Kimberly C. Mitchell, Robert A. Myers, Katherine A. Feldman, Tracy S. Duvernoy, Amy A. Bergman, Maryland Department of Health and Mental Hygiene, Veterinary Public Health, 201 W. Preston Street, 3rd floor, Baltimore, MD 21201, USA; Cyrus R. Lesser, Michael A. Cantwell, Maryland Department of Agriculture, Mosquito Control Department, 50 Harry S. Truman Parkway, Annapolis, MD 21401, USA; Heather J. Sullivan, USDA National Wildlife Research Center, Wildlife Disease Program, 4101 LaPorte Ave., Fort Collins, CO 80521, USA

Presenting author: Driscoll, Cindy

Summary: We summarize the results of West Nile Virus surveillance in Maryland.

West Nile Virus surveillance and monitoring in Maryland began in October of 1999 with the first crow (Corvus brachyrhynchos) found dead in downtown Baltimore, MD. The Maryland Department of Natural Resources (MD DNR) began immediate sampling and partnered with MD Department of Health & Mental Hygiene, MD Department of Agriculture, Maryland Zoo and Maryland’s federal military properties began coordination meetings to determine the future course of action for the state. The governor established the MD West Nile Virus Inter-Agency Task Force in the fall of 1999 and was re-named the MD Vector-Borne Disease Inter-Agency Workgroup in 2005 and interagency collaboration continues. Statewide surveillance was conducted annually from June 1 - October 31.

Wildlife: WNV activity was monitored by DNR in free-ranging and captive birds and other wildlife and testing by epitope-blocking enzyme-linked immunosorbent assay (bELISA) was conducted at the USDA Wildlife Health Laboratory in Fort Collins, CO.

Avian: Corvids dead <24 hrs were collected by various agencies and tested by reverse transcriptase polymerase chain reaction (RT-PCR) at DHMH. Horse specimens were collected by MDA and tested at DHMH by IgM-ELISA, PRNT, and RT-PCR. Mosquito pools were collected by MDA and tested by RT-PCR at DHMH. Enhanced human surveillance targeted encephalitis cases of all ages. Testing by immunosorbent assay (ELISA) and plaque reduction neutralization was conducted at DHMH. From 2002 - 2008, 292 of 4765 (6.1%) wildlife submissions were positive for WNV. Peak WNV activity in dead birds was detected in 2002. Dead bird surveillance, hotline and online reporting were discontinued at the end of 2002. The first confirmed equine WNV cases occurred in 2001 and equine activity peaked in 2003. The peak of positive mosquito pools occurred in 2003 with 117 WNV-positive and Culex as the most commonly positive species. A total of 171 human cases were detected between 2001 and 2008, with peak activity (73 cases, 1.3 cases per 100,000) in 2003. Twenty fatalities (7.4% case-fatality rate) were reported.

The Maryland Vector-borne Disease Inter-Agency Workgroup continues to shape the arboviral surveillance and management program given current priorities and funding availability. WNV is detected each year in Maryland, despite decreased numbers of cases since 2003. Although WNV has been the most prevalent arbovirus detected, other viruses of public health concern have also been detected. The sustainability of the arbovirus surveillance system is critical, particularly in the event that a novel arbovirus enters Maryland.

Acknowledgements: MD DNR; MD County Health Departments; USDA; USGS; USFWS; US Department of Defense; Centers for Disease Control and Prevention; TriState Bird Rescue and Research; Maryland Zoo
P 13. SUCCESSFUL TREATMENT OF A CANADA GOOSE (*BRANTA CANADENSIS*) WITH PRESUMED CAPTURE MYOPATHY

Rebecca Dunne and Erica Miller, Tri-State Bird Rescue & Research, Inc., 110 Possum Hollow Road, Newark, DE 19711, USA

Presenting author: Dunne, Rebecca

Summary: An adult Canada goose (*Branta canadensis*) captured during an oiled wildlife response developed clinical signs of capture myopathy and was successfully treated, rehabilitated and released.

Capture myopathy may present a risk during oil spills or other incidents involving large scale capture of susceptible wildlife. An adult Canada goose (*Branta canadensis*) was contaminated by a release of non-PCB dielectric oil and was one of 49 birds captured during the wildlife response to the incident. The bird was examined and treated in accordance with established protocols for oiled wildlife rehabilitation. The animal met medical criteria for cleaning, and it was cleaned one day post-capture. Immediately after cleaning it began to exhibit symptoms of capture myopathy. The bird was aggressively treated with IV fluids, vitamin E, methylcarbomate, gavage nutrition and physical therapy. Significant progressive improvement occurred over the next five days, and seven days post-capture the bird showed no signs of exercise intolerance. The bird was released after conditioning and veterinary examination eleven days post-capture. The case suggests that aggressive treatment at the first signs of capture myopathy can result in full recovery in wild-caught Canada geese.
P 14. ASSESSING LEAD SHOT INGESTION IN GREEN-WINGED TEAL AND NORTHERN SHOVELERS

Alan M. Fedynich, Drew A. Garrison, Autumn J. Smith, Texas A&M University-Kingsville, 700 University Blvd., MSC 218, Kingsville, TX 78363, USA; Pamela J. Ferro, Texas A&M University, College Station, TX 77843, USA; David A. Butler, Texas Parks and Wildlife Department, Bay City, TX 77414, USA; Markus J. Peterson and Blanca Lupiani, Texas A&M University, College Station, TX 77843, USA

Presenting author: Fedynich, Alan M.

Summary: The incidence of lead shot ingestion in certain species of waterfowl appears to have declined since the ban on lead shot for waterfowl hunting was put into effect.

Lead poisoning in waterfowl is primarily caused from ingestion of lead shotshell pellets spread into wetlands during hunting activities. In North America, the U.S. banned lead shotshells for hunting waterfowl in 1991. Canada followed in 1997 with more restrictive regulations. However, Mexico has not instituted restrictions. Migratory Green-winged Teal (Anas crecca) and Northern Shovelers (Anas clypeata) serve as useful biomonitors because they forage in shallow wetlands, thereby increasing the probability of being exposed to pellets that remain within their feeding zone. To learn whether Green-winged Teal and Northern Shovelers are being exposed to lead shotshell pellets, gizzards from 98 Green-winged Teal and 84 Northern Shovelers donated by hunters at the Justin Hurst Wildlife Management Area in Brazoria County, TX during the 2007–2008 hunting season were examined for ingested shot. No Green-winged Teal had lead shot, 24 (25%) had nontoxic shot or non-lead metal fragments, and 0 (0%) had steel shot, whereas, one (1%) Northern Shoveler had lead, three (4%) had steel shot, and 17 (20%) had nontoxic shot or non-lead metal fragments. Results from this study provide insight regarding exposure by Green-Winged Teal and Northern Shovelers to lead pellets in the environment.
P 15. HELMINTHS AND ECTOPARASITES OF BLACK NECKED SWAN (CYGNUS MELANOCORYPHUS MOLINA, 1872) IN CHILE

Daniel González-Acuña, Lucila Moreno; Universidad de Concepción, Facultad de Medicina Veterinaria, Casilla 537, Chillán, Chile; Mike Kinsella, Helm West Laboratory, 2108 Hilda Avenue, Missoula, MT 59801, USA

Presenting author: González-Acuña, Daniel

Summary: With the aim to know the parasitic fauna of the Black necked Swan, seven dead individuals collected in a rescue center were analyzed. We found a great variety of parasites, most of them described for the first time for this species.

The objective of this study is to obtain information about of the parasites affecting the Black necked swan (Cygnus melanocoryphus molina), and to demonstrate that it is affected by a great variety of endo and ectoparasites not described in Chile or in the species. We analyzed seven dead Black necked swans proceeding from the rescue center of the Universidad de Concepción in south central Chile. The ectoparasites were isolated and mounted in Berlese solution (Krantz, 1978. A manual of Acarology) and the lice in Canada balsam (Palma, 1978, New. Zel. Entomol. 6: 432-6). The endoparasites were extracted through parasitary necropsy and processed according to the techniques described by Pritchard & Kruse (1982, The collection and preservation of animal parasites). The identification was accomplished following the corresponding taxonomic key. The studied material was deposited in the zoological collection of the Faculty of Veterinary Science at the University of Concepción. Helminths of the class Nematoda (N= 4), Trematoda (N= 3) and Cestoda (N= 4) were isolated from the seven individuals. Four species of ectoparasites were isolated, including three of the Phthiraptera and one species of Acari. The following nematodes are new reports for the Chilean diversity: Epomidiostomun vogelsangi, Capillaria skrjabini, Avioserpens sp., the cestodes Gastrotaenia cygni, Microsomacanthus sp., Nadejdolepis sp., Retinometra sp., the trematodes Apatemon gracilis, Echinostoma trivolvis, the lice Ornithobius pricei and the mites Ingrassia cygni.

Additionally the nematode Avioserpens sp., the cestode Gastrotaenia cygni, Microsomacanthus sp., Nadejdolepis sp., Retinometra sp., the trematodes Echinostoma trivolvi, the lice Austromenonpon brevithoracicum, Anotoecus sp. and the mite Ingrassia cygni are new reports for the Black necked swan.
P 16. THE DEVELOPMENT OF A BAIT FOR THE DELIVERY OF AN ORAL BCG VACCINE FORMULATION AGAINST BOVINE TUBERCULOSIS (MYCOBACTERIUM BOVIS) TO WILD BADGERS (MELES MELES)

Sonya Gowtage, Allan Nadian, Sandrine Lesellier, Mark Chambers, Veterinary Laboratories Agency, UK, TB Research, Veterinary Laboratories Agency, Woodham Lane, Addlestone, Surrey KT15 3NB, UK; Kate Palphramand, The Food and Environment Research Agency (Fera), Woodchester Park, Tinkley Lane, Nympsfield, Gloucestershire, GL10 3UJ, UK

Presenting author: Gowtage, Sonya

Summary: This study describes the processes behind the development and evaluation of bait for the delivery of an oral BCG vaccine formulation against bovine tuberculosis, to wild badgers in the United Kingdom.

The UK Government is planning to develop a licensed oral BCG vaccine for the vaccination of wild badgers (Meles meles) in England by late 2014. The successful oral vaccination of a wildlife species requires a stable, targeted bait capable of delivering the vaccine formulation and therefore numerous competing requirements must be addressed. Bait palatability and preference studies were undertaken on captive and wild badgers in England. Captive animals were used to identify palatable food types and to refine bait design (e.g. texture) using data collected on attractiveness, uptake and handling. Candidate bait types were further screened in preference studies using a well-studied wild badger population. Measures of bait preference included daily bait disappearance rates, video surveillance data and the measurement of blood-borne bait markers in serum from trapped badgers. Preliminary data were also obtained on the attractiveness of the bait types to cattle as non-target species. To date, five bait types are being taken forward for assessment of compatibility with the vaccine formulation and for cattle preference and deployment strategy studies. The bait types fulfilled many of the required criteria and demonstrated high uptake and good handling characteristics in both wild and captive badgers. A range of palatable baits has been identified, each compatible with one or more vaccine delivery systems. Results from non-target uptake (cattle) and deployment strategy studies in badgers will reduce the number of bait candidates. The most promising candidates will be evaluated in vaccine stability and badger efficacy testing and a final product will go forward for large-scale manufacture. The production of palatable bait is key to the successful vaccination of badgers against bovine tuberculosis.

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P 17. SEVERE HOOF DEFORMITIES IN FREE-RANGING ELK IN WESTERN WASHINGTON

Sushan Han, Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164, USA; Kristin Mansfield, Washington Department of Fish and Wildlife, 2315 N. Discovery Place, Spokane Valley, WA 99216, USA; Patrick Miller, Washington Department of Fish and Wildlife, 2108 Grand Blvd., Vancouver, WA 98661, USA; Annemarie Prince, Washington Department of Fish and Wildlife, 2108 Grand Blvd., Vancouver, WA 98661, USA; Ella Rowan, Washington Department of Fish and Wildlife, 2315 N. Discovery Place, Spokane Valley, WA 99216, USA

Presenting author: Mansfield, Kristin

Summary: Elk in southwestern Washington are presenting with severely overgrown and deformed claws, and often marked emaciation, the etiology of which has not yet been elucidated.

Although reports of overgrown and deformed hooves in Roosevelt elk (Cervus elaphus roosevelti) have occurred sporadically in SW Washington for over a decade, the number and geographical distribution of such reports increased dramatically in 2008. During the winter of 2009 we undertook an investigation to better characterize the problem and examine possible etiologies. Agency biologists surveyed groups of elk and interviewed landowners to estimate the prevalence and distribution of affected elk and to plot locations of affected animals on maps. Lower limbs were collected from three affected elk that were either killed by hunters or euthanized for humane reasons. In addition, six affected elk from three locations, and three apparently unaffected elk from one location were shot and complete necropsies, radiology, routine histology, hepatic trace mineral measurements, bacteriology, virus isolation and parasitology were performed. During 2008-2009, approximately 80% of all groups observed included affected animals. Within affected herds, 30-90% of individuals were affected.

Necropsy, radiology, histology, virus isolation, and parasitology were unremarkable. Hepatic selenium and copper levels were severely deficient based on domestic livestock normal values. A variety of aerobic and anaerobic organisms were cultured, including Dichelobacter nodosus, a known cause of infectious foot rot in domestic sheep and cattle. The severe overgrowth and marked deformity of hooves from this cohort of free-ranging Roosevelt elk is unique. As it is not associated with underlying systemic disease, an etiology of toxicity, nutritional deficiency, or potentially infectious etiologies are all considered. Potential etiologies include recurrent laminitis, ergot toxicity, fescue toxicity, the effects of secondary conditions associated with severe copper and potentially severe selenium deficiency. Distantly, a genetic etiology is considered.
P 18. UTILIZING REAL-TIME PCR TO DETECT *BORRELIA BURGDORFERI* INFECTION IN *IXODES PACIFICUS*

Kimberly A. Heilig, Kristen Holt, Piper Kimball, Marin/Sonoma Mosquito and Vector Control District, 595 Helman Lane, Cotati, CA 94931, USA

Presenting author: Holt, Kristen

**Summary:** The RT-PCR protocol developed in this study is suitable for testing field-collected *Ixodes pacificus* for *Borrelia burgdorferi* infection.

Our purpose was to develop a protocol using Real-Time Polymerase Chain Reaction (RT-PCR) to test field-collected *Ixodes pacificus* ticks for *Borrelia burgdorferi*, the Lyme Disease bacterium, by conducting a Minimum Infection Rate (MIR) study. An acceptable protocol should yield a MIR comparable to those previously found in northern California. 1,806 adult *Ixodes pacificus* were collected at northern California state parks over the 2008-2009 winter season by the flannel drag method. Ticks were sorted by sex and collection location, placed in pools of five, and stored at -80°C until testing.

DNA was extracted on the Applied Biosystems 6100 Nucleic Acid PrepStation, using the NucPrep® DNA Chemistry for Tissues protocol. A positive control of heat-killed *Borrelia burgdorferi* cells was used.

RT-PCR was performed on the Applied Biosystems 7500 Real-Time PCR System, using TaqMan Chemistry. Pools with Ct values of 40 or below were considered to be positive.

Of 357 pools tested, 26 were positive for *Borrelia burgdorferi*. Assuming one positive tick per positive pool, and with a total of 1,806 individual ticks tested, the MIR found in this study was 1.44%. The RT-PCR protocol developed in this study is effective in testing *Ixodes pacificus* for infection with *Borrelia burgdorferi*. The MIR found in this study is comparable to infection rates found in previous studies conducted in northern California.
P 19. EXPERIMENTAL INFECTION OF MALLARDS (ANAS PLATYRHYNCHOS) WITH LOW-PATHOGENIC INFLUENZA VIRUSES: SUCCESSIVE CHALLENGES WITH HOMOLOGOUS AND HETEROLOGOUS SUBTYPES

E. Jourdain, G. Gunnarsson, N. Latorre-Margalef, L. Svensson, J. Waldenström, B. Olsen, Kalmar University, Kalmar SE-391 82, Sweden; J. Wahlgren, S. Sahlin, K. Falk, A. Lundkvist, Swedish Institute for Infectious Disease Control, Stockholm SE-171 82, Sweden; C. Bröjer, Swedish Veterinary Institute, Uppsala SE-751 89, Sweden

Presenting author: Jourdain, Elsa

Summary: Juvenile mallards were successively inoculated with LPAI H7N7, H7N7 again and later H5N2 during a 9-week period. They responded to the first infection with a mild fever, antibody production and viral excretion for several days whereas re-infections were only followed by occasional viral excretion.

Dabbling ducks, particularly mallards (Anas platyrhynchos), are considered the main reservoir of low-pathogenic avian influenza (LPAI) viruses. We hypothesized that individual mallards (1) are physiologically unaffected by LPAI infection and (2) excrete virus for several days after primo-infection with a given subtype but also after re-infection with a heterologous subtype. Six juvenile mallards kept in individual cages and previously equipped with subcutaneous transponders (Data Sciences International, MN USA) and temperature loggers (Maxim Integrated Products, CA USA) were inoculated with LPAI H7N7 virus (day 1). To assess subclinical effects of infection, heart rate, body temperature and activity were monitored continuously and body mass was recorded daily. To follow viral excretion, faeces, cloacal and oropharyngeal swabs were analyzed daily by RT-PCR. To detect nucleoprotein- and H5/H7-specific antibodies, serum was analyzed by HIT and ELISA. The ducks were re-infected with LPAI H7N7 and H5N2 on day 21 and 35, respectively. Body temperature increased slightly in four birds after the first H7N7 inoculation, whereas heart rate and activity were not affected. Virus was excreted continuously for 12.5 days (SD=1.4) and intermittently for another 4.0 days (SD=3.5). After both re-infections, viral excretion was observed only occasionally. Antibodies were detected from day 6. Mallards experimentally infected with LPAI viruses showed a mild physiologic response, contrary to hypothesis 1. Additionally, excretion patterns differed markedly between primo-infection and re-infections, which suggests the existence of short-term immunity to homologous but also heterologous subtypes, contrarily to hypothesis 2. Further work is needed to assess the potential effects of LPAI infection on wild mallard populations and to understand the immunological mechanisms involved when mallards are successively exposed to heterologous subtypes.

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P 20. INTERDISCIPLINARY MASTER OF SCIENCE DEGREE PROGRAM IN CONSERVATION MEDICINE

Gretchen E. Kaufman, Center for Conservation Medicine, Tufts Cummings School of Veterinary Medicine, 200 Westboro Rd., North Grafton, MA 01536, USA; Allen T. Rutberg, Center for Animals and Public Policy, Tufts Cummings School of Veterinary Medicine, 200 Westboro Rd., North Grafton, MA 01536, USA; Florina S. Tseng, Tufts Wildlife Clinic, Tufts Cummings School of Veterinary Medicine, 200 Westboro Rd., North Grafton, MA 01536, USA

Presenting author: Kaufman, Gretchen

Summary: Tufts University is developing a unique interdisciplinary professional masters degree program in Conservation Medicine designed to provide specific training, knowledge and skills for graduate students interested in pursuing a career in conservation medicine.

The Master in Conservation Medicine degree is intended to complement graduate achievement in traditional fields that contribute to conservation medicine and to better prepare the student to excel in a research or applied environment. Students from varied backgrounds will participate together in an interdisciplinary environment to complete a one year course of study centered on the integrative disciplines relevant to the field, and the research tools and research skills required for the practice of conservation medicine. All courses will be strongly case- and place-based, with an emphasis on student participation and peer-to-peer rather than didactic teaching. The student’s work will culminate in a final case study for publication. No thesis will be required. Select students will have the option to continue for a second year in a research fellowship. As the first university and the first veterinary school to establish a Center for Conservation Medicine, Tufts is well positioned to fill this critical educational niche, building on an excellent complement of conservation medicine faculty, an established public health and population medicine focus, and the unique policy expertise in the affiliated Center for Animals and Public Policy. Interdisciplinary faculty and resources will be drawn broadly from all schools at Tufts University, including Arts & Sciences, Engineering, Law and Diplomacy, Medicine and Nutrition and from the Consortium for Conservation Medicine. This program will begin in fall of 2010 and will be administered by the Tufts Center for Conservation Medicine at the Cummings School. More information is available on the website at http://www.tufts.edu/vet/ccm/. Reference: Kaufman, Gretchen E., Jonathan H. Epstein, Joanne Paul-Murphy, and Jennifer D. Modrall. Designing Graduate Training Programs in Conservation Medicine—Producing the Right Professionals with the Right Tools, EcoHealth, Published on-line 11 February, 2009.
P 21. CHRONIC WASTING DISEASE IN AN ISOLATED OUTBREAK WITH LOW PREVALENCE: ASCENDING THE SLIPPERY SLOPES OF AN EPIDEMIC CURVE IN WEST VIRGINIA

M. Kevin Keel, Richard W. Gerhold, John A. Bryan and John R. Fischer, Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; James M. Crum and Richard E. Rogers, Wildlife Resources Section, West Virginia Division of Natural Resources, P.O. Box 67, Elkins, WV 26241, USA

Presenting author: Keel, Kevin

Summary: We will discuss unusual challenges to surveillance of chronic wasting disease (CWD) in West Virginia, associated with low prevalence and geographic restriction, as well as the disease dynamics at what appears to be an early stage in the epidemic curve.

The outbreak of chronic wasting disease (CWD) in West Virginia is unusual in its very low prevalence and apparent limitation to a very small region. We hypothesize that it may have been recently established and this could help explain some of the unique aspects of the epidemiology associated with this event. Statewide surveillance for CWD among free-ranging white-tailed deer (Odocoileus virginianus) in West Virginia began in 2002. Sampling of road-killed deer was stratified across 55 deer management units (county political subdivisions). After the first positive was identified in Hampshire County in September 2005, a combination of samples from hunter-killed deer and special collections has been required to define the affected population and prevalence of the disease. Samples are tested by enzyme linked immunosorbent assay (ELISA) with confirmation by immunohistochemistry (IHC). Sex, age, clinical signs and location are recorded for statistical analysis. Results are also examined through a GIS database. Of the 5,265 deer examined from Hampshire County, 38 positives were collected by hunters (n=13), special collections (n= 23) or vehicle-collisions (n=2). They included 17 does (mean age 2.7Y) and 20 bucks (mean age 2.5Y). Three were approximately nine months old. The prevalence within two miles of positives is 2.3%. Surveillance of hunter-killed deer has been inadequate to define the affected population due to the inability to acquire sufficient samples in the small area known to be affected. The low prevalence of disease in a very small area has resulted in the necessity of more focused collections within a close proximity zone. Over three years of intensive surveillance the affected area remains localized though the size of the affected area is slowly expanding.
P 22. INDENTIFICATION OF MULTIPLE SPECIES APICOMPLEXAN PROTOZOAN MENINGOENCEPHALITIS IN HARBOR SEALS (PHOCA VITULINA) OF THE PACIFIC NORTHWEST

Dyanna M. Lambourn and Steven J. Jeffries, Washington Dept. of Fish and Wildlife, Marine Mammal Investigations, 7801 Phillips Rd. SW, Lakewood, WA 98498, USA; Stephan A. Raverty, Animal Health Center, 1767 Angus Campbell Road, Abbotsford, BC, V3G 2M3, Canada; Jessica Huggins, John Calambokidis, Cascadia Research, 218 1/2 W 4th Ave., Olympia, WA 98501, USA; Mike Garner, Northwest Zoo Path, 654 W. Main St., Monroe, WA 98272, USA; Melissa Miller, Marine Wildlife Veterinary Care and Research Center, California Dept. of Fish and Game, Santa Cruz, CA 95060, USA; Pat Conrad, Dept. of Pathology, Microbiology and Immunology, 5311 Vet Med 3A, School of Veterinary Medicine, University of California, Davis, CA 95616, USA; Micheal E. Griggs, National Institutes of Health, NIAID 4 Center Drive Rm B1-06, Bethesda, MD 20892, USA

Presenting author: Lambourn, Dyanna

Summary: Increasing numbers of stranded and necropsied harbor seals (Phoca vitulina) in the Pacific Northwest have been diagnosed with protozoal meningoencephalitis due to either individual or mixed infections with Sarcocystis spp., Toxoplasma gondii, and/or Neospora spp. As part of ongoing investigations of the health status of harbor seals (Phoca vitulina) in the Pacific Northwest, comprehensive necropsies have been conducted on moribund and dead harbor seals collected. Based on histopathology, tissues from animals diagnosed with protozoal meningoencephalitis were submitted to a reference lab for additional molecular characterization as to species and genotype. Washington Department of Fish and Wildlife staff or other stranding network responders conducted complete necropsies on dead harbor seals. Complete sets of tissues are collected at necropsy for histopathology, in 10% neutral buffered formalin and submitted for diagnostic evaluation. Paired and often replicate samples are also placed in whirlpak bags and either kept cold or frozen for ancillary diagnostics. Sera and pericardial fluid are also collected for serology. Serology and culture of fresh brain tissue were submitted to University of California. Molecular evaluation of infected tissue by PCR for ITS1, NTS2, B1, and ITSIS00 was conducted at National Institute of Health. Most consistent microscopic finding was granulomatous to nonsuppurative meningoencephalitis with occasional necrosis and intralesional protozoa consistent with Apicomplexa. Reactive changes in lymph nodes and protozoa were rarely detected within medullary histiocytes. Immunohistochemistry disclosed individual and occasionally mixed protozoal infections. Cell culture and PCR results were positive for either T. gondii genotype I, II, X, or an non-archetypal genotypes, Sarcocystis spp., and Neospora spp. This case series is believe to represent the first detection of an Type I and non-archetypal T. gondii genotype in marine mammals and is distinct to the genotypes X and II, as previously detected in harbor seals and sea otters (Enhydra lutris) in California. This case series also documents the first detection of neosporosis in marine mammals. Currently, there is insufficient information on the natural history of these parasites to assess the implications on host population status, transmission, or pathogenesis.

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P. Latchman, Kenneth Dive Center, St. Kitts, West Indies; M. Sullivan, St. Kitts Reef Ecology Watch Group; R. Stimmelmayr, Ross University School of Veterinary Medicine, PO Box 334, St. Kitts, West Indies; Veterinary Sciences, Interior Aleutian Campus, CRCD, University of Alaska Fairbanks, P.O Box 99775, USA

Presenting author: Stimmelmayr, Raphaela

Summary: Shark attacks are an important cause of fatal and non-lethal injuries in sea turtles utilizing St. Kitts waters.

On St. Kitts similar to other Caribbean islands traditional sea turtle harvest occurs seasonally. In water techniques include netting and spear fishing of foraging green (Chelonia mydas) and hawksbill turtles (Eretmochelys imbricata). To gain insight into local threats to sea turtles we recorded types and causes of injury in free-ranging sea turtles. As part of a large marine ecosystem survey project (2006-2008), sightings of sea turtles were recorded during roving snorkel (day), dive (night/day), and boat (day) surveys. Data collected included species, estimated straight carapace length (cm), type and location of injury and abnormalities. A total of 144 turtle sightings were recorded. No injuries and/or other abnormalities were observed in juvenile sea turtles. Injuries and abnormalities observed in adults were missing hind leg flipper (n=1; hawksbill), cracked tail shell (n=1; hawksbill); barnacles (n=1), discolored shell (n=1), fatal shark bites (n=2; hawksbill; green turtle) and fibropapillomatosis (n=1; green turtle). We did not observe any injuries on sea turtles that could be directly linked to local traditional harvest practices. Shark bite related injury and death were the leading cause (43%) among observed injuries. Our current observation of a severe case of cutaneous fibropapillomatosis in an adult resident green turtle confirms previous sightings by local marine knowledge holders (Kenneth Samuels pers. commun.). Marine turtle fibropapillomatosis has a circumtropical distribution including the Caribbean region.

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P 24. SURVEY OF AVIAN PARAMYXOVIRUS INFECTIONS IN WILD WATERFOWL IN KOREA

H.R. Lee, S.H. Byun, Avian Disease Laboratory, College of Veterinary Medicine, Chungbuk National University, Cheonju, 361-763, Korea; K.S. Choi, Avian Disease Division, National Veterinary Research and Quarantine Service, Anyang, 430-834, Korea; J.H. Shin, Ecology Research Department, National Institute of Environmental Research, Incheon, 404-708, Korea; I.P. Mo, Avian Disease Laboratory, College of Veterinary Medicine, Chungbuk National University, Cheonju, 361-763, Korea

Presenting author: Lee, Hae Rim

Summary: During this surveillance, 15 avian paramyxoviruses were isolated from wild waterfowl and further classified into three different serotypes including serotype 1 which is very closely related with the poultry population.

After outbreaks of highly pathogenic avian influenza (AI) in Korea, intensive surveillance of waterfowl for AI has been conducted. Many low pathogenic AI viruses were reported during this campaign, and also unknown viruses with hemmaglutination activity were isolated. Therefore, this study was conducted to identify these unknown viruses isolated from waterfowls. A variety of samples including feces, swabs and blood were collected from waterfowl or their natural habitats. These samples were treated with antibiotics and inoculated into 9- to 11- day-old embryonated specific pathogen free eggs. Harvested viruses in allantochorionic fluid were examined with hemagglutination test and RT-PCR for detecting AI. Non-AI hemagglutinating agents were tested with RT-PCR for Newcastle disease virus and serologically with a panel of APMV reference antisera. 15 isolates which were not AI viruses but had hemagglutination activity are determined as APMVs; nine APMV serotype-1, tow APMV serotype-4, and one APMV serotype-6. Another three isolates were yet to identify serotype with their unspecific reaction. This is the first time to survey APMV distribution in the five geographically different wild bird habitats. Total 15 APMVs were isolated and the predominant APMV was serotype 1 (Newcastle disease virus) which is the most important serotype in poultry. From this study, we found that different serotypes of APMV exist in the waterfowl and further study will be needed in the area of molecular ecology between wild birds and domestic poultry, especially APMV.
P 25. CHARACTERIZATION OF TEMPORAL AND SPATIAL DISTRIBUTION OF VIRUSES IN MOOSE AND CARIBOU THROUGHOUT ALASKA

Camilla Lieske, Wildlife Toxicology Laboratory, Institute of Arctic Biology, P.O. Box 75700, Fairbanks, AK 99775, USA; Kimberlee B. Beckmen, Alaska Department of Fish & Game, Division of Wildlife Conservation, 1300 College Road, Fairbanks, AK 99701, USA

Presenting author: Beckmen, Kimberlee

Summary: Since 2001 there has been an increase in serum prevalence of the respiratory disease complex viruses in free-ranging caribou and moose throughout Alaska.

Moose (Alces alces) and caribou (Rangifer tarandus) are important subsistence resources. Previous studies on the Northern Alaska Peninsula caribou herd found an apparent emergence of high antibody prevalence to respiratory disease complex viruses between 1999 and 2001. The goal was to characterize temporal and spatial distribution of viruses in moose and caribou throughout Alaska. Using a serologic database of 3655 caribou (collected 1975-2007) and 2330 moose (collected 1968-2007) the serum antibody prevalence to the four viruses considered to comprise the respiratory disease complex viruses (Bovine Respiratory Syncytial Virus (BRSV), Infectious Bovine Rhinotracheitis (IBR), and Parainfluenza-3 Virus (PI3) plus Bovine Viral Diarrhea (BVD)) were determined. For consistency across all time periods, serologic testing by serum neutralization was conducted at the Wyoming Veterinary Diagnostic Laboratory. Since more precise spatial data were not available, prevalence of exposure was reported for caribou by caribou herd and for moose by Game Management Unit (GMU). Prevalence rates <15% were noted in caribou herds before 2001 for BRSV, IBR and PI3. Since then, herds were found with moderate to high prevalences (affecting up to 90% of the individuals). In moose, there is a similar pattern of recent increase in prevalence of BRSV and IBR. The causes of the recent increase in respiratory complex viruses could not be determined. Reasons for changes in prevalence include exposure of disease to a naïve population, increase in herd size (with subsequent increase in potential contact to positive individuals), changes in immune function of affected herds, and changes in the environment leading to increased transmission. This study illustrates the importance of disease monitoring in populations for the timely identification of emerging health problem.

Acknowledgements: This study could not have been conducted without the major contribution of Randy Zarnke for establishing the serology database and serum archive.
P 26. AN EMERGENCY RESPONSE TO THE DETECTION OF PSEUDORABIES IN MICHIGAN USING THE INCIDENT COMMAND SYSTEM (ICS)

David R. Marks, USDA-APHIS-WS Wildlife Disease Program, 2803 Jolly Rd. Suite 100, Okemos, MI 48864, USA; Daniel E. Harpster, USDA-APHIS-VS, 12927 Stonecreek Drive, Pickerington, OH 43147, USA

Presenting author: Marks, David

Summary: A case study of how the Incident Command System (ICS) was applied when Pseudorabies was detected in several captive game ranches, as a model for future emergency responses such as FAD introductions in wildlife populations.

In 2008, Pseudorabies virus (PRV) was detected in several swine on private hunting ranches in Michigan. The situation threatened the state’s PRV-free status and required response from several agencies. An Incident Command System (ICS) was established to manage the response activities, serving as a model for future situations. With the detection of PRV at a captive hunting ranch, the state quickly recognized a rapid and large-scale response would be necessary. As several agencies would be involved and the amount of workload would be great, an Incident Management Team was established. Recently, both federal and state agencies have received training on ICS. This situation also presented an opportunity to apply ICS in a real-world situation. The response included three major actions: identifying and testing herds linked to the index herd (trace surveillance), identifying and testing swine within five miles of PRV positive facilities, and depopulating the PRV positive facilities. Four facilities were found to be PRV positive and were directly linked to one another through trade. The facilities were depopulated and no domestic swine tested positive in the surrounding areas (n=1,198). Eight feral swine within five miles of the index facility have tested positive for PRV since the incident. Although the overall outcome of the response was successful, many issues arose concerning how the ICS functioned. Some examples include: communication breakdowns (reporting to traditional supervisors, not according to ICS structure), inadequate ICS training/experience for some team members, ICS forms not applicable to disease response situations, and staff not fully devoted to incident (still had normal job duties). The situation brought these weaknesses to the front and the lessons learned will hopefully prove beneficial for future emergency responses.
P 27. CLINICAL AND PATHOLOGICAL ASSESSMENT OF WEST NILE VIRUS INFECTION IN THE AMERICAN (CORVUS BRACHYRHYNCHOS) AND FISH CROW (C. OSSIFRAGUS)

Nicole Nemeth, Jeret Benson, Angela Bosco-Lauth, Jack Muth, Terry Campbell, Janice Bright, Terry Spraker, and Richard Bowen, Colorado State University, 4801 Rampart Rd., Fort Collins, CO 80523, USA; Thomas Gidewski, USDA/Veterinary Services, 4101 Laporte Ave., Fort Collins, CO 80521, USA

Presenting author: Nemeth, Nicole

Summary: Differences in clinical and pathological responses to West Nile virus (WNV) infection exist between American and fish crows; hematologic responses and patterns of viral pathogenesis may reveal underlying reasons for variation in infection outcome in these species. Numerous North American corvid species are highly susceptible to WNV infection, with potentially severe consequences on individual and population health. We sought to better understand and compare the clinical course, clinical pathology, virology, and pathogenesis of WNV infection in two North American crow species. American (Corvus brachyrhynchos) (AMCR) and fish crows (C. ossifragus) (FICR) were experimentally inoculated with WNV by subcutaneous injection. For three days prior to inoculation and during the acute phase of infection (1-6 days post-inoculation; DPI), clinical observations were made, including videos (activity level assessment), hydration, electrocardiogram, fecal examination, neurological examination, blood chemistries and cell counts, and body temperature and weight. Viral titers in blood were determined daily, and presence of neutralizing antibodies was determined at 5 and 6 DPI. Birds were euthanized on 6 DPI and necropsies performed for gross and histopathologic assessment and determination of viral titers in tissues. Unlike FICR, AMCR were inactive by 6 DPI, with delayed postural and myotactic reflexes. All crows experienced decreased thrombocytes, glucose and hemoglobin; AMCR had lymphocytosis. Mean peak viremias were 10e5.9 (FICR) and 10e9.2 PFU/ml serum (AMCR); titers were higher in AMCR tissues, especially liver, kidney, pancreas, small intestine and brain. While analyses are pending, including pathological comparison between AMCR and FICR, results suggest that although the effects of WNV infection in crows and other birds are systemic, specific systems (e.g., nervous) are more affected in AMCR than FICR. In addition, differences in blood cell counts and chemistry may support decreased neurologic function and inability to control viral replication in AMCR. This may also correlate with weakened and delayed humoral immune responses in AMCR versus FICR.

Acknowledgements: We thank Christy Yoder and Gordon Gathright of the National Wildlife Research Center for providing crows and crow care prior to the study.
P 28. FIRST REPORT OF A SUITE OF TICK-BORNE INFECTIONS IDENTIFIED IN MONGOLIAN REINDEER (RANGIFER TARANDUS)

Sophia Papageorgiou, Janet E. Foley, University of California, Davis, CA 95616, USA; Tsetseg Battsetseg, Institute of Veterinary Medicine, Zaison, Ulaanbaatar, Mongolia

Presenting author: Papageorgiou, Sophia

Summary: Mongolian reindeer have low body condition scores (BCS), appear debilitated, and have musculo-skeletal problems that may be associated with exposure to and/or infection of three tick-transmitted diseases.

Health assessments of Mongolian reindeer (Rangifer tarandus) indicate the herds have poor BCS, lameness, and reproductive issues. Tick-transmitted infections may contribute to the health problems in these reindeer. This cross-sectional field investigation measures infection prevalence of, and identifies risk factors for, tick-borne infections in these animals. Blood and skin samples from reindeer were taken using manual restraint. Blood smears were made, and serum pulled from clotted blood in red top tubes. Samples were transported to UlanBataar, Mongolia and stored at -20°C until transport to the U.S. Serum and whole blood samples were analyzed for Borrelia spp., Anaplasma spp., and Rickettsia spp. using IFA and PCR respectively. PCR was performed for A. ovis, and positive samples sequenced. Physical examinations were performed on 30 animals. Data analyses were done using a variety of statistical programs, with statistical significance at p≤0.05.

128 blood and 90 skin samples were collected. Seroprevalence ranged from 35.4% to 51.4% for Borrelia spp., 50% to 100% for Anaplasma spp., 25% to 76.9% for Rickettsia spp., and 53.2% were A. ovis PCR positive. Serologic coinfection of all three organisms was seen in 26.3%, n=35, of the animals tested. We identified a high seroprevalence of a suite of tick-borne organisms and high prevalence of active infection of A. ovis, all of which may be contributing to adverse health conditions in Mongolian reindeer. This small isolated population migrating within a closed ecosystem may be experiencing elements of the ‘extinction vortex’, inbreeding and decreased genetic diversity, adverse environmental conditions, and skewed demographics, coupled with infectious diseases that may play a role in reduced herd health.

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P 29. HELMINTH PARASITES OF ANATIDAE IN IRAN

Nader Pestehechian, Dalimi asl Abdolhosin, Department of Parasitology, Medical School, Isfahan University of Medical Sciences, Hezar Jerib St., Isfahan (81746 -73461), Iran

Presenting author: Pestehechian, Nader

Summary: The accurate identification of parasites has important implications for many areas of parasitology, including systematics, taxonomy, ecology and epidemiology. Fundamental research is also central to diagnosis, treatment, and control of the diseases they cause.

The role of migrating aquatic birds in distribution of parasites, especially those that are common in human and wild and domestic animals, is well known. A total of 187 ducks belonging to five species of wild ducks and two species of domestic ducks were collected.

After necropsy, different organs were inspected for the evidence of helminthic infections. Helminths were preserved in formalin, stained, drawn by camera lucida and photographed. The taxonomic study was carried out by key identification and measuring different parts of the body of hemithis. The collected data were compared with different records in the world.

Results showed that 88% of examined ducks were infected with various types of helminthes. A total of 35 species of helminths were recorded. After each parasite the number indicates the species of the host: 1=Mallard (Anas platyrhynchos), 2= pochard, 3=Gadwall (Anas strepera), 4=Teal, 5=Shelduck (Tadorna sp.), 6=domestic duck. Cotylurus cornatus:1,4, means this parasite has been found in Mallard and Teal. Paramonostomum pseudalveatum:1,2,3,4,5.


Paramonostomum pseudalveatum and Notocotylus attenuatus were the most common trematodes. Amidostomum anseris was the most common nematode and Sobolevicanthus gracilis was the most common cestode with respect to the number of infected wild aquatic birds. Among these parasites, the four following species had a zoontic importance: Trichobilharzia sp., Hypoderaum conoideum, Echinostoma parvulum, and Echinostoma revolutum. In conclusion, a total of 35 species were reported in the Gavkhoni pool and Zayandehrood River, situated in the Isfahan region of central Iran. Aquatic birds as definitive hosts of helminths play an important role in epidemiology of worm diseases and are important in hygiene in humans and aquatic birds.

Acknowledgements: Thanks to Dr. Mobedi Iraj and Dr. Dalimi Asl Abdolhosin for providing some of the key identification used in this study and helping me with accurate identification of helminths.
P 30. HELMINTH PARASITES OF STRAY DOGS FROM THE ISFAHAM REGION OF IRAN

Nader Pestehchian, Hossein Hejazi, Hosnali Yosefi, Jahangir Abdi, Department of Parasitology and Mycology, Isfahan University of Medical Sciences, Hezar Jerib St., Isfahan (81746 -73461), Iran

Presenting author: Pestehchian, Nader

Summary: The accurate identification of parasites has important implications for many areas of parasitology, including systematics, taxonomy, ecology and epidemiology. Fundamental research is also central to diagnosis, treatment, and control of the diseases they cause.

The role of stray dogs in distribution of parasites specially those that are common in human and domestic animals is well known. In the present study helminth parasites of stray dogs from the Isfahan region were isolated and identified and their prevalence was determined. This study was conducted from June 2004 until March 2007. After accommodation with municipality and bioenvironmental and police, 237 stray dogs have been killed and collected. After necropsy, the digestive tracts and abdominal cavity were inspected for the evidence of helminthic infections. Helminth isolates were preserved in formalin or glycerine-alcohol. All species were stained and finally all species were drawn by camera lucida. The taxonomic study was carried out by measuring different parts of the body of heminths and by key identification, then the collected data were compared with different records in the world. Results showed 76% of dogs were infected with various helminths. A total of 7 species of nematoda and 7 species cestoda were recorded: Toxocara canis (27.5%), Toxocara leonina (14.6%), Rictularia affinis (9.5%), Trichuris vulpis (9.5%), Physaloptera preputialis (1.7%), Uncinaria stenocephala (1.7%), Oxyuris spp. (1.7%), Echinococcus granulosus (12.3%), Taenia multiceps (34.2%), Taenia hydatigena (28.5%), Taenia ovis (14.2%), Mesocestoides lineatus (6.6%), Dipylidium caninum (11.4%), Joyuxiella echinorhincoides (4.7%).

Stray dogs are definitive hosts of helminthic parasites and play an important role in epidemiology of hydatidosis, taeniasis, visceral and ophthalmic and cutaneous toxocariasis and are important in human and animal hygiene. Treatment for helminths or countinuing the stray dogs killing project could be important strategies for control of the zoonotic parasites in the Isfahan region.

Acknowledgements: Thanks to Dr Mobedi Iraj for providing some of some of the key identification used in this study and helping me.
P 31. ABDOMINAL TELEMETRY IMPLANT DISPLACEMENT AND LOSS OF A VANCOUVER ISLAND MARMOT (MARMOTA VANCOUVERENSIS)

Stephen Raverty and Erin Zabek, Animal Health Center, 1767 Angus Campbell Road, Abbotsford, BC, V3G 2M3, Canada; Malcolm McAdie, Vancouver Island Marmot Recovery Program, 2080 Labieux Road, Nanaimo, BC, V9T 6J9, Canada; Helen Schwantje, Ministry of Environment, 2975 Jutland Road, Victoria, BC, V8W 9M1, Canada

Presenting author: Raverty, Stephen

Summary: Post-mortem examination of a Vancouver Island Marmot recovered from the wild disclosed colonic impaction and secondary septicemia due to displacement and colonic compression by a surgically implanted abdominal telemetry device.

To obtain data on the natural history and facilitate tracking or recovery of Vancouver Island marmots post introduction to the wild, animals are routinely implanted with an abdominal telemetry device. Although deleterious effects of implants are rare, potential adverse consequences should be part of the risk assessment with endangered species recovery programs. Baseline biologic information and potential disease processes of concern to Vancouver Island marmots has been compiled through establishment of a comprehensive and systematic necropsy protocol, which includes gross examination, photography, morphometrics, and radiography, and selection of tissues for histopathology, routine and selective bacterial culture, molecular studies (polymerase chain reaction), heavy metal and vitamin A analysis of the liver, parasitology and archiving of tissues for additional ancillary studies. Between 1998 and 2007, 60 animals were examined. This case report describes the findings of a 3.0 kg male marmot presented for post-mortem examination in July 2007. Necropsy disclosed displacement and lodgement of an implant from the cranial abdomen to pelvic inlet with compression and partial obstruction of the colon. At the site of impact, there was ulcerative colitis and throughout the abdomen, there was a diffuse fibrinous peritonitis with multiple serosal adhesions. Factors which may have contributed to the loss of this individual include the recent change from a larger diameter devise used routinely in the past (Telonis) to a smaller unit coated with a hard polymer (Holohil). In addition, this animal has just emerged from hibernation and with the loss of abdominal (pelvic) fat stores and renewed motility of the gastrointestinal tract, may have facilitated displacement of the devise to the pelvis of this animal.
P 32. PUTATIVE HERPESVIRAL ULCERATIVE ESOPHAGITIS IN A STRANDED YEARLING HARBOUR PORPOISE (*PHOCEONA PHOCEONA*) FROM BRITISH COLUMBIA, CANADA

Stephen Raverty and John Robinson, Animal Health Center, 1767 Angus Campbell Road, Abbotsford, BC, V3G 2M3, Canada; Lisa Spaven, Graeme Ellis and John Ford, Pacific Biologic Station, Department of Fisheries and Oceans, 3190 Hammond Bay Road, Nanaimo, BC, V9T 6N7, Canada; Anna Hall, 2202 Main Mall, University of British Columbia, Vancouver, BC, V6T 1Z4, Canada; Ole Nielsen, Central & Arctic Region, Department of Fisheries and Oceans, 501 University Crescent, Winnipeg, MB, R3T 2N6, Canada

Presenting author: Raverty, Stephen

Summary: Post-mortem examination of a stranded male yearling harbor porpoise disclosed multifocal to coalescing ulcerative and erosive esophagitis with rare intranuclear inclusions and a previously undescribed herpesvirus was detected by polymerase chain reaction.

As part of an ongoing effort to establish baseline information on pathologic findings of stranded harbour porpoises (*Phoceaena phoceaena*) along the British Columbia coastline, animals are recovered and comprehensive necropsies undertaken. Over the last 10 years, 148 porpoises have been examined and to date, no viral pathogens have been documented. On September 12, 2008 a yearling male harbour porpoise was recovered from the Esquimalt Lagoon, Vancouver Island, British Columbia. The animal was transported to a diagnostic laboratory and a necropsy conducted. Representative tissues were collected for histopathology, heavy metal and vitamin A analysis, routine bacteriology, and molecular screening by polymerase chain reaction for Brucella spp, morbillivirus and herpesvirus. A replicate set of tissues was forwarded to an outside reference for attempted virus isolation. Tissue homogenates were inoculated on SLAM cells and evaluated for cytopathic effect. The esophageal mucosa featured numerous ulcers, erosions and cleft formation and in rare cells, there is mild karyomegally with a poorly circumscribed amphophilic intranuclear inclusion. PCR of the ulcer was positive with primers for universal herpesvirus and no cytopathic effect was detected in tissue culture. Previous case reports of herpesviral infections in cetaceans include an encephalitis in a harbour porpoise, genital infection in a male harbour porpoise, and disseminated viremia in an Atlantic bottlenose dolphin (*Tursiops truncatus*) and belugas (*Delphinapterus leucas*). The esophageal presentation in this case is unusual and reminiscent of a number of herpesviral infections in humans, livestock and companion animals. There were no apparent lesions which may have predisposed this animal to infection and implications for overall population health status are unknown.
P 33. INFECTION DYNAMICS OF TWO NORTH AMERICAN TRYPANOSOMA CRUZI RESERVOIRS (PROCYON LOTOR AND DIDELPHIS VIRGINIANA) WITH GENETICALLY DISTINCT ISOLATES OF THE PARASITE

Dawn M. Roellig, Department of Infectious Diseases and Southeastern Cooperative Wildlife Disease Study, Department of Population Health, The University of Georgia, Athens, GA 30602; Angela Ellis, Veterinary Diagnostic Laboratory, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602; Michael J. Yabsley, D. B. Warnell School of Forestry and Natural Resources and Southeastern Cooperative Wildlife Disease Study, Department of Population Health, The University of Georgia, Athens, GA 30602

Presenting author: Yabsley, Michael

Summary: Experimental infections of two North American wildlife reservoirs indicate that infection dynamics of various T. cruzi strains can differ considerably which should be considered when investigating the epidemiology of Chagas disease in the United States. Trypanosoma cruzi, the causative agent of Chagas’ disease, has a wide host and geographic range. Within the various host species, the genotype of the parasite may vary and an association between genotype and host and geographic range. Within the various host species, the genotype of the parasite may vary and an association between genotype and host has been strongly supported by molecular typing of isolates from autochthonously infected wild and domestic animals and humans. Individuals (n=2 or 3) of each species were intraperitoneally or intravenously inoculated with 1x10^6 culture-derived T. cruzi trypomastigotes of Tc IIa (North America-raccoon, Procyon lotor), Tc I (NA-opossum, Didelphis virginiana), Tc IIb (South America-human), or both Tc I and IIa. Blood was collected every 3-4 days post-inoculation (DPI) for direct and molecular detection of T. cruzi. Plasma or serum was used for detection of anti-T. cruzi antibodies in an indirect IFA. At euthanasia (28 DPI, 56 DPI, or 112 DPI), tissues were collected for PCR amplification of T. cruzi DNA and histopathologic analysis. Raccoons became infected with all three T. cruzi strains, while opossums only became infected with TcI and TcIIb. Although opossums were susceptible to TcIIb, infection dynamics were different compared with TcI. Opossum parasitemias gradually increased and declined rapidly; whereas, parasitemias peaked sooner in raccoons which maintained relatively high parasitemia for 5 weeks. Differences in susceptibility to distinct genotypes were demonstrated. Virginia opossums that were solely infected with TcI or dually-inoculated with TcI and IIa were parasitemic and had patent infections. Variation between experimental groups may represent differences in the Virginia opossum’s reservoir competency and is further supported by molecular typing studies that have only isolated TcI from the species. While raccoons were able to develop a patent infection when inoculated with TcI, IIa, and IIb, the highest parasitemia from a single isolate inoculation was with TcIIa.

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P 34. LONGITUDINAL ANTIBODY RESPONSES OF RACCOONS NATURALLY EXPOSED TO MULTIPLE SUB-TYPES OF INFLUENZA A VIRUS

J.J. Root, K.T. Bentler, H.J. Sullivan, U.S. Department of Agriculture, Wildlife Services, National Wildlife Research Center (USDA/APHIS/WS), 4101 La Porte Avenue, Fort Collins, CO 80521, USA; B.J. Blitvich, Department of Veterinary Microbiology and Preventive Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA 5001, USA; R.G. McLean, A.B. Franklin, U.S. Department of Agriculture, Wildlife Services, National Wildlife Research Center (USDA/APHIS/WS), 4101 La Porte Avenue, Fort Collins, CO 80521, USA

Presenting author: Root, Jeff

Summary: Antibodies to Influenza A virus in naturally exposed raccoons appear to have a long duration of detectability.

The longevity of detectable antibody responses of wildlife to influenza A virus exposure is largely unknown, but could be important information for surveillance programs and informing management decisions. The longitudinal antibody response of raccoons (Procyon lotor) to influenza A virus was assessed in naturally exposed raccoons. Raccoons were held in captivity for up to 279 days and bled on 10 occasions during this interval. All raccoons (n = 7) were exposed to influenza A virus at an unknown time prior to being brought into captivity. Serum samples were tested for antibodies to influenza A virus by a blocking ELISA technique. Although titer declines were noted in most animals over time, all animals maintained detectable antibodies for the duration of this study, which indicated that influenza A antibodies in raccoons typically will remain detectable for a minimum of nine months. However, the actual duration of detectable antibodies is likely much longer. Hemagglutination-inhibition (HI) and neuraminidase-inhibition (NI) tests indicated that most of these raccoons were exposed to multiple subtypes of influenza A virus. These data will be of importance to surveillance programs, as the duration of naturally acquired antibodies to influenza A virus in wildlife populations is largely unknown.
P 35. CALCITRIOL IS PRODUCED DURING URSINE HIBERNATION DESPITE PROLONGED ANURIA

Rita L. Seger and Robert C. Causey, Department of Animal and Veterinary Sciences, and Frederick A. Servello, Department of Wildlife Ecology, University of Maine, Orono, Maine, USA; Randal A. Cross and Walter J. Jakubas, Maine Department of Inland Fisheries and Wildlife, Bangor, Maine, USA; Michael F. Holick and Tai C. Chen, Boston University Medical Center, Boston, Massachusetts, USA; Caren M. Gundberg and Thomas O. Carpenter, Yale University School of Medicine, New Haven, Connecticut, USA; Clifford J. Rosen, Maine Medical Center Research Institute, Scarborough, Maine, USA. Author contact: rita.seger@umit.maine.edu

Presenting author: Seger, Rita L.

Summary: Despite prolonged anuria, hibernating black bears produce calcitriol, which may be important in suppressing unloading-induced bone resorption.

Black bears (Ursus americanus) remain anuric during approximately six months of hibernation. Urea nitrogen is recycled by an unknown mechanism. The means by which the ursine kidney ceases and resumes urine production is unknown. The status of other renal functions is also unknown, including the production of calcitriol (1,25(OH)2 vitamin D). This report represents a subset of a larger study that analyzed a panel of bone metabolic markers in serum collected from free-ranging female black bears during active season (mid-May through June) and hibernation (mid-January through March), during 2005 through 2007 (Seger, 2009, Univ Maine). 25-hydroxy vitamin D [25(OH)D] was measured by high performance liquid chromatography in samples collected in 2005 and 2006. Calcitriol was measured by dual-antibody radioimmunoassay, following mini-column extraction, in samples collected in 2006 and 2007. Ages of the bears were known or determined by cementum annuli. Mean(SD) 25(OH)D was greater (p=0.003) during winter [24.9(15.7)ng/ml, n=39] than spring [14.1(9.2)ng/ml, n=16]. Mean(SD) calcitriol was greater (p=0.048) during spring [103.09(59.28)pg/ml, n=15] than winter [71.97(46.87)pg/ml, n=39]. In hibernating bears, calcitriol correlated positively with age (r2=0.39, p<0.001), and age-adjusted calcitriol correlated negatively with serum calcium adjusted for albumin (r2=0.19, p=0.013, n=31). Hibernating bears in this study, estimated to have been in the winter den for 8 to 18 weeks, demonstrated continued production of calcitriol. Serum levels were substantially less than during the active season, and the correlation with age suggests that functional renal mass may be a determinant of calcitriol production during ursine hibernation. The negative correlation of calcitriol with serum calcium suggests that calcitriol may be important in suppressing unloading-induced bone resorption in hibernating bears.

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P 36. WATERBIRD MORTALITY FROM BOTULISM TYPE C IN NAMDONG WATER RESERVOIRS

J.H. Shin, Ecology Research Department, National Institute of Environmental Research, Incheon 404-708, Korea; S. H. Byun, Avian Disease Laboratory, College of Veterinary Medicine, Chungbuk National University, Cheongju 361-763, Korea; J.Y. Yi, Ecology Research Department, National Institute of Environmental Research, Incheon 404-708, Korea; N.R. Shin, Center for Infectious Diseases, National Institute of Health, Korea Centers for Disease Control and Prevention, Seoul 122-701, Korea; I.P. Mo, Avian Disease Laboratory, College of Veterinary Medicine, Chungbuk National University, Cheongju 361-763, Korea; J.H. Kim, H.M. Chung, Ecology Research Department, National Institute of Environmental Research, Incheon 404-708, Korea

Presenting author: Shin, Heong-Wha

Summary: We describe an outbreak of avian type C botulism at Namdong water reservoirs in Incheon, South Korea.

From October 2008 to March 2009, high mortality of waterbirds occurred in the Namdong water reservoirs used for retarding basin and drainage of treated sewage located in Incheon. These sites are important habitat of migratory waterbirds and are surrounded by industrial complexes and reclaimed land for city development. The clinical signs of the sick birds were observed in situ and recorded on photographs. Moribund birds were captured manually and blood was taken from either heart or wing vein. Fourteen live birds with paralysis and 53 carcasses were collected. After each necropsy, egg inoculation test, RT-PCR and direct bacterial culture were performed for detection of avian influenza and avian cholera. Sera, gastric fluids, small intestines, and maggots from the carcasses were tested for botulinum toxin type C. The presence of botulinum toxin in the animal specimens was determined by the mouse bioassay. Histologically, no specific lesions presenting the causes of death were observed in any of the tissues examined. Two low pathogenic avian influenza viruses were isolated from Common Teals. Type C neurotoxin was directly detected by a mouse bioassay in animal specimens. This case in the Namdong water reservoirs is the largest outbreak caused by type C botulinum ever observed in Korea so far. Approximately 2,500 dead wild waterbirds were counted. Most of affected birds belonged to filter-feeding and dabbling ducks (96.3%). The botulinum type C toxins were detected from sera of Common Teal (Anas crecca), Pintail (Anas acuta) and Spot-billed Duck (Anas poecilorhyncha), maggots from carcasses and an intestinal culture supernatant. Also Low pathogenic avian influenza viruses were detected simultaneously.

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P 37. CHARACTERIZATION OF UPLAND GAMEBIRD FACILITIES IN THE UNITED STATES: POTENTIAL FOR HUMAN AND WILD AND DOMESTIC BIRD INTERACTIONS

Katharine E. Slota, Colorado State University, Dept. Environmental and Radiological Health Sciences, 1618 Campus Delivery, Colorado State University, Fort Collins, CO 80523, USA; Ashley E. Hill, Colorado State University, Dept. of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO 80523-1678, USA; Richard A. Bowen, Colorado State University, Dept. of Biomedical Sciences Colorado State University, Fort Collins, CO 80523-1680, USA; Thomas J. Keefe, Colorado State University, Dept. Environmental and Radiological Health Sciences, 1618 Campus Delivery, Colorado State University, Fort Collins, CO 80523, USA; Kristy L. Pabilonia, Colorado State University, Dept. Microbiology, Immunology, Pathology, College of Veterinary Medicine and Biomedical Science, Colorado State University, Fort Collins, CO 80523-1644, USA

Presenting author: Pabilonia, Kristy

Summary: Our study describes common practices associated with raising and releasing upland gamebirds in the United States and the potential implications of such practices on human, wild, and domestic bird health.

Due to the large numbers of birds being raised and released, upland gamebird facilities may represent an increased opportunity for interactions between domestic birds and humans and wildlife. Growth of this industry may have implications for wildlife disease events and the examination of common practices used by such facilities is important. We constructed a list of persons that held current, state-issued permits to keep, breed, or release upland gamebirds in the United States. We surveyed 218 randomly selected permit holders over the telephone. Surveys consisted of 61 questions and addressed bird movement, health, flock/release environment, and common practices used by release facilities. Facilities were stratified into three types based on self reported purposes for permits. Differences were identified between commercial, release, and hobby type facilities. The median number of birds released in the past 12 months was 600 (IQR 178.5-2500). Pheasant (Phasianus sp.) was the most frequent type of bird released but quail were released in the greatest number. Release facilities estimated a median of 65% of released pheasant and quail were actually harvested. Upland gamebird facilities promoted opportunities for interactions between wild birds and domestic birds. Permit holders reared birds outdoors and observed wild birds in their flock area. Permit holders employed practices that attract wild birds such as placing feeders on release land. Keeping or releasing waterfowl in concurrence with upland gamebirds was not uncommon. Encouraging disease surveillance for facilities that rear birds for release may help reduce the potential for disease transmission between domestic and wild birds.

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Cooperative funding from United States Center for Disease Control and Prevention; State Wildlife Agencies; Colorado State University Veterinary Diagnostic Lab Staff; Colorado Avian Disease Surveillance Upland Gamebird Clients; North American Gamebird Association National Poultry Improvement Plan; Texas Gamebird Association
P 38. OUTBREAK OF SEPTICEMIC SALMONELLOSIS CAUSED BY SALMONELLA HESSAREK IN MIGRATING SONG THRUSHES (TURDUS PHILOMELOS)

R. Velarde, Servei d’Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain; C. Porroero, Centro de Vigilancia Sanitaria Veterinaria (VISAVET), Universidad Complutense, Avenida Puerta de Hierro s/n, 28040 Madrid, Spain; I. Marco, Servei d’Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain; M. García, S. Téllez, L. Domínguez, Centro de Vigilancia Sanitaria Veterinaria (VISAVET), Universidad Complutense, Avenida Puerta de Hierro s/n, 28040 Madrid, Spain; R. Aymí, Institut Català d’Ornitologia, Museu de Ciències Naturals, Passeig Picasso, s/n, 08003 Barcelona, Spain; S. Lavín, Servei d’Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain

Presenting author: Marco, Ignasi

Summary: To date Salmonella hessarek has only been reported causing outbreaks in starlings. A new host-adaptation of the serotype S. hessarek is suspected since the disease almost exclusively affected song thrushes.

Outbreaks of infection by Salmonella hessarek have been reported only in starlings (Sturnus vulgaris), in Israel in 1977 and during the winter of 2005 in Spain and Italy. From February to March of 2009, an outbreak of septicemic salmonellosis affected mostly migrating Song Thrushes (Turdus philomelos) over a large area of the northeast of Spain. Necropsies from thirty dead birds were performed and routine histopathological studies were done. Spleens samples taken for microbiological culture were processed as follow. Culture of bacteria was made according to ISO 6579:2002 Annex D which is the method recommended by the EU’s CRL (European Union Community Reference Laboratory) for Salmonella. Colonies of presumptive Salmonella were subcultured on Columbia 5% sheep blood agar (bioMérieux) and incubated for 24h ± 3h at 37°C ± 1°C. Identification of isolates were confirmed as Salmonella spp. by a commercially available biochemical method: Enterotube TM II (BD BBL TM). Serological typing was performed based on the Kauffmann-White scheme. Birds were found sick or dead in open fields or roads. A poor body condition, marked splenomegaly with microscopic multifocal necrosis with fibrin, pectoral multifocal myonecrosis, and thrombosis with intravascular extracellular and intracellular aggregates of Gram-negative bacteria were the main findings. Fifteen isolates of Salmonella recovered from the spleen samples were identified as Salmonella enterica ssp. enterica serotype hessarek. This is the first time S. hessarek has been associated to an outbreak of salmonellosis in Song Thrushes. The source of this epizootic remains poorly understood. Outbreaks of infection covering large geographical areas, as in our case, are difficult to explain. A new host-adaptation of the serotype is suspected since the disease almost exclusively affected this species.
P 39. STAGES OF FETAL DEVELOPMENT IN CALIFORNIA SEA LIONS (ZALOPHUS CALIFORNIANUS)

Elizabeth A. Wheeler, Frances M.D. Gulland, Denise J. Greig, The Marine Mammal Center, 2000 Bunker Road, Sausalito, CA 94965, USA; Tracey Goldstein, VM: Wildlife Health Center, University of California, Davis, CA 95616, USA

Presenting author: Wheeler, Elizabeth

Summary: Documentation of fetal developmental stages in California sea lions is important for characterizing potential risks from exposure to toxins, contaminants, and infectious diseases. Abortion and premature parturition are common in California sea lions (Zalophus californianus), however limited data on fetal development makes it difficult to evaluate their etiology. A better understanding of fetal stages may aid in evaluating exposure risks to infectious and non-infectious insults in the developing fetus. Opportunistic examination of fetal development stages was performed by measuring, weighing and photo-documenting aborted and dead in-utero fetuses from stranded dams admitted to The Marine Mammal Center over an 11 year period. Admission spanned the full nine month gestation period, following a three month embryonic diapause. Whole body weights, standard lengths, axillary girths, and fetal features were recorded and photographs were taken of developing characteristics (whiskers, nails, hair growth). Variation in fetal features was compared across the three trimesters and length and growth modeled over time. Seventy-six fetuses were examined and compared from 1998 through early 2009: 6 in the first trimester (October – December), 20 in the second trimester (January – March), and 50 in the third trimester (April – June). Variations during the three trimesters, based on weighing and measuring individuals will be graphed and evaluated. Known peak pupping estimates on Channel Island rookeries (June 15th), and the presence of synchronized parturition and delayed implantation allow predictions of trimester stages. By documenting this variation in growth and fetal development, we hope to better characterize these developmental stages. This allows the potential for predicting effects and assessing risk to fetuses from exposure to toxins, contaminants, and infectious diseases, as well as extrapolating actual implantation dates.
P 40. DESCRIPTION OF NOVEL BABESIA SPECIES AND ASSOCIATED LESIONS FROM COMMON MURRES (URIA AALGE) FROM CALIFORNIA

Michael J. Yabsley, D.B. Warnell School of Forestry and Natural Resources and Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens, GA 30602, USA; Ellis Greiner, Department of Infectious Diseases and Pathology, College of Veterinary Medicine, University of Florida, Gainesville, FL 32610, USA; Florina S. Tseng, Tufts Cummings School of Veterinary Medicine, North Grafton, MA 01536, USA; Michael M. Garner, Northwest ZooPath, 654 West Main, Monroe, WA 98296, USA; Robert W. Nordhausen, Electron Microscopy Laboratory, California Animal Heath and Food Safety Laboratory, Davis, CA 95616, USA; Michael H. Ziccardi, Wildlife Health Center, School of Veterinary Medicine, University of California, Davis, CA 95616, USA; Dori L. Borjeson and Shannon Zabolotzky, Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California, Davis, CA 95616, USA

Presenting author: Yabsley, Michael

Summary: A novel, potentially pathogenic, Babesia species is described from common murres from California.

Despite being common among mammals, there are few descriptions of piroplasms in avian hosts. Currently, there are only 14 valid avian Babesia species described from 14 avian families. In this report, a novel Babesia species is described from 3 common murres (also known as common guillemots) (Uria aalge) from California. In 1997, a common murre was received at the International Bird Rescue Research Center in Berkeley, California. In July and August 2007, two adult common murres presented to the San Francisco Bay Oiled Wildlife Care and Education Center in Fairfield, California, one with a history of emaciation and hyperpnea and the other presented completely covered in dark oil, but was otherwise normal on initial physical exam. Blood smears from these three birds revealed infection with intraerythrocytic parasites. To characterize the piroplasms, regions of the 18S and 5.8S rRNA genes and the ITS-1 and ITS-2 regions were sequenced. This is the first report of Babesia sp. from alcid birds (Order Charadriiformes). Histologic lesions were observed in one bird. Genetically, this Babesia was most similar to B. poelea with 99.3%, 85.2%, 97.4%, and 89.1% similarity in the 18S rRNA, ITS-1, 5.8S rRNA, and ITS-2 regions, respectively. Only one other Babesia species has been reported from charadriiforms, i.e., B. bennetti in yellow-billed gulls. The murre Babesia, although morphologically similar to B. bennetti, can be differentiated in its possession of smaller, on average, round and amoeboid forms compared with B. bennetti. Furthermore, 18S rRNA gene sequences from these 2 species were considerably different. Genetically, the murre Babesia was most similar to B. poelea, but can be differentiated in having numerous nucleotide substitutions.

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# Program at a Glance

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<td>Victoria Room</td>
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<td><strong>5:30 – 7:00</strong></td>
<td>Student Mentor Kick-off</td>
<td>Semiahmoo Ballroom</td>
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<td><strong>7:00 - 10:00</strong></td>
<td>Welcome Reception</td>
<td>Semiahmoo Ballroom</td>
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<td><strong>8:30 – 10:00</strong></td>
<td>Wildlife Health from Land to Sea: Impacts of a Changing World</td>
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<td><strong>10:30 – 12:00</strong></td>
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<td>Semiahmoo Ballroom</td>
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<td><strong>4:00 - 4:45</strong></td>
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<td><strong>4:45 - 5:00</strong></td>
<td>WDA 2010 Argentina</td>
<td>Semiahmoo Ballroom</td>
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<tr>
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<td><strong>6:00 – 7:00</strong></td>
<td>AAWV Business Meeting</td>
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<td></td>
<td><strong>6:00 - 7:00</strong></td>
<td>CAZVW Business Meeting</td>
<td>Salt Spring Saturna</td>
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<td></td>
<td><strong>11:45</strong></td>
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