56th Annual
Wildlife Disease Association Conference

August 12-17, 2007
YMCA of the Rockies
Estes Park, Colorado

Program & Abstracts
THANK YOU TO OUR SPONSORS

National Park Service
Colorado Division of Wildlife
USDA/APHIS – Wildlife Services, Wildlife Health Program

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E.I. Medical Imaging
International Wildlife Health Institute
PneuDart
Safe-Capture International
C. W. Schiller Wildlife Artistry & Bronze Sculpting
Jax Farm & Ranch
Sportsman’s Warehouse
Trail Ridge Winery
New Belgium Brewing Company
Odell Brewing Company
Coopersmiths Pub & Brewery
Estes Park Brewery
WDA 2007 OFFICERS & COUNCIL

President ........................................................................................................Scott Wright
Vice-President .............................................................................................Michael Miller
Secretary......................................................................................................Margaret Wild
Treasurer ..................................................................................................... Carol Meteyer
Past-President ...........................................................................................Torsten Mörner
Executive Manager...........................................................................................Ed Addison
Journal Editor ......................................................................................Elizabeth Howerth
Journal Editor ........................................................................................David Stallknecht
Website Editor......................................................................................... Michael Ziccardi
Supplement Editor .......................................................................................... Pauline Nol

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Markus Peterson                   Marcela Uhart                                  Dolores Gavier-Widén

Student Member of Council
Leslie Reperant

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Africa .................................................................Elizabeth Wambwa
Australasia..............................................................Pam Whiteley
Europe..............................................................................Dolores Gavier-Widén
Nordic...............................................................Erik Ågren
Wildlife Veterinarian .......................Kirsten Gilardi
2007 PLANNING COMMITTEE

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Margaret Wild
Michael Miller
Jenny Powers

Organizing Committee
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Laurie Baeten  Bruce Heath  Jack Rhyany  Mary Kay Watry
Lynn Creekmore  Vicki Jameson  Bridget Schuler  Mary Wright
Terry Creekmore  Bill Lance  Terry Spraker  Lisa Wolfe
Tom DeLiberto  Bob McLean  Andrea Torres  Bruce Wunder
Colleen Duncan  Pauline Nol  Sue VandeWoude

Session Moderators & Workshop Chairs
Laurie Baeten  Jerome Freier  Jack Rhyany  Andrea Torres
Todd Cornish  Vicki Jameson  Philip Rice  Sue VandeWoude
Lynn Creekmore  Emily Jenkins  Shawn Riley  Kurt VerCauteren
Jack Cully  Bill Lance  Tonie Rocke  Mary Kay Watry
Josh Dein  Bob McLean  Jeff Root  Margaret Wild
Tom DeLiberto  Michael Miller  Chris Soderquist  Lisa Wolfe
Matthew Farnsworth  Pauline Nol  Terry Spraker  Mary Wright
Alan Franklin  Jenny Powers  Dick Stroud  B. Zimmerman

Local Color
History of Estes Park by Billy Ward from the Stanley Hotel
The story of Jack Slade and Virginia Dale by Jack Rhyan
An overview of the geology of Rocky Mountain National Park by Rainey Kreis, Education Ranger at Rocky Mountain National Park
Fortress Rocks by Jack Rhyan
Ghosts of the Stanley Hotel by Billy Ward and Other local Stories by Jack Rhyan
Brief histories of WDA and its awards by Ed Addison, Todd Cornish, and others

Conference Supporters
Mike Smith, Cami Sebern, Dan Deblasio and YMCA of the Rockies staff; Laura Tanaka, Helen VanDeMark, Janelle Armentrout, and Colorado State University Conference Services staff; Mark Hansen, Margie Michaels, Michelle Gallagher, Danny Martin, Debi Reep, Vaughn Baker and Rocky Mountain National Park; Sandy Lockman, Alice Johnson and Lake Shore Lodge; Baxter Black; Ray Devera and Jansport

Conference logo by Terry Creekmore
EXHIBITORS
Visit exhibitors in the Hobbs & Sweet rooms inside the Walter G. Ruesch Auditorium
Monday/Tuesday 8:00a–5:00p; Wednesday 8:00a–12:00p

Wildlife Pharmaceuticals
ChemBio Diagnostic Systems
Stevan Logsdon Jewelry
American Association of Wildlife Veterinarians
Chemical Immobilization Data Standardization Initiative

CONTINUING EDUCATION

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

See registration desk for continuing education forms
WDA 2007 DETAILED CONFERENCE PROGRAM

Welcome Reception - Sunday, August 12
A welcome reception Sunday evening in the YMCA Walnut Dining Room will include light desserts as well as complimentary wine and beer. This will be an opportunity to renew old acquaintances, make new ones, and for mentors to meet their students. In keeping with recent tradition, there will be a student/mentor only reception from 7:00p – 7:30p and open to all registrants from 7:30p – 10:00p.

Picnic - Monday, August 13
The picnic on Monday evening will take place at the Upper Cookout on the grounds of the YMCA, along with the meal will be complimentary beer. The picnic will provide an opportunity for informal interaction among registrants in an outdoor setting. The Hi-Beams, a local band, will entertain us for the evening. Safe-Capture International will sponsor a fun competition to test your field skills in wildlife immobilization-and to find that next generation of wildlife experts! Dress in layers for the cool and ever-changing weather, and bring tennis shoes for a potential softball or volleyball game.

Auction - Tuesday, August 14
The auction on Tuesday evening, held in the Walter G. Ruesch Auditorium is likely to be a major source of entertainment at the meeting and will include hors d’oeuvres and complimentary wine and beer. This year, proceeds from the auction will be donated to the Thorne - Williams Memorial Award Fund.

Field Trips - Wednesday, August 15 (12:30p-5:00p)
- A tour of the local (Fort Collins) wildlife research facilities
- Rocky Mountain National Park activities:
  - High-country hiking
  - Family hiking
  - Wildflower hike
  - History of Rocky Mountain National Park and Estes Park
  - Driving tour of Rocky Mountain National Park
  - Elk viewing tour in Rocky Mountain National Park

Banquet - Thursday, August 16
The conference banquet, including a cash bar will occur at the Lake Shore Lodge in Estes Park. Highlights, in addition to the meal featuring trout and bison, will include presentations of major WDA awards, as well as entertainment from Baxter Black cowboy poet and humorist. WDA awards include presentation of the Distinguished Service Award, the Emeritus Award and the infamous Duck Award to the unfortunate recipient recognized to have made the biggest blunder at the conference! New to this year, the first Tom Thorne and Beth Williams Memorial Award will be presented. Transportation to the banquet will be provided from the YMCA.
## SUNDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:30a</td>
<td>Editorial Board Meeting</td>
<td>Location TBA 8:30a-12:00p</td>
</tr>
<tr>
<td>12:00p</td>
<td>Lunch (Editorial Board &amp; Council)</td>
<td></td>
</tr>
<tr>
<td>1:00p</td>
<td>WDA Council Meeting</td>
<td>Location TBA 1:00p-5:00p</td>
</tr>
<tr>
<td>3:00p</td>
<td>Registration</td>
<td>Walter G. Ruesch Auditorium 3:00p-8:00p</td>
</tr>
<tr>
<td>7:00p</td>
<td>Student/Mentor Reception</td>
<td>Walnut Dining Room 7:00p-7:30p</td>
</tr>
<tr>
<td>7:30p</td>
<td>Welcome Reception</td>
<td>Walnut Dining Room 7:30p-10:00p</td>
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## MONDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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</thead>
<tbody>
<tr>
<td>7:30a</td>
<td>Registration</td>
<td>Walter G. Ruesch Auditorium 7:30a-4:00p</td>
</tr>
<tr>
<td>8:00a</td>
<td>Coffee</td>
<td>Walter G. Ruesch Auditorium</td>
</tr>
<tr>
<td>8:30a</td>
<td>Conference Welcome</td>
<td>Walter G. Ruesch Auditorium</td>
</tr>
</tbody>
</table>

### 8:45A-10:00A ECOLOGY OF WILDLIFE DISEASES

**CARLTON HERMAN FOUNDERS FUND LECTURE**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:45a</td>
<td>André A. Dhondt</td>
<td>[1] MYCOPLASMAL CONJUNCTIVITIS IN HOUSE FINCHES: HOST &amp; DISEASE DYNAMICS IN THE INTRODUCED &amp; NATIVE RANGE OF THE HOST</td>
</tr>
<tr>
<td>9:45a</td>
<td>Michael Bull</td>
<td>[4] CLIMATE CHANGE &amp; THE IMPACTS ON TICK-LIZARD INTERACTIONS &amp; HEMOGREGARINE TRANSMISSION IN AUSTRALIA</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Time</th>
<th>Break, Visit Exhibitors (Hobbs &amp; Sweet Rooms in Walter G. Ruesch Auditorium)</th>
</tr>
</thead>
</table>

### 10:30A-11:45A ECOLOGY OF WILDLIFE DISEASES, CONTINUED

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30a</td>
<td>Andy Dobson</td>
<td>[5] THE TRANSMISSION DYNAMICS OF CDV IN SERENGETI LIONS: ESTIMATING TRANSMISSION &amp; MODELS FOR MULTI-HOST DYNAMICS</td>
</tr>
<tr>
<td>11:00a</td>
<td>Stephanie F. Gebert</td>
<td>[7] A LONGITUDINAL STUDY OF FACTORS AFFECTING HELMINTH PREVALENCE IN FIELD VOLES IN NORTHUMBERLAND, UK</td>
</tr>
<tr>
<td>11:15a</td>
<td>Emily Jenkins</td>
<td>[8] ECOLOGY OF DISEASES OF COLONY NESTING BIRDS IN SASKATCHEWAN, CANADA</td>
</tr>
<tr>
<td>11:30a</td>
<td>Karoun H. Bagamian</td>
<td>[9] A MANIPULATIVE EXPERIMENT TO MONITOR TRANSMISSION OF SIN NOMBRE HANTAVIRUS IN DEER MOUSE POPULATIONS UNDER NATURAL FIELD CONDITIONS</td>
</tr>
</tbody>
</table>
## MONDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>11:45a</td>
<td>Introduction of the Tom Thorne &amp; Beth Williams Award</td>
</tr>
<tr>
<td>12:00p</td>
<td>Lunch Break</td>
</tr>
<tr>
<td>1:00p-2:45p</td>
<td><strong>Sociopolitical Challenges of Wildlife Disease Management</strong></td>
</tr>
<tr>
<td>1:00p</td>
<td>Daniel J. Decker</td>
</tr>
<tr>
<td>1:15p</td>
<td>Terry J. Kreeger</td>
</tr>
<tr>
<td>1:30p</td>
<td>Ken Kingdon</td>
</tr>
<tr>
<td></td>
<td>[12] Challenges &amp; successes of managing bovine tuberculosis in a multi-jurisdictional environment in the Riding Mountain National Park region, Manitoba, Canada</td>
</tr>
<tr>
<td>1:45p</td>
<td>Marcela Uhart</td>
</tr>
<tr>
<td>2:00p</td>
<td>Alonso Aguirre</td>
</tr>
<tr>
<td></td>
<td>[14] The effects of species diversity on directly transmitted diseases</td>
</tr>
<tr>
<td>2:15p</td>
<td>Edward M. Addison</td>
</tr>
<tr>
<td>2:30p</td>
<td>Shawn J. Riley</td>
</tr>
<tr>
<td></td>
<td>[16] A learning laboratory to promote integration of insights from biological &amp; human dimensions for wildlife disease management</td>
</tr>
<tr>
<td>2:45p-3:45p</td>
<td><strong>Poster Session One [100-130] (see pg. 68) &amp; Break</strong></td>
</tr>
<tr>
<td>3:45p-5:00p</td>
<td><strong>Managing Wildlife Diseases</strong></td>
</tr>
<tr>
<td>3:45p</td>
<td>Craig Stephen</td>
</tr>
<tr>
<td>4:15p</td>
<td>Hamish McCallum</td>
</tr>
<tr>
<td></td>
<td>[18] Managing facial tumour disease in the Tasmanian devil: A disease suppression trial</td>
</tr>
<tr>
<td>4:30p</td>
<td>Roni King</td>
</tr>
<tr>
<td></td>
<td>[19] A model for optimizing the application of oral rabies vaccination in Israel, based on red fox population spatial dynamics</td>
</tr>
<tr>
<td>4:45p</td>
<td>Daniel M. Tompkins</td>
</tr>
<tr>
<td></td>
<td>[20] Orally delivered bacille Calmette-Guérin (BCG) vaccine protects wild free-living brushtail possums against bovine tuberculosis</td>
</tr>
<tr>
<td>5:00p</td>
<td>AAWV member meeting</td>
</tr>
<tr>
<td></td>
<td>Walter G. Ruesch Auditorium 5:00p–6:00p</td>
</tr>
<tr>
<td>6:00p</td>
<td>Picnic Dinner</td>
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<td></td>
<td>Upper Cookout picnic area 6:00p–10:00p</td>
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<tr>
<td>Time</td>
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</tr>
<tr>
<td>7:30a</td>
<td>Prayer Breakfast</td>
</tr>
<tr>
<td>7:30a</td>
<td>Registration</td>
</tr>
<tr>
<td>8:00a</td>
<td>Coffee</td>
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</tbody>
</table>

### 8:30-10:00 Managing Wildlife Diseases, Continued

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>8:30a</td>
<td>Marc Artois</td>
<td>[21] Lessons learned from highly pathogenic avian influenza in Europe</td>
</tr>
<tr>
<td>8:45a</td>
<td>Kimberlee Beckmen</td>
<td>[22] Managing the adverse impacts of the biting dog louse on wolves in Alaska</td>
</tr>
<tr>
<td>9:00a</td>
<td>Victoria Patrek</td>
<td>[23] The effects of supplemental feeding on stress levels in elk</td>
</tr>
<tr>
<td>9:30a</td>
<td>Jack Cully</td>
<td>[25] Spatial dynamics of plague in three black-tailed prairie dog complexes</td>
</tr>
<tr>
<td>9:45a</td>
<td>Tonie E. Rocke</td>
<td>[26] Evidence of enzootic plague impacts on black-footed ferret survival in Montana</td>
</tr>
</tbody>
</table>

### 10:00a Break & Visit Exhibitors (Hobbs & Sweet Rooms in Walter G. Ruesch Auditorium)

### 10:30a–12:00p Terry Amundson Award Student Presentations

#### WDA Graduate Student Research Recognition Award Winner

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30a</td>
<td>Shelly Lachish</td>
<td>[27] Using CMR models to detect disease impacts &amp; patterns of infection in a Tasmanian devil population affected by devil facial tumour disease</td>
</tr>
<tr>
<td>10:45a</td>
<td>Justin D. Brown</td>
<td>[28] Comparative susceptibility of waterfowl &amp; gulls to highly pathogenic avian influenza H5N1 virus</td>
</tr>
<tr>
<td>11:00a</td>
<td>Rebecca N. Dailey</td>
<td>[29] Tumbleweed shield lichen (Xanthoparmelia chlorochroa) toxicity</td>
</tr>
<tr>
<td>11:15a</td>
<td>Julian Drewe</td>
<td>[30] Establishing the role of intra-specific social interactions &amp; social networks in the transmission of tuberculosis within a wild animal population</td>
</tr>
<tr>
<td>11:30a</td>
<td>David R. Edmunds</td>
<td>[31] Survival rates &amp; causes of mortality of chronic wasting disease positive &amp; negative white-tailed deer in Wyoming</td>
</tr>
<tr>
<td>11:45a</td>
<td>Christina Faust</td>
<td>[32] Influence of bivalves on the persistence of avian influenza virus in water</td>
</tr>
</tbody>
</table>

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<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>12:00p</td>
<td>Lunch Break</td>
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</tbody>
</table>
# TUESDAY

## 1:00p–2:30p Terry Amundson Award Student Presentations, Continued

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>1:00p</td>
<td>Richard W. Gerhold</td>
<td><strong>[33] Identification of Cryptic Species in the Trichomonas Gallinae</strong> Morphological Complex by Molecular Characterization</td>
</tr>
<tr>
<td>1:15p</td>
<td>Stephanie S. Godfrey</td>
<td><strong>[34] Social Connectivity and Parasite Transmission in Populations of a Territorial Reptile, The Tuatara</strong></td>
</tr>
<tr>
<td>1:45p</td>
<td>Caroline Millins</td>
<td><strong>[36] Wild Bird Surveillance for Detection of West Nile Virus Activity in Rural Areas of Saskatchewan, Canada</strong></td>
</tr>
<tr>
<td>2:00p</td>
<td>Ryan J. Monello</td>
<td><strong>[37] Biotic &amp; Abiotic Predictors of Tick (Dermacentor Variabilis) Abundance &amp; Engorgement on Free-Ranging Raccoons</strong></td>
</tr>
</tbody>
</table>

## 2:30p–3:30p Student Poster Presentations [131-159] (see pg. 86) & Break

## 3:30p–5:00p Terry Amundson Award Student Presentations, Continued

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>3:30p</td>
<td>Kris Murray</td>
<td><strong>[39] Does Chytridiomycosis Still Kill Frogs 30 Years After Invasion &amp; Declines?</strong></td>
</tr>
<tr>
<td>3:45p</td>
<td>Nicole Nemeth</td>
<td><strong>[40] The Effects of West Nile Virus on Raptors at a Rehabilitation Facility in Colorado</strong></td>
</tr>
<tr>
<td>4:00p</td>
<td>Paul T. Oesterle</td>
<td><strong>[41] Experimental Infection of Cliff Swallows with Varying Doses of West Nile Virus</strong></td>
</tr>
<tr>
<td>4:15p</td>
<td>Leslie A Reperant</td>
<td><strong>[42] Red Foxes Are Susceptible to Infection with a Swan Isolate of Highly Pathogenic Avian Influenza H5N1 Virus</strong></td>
</tr>
<tr>
<td>4:30p</td>
<td>Amanda Jo Williams</td>
<td><strong>[43] Changes in Immunocompetence of the Gray Catbird During an Experimental West Nile Virus Infection</strong></td>
</tr>
<tr>
<td>4:45p</td>
<td>Carin Kistler Williams</td>
<td><strong>[44] The Effects of Aflatoxin on Three Dove Species</strong></td>
</tr>
</tbody>
</table>

## 5:00p WDA Business Meeting Walter G. Ruesch Auditorium 5:00p–6:00p

## 7:00p Auction Walter G. Ruesch Auditorium 7:00p–10:00p
### Wednesday

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
<th>Details</th>
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<tbody>
<tr>
<td>7:30a</td>
<td>Registration</td>
<td>Walter G. Ruesch Auditorium</td>
<td>7:30a-12:00p</td>
</tr>
<tr>
<td>8:00a</td>
<td>Coffee</td>
<td>Walter G. Ruesch Auditorium</td>
<td></td>
</tr>
<tr>
<td><strong>8:30a-10:00a Concurrent Session - Avian Species</strong> (Walter G. Ruesch Auditorium)</td>
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<tr>
<td>8:30a</td>
<td>Catherine Soos</td>
<td></td>
<td>AVIAN CHOLERA IN CANADA’S EASTERN ARCTIC: EMERGENCE OF AN OLD DISEASE IN A NEW ENVIRONMENT</td>
</tr>
<tr>
<td>8:45a</td>
<td>Frederick A. Leighton</td>
<td></td>
<td>EPIDEMIC MORTALITY IN DOUBLE-CRESTED CORMORANTS AND THE “REVENGE OF THE TREES” HYPOTHESIS</td>
</tr>
<tr>
<td>9:00a</td>
<td>Charles R. Brown</td>
<td></td>
<td>BIRD MOVEMENT PREDICTS BUGGY CREEK VIRUS INFECTION IN INSECT VECTORS</td>
</tr>
<tr>
<td>9:15a</td>
<td>Jennifer C. Owen</td>
<td></td>
<td>EFFECTS OF MIGRATORY STRESS &amp; TESTOSTERONE ON THE RECRUDESCENCE OF LATENT WEST NILE VIRUS INFECTIONS IN THE GRAY CATBIRD</td>
</tr>
<tr>
<td>9:30a</td>
<td>Colin Gillin</td>
<td></td>
<td>PRELIMINARY FINDINGS OF LONG-BILLED HAWK SYNDROME IN OREGON RED-TAILED HAWKS</td>
</tr>
<tr>
<td>9:45a</td>
<td>Mark L. Drew</td>
<td></td>
<td>WEST NILE VIRUS IN IDAHO: PUBLIC &amp; GOVERNMENT RESPONSE TO MORTALITY IN WILDLIFE, HORSES &amp; HUMANS IN 2006</td>
</tr>
<tr>
<td><strong>8:30a-10:00a Concurrent Session - Terrestrial Carnivores</strong> (Wind River)</td>
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<tr>
<td>8:30a</td>
<td>Richard N. Brown</td>
<td></td>
<td>PATHOGENS ASSOCIATED WITH FISHER POPULATIONS IN NORTHERN CALIFORNIA</td>
</tr>
<tr>
<td>8:45a</td>
<td>Mourad W. Gabriel</td>
<td></td>
<td>PATHOGENS ASSOCIATED WITH MESOCARNIVORES THAT ARE SYMPATRIC TO A POPULATION OF FISHERS IN NORTHERN CALIFORNIA</td>
</tr>
<tr>
<td>9:00a</td>
<td>Vic Simpson</td>
<td></td>
<td>INCREASING INTRASPECIFIC AGGRESSION IN AN EXPANDING OTTER POPULATION</td>
</tr>
<tr>
<td>9:15a</td>
<td>Rodrigo S. P. Jorge</td>
<td></td>
<td>LEISHMANIA SPP. IN WILD CARNIVORES CAPTURED IN THE PANTANAL, BRAZIL</td>
</tr>
<tr>
<td>9:30a</td>
<td>Nadine Lamberski</td>
<td></td>
<td>PREVALENCE OF SELECTED INFECTIOUS DISEASES IN BLACK-FOOTED CATS &amp; SYMPATRIC CARNIVORES IN THE NORTHERN CAPE: PRELIMINARY RESULTS</td>
</tr>
<tr>
<td>9:45a</td>
<td>Melody E. Roelke</td>
<td></td>
<td>CLINICAL &amp; PATHOLOGICAL CONSEQUENCES OF FELINE IMMUNODEFICIENCY VIRUS INFECTION IN WILD AFRICAN LIONS IN BOTSWANA</td>
</tr>
<tr>
<td>10:00a</td>
<td>Break &amp; Visit Exhibitors</td>
<td>Hobbs &amp; Sweet Rooms in Walter G. Ruesch Auditorium</td>
<td></td>
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</tbody>
</table>
## 10:30a-12:00p Concurrent Session - Terrestrial Ungulates (Walter G. Ruesch Auditorium)

<table>
<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>10:30a</td>
<td><em>E. Frances Cassirer</em></td>
<td>[57] Biochemical &amp; molecular characteristics of Pasteurella spp. &amp; Mannheimia spp. isolated from bighorn &amp; domestic sheep in Hells Canyon</td>
</tr>
<tr>
<td>10:45a</td>
<td><em>Scott C. Bender</em></td>
<td>[58] Scrapie genetic findings in a herd of desert bighorn sheep</td>
</tr>
<tr>
<td>11:00a</td>
<td><em>A. Christy Wyckoff</em></td>
<td>[59] Feral swine contact with domestic swine: Potential for disease transmission</td>
</tr>
<tr>
<td>11:15a</td>
<td><em>Christian Gortazar</em></td>
<td>[60] Bovine tuberculosis ecology in Doñana National Park, Spain: The role of wild ungulates as disease reservoirs in the last Iberian lynx strongholds</td>
</tr>
<tr>
<td>11:30a</td>
<td><em>Brett T. Elkin</em></td>
<td>[61] Description of an outbreak of tuberculosis &amp; subsequent epidemiological investigation in a captive breeding herd of wood bison</td>
</tr>
<tr>
<td>11:45a</td>
<td><em>John S. Nishi</em></td>
<td>[62] Lessons learned from the Hook Lake Wood Bison Recovery Project: Relevance &amp; application to the larger issue of northern diseased bison in Canada</td>
</tr>
</tbody>
</table>

## 10:30a-12:00p Concurrent Session - Carnivores & Rodents (Wind River)

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<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>10:30a</td>
<td><em>Mark W. Cunningham</em></td>
<td>[63] Epizootiology of generalized demodicosis in a Florida black bear population</td>
</tr>
<tr>
<td>10:45a</td>
<td><em>T. Winston Vickers</em></td>
<td>[64] Unusually high prevalence of ceruminous gland carcinomas in Channel Island foxes on Santa Catalina Island, California</td>
</tr>
<tr>
<td>11:00a</td>
<td><em>Nathan C. Nieto</em></td>
<td>[65] Evaluation of Sciurids as ecologically significant hosts for Anaplasma Phagocytophilum in California</td>
</tr>
<tr>
<td>11:15a</td>
<td><em>Pablo M. Beldomenico</em></td>
<td>[66] The dynamics of health in field vole populations: A haematological perspective</td>
</tr>
<tr>
<td>11:30a</td>
<td><em>Amy J. Kuenzi</em></td>
<td>[67] Sin Nombre virus (SNV) &amp; deer mice dynamics in a paired sylvan &amp; peridomestic population in Montana</td>
</tr>
<tr>
<td>11:45a</td>
<td><em>Tony Schountz</em></td>
<td>[68] Regulatory T cell-like responses in deer mice persistently-infected with Sin Nombre virus</td>
</tr>
</tbody>
</table>

### Special Events

- **12:00p**: Pick-up Sack Lunches  
  - Walter G. Ruesch Auditorium  
  - 12:00p-12:30p

- **12:30p**: Field Trips  
  - Various Locations  
  - 12:30p-5:00p
<table>
<thead>
<tr>
<th>Time</th>
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<th>Location</th>
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<tbody>
<tr>
<td>7:30a</td>
<td>Registration</td>
<td>Walter G. Ruesch Auditorium 7:30a-8:30a</td>
</tr>
<tr>
<td>8:00a</td>
<td>Coffee</td>
<td>Walter G. Ruesch Auditorium</td>
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</table>

### 8:30A-9:45A Concurrent Session - Parasitic Diseases (Walter G. Ruesch Auditorium)

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:30a</td>
<td>Michael J. Yabsley</td>
<td>NATURAL &amp; EXPERIMENTAL INFECTION OF WHITE-TAILED DEER WITH AN <em>EHRLICHA</em> SP. FROM THE UNITED STATES CLOSELY RELATED TO <em>EHRLICHA RUMINANTIUM</em></td>
</tr>
<tr>
<td>8:45a</td>
<td>I-M. Vilcins</td>
<td>DETECTING TICK-BORNE PATHOGENS IN AUSTRALIAN TICKS</td>
</tr>
<tr>
<td>9:00a</td>
<td>Susan Kutz</td>
<td>GIARDIA ASSEMBLAGE A: HUMAN GENOTYPE IN MUSKOXEN IN THE CANADIAN ARCTIC</td>
</tr>
<tr>
<td>9:15a</td>
<td>Jonas Malmsten</td>
<td>HAIR LOSS IN THE SCANDINAVIAN MOOSE POPULATION IN 2006-2007</td>
</tr>
<tr>
<td>9:30a</td>
<td>Soraya Naem</td>
<td>AN INVESTIGATION ON THE PARASITES OF OSTRICH BY SCREENING EGGS IN FECES, ISFAHAN, IRAN</td>
</tr>
</tbody>
</table>

### 8:30A-9:45A Concurrent Session - Eclectic Species (Wind River)

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:30a</td>
<td>Jamie Voyles</td>
<td>ELECTROLYTE DEPLETION &amp; OSMOTIC IMBALANCE IN AMPHIBIANS WITH CHYTRIDIOMYCOSIS</td>
</tr>
<tr>
<td>8:45a</td>
<td>Philip Ladds</td>
<td>PATHOLOGY OF YOUNG CAPTIVE CROCODILES</td>
</tr>
<tr>
<td>9:00a</td>
<td>Greta S. Aeby</td>
<td>ASPECTS OF THE EPIZOOTIOLOGY OF <em>ACROPORA</em> WHITE SYNDROME ON REEFS ACROSS THE INDO-PACIFIC OCEAN</td>
</tr>
<tr>
<td>9:15a</td>
<td>Thierry M. Work</td>
<td>DISTRIBUTION &amp; MORPHOLOGY OF GROWTH ANOMALIES IN <em>ACROPORA</em> FROM THE INDO-PACIFIC</td>
</tr>
<tr>
<td>9:30a</td>
<td>Valerie Shearn-Bochsler</td>
<td>SAXITOXIN POISONING AS A CAUSE OF MORTALITY IN COMMON TERNS DURING THE 2005 SEVERE HARMFUL ALGAL BLOOM OFF THE SOUTHERN NEW ENGLAND COAST</td>
</tr>
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9:45a–11:00a Poster Session Two [160-193] (see pg. 103) & Break
# THURSDAY

## 11:00a–12:00p Concurrent Session - Case Reports (Walter G. Ruesch Auditorium)

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:00a</td>
<td>Christopher A. Whitter</td>
<td>[79] Metastatic Carcinoid in a Wild Mountain Gorilla</td>
</tr>
<tr>
<td>11:15a</td>
<td>Maria C. Tosta</td>
<td>[80] Pasteurellosis in a Great Anteater</td>
</tr>
<tr>
<td>11:30a</td>
<td>Abelardo Morales</td>
<td>[81] Gastritis Ulceration Syndrome in <em>Pteronura brasiliensis</em> associated with <em>Helicobacter pylori</em></td>
</tr>
<tr>
<td>11:45a</td>
<td>Aleksija Neimanis</td>
<td>[82] Sheep-Associated Malignant Catarrhal Fever in Free-Ranging Moose in Saskatchewan, Canada</td>
</tr>
</tbody>
</table>

## 11:00a–12:00p Concurrent Session - Marine Species (Wind River)

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:00a</td>
<td>Tracey Goldstein</td>
<td>[83] The Role of the Biotoxin Domoic Acid in Reproductive Failure in California Sea Lions on San Miguel Island</td>
</tr>
<tr>
<td>11:15a</td>
<td>Ole Nielsen</td>
<td>[84] Isolation &amp; Preliminary Characterisation of a Morbillivirus Responsible for an Outbreak of Distemper in Seals from Maine</td>
</tr>
<tr>
<td>11:30a</td>
<td>Felicia B. Nutter</td>
<td>[85] Update on Northern Fur Seal Strandings Along the Central California Coast Since 1975</td>
</tr>
<tr>
<td>11:45a</td>
<td>Scott H. Loeffler</td>
<td>[86] Infection of Beef Cattle with <em>Mycobacterium pinnipedi</em> Due to Cattle Grazing in Coastal Areas in Close Contact with New Zealand Fur Seals – Two Cases Studies</td>
</tr>
</tbody>
</table>

**12:00p** LUNCH BREAK

## 1:00p–2:30p New Tools for Wildlife Disease Management

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:00p</td>
<td>Julie A. Blanchong</td>
<td>[87] Landscape Genetics &amp; the Spatial Distribution of Chronic Wasting Disease</td>
</tr>
<tr>
<td>1:45p</td>
<td>Andrea D. Phillott</td>
<td>[90] Infected <em>Litoria rheocola</em> Presenting Clinical Signs of Amphibian Chytridio-Mycosis Have Comparable Detectable QPCR Values to Infected, Aclinical Frogs</td>
</tr>
<tr>
<td>2:00p</td>
<td>Mark W. Atkinson</td>
<td>[91] Application of a Novel Virus Detection System in Rocky Mountain Bighorn Sheep in Montana</td>
</tr>
<tr>
<td>2:15p</td>
<td>Rachael Y. Dudaniec</td>
<td>[92] The Use of Microsatellites to Inform Future Management of a Deadly Fly Parasitising Darwin’s Finches, Galápagos Islands</td>
</tr>
</tbody>
</table>
### THURSDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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</thead>
<tbody>
<tr>
<td>2:30p</td>
<td>Preview of WDA 2008 Conference &amp; Passing of the Presidential Gavel</td>
</tr>
<tr>
<td>2:45p</td>
<td>Break</td>
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</tbody>
</table>

**3:15p–5:00p NEW TOOLS FOR WILDLIFE DISEASE MANAGEMENT, CONTINUED**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker &amp; Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>3:15p</td>
<td>Todd K. Shury [93] Preliminary Evaluation of Blood-Based Assays for the Diagnosis of Bovine Tuberculosis in Elk from the Riding Mountain National Park Region</td>
</tr>
<tr>
<td>3:30p</td>
<td>Kurt C. VerCauteren [94] Sentinel-Based Surveillance of Coyotes to Detect Bovine Tuberculosis in Michigan</td>
</tr>
<tr>
<td>4:00p</td>
<td>Pauline Nol [96] Immunologic Responses &amp; Protection in Elk Vaccinated with Brucella abortus Strain RB51 Over-Expressing SOD &amp; WboA &amp; Challenged with Virulent B. abortus</td>
</tr>
<tr>
<td>4:15p</td>
<td>Bonnie L. Raphael [97] Comparison of Different Methods of Administration of Canine Distemper Vaccine to African Wild Dogs</td>
</tr>
<tr>
<td>4:30p</td>
<td>Joseph K. Gaydos [98] Developing a Surgical Technique for Implanting Transmitters in Western Grebes</td>
</tr>
<tr>
<td>4:45p</td>
<td>F. Joshua Dein [99] An Introduction to Wildlife Disease Informatics</td>
</tr>
<tr>
<td>5:30p</td>
<td>Buses Depart for Banquet Walter G. Ruesch Auditorium 5:30p-5:45p</td>
</tr>
<tr>
<td>6:00p</td>
<td>Banquet Lake Shore Lodge, Estes Park 6:00p-10:00p</td>
</tr>
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### FRIDAY

<table>
<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>7:30a</td>
<td>Registration Walter G. Ruesch Auditorium 7:30a-8:30a</td>
</tr>
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**8:30a–11:30a Workshops**

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<thead>
<tr>
<th>Topic</th>
<th>Location</th>
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<tbody>
<tr>
<td>Spatial Epidemiology: Techniques &amp; Applications (see pg. 124)</td>
<td>Main Auditorium (WGRA)</td>
</tr>
<tr>
<td>Wildlife Forensics (see pg. 125)</td>
<td>Bilheimer/Dodge (WGRA)</td>
</tr>
<tr>
<td>New Field Anesthesia Techniques &amp; Drugs [194-198] (see pg. 126)</td>
<td>Hobbs (WGRA)</td>
</tr>
<tr>
<td>Learning Lab: A Wildlife Disease Managers' Model (see pg. 130)</td>
<td>Sweet (WGRA)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:30a</td>
<td>Lunch</td>
</tr>
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**12:00p–3:00p Workshops**

<table>
<thead>
<tr>
<th>Topic</th>
<th>Location</th>
</tr>
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<tbody>
<tr>
<td>Chronic Wasting Disease [199-207] (see pg. 131)</td>
<td>Main Auditorium (WGRA)</td>
</tr>
<tr>
<td>Avian Influenza [208-217] (see pg. 137)</td>
<td>Bilheimer/Dodge (WGRA)</td>
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<tr>
<td>Wildlife Disease Informatics [218] (see pg. 143)</td>
<td>Hobbs (WGRA)</td>
</tr>
<tr>
<td>Plague Ecology [219-220] (see pg. 144)</td>
<td>Sweet (WGRA)</td>
</tr>
<tr>
<td>3:00p Ice Cream Social</td>
<td>Walter G. Ruesch Auditorium 3:00p-3:30p</td>
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<td><strong>ECOLOGY OF WILDLIFE DISEASES</strong>&lt;br/&gt;Moderator: Michael Miller</td>
<td>pg. 16–20</td>
<td>[1–9]</td>
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<tr>
<td><strong>SOCIOPOLITICAL CHALLENGES OF WILDLIFE DISEASE MANAGEMENT</strong>&lt;br/&gt;Moderator: Margaret Wild</td>
<td>pg. 20–23</td>
<td>[10–16]</td>
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<tr>
<td><strong>MANAGING WILDLIFE DISEASES</strong>&lt;br/&gt;Moderator: Jenny Powers</td>
<td>pg. 24–28</td>
<td>[17–26]</td>
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<td><strong>TERRY AMUNDSON AWARD STUDENT PRESENTATIONS</strong>&lt;br/&gt;Moderator: Todd Cornish</td>
<td>pg. 29–37</td>
<td>[27–44]</td>
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<tr>
<td><strong>AVIAN SPECIES</strong>&lt;br/&gt;Moderator: Bob McLean</td>
<td>pg. 38–40</td>
<td>[45–50]</td>
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<td><strong>TERRESTRIAL CARNIVORES</strong>&lt;br/&gt;Moderator: Pauline Nol</td>
<td>pg. 41–43</td>
<td>[51–56]</td>
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<td><strong>TERRESTRIAL UNGULATES</strong>&lt;br/&gt;Moderator: Lisa Wolfe</td>
<td>pg. 44–46</td>
<td>[57–62]</td>
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<tr>
<td><strong>CARNIVORES &amp; RODENTS</strong>&lt;br/&gt;Moderator: Kurt VerCauteren</td>
<td>pg. 47–49</td>
<td>[63–68]</td>
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<tr>
<td><strong>PARASITIC DISEASES</strong>&lt;br/&gt;Moderator: Jack Rhyan</td>
<td>pg. 50–52</td>
<td>[69–73]</td>
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<tr>
<td><strong>ECLECTIC SPECIES</strong>&lt;br/&gt;Moderator: Jeff Root</td>
<td>pg. 52–54</td>
<td>[74–78]</td>
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<td><strong>CASE REPORTS</strong>&lt;br/&gt;Moderator: Andrea Torres</td>
<td>pg. 55–56</td>
<td>[79–82]</td>
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<td><strong>MARINE SPECIES</strong>&lt;br/&gt;Moderator: Terry Spraker</td>
<td>pg. 57–58</td>
<td>[83–86]</td>
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<tr>
<td><strong>NEW TOOLS FOR WILDLIFE DISEASE MANAGEMENT</strong>&lt;br/&gt;Moderators: Bill Lance &amp; Lynn Creekmore</td>
<td>pg. 59–65</td>
<td>[87–99]</td>
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The Wildlife Disease Association *Conference Program and Abstracts* booklet is distributed to all meeting attendees. Abstracts were lightly edited to comply with formatting and space limits, but otherwise were printed as submitted. The Wildlife Disease Association does not regard this *Conference Program and Abstracts* booklet as a publication, and abstracts included herein should not be cited in scientific literature.
CARLTON HERMAN FOUNDERS FUND LECTURE


André A. Dhondt
Cornell University, Ithaca, NY, USA

One example of a pathogen’s successful jump between hosts is *Mycoplasma gallisepticum*, which jumped from poultry to house finches (*Carpodacus mexicanus*) in early 1994. This new disease spread rapidly in the eastern (introduced) part of the finch’s range, but after reaching western (native) finch range in 2002 it spread much more slowly. *Mycoplasma gallisepticum* also causes disease in other finch species, but these seem to be spill-over infections. The study system is interesting in that the house-finch strain of *Mycoplasma gallisepticum* is most likely a novel strain (causing only mild clinical signs in poultry) that emerged recently and invaded a new host that itself was introduced in 1940 in eastern North America. House finches increased about $10^6$-fold in 60 years. They are a mobile, patchily distributed, seasonally breeding social species. As the bacterium cannot survive outside a host for more than a few days, transmission occurs primarily through direct contact and/or through fomites, less through vertical transmission. Disease severity varies with transmission route. Disease prevalence shows strong seasonal fluctuations, although amplitude and cycle vary geographically. To understand and model *Mycoplasma gallisepticum* dynamics in house finches, we combine data from three lines of investigation: volunteers to describe disease prevalence at large geographic scales; intense capture-mark-recapture studies in local populations to determine effects of disease on survival and behavior; and controlled experimental infections in captivity to understand factors influencing disease course in individuals in controlled conditions. I will present recent advances obtained by our multi-disciplinary team in understanding disease dynamics using results from all three lines of investigation, emphasizing differences in disease dynamics between eastern and western finch populations and the role of other host species.


Charles Van Riper III1, Paul Super2, Chris O’Brien1, Grant Ballard3, Geoff Guepel3
1USGS/SBSC, University of Arizona, Tucson, AZ, USA; 2Great Smoky Mountain National Park, Lake Junaluska, USA; 3Point Reyes Bird Observatory, Stinson Beach, CA, USA

In western North America, patterns of blood parasite infections in birds evolved within a landscape of heterogeneous and patchy environments. We asked the question: “What long-term impact do blood parasites have on bird populations in a California coastal scrub ecosystem?” We sampled a color-marked population of passerine birds at Point Reyes, CA, for hematozoa infections during the years 1984-1990, and then followed the productivity of known individuals over the next 15 years. *Haemoproteus* and *Leucocytozoon* were the most commonly encountered infections and *Haemoproteus* transmission varied the most among all parasite groups for all years. We then compared productivity and calculated fitness between infected and non-infected individuals of each avian host species over the next 15 year period (1990-2005). *Leucocytozoon* negatively impacts productivity, while infection with *Haemoproteus* did not show any long-term effect. Birds that were NOT infected with *Leucocytozoon* fledged a greater number of young, produced more eggs, hatched more young, and acquired more mates; however, these same birds did not show a significant increase in number of nests or number of young recruited into the local population when compared to infected individuals. A comparison of hematozoa epizootiology among parasite species revealed, that because of appropriate vectors, a significantly lower prevalence of certain blood parasite groups occurred within the California coastal scrub ecosystem.

Rodrigo K. Hamede, Hamish McCallum, Menna Jones
University of Tasmania, Hobart, Tasmania, Australia

Devil facial tumor disease (DFTD), is an emerging infectious cancer thought to be spread by biting that is causing ongoing, severe population decline of the Tasmanian devil (Sarcophilus harrisii). There are explicit concerns that DFTD might cause local or regional extinctions. Whether extinction is likely depends on patterns of contact rates and their relationship to host density. We used two different data sets, the first consisting of field observations of contact and biting behavior around prey carcasses and, the second a three-year longitudinal series of injuries in a marked devil population, to investigate contact rates. During feeding interactions at carcasses, contact rates were significantly positively associated with population density and subadults bit more frequently than adult males and females. In contrast, injuries from the marked devil population suggested that biting increased markedly during mating season and that such bites occurred more frequently in adult males and females than in subadults. Most bites recorded in both data sets occurred on the head and the majority of injuries resulted in dermal layer penetrating wounds, suggesting a strong relationship between location and severity of contact and tumor location. Although contact rates around carcasses increased with population density, our results suggest that mating season is the key period for disease transmission. If most bites occur during mating interactions, DFTD transmission is likely to be frequency-dependent disease, which means that there would be no threshold host density for disease persistence, and disease-induced extinction is possible.

[4] CLIMATE CHANGE & THE IMPACTS ON TICK-LIZARD INTERACTIONS & HEMOGREGARINE TRANSMISSION IN AUSTRALIA

Michael Bull, Greg Kerr, Jaro Guzinsky
Flinders University, Adelaide, South Australia, Australia

Australian lizards are often infected with ticks. These transmit hemogregarine parasites, Hemolivia mariae, that infect lizard red blood cells. The sleepy lizard, Tiliqua rugosa, is a large skink that is widespread in semi-arid regions of southern Australia. Ticks waiting for hosts have a high risk of desiccation. Unsurprisingly, over a 25 year study, infestation intensity of one tick species, Bothriocroton hydrosauri, was lower following years of low rainfall. More intriguingly, the opposite trend was found for a second tick species, Amblyomma limbatum. That trend may result from the higher incidence of refuge sharing by the lizard hosts in very hot and dry years, thus enhancing the opportunities for tick transmission, and increasing tick survival by decreasing the time to find the next host. We have used polymorphic microsatellite DNA loci to show tick dispersal is restricted, and we have used on-board GPS trackers to explore the social network of host individuals, and to deduce cross-host transmission opportunities. We show that ticks and hemogregarines have potential impacts on lizard fitness, but that Amblyomma limbatum is a more effective vector of H. mariae. Climate change might affect the two tick species differently but could potentially increase the parasite pressure on the lizard population.

Andy Dobson¹, Meggan Craft², Peter Hawthorne², Craig Packer², Sarah Cleaveland³.
¹Princeton University, Princeton, NJ, USA; ²University of Minnesota, Minneapolis, MN, USA; ³University of Edinburgh, Roslin, Midlothian, Scotland

An epidemic of canine distemper swept through the Serengeti lion population in 1994. Detailed information on the time course of the epidemic is available for the sub-section of the lion population that has been studied by the Serengeti Lion Project. In this talk we will present details of ways to estimate transmission rates for CDV in lions; these methods explicitly acknowledge that the lions are distributed as distinct social groups with limited contact between groups. In the second half of the talk we will describe some spatially explicit models for lions, hyenas, and jackals that explore the consequences for disease transmission when more than one potential host species is present.


Viviane Hénaux, Andrew J. Tyre, Larkin A. Powell
University of Nebraska-Lincoln, Lincoln, NE, USA

Emergent diseases posing significant health risks to humans are appearing with increasing frequency. In many cases, diseases involve birds as primary hosts, raising the possibility that migrating birds can spread the disease faster over greater distances. In order to understand the connection between migration and disease dynamics, we studied avian cholera in lesser snow geese Chen caerulescens as a model system. Although this highly contagious disease kills thousands of waterfowl annually in North American wetlands, the source of the bacteria Pasteurella multocida remains unclear. Two non-exclusive hypotheses involve either migrating carrier birds or epizootic wetland sites as the source of the disease. We investigated several scenarios of disease diffusion within the goose population by developing a spatially explicit model of the host-parasite interaction: we nested a within-host model describing the dynamics of the parasite population over the course of an infection in a spatial epidemiological model characterizing the transmission of the disease within the host population. We tested predictions concerning the source of the disease and the transmission probability of the disease over any migration distance against observed patterns of avian cholera outbreaks through the migration corridors. Selected scenarios allow a better understanding of the role of carrier birds in the transmission patterns of avian cholera and, more broadly, of infectious diseases within populations of migrating birds. We believe our population model's predictions of disease dynamics will be useful to agencies preparing to respond to disease outbreaks in North America.
[7] A LONGITUDINAL STUDY OF FACTORS AFFECTING HELMINTH PREVALENCE IN FIELD VOLES IN NORTHUMBERLAND, UK

Stephanie F. Gebert, Sandra Telfer, Pablo Beldomenico, Lucasz Lukomski, Steve Paterson, Mike Begon
University of Liverpool, Liverpool, UK

This project is part of a large multi-pathogen study of wild rodents that has been conducted in a man made forest in Northumberland, UK, between March 2005 and March 2007. It is a capture mark recapture study with field voles, *Microtus agrestis*, being trapped every four weeks at three sites throughout the forest, with a sampling efficiency of 70-80%. On first capture each vole was individually and permanently marked to allow infections to be followed within individuals. During each trap session the sex, weight, body condition and reproductive status was recorded for each vole and a fecal sample was collected. This study is one of the first to use fecal egg counts to estimate helminth infestations within individual hosts and follow the course of infection within those individuals through time. There are two families of cestodes and two nematode species that have been identified within the fecal samples. We investigate and discuss the importance of population level factors including density, season, site and weather on helminth prevalence. We also consider the importance of individual factors including sex, age and reproductive status on helminth prevalence and whether particular individuals or groups of individuals are more likely to have a helminth infestation. These data also offer the opportunity to investigate interactions between helminth groups within individual hosts.

[8] ECOLOGY OF DISEASES OF COLONY NESTING BIRDS IN SASKATCHEWAN, CANADA

Heather Fenton¹, Christopher Somers², Catherine Soos¹,³, Emily Jenkins¹,³, Frederick Leighton¹,⁴, Lydden Polley¹, Brent Wagner¹, Manuel Chirino¹
¹University of Saskatchewan, Saskatoon, SK, Canada; ²Department of Biology, University of Regina, Regina, SK, Canada; ³Environment Canada, Saskatoon, SK, Canada; ⁴Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada

We investigated pathogens and patterns of disease in American white pelicans (*Pelecanus erythrorhynchos*) and double-crested cormorants (*Phalacrocorax auritus*) at two boreal and two prairie sites in Saskatchewan, Canada. Outbreaks of avian cholera, botulism Type C, and Newcastle’s disease are common in cormorants at a boreal site, but have not been extensively investigated in the prairie region. We examined carcasses of birds found during colony inspections, and those of 49 healthy adult cormorants that were shot. In the latter, differences in parasite community and intensity among the sites were partly explained by differences in diet and population size, demonstrating the role of parasites as sentinels for local ecosystems. We also collected samples from live birds to test for West Nile virus, avian influenza virus, and avian paramyxovirus (results pending). *Pasteurella multocida* was recovered from two of twenty choanal swabs from healthy juvenile cormorants at a boreal site (but not in twelve samples collected from the two prairie sites), and preceded an outbreak of avian cholera that killed ~20% of juveniles at this boreal site in August 2006. At the prairie sites, West Nile Virus was detected in tissues from five of six pelicans that displayed neurological symptoms. We continue to investigate geographic and temporal patterns of disease outbreaks and parasite intensity in colony nesting birds in Saskatchewan, complementing ongoing investigation of host genetics, behavior, and diet. Such investigations are important for wildlife management and conservation in a future of climate change and habitat disturbance, and to explore the role of wildlife in the ecology of diseases with significance for public health and agriculture.
[9] A MANIPULATIVE EXPERIMENT TO MONITOR TRANSMISSION OF SIN NOMBRE HANTAVIRUS IN DEER MOUSE POPULATIONS UNDER NATURAL FIELD CONDITIONS

Karoun H. Bagamian¹, James N. Mills², Richard J. Douglass³
¹Emory University, Atlanta, GA, USA; ²Centers for Disease Control & Prevention, Atlanta, GA, USA; ³Montana Tech, Butte, MT, USA

Hantavirus pulmonary syndrome (HPS) is a frequently fatal rodent-borne zoonosis caused by Sin Nombre virus (SNV). The natural host of SNV is the deer mouse (Peromyscus maniculatus). Soon after the initial outbreak of HPS in the southwestern United States in 1993, investigators began long-term ecological studies of the dynamics of infection with SNV in deer mouse populations. While these mark-recapture studies have answered many questions, they have also directed attention to new inquiries that can only be answered using controlled experiments. Because laboratory research on SNV in the natural host can only be conducted in maximum containment (BL-4) laboratories, controlled studies of transmission of SNV are rare; a few experiments in “outdoor laboratories” have been unsuccessful at demonstrating transmission of SNV in caged deer mice. These results may be related to the unnatural environment of the cages. We have constructed .25 ha enclosures in natural deer mouse habitat in Montana in which we are able to manipulate the abundance of animals of known SNV infection status; we are able to conduct virological assays (ELISA and PCR) on site. In a pilot study last summer we were able to achieve SNV transmission among our experimental deer mouse populations. This season (beginning in May) we will conduct studies investigating the effects of factors hypothesized to be associated with SNV transmission including host population density, age, sex, reproductive status, and the presence of other species. These results will be presented.


Daniel J. Decker¹, Shawn Riley², Margaret Wild³, Kirsten Leong³
¹Cornell University, Ithaca, NY, USA; ²Michigan State University, East Lansing, MI, USA; ³National Park Service, Fort Collins, CO, USA

What’s at stake in wildlife health and disease management? Ecosystem health is a prime concern, but so are credibility of the wildlife profession and sustaining wildlife as a valued “resource.” This claim should not be surprising as a growing list of diseases affecting wildlife lead to real or perceived impacts on human health and safety, economic values, and esthetic attributes of ecosystems. Wildlife health and management specialists recently articulated a model depicting ecological and social dimensions of the wildlife disease management system highlighting integration of these considerations. We use this model to explore how consideration of types of impacts, scale, limits/capacity, and decision processes in management reveals the significance of social, cultural and economic aspects of wildlife disease management using three examples: chronic wasting disease, plague, and highly pathogenic avian influenza. We also consider collateral effects of management (real or perceived effects created by interventions to manage disease) to demonstrate how such effects can have greater impact than the disease. We reveal similarities and differences in the human dimensions of management interventions for different wildlife disease situations. We conclude that even for diseases in wildlife shown by wildlife health and public health professionals to pose minimum risk of transmission from wildlife to humans and domestic animals, various human dimensions considerations may nevertheless affect public perception of risk, trust of management, and regard for wildlife. The consequences of not dealing effectively with this aspect of disease management can have far-reaching implications for the entire field of wildlife “resource” conservation and management.

Terry J. Kreeger
Wyoming Game & Fish Department, Wheatland, WY, USA

Federal and state governments have been largely successful in eradicating brucellosis in domestic cattle. Today, elk and bison in the Greater Yellowstone Area represent the last nidus of brucellosis, which conflicts with the federal goal of eradication. Thus far, the only “tools” used to eradicate brucellosis have been vaccination and test and slaughter. Other tools could include: (1) shutting down elk feedgrounds to reduce disease transmission; (2) removing problem elk that have a higher probability of coming into contact with cattle; (3) removing cattle from public lands; (4) re-establishing historic elk migration routes; (5) developing and implementing more efficacious brucellosis vaccines for elk and bison; (6) managing cattle through vaccination and physical separation from elk and bison; and (7) using contraceptives to decrease pregnancies and, thus, abortions. Regardless of what, if any, tools are employed, the public probably will have to accept fewer elk numbers in northwest Wyoming which will mean less hunting and less opportunities for viewing wildlife. All solutions will take decades to implement and become effective.

[12] CHALLENGES & SUCCESSES OF MANAGING BOVINE TUBERCULOSIS IN A MULTI-JURISDICTIONAL ENVIRONMENT IN THE RIDING MOUNTAIN NATIONAL PARK REGION, MANITOBA, CANADA

Ken Kingdom¹, Todd Shury², John Whitaker³, Ryan K. Brook⁴
¹Riding Mountain National Park, MB, Canada; ²Parks Canada, Saskatoon, SK, Canada; ³Riding Mountain Biosphere Reserve, Erickson, MB, Canada; ⁴University of Manitoba, Winnipeg, MB, Canada

Disease management across a multi-jurisdictional landscape is always a challenge. Beginning in 1991, bovine tuberculosis (TB) (Mycobacterium bovis) was found in several cattle herds on farms surrounding Riding Mountain National Park, Manitoba, Canada. Subsequent testing of wildlife indicated that Wapiti (Cervus elaphus) and White-tailed Deer (Odocoileus virginianus) also carried the disease, and may be acting as a disease reservoir. This led to demands from some stakeholders that the elk herd be destroyed or fenced inside the Park. As the disease was found in both domestic livestock, and in wildlife both inside and outside the National (Federal) Park, coordinated management actions required the cooperation of 4 government agencies or departments. Initially, each agency had a different set of operating procedures, management interests, and stakeholder groups that they interacted with. At the same time, local stakeholders around the National Park felt that their own particular needs were not being met, and demanded greater input into the decision making process. A flexible, adaptive approach combined with close working relationships of field staff for each government agency led to the formation of a multi-stakeholder management process. Despite several on-going challenges including facilitating the participation of Aboriginal people in the process, and sustaining the interest and efforts of all participants given the re-acquisition of TB-free status in domestic livestock, the program has had considerable success in management of TB on the landscape. The presentation reviews the process and management structures developed to manage this complex disease in a challenging management environment.
[13] DOMESTIC ANIMAL MANAGEMENT & WILDLIFE HEALTH IN INDIGENOUS COMMUNAL LANDS OF BOLIVIA

Rodolfo Nallar¹, Erika Alandia¹, Erik Eulert¹, Jorge Zapata¹, Fabian Beltran¹, Sixto Angulo¹, Lena Patiño¹, Marcela Uhart², W. B. Karesh³
¹Wildlife Conservation Society, Bolivia; ²Wildlife Conservation Society, Argentina; ³Wildlife Conservation Society, USA

In the Bolivian tropical lowlands, the sustenance of indigenous communities has been traditionally based on hunting, fishing and fruit collection. Recently however, some of their feeding habits have been modified due to the loss of habitats and hence, the decrease in availability of natural foods. These changes respond to incorrectly applied development policies that have debilitated local capacities and introduced new inappropriate technologies. Another factor has been the introduction of domestic animal rearing programs without providing basic management and husbandry criteria. The latter fact has triggered epidemics, causing losses of domestic animal herds, and threatening wildlife populations. Because in Bolivia many communities are established within protected areas, disease prevention and control become of core significance. Domestic animal diseases have the potential to significantly affect wildlife populations as well as human livelihoods (directly or by decreasing the amount of game available), jeopardizing the nutritional wellbeing of communities which depend on hunting for food. At present, we are focusing on 3 different sites in Bolivia, ranging from the Andean highlands to the dry temperate forest of the Chaco and tropical lowlands of Madidi. The objective of our work is to improve domestic animal management, which will allow us to a) prevent infectious disease transmission amongst domestic animals, wildlife and humans, b) reduce hunting pressure and c) support community livelihoods and the sustainable development of these areas. We will discuss results of the first two years of our community programs, highlighting difficulties encountered, challenges for the future and successes achieved.

[14] THE EFFECTS OF SPECIES DIVERSITY ON DIRECTLY TRANSMITTED DISEASES

Gerardo Suzán¹, Andres Gómez², Alonso Aguirre³
¹Universidad Nacional Autónoma de México, Ciudad Universitaria, Mexico; ² Columbia University, New York, NY, USA; ³Wildlife Trust, New York, NY, USA

The world is currently facing unprecedented levels of biodiversity loss and the consequences of such loss have become an important issue for ecological and epidemiological research. Recent studies hypotheses have suggested that high species richness may reduce the prevalence of some vector-borne diseases (“the dilution effect hypothesis”), however, the effects of species diversity loss on directly transmitted diseases is barely known. We describe different pathways through which diversity can influence infection rates of directly transmitted diseases with different outcomes at different spatial and temporal scales. Our analysis suggests that that environmental variables like global change or habitat fragmentation influence infectious disease dynamics and other community attributes, such as species richness, dominance, species composition, and functional diversity, also have significant influence on infection prevalence but that the buffering effect of high species richness may dominate in long-term biotic relations. These relationships have important consequences for public and animal health and for conservation biology.

Edward M. Addison
Ecolink Science, Aurora, ON, Canada

Negative and positive impacts of fragmentation of habitats and isolation of populations are both well documented in the scientific literature. Negative impacts are given much credence in resource management agencies when developing policies and programs about such things as ‘wildlife corridors’. Concomitantly, discussions of benefits of fragmentation and isolation are often discounted as being irrelevant. Managers of wildlife from a habitat perspective seem much less likely to acknowledge benefits of fragmentation than do those managing wildlife from a health perspective, particularly when specialists in wildlife health are managing wildlife in a reactive mode to control spread of parasites and diseases. Reasons and examples are given as to why we require a much more inclusive discussion of the contrasting values of fragmentation when developing resource management policies and programs.

[16] A LEARNING LABORATORY TO PROMOTE INTEGRATION OF INSIGHTS FROM BIOLOGICAL & HUMAN DIMENSIONS FOR WILDLIFE DISEASE MANAGEMENT

Shawn J. Riley1, Chris Soderquist2, Philip Rice3
1Michigan State University, East Lansing, MI, USA; 2Pontifex Consulting, Hanover, NH, USA; 3Sustainability Institute, Hartland, VT, USA

Effective wildlife disease management (WDM) requires a systemic orchestration – timing and magnitude of implementation – of policies that strategically apply insights from biological and human dimensions of the broader system in which WDM occurs. Opportunities to prompt decision-makers to use quantitative information while giving weight to qualitative information may minimize unforeseen collateral impacts from disease management efforts. The objective of this study was to develop an interactive systems model for use in learning about WDM. Wildlife management and wildlife disease specialists participated in a series of workshops and interviews to articulate their perspective of the WDM system, guided by a focus question: “When a wildlife disease issue arises or is anticipated, what suite of factors needs consideration and how do these play into the approach taken?” Chronic wasting disease (CWD) management was used as a model system. The learning lab portrays effects of CWD on two adjacent deer populations, as well as the effect of hunting or other herd management actions. The lab emphasizes consideration of human dimensions components contributing to perceived impacts of wildlife disease and management efforts, including: tolerance thresholds for perceived disease risks to wildlife, domestic animals, and humans; social acceptability of management options; and the effect of information and communication efforts. Users of the lab balance management actions against budgetary considerations and effect on the disease population. We demonstrate the systems model and discuss its application as a tool for education and decision-aiding, and explore how the learning lab may facilitate communication among wildlife managers.
WILDLIFE HEALTH MANAGEMENT: DEVELOPING THE “COLORADO CHARTER”

Craig Stephen
Centre for Coastal Health, Nanaimo, BC, & University of Calgary, AB, Canada

It has been said that the care of the sick has taught us how to protect the healthy. By studying wildlife disease, we have learned how to keep animals healthy through the judicious use of drugs, chemicals, vaccines, and population management. But health management is more than dealing with disease. Health is a capacity that allows populations to access the needs for daily living, cope with stress and change, and meet the aspirations of society for productivity, ecological services and sustainability. The Ottawa Charter for Health Promotion was presented in 1986 as a health model inextricably linking individuals and their environments. It emphasized the interactions of the social, individual and environmental determinants of health. Wildlife health has been slow to adopt this approach, marginalizing its relevance to wildlife management. Many of the contentious issues challenging wildlife health decisions are not to be found in inadequate knowledge of pathology and pathogens. Rather it is the human dimensions of values and policies intertwined with the systems dimensions of complexity and unpredictability that make clear cut wildlife health management decisions elusive. Failing to consider the biomedical aspects of wildlife health along with the 4 P’s of health management (people, policy, participatory, promotion) will minimize the role wildlife health professionals play in management decisions. The methods and perspectives of health promotion can serve as a model from which wildlife health can move into the next generation where capacity to discover the causes of disease are exceeded by skills to protect and promote health by an integrated, interdisciplinary approach.

MANAGING FACIAL TUMOUR DISEASE IN THE TASMANIAN DEVIL: A DISEASE SUPPRESSION TRIAL

Menna Jones1,2, Hamish McCallum1
1University of Tasmania, Hobart, Australia; 2Department of Primary Industries & Water, Hobart, Australia

The Tasmanian devil (Sarcophilus harrisii) is the largest surviving marsupial carnivore, but is threatened by an infectious cancer, spread by a transmissible cell line. The disease has caused reductions of up to 90% in affected populations and has now spread across the majority of the range of the devil. Without a vaccine or a field deliverable treatment, management options are severely limited. One possibility is that, by removal of infected individuals, we may reduce $R_0$ to below one, thus eliminating the disease. We are trialing this strategy on the Forestier Peninsula, 160 km² in area, connected to mainland Tasmania only by a single bridge. The experiment has been progress since June 2004. By April 2007, 111 infected devils had been removed and euthanized, from an estimated population of 250 individuals. This disease suppression has influenced the epidemic, with significantly fewer large tumors being found than at the start of the trial. Despite the removals, population density has remained high, without the declines evident in other diseased populations. The age structure of the population has remained similar to the pre-disease structure, whereas in other diseased populations, animals older than two years are almost absent. There is some evidence that spatial progress may have slowed. However, disease prevalence remains high and it is too early to determine whether or not the suppression will successfully eliminate the disease from the peninsula.
[19] A MODEL FOR OPTIMIZING THE APPLICATION OF ORAL RABIES VACCINATION IN ISRAEL, BASED ON RED FOX POPULATION SPATIAL DYNAMICS

Amit Dolev1,2, Amir Perelberg3, Roni King4, David Saltz1,4

1Ben-Gurion University, Israel; 2Northern R&D, Kiryat Shmona, Israel; 3Israel Mammals Research Center, Tel Aviv, Israel; 4Israel Nature and Parks Authority, Jerusalem, Israel

The red fox (Vulpes vulpes) is the main vector of rabies in Israel. In the past six years the implementation of an oral rabies vaccination (ORV) program has successfully prevented rabies outbreaks. The bait containing the vaccine is uniformly spread over the landscape by aircraft. We hypothesized that fox densities in Israel vary greatly over space due to anthropogenic influences and that their movement patterns are not random and are directed by the interaction between landscape characteristics and the foxes’ behavior. This, in turn, suggests that a non-uniform spreading of ORV may be more efficient. We tested these predictions using a spatially realistic individual-based model for the dynamics of rabies deriving the parameters for the model from a 3-year field study of foxes. The field study focused on the spatial dynamics of 77 radio-collared red foxes in the Galilee region in northern Israel. Specifically we compared between "farm foxes" (those captured in the vicinity of settlements with poultry farms) and rural foxes (captured in regions away from poultry farms) in terms of densities, dynamics, and movement patterns. We then used the model to assess the efficiency of various aerial spreading patterns of ORV baits in eliminating and preventing future rabies outbreaks. The most efficient (in terms of efforts vs. results) pattern was based on rabies-free belts deployed along potential penetration corridors from neighboring countries. These belts required the scattering of ORV baits on only 25-40% of the total area currently vaccinated.

[20] ORALLY DELIVERED BACILLE CALMETTE-GUÉRIN (BCG) VACCINE PROTECTS WILD FREE-LIVING BRUSHTAIL POSSUMS AGAINST BOVINE TUBERCULOSIS

Daniel M. Tompkins, Dave Ramsey

Landcare Research, Dunedin, New Zealand

Bovine tuberculosis (Mycobacterium bovis) in wild animals is a world-wide problem, with wildlife acting as reservoirs for both domestic animal and human infections. Culling wildlife provides insufficient control in many cases. In New Zealand, the principal wildlife reservoir of infection for cattle and farmed deer is the introduced Australian brushtail possum (Trichosurus vulpecula). While an extensive of possum culling program over the past decade has been a major factor in an 85% reduction in infected cattle herds, this strategy has not reduced the total area in which bovine Tb is endemic in wildlife (now extending over 40% of the country). Additional strategies of disease control are thus required, with vaccination against disease being an attractive option to reduce the tuberculosis burden in possum populations. While bacille Calmette-Guérin (BCG) is currently administered in humans via intradermal injection, oral bait vaccination is the only feasible means of disease management in wildlife reservoirs. However, this delivery route is more challenging given the need for sufficient live bacilli to reach sites of mucosal immune induction in the gastrointestinal tract in the face of degradation by gastric hydrolysis. Previous trials demonstrated that orally delivered BCG vaccine based on lipid encapsulation of live bacilli induced a significant level of protection against bovine Tb in caged possums. Here we extend this research to possums in the field, and provide the first evidence that such a vaccine also induces a significant and operationally viable level of protection against bovine Tb in a wild, free-living animal population.
[21] LESSONS LEARNED FROM HIGHLY PATHOGENIC AVIAN INFLUENZA IN EUROPE

Marc Artois1, Dominique Bicout1, Jérome Coppale2, Jean Hars3, T. Mörner4
1Ecole nationale vétérinaire de Lyon, Marcy l’Etoile, France; 2Ecole nationale des services vétérinaires, Marcy l’Etoile, France; 3Unité sanitaire, Gieres, France; 4National Veterinary Institute, Uppsala, Sweden

In 2006, the incursion of Highly Pathogenic Avian Influenza in Europe among wildfowl was a new illustration of the health risk presented by wildlife for humans and domestic animals. In order to better anticipate similar incursions, and avoid drift from poor public communication, we described the way such a sanitary risk was studied and managed in the past in Europe for HPAI and other wildlife diseases and have attempted to identify a broad approach allowing anticipating such events based on four main “lessons”: 1) investigation of the pathogen, 2) identification of the reservoir host, 3) management of the risk(s), 4) public communication on the risk and its management. We advocate an improvement of the collaborative approach between field biologists, virologists, wildlife veterinarians, and also veterinary and public health officers. We further argue that wildlife disease investigation and management should be considered as a field of professional skill and scientific expertise within the veterinary profession.

[22] MANAGING THE ADVERSE IMPACTS OF THE BITING DOG LOUSE ON WOLVES IN ALASKA

Kimberlee Beckmen, Craig Gardner, Mark McNay
Alaska Department of Fish & Game, Fairbanks, AK, USA

The biting dog louse (Trichodectes canis) was first identified in Alaska on a coyote (Canis latrans) and wolves (C. lupus) on the Kenai Peninsula during the winter of 1981–82. Wildlife managers attempted to eliminate it by administering ivermectin injections during live-capture and with ivermectin-treated baits. This effort was unsuccessful because of the difficulty in treating all exposed individuals. In 1998, trappers reported wolves and coyotes with lice in south-central. Treatment attempts were similarly unsuccessful. When lice were detected in wolves north of the Alaska Range in March 2004, a cost-effective means of management rather than eradication of lice infestation was sought. In spring 2005 all members of an infected pack were radio-collared and treated. After emergence from the den, pups were treated at two week intervals with ivermectin-impregnated baits dropped from a Supercub. In December, pups were live-captured, ear-tagged assessed for lice, and released. Pelts from marked wolves obtained from trappers were subjected to hide digestion to detect occult infestations. The pack was determined to be louse-free. During 2005-06, 1-2 wolves in each of 11 packs were examined and radio-collared. Ivermectin-baits were distributed at the dens and rendezvous sites of 5 infected packs during May-August. During the winter, 1-3 wolves were examined from each of 8 radio-collared packs. None of the wolves from treated packs had lice or hair loss suggestive of lice. Preliminary results suggest that distribution of ivermectin-impregnated baits is efficacious in production normal pelt quality wolves during the trapping season.
[23] THE EFFECTS OF SUPPLEMENTAL FEEDING ON STRESS LEVELS IN ELK

Victoria Patrek1, Paul C. Cross2, Scott Creel1, Mark Taper1, Eric Maichak3, Jill Miller4
1Montana State University, Bozeman, MT, USA; 2US Geological Survey, Bozeman, MT, USA; 3Wyoming Game & Fish Department, Jackson, WY, USA; 4Wyoming Game & Fish Department, Pinedale, WY, USA

In 23 areas around Wyoming elk, Cervus elaphus, are fed throughout the winter by state and federal agencies. Elk utilizing feedgrounds are plagued with brucellosis, a bacterial disease caused by Brucella abortus, which is transmitted primarily during abortion events. The aggregation of elk during the peak transmission period sustains the high prevalence of brucellosis observed in these populations. Beyond creating the opportunity for transmission, the aggregation of elk on feedgrounds may have additional effects on transmission and susceptibility to disease. Chronically high stress levels are known to suppress the immune system and reduce reproductive success; thus it is possible that the stress levels experienced by elk on feedgrounds contribute to transmission and susceptibility to brucellosis. Stress levels are probably affected by snowpack, time of year, and density. In this study we use fecal glucocorticoids (fGC) as a measure of stress levels in elk. The aim of our research is to investigate how stress levels are associated with snowpack and density of individuals on the feedground within and among populations. Preliminary results suggest that elk on Wyoming feedgrounds have fGC levels ~57% higher than elk in wild populations. In 2007, we collected fecal samples from 16 feedground populations and from 5 unfed elk populations. Here we present the results on what factors explain the variation in stress levels of that study and how this may affect disease dynamics.

[24] THE FUTURE OF ORAL WILDLIFE RABIES VACCINATION?

Charles E. Rupprecht1, Dennis Slate2
1Centers for Disease Control & Prevention, Atlanta, GA, USA; 2US Department of Agriculture- Wildlife Services, Concord, NH, USA

Rabies remains one of the most significant wildlife diseases from a global perspective. In contrast to a historical reliance upon population reduction as a primary means of disease control, the development of the concept of oral immunization has provided an important adjunct in the modern wildlife management arsenal. To date, such biologicals deployed in the field have consisted of either modified-live or recombinant rabies virus vaccines. Clearly, establishment of programs for the strategic distribution of such vaccine-laden baits has led to substantial progress in rabies elimination among free-ranging carnivores in both Europe and North America. Nevertheless, no vaccine in common use is equally effective for all intended species. Moreover, practical usage related to the relative abundance of the targeted host and potential non-target competition requires applied bait densities that may exceed 100 baits/km² in some habitats. In addition, less than ideal perceptions may remain over the environmental repercussions of certain introduced foreign entities. Given what is understood currently about the immunology of oral vaccination, it is unlikely that reliance upon inactivated immunogens will prove feasible any time soon, coupled with the severe limitations in cost-effective commercial production. Future efforts focused upon greater pathogen discovery in the taxa of interest may provide more selective examples of agents for consideration, with lesser potential public health or veterinary ramifications than prior choices. For example, exploitation of enzootic rabies viruses selectively modified via reverse genetics, or a renewed concentration upon recombinant canine adenoviruses, may provide alternative biological products in the near future.
[25] **SPATIAL DYNAMICS OF PLAGUE IN THREE BLACK-TAILED PRAIRIE DOG COMPLEXES**

Jack Cully¹, Tammi Johnson²

¹Kansas Cooperative Fish & Wildlife Research Unit-Kansas State University, Manhattan, KS, USA; ²University of Montana, Missoula, MT, USA

Sylvatic plague, caused by the bacterium *Yersinia pestis*, has been one of the most serious threats to the conservation of black-tailed prairie dogs since the two species came into contact in the middle of the last century. Since 1999, we have monitored black-tailed prairie dog colony dynamics (growth and decline) at the Kiowa and Rita Blanca National Grasslands (73 colonies) in New Mexico, Oklahoma, and Texas, the Cimarron National Grassland (60 colonies) in SW Kansas, and the Comanche National Grassland (157 colonies) in SE Colorado. We documented plague epizootics at all three grasslands and were able to record the spread of plague by carefully mapping active prairie dog colonies at each grassland during 1999 and annually from 2001 to 2006. At each grassland, plague epizootics first appeared at a limited number of colonies in a small area and then spread in a regular pattern to additional colonies over periods of 2-5 years. Our results demonstrate that at the three grasslands, careful monitoring can reveal the local beginning of plague activity that would provide opportunities for intervention such as burrow dusting to control fleas at nearby colonies. Similar flea control has been used successfully to curtail epizootics at other sites.

[26] **EVIDENCE OF ENZOOTIC PLAGUE IMPACTS ON BLACK-FOOTED FERRET SURVIVAL IN MONTANA**

Tonie E. Rocke¹, Marc R. Matchett², Dean Biggins³

¹National Wildlife Health Center, Madison, WI, USA; ²US Fish & Wildlife Service, Lewistown, MT, USA; ³US Geological Survey, Fort Collins, CO, USA

Black-footed ferrets (*Mustela nigripes*) were first reintroduced to Montana in 1994 on prairie dog complexes at the UL Bend National Wildlife Refuge and later on BLM-managed lands north of UL Bend. Epizootics of plague (*Yersinia pestis*) in this area, reduced prairie dog populations by 75% from 1992-1996. From 1994 through 2003, nearly 300 ferrets were released and at least 197 wild-born kits were observed, yet by spring 2004, only 8 ferrets were present. Black-footed ferrets are highly susceptible to plague acquired either via flea-bite or consumption of infected prey. Given this poor ferret survival, even in the absence of epizootic plague on some prairie dog colonies, we hypothesized that low (enzootic) levels of plague may be affecting ferret survival. We tested this hypothesis by dusting prairie dog burrows with Deltamethrin and by vaccinating black-footed ferrets to protect them from plague exposure. Ferret survival was monitored on comparable dusted and non-dusted prairie dog colonies. Half of all resident and released ferrets at each site were vaccinated against plague; the other half received a placebo. Results from logistic regression analysis of data from 131 ferrets, spanning 208 survival intervals, demonstrated that both pesticide application and vaccination improved ferret survival roughly two times over that of non-vaccinated animals living on non-dusted colonies. These results provide evidence that enzootic plague occurs in prairie dog colonies in these study areas and significantly impacts black-footed ferret survival. With this knowledge, we can now develop effective management steps to enhance recovery of endangered black-footed ferrets.
WDA GRADUATE STUDENT RESEARCH RECOGNITION AWARD WINNER

[27] USING CMR MODELS TO DETECT DISEASE IMPACTS & PATTERNS OF INFECTION IN A TASMANIAN DEVIL POPULATION AFFECTED BY DEVIL FACIAL TUMOUR DISEASE

Shelly Lachish¹, Menna Jones², Hamish McCallum²
¹University of Queensland, Brisbane, Queensland, Australia; ²University of Tasmania, Hobart, Tasmania, Australia

The Tasmanian devil (Sarcophilus harrisii) is the largest extant marsupial carnivore. A debilitating facial cancer first detected in 1996, devil facial tumour disease (DFTD), has now spread over most of the Tasmanian devil’s range, causing major population declines in affected populations. We used Cormack-Jolly-Seber and multi-state mark-recapture models to determine the impact of DFTD on age- and sex-specific apparent survival rates and to investigate patterns of infection rates in a population of Tasmanian devils in eastern Tasmania. Disease impact on population growth rate was investigated using reverse-time mark-recapture models. The arrival of DFTD triggered immediate major declines in apparent survival rates of adults and subadults, resulting in a marked, ongoing decline in the population growth rate of the previously stable population. The probability of transition from susceptible to infected classes increased through time and with disease prevalence, suggesting that the force of infection in the population is increasing and that the epidemic is not subsiding. Increasing infection rates also indicate that subadults will soon be more likely to develop into diseased adults than healthy adults. These results suggest that this disease may lead to the local extinction of this population.

[28] COMPARATIVE SUSCEPTIBILITY OF WATERFOWL & GULLS TO HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 VIRUS

Justin D. Brown¹, David E. Swayne², David E. Stallknecht¹
¹Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA; ²US Department of Agriculture-Agricultural Research Service, Athens, GA, USA

Wild avian species in the Orders Anseriformes (ducks, geese, swans) and Charadriiformes (gulls, terns, shorebirds) have traditionally been considered the natural reservoirs for avian influenza viruses (AIV) and morbidity or mortality is rarely associated with AIV infection in these hosts. However, since 2002 highly pathogenic avian influenza (HPAI) H5N1 viruses have caused mortality in numerous wild avian species throughout Eurasia. Based on mortality data from field reports, some of these viruses are highly virulent for certain species of anseriforms. In this study, thirteen species of anseriforms and charadriiforms were inoculated intranasally with A/Whooper Swan/Mongolia/244/05 (H5N1) avian influenza virus (AIV) to evaluate the range of viral shedding and pathology within these two avian orders. Species-related differences in morbidity, mortality, viral shedding, and pathology exist between the examined species. Based on mortality and the distribution of virus, these species were separated into three general categories: 1) 100% mortality with viral antigen disseminated in the vasculature and/or parenchyma of numerous visceral organs, 2) high mortality with antigen primarily distributed in the brain, pancreas, adrenal glands and/or heart, and 3) No mortality and no viral antigen was detected. Where possible, the majority of our experimental infection results are consistent with field data from H5N1 HPAI virus outbreaks. Species-related differences in susceptibility and viral shedding are vital to understanding the epidemiology of H5N1 HPAI virus in wild waterfowl and in developing control efforts, biosecurity plans, and surveillance needs worldwide.
[29] TUMBLEWEED SHIELD LICHEN (XANTHOPARMELIA CHLOROCHROA) TOXICITY

Rebecca N. Dailey¹, Merl F. Raisbeck¹, Don Montgomery¹, James T. Ingram², Roger Siemion¹, Marce Vasquez³
¹University of Wyoming, Laramie, WY, USA; ²Colorado State University, Fort Collins, CO, USA

Toxicity following ingestion of the vagrant, foliose lichen Xanthoparmelia chlorochroa has been identified as the putative etiology in the death of elk (Cervus elaphus) at the Red Rim-Daley Wildlife Habitat Management Area in Wyoming during the winter of 2004. Reports of this particular lichen species being toxic to mammals are extremely rare. The objective of this feeding study was to determine if X. chlorochroa collected from various locations throughout Wyoming and/or seasons would induce the specific syndrome seen in Red Rim-Daley 2004 poisoned elk. Four treatment groups consisting of three adult Rambouillet ewes were fed lichen collected from (1) Red Rim-Daley WHMA immediately following the die-off in March 2004 (2) Red Rim-Daley WHMA collected in October 2005 (3) Bureau of Land Management McCulloch Peaks grazing area in February 2006 and (4) Monolith Ranch Hunter Management Area in May 2006. Ewes were examined for congruence of signs, clinical pathology and post mortem lesions among lichen groups and with the Red Rim-Daley elk. Clinical signs varied significantly among lichen groups; however, all ewes exhibited a transient spike in serum creatine kinase activity as well as mild skeletal myopathy. Based on clinical signs the toxicity of X. chlorochroa does vary by collection location and/or season.


Julian Drewe¹, Gareth Pearce¹, Tim Clutton-Brock¹, Gillian Dean² Anita Michel³
¹University of Cambridge, Cambridge, UK; ²Veterinary Laboratories Agency, Weybridge, UK; ³Onderstepoort Veterinary Institute, Pretoria, South Africa

Investigation of socially-mediated infectious disease transmission in wild animals is often constrained by lack of empirical data on social interactions. We present data from an ongoing study of bovine tuberculosis (Mycobacterium bovis infection; bTB) in a population of wild meerkats (Suricata suricatta) habituated to the close presence of researchers in the South African Kalahari. Prevalence and location of bTB infection were quantified in 14 neighbouring meerkat social groups in a cross-sectional study of 150 meerkats. A longitudinal study sampling 80 meerkats in five social groups approximately every three months over two years commenced in 2006. The bTB status of individually-identifiable meerkats was established through serological testing and microbial culture of tracheal wash samples and submandibular lymph node aspirates. Testing has shown serological evidence of exposure to bTB in 9.2% (15/163) of meerkats sampled, with 2.0% of meerkats being classified as infectious to others (2/102 tracheal washes cultured positive for M. bovis). Social network analysis (SNA) of detailed daily observations of intra- and inter-group interactions has identified frequency and duration of temporary inter-group movements of males searching for mates as important in transmission of bTB. Epidemiological modelling demonstrated that variations in intra-group social interactions help explain differences in bTB transmission rates. Social network analysis appears useful for determining which social interactions account for observed variation in transmission rates of bTB in wild animal populations. Our data are being used to develop a predictive model for quantifying disease transmission risk, which may have implications for bTB control in other social mammal species.
[31] SURVIVAL RATES & CAUSES OF MORTALITY OF CHRONIC WASTING DISEASE POSITIVE & NEGATIVE WHITE-TAILED DEER IN WYOMING

David R. Edmunds¹, Frederick G. Lindzey¹, Ronald G. Grogan¹, Walter E. Cook², Terry J. Kreeger³, Todd E. Cornish¹
¹University of Wyoming, Laramie, WY, USA; ²Wyoming Livestock Board, Cheyenne, WY, USA; ³Wyoming Game & Fish Department, Wheatland, WY, USA

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy of mule deer (Odocoileus hemionus), white-tailed deer (Odocoileus virginianus), Rocky Mountain elk (Cervus elaphus nelsoni), and moose (Alces alces). Transmission and geographic spread of CWD are poorly understood. Our long term objectives are to determine effects of CWD on behavior and survival of white-tailed deer (WTD) and provide information on spread of CWD. Deer were captured as fawns, tested for CWD, marked with ear tag radio-transmitters, and recaptured on a yearly basis to re-test for CWD and replace radio-transmitters with global positioning system collars. In five years, we have captured, marked and CWD tested 154 WTD. The overall CWD prevalence is 27% (37/136). Based on Kaplan-Meier annual survival analysis, survival rates are lowest for adult CWD-positive deer (0.29; female = 0.22; male = 0.40). Annual survival rates are significantly lower for adult CWD-positive deer than CWD-negative deer ($\chi^2_1 = 8.85$, $p = 0.00293$) and adult female CWD-positive deer than female CWD-negative deer ($\chi^2_1 = 8.39$, $p = 0.00377$). For deer where cause of death and final CWD status was determined, hunter harvest (22), capture-related mortality (15), clinical CWD (12), predation (5), vehicle collision (5), epizootic hemorrhagic disease or adenovirus (5), entanglement in fence (2), and drowning (1) are the major causes of mortality. The proportion of mortalities that were CWD-positive was higher than expected ($\chi^2_1 = 5.59$, $p = 0.01807$). Our data suggests CWD is a major cause of WTD mortality, either directly or indirectly, and may limit WTD population growth.

[32] INFLUENCE OF BIVALVES ON THE PERSISTENCE OF AVIAN INFLUENZA VIRUS IN WATER

Christina Faust¹, Justin D. Brown², David E. Stallknecht²
¹University of Georgia, Athens, GA, USA; ²Southeastern Cooperative Wildlife Disease Study- University of Georgia, Athens, GA, USA

Although the transmission of avian influenza virus (AIV) is dependent on an indirect fecal-oral route involving fecal-contaminated water, little is known about the persistence of AIV in aquatic environments. Studies have shown that the infectivity of AIV is temperature, pH and salinity dependent; however, biotic factors have not been studied. The objective of this study is to examine the influence of filter feeding bivalves on the infectivity of AIV in water. In experiments, freshwater clams, Corbicula fluminea, were used as model bivalves and collected locally. For each trial, clams were rinsed and individually placed in a tissue culture flasks (n=20) containing distilled water that was inoculated (1:100) with low pathogenic avian influenza virus. Water samples were taken a minimum of three times during 48 hours, and after each trial the clams were processed for microscopic examination with immunohistochemistry (IHC) and in situ hybridization. The virus titer of the water samples was quantified by titration in primary cultures of chicken embryo fibroblasts. The virus titer decreased (compared to control flasks) or was undetectable in all 20 flasks where clams were present. Rapid decreases in virus titers at varying time points suggested the decrease in titer was due to water filtration by clams. The results of this study suggest that biotic factors within the environment, specifically filter feeders, impact the persistence, and thus infectivity, of AIV. Studying the impact of filter feeders on the epidemiology of AIV will help develop an understanding of the maintenance of AIV within wild aquatic bird populations.
[33] IDENTIFICATION OF CRYPTIC SPECIES IN THE TRICHOMONAS GALLINAE MORPHOLOGICAL COMPLEX BY MOLECULAR CHARACTERIZATION

Richard W. Gerhold, Michael J. Yabsley, John R. Fischer
Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA

Avian trichomonosis, caused by Trichomonas gallinae, is reported from most continents and has caused significant population impacts in several avian species. The parasite has a wide spectrum of virulence, which is hypothesized to be controlled genetically; however, genetic sequence analysis of T. gallinae isolates has not been investigated. To determine if a genetic association among virulent and avirulent isolates or a distinct host-parasite association existed, clinically virulent (N=16) and avirulent (N=22) T. gallinae isolates were cultured from eight free-ranging avian species originating from a widespread geographical range within the United States. The 5.8S rRNA and surrounding internal transcribed spacer (ITS) regions were amplified by PCR from extracted trichomonad DNA and the sequences of the 375 bp amplicons were analyzed and compared. A genetic difference was not apparent among virulent and avirulent isolates nor was there a distinct host-parasite association. However, the results of the sequence analysis strongly suggest that there are at least two different species within the T. gallinae morphologic complex. One group demonstrated high nucleotide homology to the three T. gallinae sequences available in GenBank; whereas the other group had at least thirty-one nucleotide polymorphisms compared to the T. gallinae GenBank isolates and was more closely related to T. vaginalis (99%) than to T. gallinae (92%). Sequence analysis of both the 18S rRNA and alpha-tubulin genes, from a subset of the isolates, supports the ITS sequence results.

[34] SOCIAL CONNECTIVITY AND PARASITE TRANSMISSION IN POPULATIONS OF A TERRITORIAL REPTILE, THE TUATARA

Stephanie S. Godfrey¹, Jennifer A. Moore², C. Michael Bull¹, Nicola J. Nelson², Jens Krause³, Richard James⁴
¹Flinders University, Australia; ²Victoria University of Wellington, New Zealand; ³University of Leeds, UK; ⁴University of Bath, UK

Understanding what factors influence the dynamics of parasite transmission is integral to the management of wildlife diseases. Social interactions or association among individuals can provide opportunities for parasite transmission, hence social organization may be an important factor in disease transmission. In this study, we use social network analysis to examine how social connectivity influences parasite transmission in a threatened reptile, the tuatara (Sphenodon punctatus). Tuatara are the only extant members of an ancient reptilian order (Sphenodontia), and occur on off-shore islands of New Zealand. Tuatara have a stable, territorial social system, where males actively defend their territory from other males, and compete for females. Tuatara are also host to a diversity of parasites, including ectoparasites (ticks and mites), blood parasites (haemogregarines), and intestinal parasites. We collected detailed information on territory structure, mating patterns and parasite loads of individuals within three study populations on Stephens Island over a two year period, and analyzed these data using social network methods. We predict that individuals with a higher level of social connectivity (ie. interact with a greater number of individuals) will be more likely to be infected by parasites and have higher parasite loads, than those individuals with lower levels of “connectivity”. We discuss the role these individuals can play in disease transmission dynamics.
[35] THE ECOLOGY OF *E. COLI* & OTHER *ENTEROBACTERIACEAE* ISOLATES FROM FREE-RANGING BIRDS & CHICKENS IN SAN LUIS, COSTA RICA

Sonia M. Hernandez-Divers, Natasha James, Ron Carroll, and Susan Sanchez
University of Georgia, Athens, GA, USA

Conservation efforts like sustainable agriculture (shade-grown coffee), have been promoted to preserve avian diversity in Costa Rica. However, shade-grown coffee plantations may act as ecological sinks, as they are islands of attractive habitat that serve as a point of contact with backyard chickens which have been found to have high prevalence of poultry pathogens. This study investigates the antimicrobial resistance profiles of *Enterobacteriaceae* isolates of wild birds and free-roaming chickens living in coffee plantations, and wild birds living in forest patches. We hypothesized that fecal bacteria isolated from chickens and birds living in shade-grown coffee plantations would have a higher prevalence of phenotypic antimicrobial resistance and display a higher prevalence of resistance genes. Avian fecal samples were collected and plated on enteric selective media. Isolates were identified via standard biochemical tests. The phenotypic antimicrobial resistance profile was determined as “growth” or “no growth” on antibiotic impregnated media. The Minimum Inhibitory Concentration was then determined for those isolates displaying resistance in the previous tests. We utilized PCR techniques to determine the presence of Class I Integron (*intI, 5’-3’* and *Tet(A)*) in each isolate to elucidate potential mechanisms of resistance. Chicken isolates display both a high prevalence of resistance to tetracycline and ceftiofur. Birds living in forest display a significantly different antimicrobial resistance profile than chickens termed “baseline” resistance. Birds inhabiting coffee plantations display a pattern of antimicrobial resistance similar to forest-dwelling birds; however, they have a higher prevalence of resistance to tetracycline. Is exposure to chickens responsible for this acquired resistance?

[36] WILD BIRD SURVEILLANCE FOR DETECTION OF WEST NILE VIRUS ACTIVITY IN RURAL AREAS OF SASKATCHEWAN, CANADA

Caroline Millins¹, Phil Curry², Alex Reid¹, Peter Buck³, Ted Leighton¹

¹Canadian Cooperative Wildlife Health Centre and Western College of Veterinary Medicine, Saskatoon, SK, Canada; ²Saskatchewan Health, Regina, SK, Canada; ³Public Health Agency of Canada, Ottawa, ON, Canada

Dead corvid surveillance for West Nile virus (WNV) has been widely used as a method of early detection of virus activity in seasonally endemic regions of North America. However, in rural areas, with low human population density, detection and testing of dead corvids can be low. Rural populations represent approximately one third of the total population in Saskatchewan. A seroprevalence study from the south of the province found a six times higher odds of infection in rural compared to urban residents. As an alternate method of wild bird surveillance in rural areas, a study sampling resident House Sparrows, was designed and carried out in rural southeast Saskatchewan. Sixty House Sparrows were sampled each week for 10 weeks from May 30 2006. All birds tested negative for WNV. Mosquito trapping in the study area found low numbers of the main enzootic and bridge vector *Culex tarsalis* and all mosquito pools tested negative for WNV. However, 15 WNV positive mosquito pools were trapped in the nearby city of Estevan, just 85km southeast of the study area. One of 16 dead corvids were submitted from the city of Regina, 100km northwest of the study site was infected with WNV. The combined results of mosquito and bird surveillance in southeast Saskatchewan, suggests sharp differences in WNV activity on a local scale. This finding has important implications for the distribution and allocation of WNV surveillance resources.
BIOTIC & ABIOTIC PREDICTORS OF TICK (*DERMACENTOR VARIABILIS*) ABUNDANCE & ENGORGEMENT ON FREE-RANGING RACOONS

Ryan J. Monello, Matthew E. Gompper  
University of Missouri, Columbia, MO, USA

We examine the relative importance of abiotic and biotic factors on the ability of adult *Dermacentor variabilis* ticks to attach and engorge with blood across 10 populations of free-ranging raccoons (*Procyon lotor*). We developed *a priori* models that represented explicit hypotheses based on the literature and tested the ability of these models to explain non-replete and replete (engorged with blood) tick infestation using generalized linear models and Akaike’s Information Criterion. Abiotic models that included month and site clearly provided a better fit for non-replete tick abundance data, while biotic models with host age and sex covariates best fit replete tick data. Abiotic models of non-replete abundance were superior to biotic models because of large seasonal and site fluctuations in non-replete abundance that masked differences due to host characteristics. The finding that the best-fitting models of replete tick abundance included only age and sex suggest that once a tick has reached a host, host-parasite interactions are the primary determinant of full engorgement by female ticks. The strength of age and sex as strongly predictive variables reflects increased abundance of ticks on males, increasing intensity of parasitism with age except in the oldest age class where abundance declines, and relationships between replete and non-replete tick abundance across females and males that are linear and non-linear, respectively. Non-linear patterns among males as well as the lack of large fluctuations in replete abundance despite high tick prevalence among all raccoons suggest density dependence deserves increased attention as a possible mechanism regulating engorgement by ticks.

USE OF WHITE-TAILED DEER AS SENTINELS FOR *BORRELLIA* SPP. IN THE EASTERN UNITED STATES

Jessica H. Murdock¹, Michael J. Yabsley¹, Chandrashekar Ramaswamy², Tom O’Connor², Susan E. Little³  
¹Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA: ²IDEXX Laboratories, Westbrook, ME, USA; ³Oklahoma State University, Stillwater, OK, USA

In the United States, Lyme disease, caused by the spirochete *Borrelia burgdorferi*, is most common in the northern and western United States and is vectored by the blacklegged tick (*Ixodes scapularis* and *Ixodes pacificus*). Lyme disease causes an erythema migrans rash, fever, fatigue, and headache and can cause chronic sequelae (e.g., heart palpitations, arthritis, etc). In the southern United States, a Lyme-like disease has been reported which may be caused by *B. lonestari*, a spirochete transmitted by the lone star tick (*Amblyomma americanum*) and naturally infects white-tailed deer (*Odocoileus virginianus*). The object of this project was to determine the usefulness of deer as sentinels for these *Borrelia* spp. To date, 447 white-tailed deer from 19 states were tested for anti-*Borrelia* antibodies using a *B. lonestari* whole-cell antigen indirect immunofluorescent antibody test (IFAT). By IFAT, 97 (21.7%) were positive for anti-*Borrelia* antibodies at a 1:64 dilution. To determine the prevalence of *B. burgdorferi*, samples were tested using a highly specific IDEXX 4Dx SNAP test. By SNAP, 33 (7.4%) were positive. Seventeen deer were positive by both assays, but 16 *B. burgdorferi*-positive deer were IFAT negative suggesting that IFAT testing alone is not sufficient to detect *B. burgdorferi* exposure. The majority of *B. burgdorferi*-positive deer were from northern-tier states, which corresponds with the risk of human Lyme disease. These data indicate that deer are exposed to *Borrelia* spp. and could be used as sentinels. Future work will be conducted to test additional samples and to develop a *B. lonestari*-specific assay.
[39] DOES CHYTRIDIOMYCOSIS STILL KILL FROGS 30 YEARS AFTER INVASION & DECLINES?

Kris Murray\textsuperscript{1}, Rick Speare\textsuperscript{2}, Hamish McCallum\textsuperscript{3}, Ruth Campbell\textsuperscript{2}

\textsuperscript{1}University of Queensland, St Lucia, Brisbane, Queensland, Australia; \textsuperscript{2}James Cook University, Townsville, Queensland, Australia; \textsuperscript{3}University of Tasmania, Hobart, Tasmania, Australia

Chytridiomycosis, caused by infection with the chytrid fungus \textit{Batrachochytrium dendrobatidis} (Bd), is an emerging infectious disease of amphibians implicated in global declines and extinctions. Research on this disease has been biased towards populations or species that have suffered or are suffering declines. However, little research has been carried out on populations that have survived and begun to recover and in which Bd has become endemic. We are investigating the epidemiology of Bd infections in frog populations along rainforest streams in south-east Queensland, Australia, where two frog species went extinct at the time of Bd invasion. Despite the presence of the fungus for at least 29 years in this area, several endangered species have persisted and begun to recover post-decline, prompting suggestions that they may have become resistant to infections or disease. In a mark-recapture study, we identified Bd zoospores on 65 of 334 (19.5\%) swabs taken from 6 frog species between September 2006 and February 2007. Prevalence of infections varied dramatically between species and decreased significantly as summer progressed. Uninfected frogs of one endangered species, \textit{Litoria pearsoniana}, were 3.86 (odds ratio 95\% CI = 1.14-16.98) times more likely to be recaptured than infected frogs. The best mark-recapture model included infection status and time as additive factors influencing \textit{L. pearsoniana} survival (QAICc = 0.676). Model averaged monthly survival estimates were ~20\% lower for infected frogs. Chytridiomycosis therefore remains a substantial source of mortality and a potential threatening process well after initial epidemics have passed and infection has become endemic.

[40] THE EFFECTS OF WEST NILE VIRUS ON RAPTORS AT A REHABILITATION FACILITY IN COLORADO

Nicole Nemeth\textsuperscript{1,2}, Gail Kratz\textsuperscript{3}, Rebecca Bates\textsuperscript{3}, Judy Scherpelz\textsuperscript{3}, Eric Edwards\textsuperscript{2}, Richard Bowen\textsuperscript{1}, Nick Komar\textsuperscript{2}

\textsuperscript{1}Colorado State University, Fort Collins, CO, USA; \textsuperscript{2}Centers for Disease Control & Prevention, Fort Collins, CO, USA; \textsuperscript{3}Rocky Mountain Raptor Program, Fort Collins, CO, USA

West Nile virus (WNV) infection, and associated disease and mortality, has been documented in numerous North American raptor species. Information regarding clinical presentation and long-term outcome of infected raptors is important for assessment of the potential impacts of WNV on raptor populations. Twenty-two species of raptors admitted to rehabilitation facilities from 2002-05 were tested for WNV exposure and acute infection. Clinical syndromes, sequelae and rehabilitation outcomes were recorded. WNV-specific antibody titers were monitored for 4 years in seven species of captive raptors. Forty-two percent (132/314) of admitted raptors had been exposed to WNV, and 14.6\% (46/314) were diagnosed with acute infection. West Nile virus-positive raptors were less likely to be released (79/132, 59.8\%) than negative raptors (138/182, 75.8\%), and more likely to die or be euthanized (47/132, 35.6\% for WNV-positive versus 32/182, 17.6\% for negative). Clinical syndromes varied among species. Great horned owls (\textit{Bubo virginianus}) and red-tailed hawks (\textit{Buteo jamaicensis}) were more likely to have neurological manifestations, while neurological disease was less likely in American kestrels (\textit{Falco sparverius}) and Swainson’s hawks (\textit{Buteo swainsonii}). Naturally-induced WNV antibody levels remained unchanged for \textgreater 46 months in some raptors, while in others \textgreater 4-fold rise in antibody titer, indicating re-exposure, occurred without recurrence of clinical disease. These results suggest that free-ranging raptors are frequently exposed to WNV and that clinical syndromes are more severe in certain species, leading to population reductions. West Nile virus has potentially devastating effects on raptors. Once exposed to WNV, surviving raptors benefit from protective antibody for \textgreater 4 yr post-exposure.
[41] EXPERIMENTAL INFECTION OF CLIFF SWALLOWS WITH VARYING DOSES OF WEST NILE VIRUS

Paul T. Oesterle1, Nicole Nemeth2, Cynthia Smeraski2, Kevin Bentler1, Heather Sullivan1, Ginger Young1, Kaci VanDalen1, Richard Bowen2, Larry Clark1, Robert G. McLean1, Jeffrey S. Hall1
1US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 2Colorado State University, Fort Collins, CO, USA

Cliff swallows (Petrochelidon pyrrhonata) may serve as reservoir hosts in West Nile virus (WNV) transmission. Cliff swallows often nest in large colonies, and in northern Colorado, cliff swallows begin nesting in late May. These colonies are often associated with mosquito breeding habitat. This close proximity of colonies to mosquito breeding sites and their insectivorous feeding behavior may predispose cliff swallows to WNV infection. To evaluate the potential role of cliff swallows as amplifying hosts, and assess their response to various doses of WNV, we subcutaneously inoculated 40 (65 – 80 days post-hatch) cliff swallows with four concentrations WNV (10^{1.0}, 10^{1.5}, 10^{2.5}, and 10^{3.5} plaque forming unit (PFU); 10 birds/dose). Serum samples and oral swabs were collected every 2 days for 8 days post-inoculation (DPI), with additional sampling on 14, 15 and 17 DPI. There was an association between inocula concentration and the likelihood of becoming viremic, but the concentration did not appear to have an effect on peak viremia titers in infected individuals. The average peak viremia across groups was 10^{6.3} PFU/ml serum on 3 DPI (range 10^{3.4} to 10^{6.9} PFU/ml serum), suggesting that cliff swallows develop viremias sufficient to infect mosquitoes. In addition, viral shedding was detected in oral swabs from 1 - 8 DPI with an average peak titer of 10^{4.4} PFU on 7 DPI (range < 10^{0.7} to 10^{5.7} PFU). The natural history of cliff swallows and the results from this study indicate that these passerines may play an important role in the early seasonal amplification of WNV.

[42] RED FOXES ARE SUSCEPTIBLE TO INFECTION WITH A SWAN ISOLATE OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 VIRUS

Leslie A Reperant1, Geert van Amerongen2, Marco W.G. van de Bildt2, Guus F. Rimmelzwaan2, Albert D.M.E. Osterhaus2, Andrew P. Dobson1, Thijs Kuiken2
1Princeton University, Princeton, NJ, USA; 2Erasmus Medical Centre, Rotterdam, The Netherlands

Since the re-emergence of highly pathogenic avian influenza (HPAI) H5N1 virus in 2002, various carnivore species have been found infected after eating bird carcasses. The infection resulted in a systemic disease, described notably in big felids and domestic cats, and in a domestic dog. The expanding host range and high virulence of HPAI H5N1 virus in carnivores raise not only concerns for endangered species but also questions about the potential role of carnivores in the local spread of the disease and in the transmission of the virus to other species. The red fox (Vulpes vulpes) is an abundant and widespread canid with increasing populations in Europe. It is an opportunistic carnivore which may become exposed to HPAI H5N1 virus after consumption of infected birds. We experimentally assessed the susceptibility of red foxes to infection with a Qinghai-like HPAI H5N1 virus isolated from a wild swan (Cygnus sp.). Foxes infected intra-tracheally shed virus via the pharynx up to 7 days post-inoculation and developed extensive lesions of acute broncho-interstitial pneumonia. Focal encephalitis associated with the presence of the virus was observed in the cerebrum of one fox. Foxes fed with infected chicks shed virus via the pharynx up to 5 days post-inoculation, and developed only small areas of pulmonary consolidation. These results suggest that although a productive infection is observed with up to 7 days of viral shedding, the natural route of exposure may not result in extensive lesions and death in this species, potentially facilitating the local dispersal of the virus.
[43] CHANGES IN IMMUNOCOMPETENCE OF THE GRAY CATBIRD DURING AN EXPERIMENTAL WEST NILE VIRUS INFECTION

Amanda Jo Williams¹, Jennifer C. Owen¹, Frank R. Moore¹, Mary Garvin²
¹University of Southern Mississippi, Hattiesburg, MS, USA; ²Oberlin College, Oberlin, OH, USA

Bacterial and fungal infections are attacked primarily by the innate immune system, while the energetically more expensive acquired immune system is principally responsible for virus killing. The up regulation of the acquired immune system of birds infected with a viral pathogen may cause an energetic trade-off resulting in a reduction in innate immune capabilities. To test this, we experimentally infected 11 hatching-year male Gray Catbirds (Dumetella carolinensis) with West Nile virus and measured the activity of the immune system before, during, and after infection. Eight uninfected conspecifics were used as controls for seasonal and stress-related variation in immunocompetence. Innate immunity was quantified using a microbicidal assay, a technique that correlates immunocompetence with the ability of a bird’s blood to kill a panel of microbes (Staphylococcus aureus, Candida albicans, and two strains of Escherichia coli). Acquired immunity was measured as the virus clearance rate for each bird. Infected birds are expected to have lower bacterial and fungal-killing rates than uninfected birds due to a shift in resources away from innate immunity in the West Nile-challenged birds. Similarly, within the infected birds, those with higher virus clearance rates are predicted to have lower bacterial and fungal-killing abilities. These results will be discussed in the context of understanding the potential for secondary infections to affect birds experiencing a West Nile infection.

[44] THE EFFECTS OF AFLATOXIN ON THREE DOVE SPECIES

Carin Kistler Williams, Scott E. Henke, Alan M. Fedynich, Jamie C. Laurenz
Caesar Kleberg Research Institute-Texas A&M University, Kingsville, TX, USA

Aflatoxin is a metabolic by-product produced by Aspergillus molds that grow on grains such as corn and peanuts. Acute exposure to aflatoxin results in liver damage, suppressed growth, and immune system suppression in many species. We compared the effects of aflatoxin on three columbid species to determine the consequences of exposure to aflatoxin and species differences in susceptibility and recovery. Twenty-four rock pigeons (Columba livia), white-winged doves (Zenaida asiatica), and Inca doves (Columbina inca) received 0.06 mg/kg aflatoxin in DMSO orally. Control groups (N=24 for each species) received the same volume of DMSO only. Susceptibility was determined by comparing control and treatment group mortality, spleen weight, splenocyte proliferation, and liver tissue damage 2, 9, and 30 days post-exposure. Mortality among treated birds was 4% in pigeons, 8% in white-winged doves, and 45% in Inca doves. No control birds died during the experiment. Spleen sizes in treated birds tended to be 85% the size of those in control birds though the trend was not significant. Splenocyte proliferation in treated birds tended to be 90% of that in control birds at day 2, and 94–98% by day 30, but the difference was not significant. No significant treatment trends were observed in liver lesions. This research will enhance our understanding of the impacts of aflatoxin on wild birds.
AVIAN CHOLERA IN CANADA’S EASTERN ARCTIC: EMERGENCE OF AN OLD DISEASE IN A NEW ENVIRONMENT

Grant Gilchrist1, Catherine Soos2, Isabel Buttler3, André Dallaire4, David Blehert5, Stéphane Lair4
1Environment Canada, Ottawa, ON, Canada; 2Environment Canada, Saskatoon, SK, Canada; 3Carleton University, Ottawa, ON, Canada; 4Canadian Cooperative Wildlife Health Centre, St. Hyacinthe, QC, Canada; 5National Wildlife Health Center, Madison, WI, USA

In North America, avian cholera outbreaks caused by Pasteurella multocida appear to be occurring with increasing frequency and spreading to new regions, particularly in Canada’s north and east coast. Prior to 2004, avian cholera had rarely been detected in northern Hudson Bay, however regular massive outbreaks occur in snow geese nesting on Banks Island, Northwest Territories. Since it was first detected on East Bay Island in 2004, there have been increasingly large outbreaks in common eiders each year. In 2006, over 3,500 eiders died (>30% of nesting females) between late June and early August. Small numbers of other species including gulls and geese were also affected. Most birds had lesions suggestive of septicemia, with positive isolation of P. multocida. Serotype 1 was the main cause of mortality in 2005, and serotyping of 2006 isolates is currently underway (however both serotypes 1 and 3/4 have been identified to date). The extent of mortality may have significant conservation implications to northern populations which may have difficulty recovering following repeated largescale outbreaks. Field investigations in 2007 will attempt to identify carrier status in common eiders prior to anticipated outbreaks, and determine whether the bacterium can overwinter in the Arctic environment. Furthermore, in a larger interagency investigation involving agencies in Canada and the US, we are beginning to evaluate genomic variation and degree of relatedness of cholera outbreaks across Canada, using novel DNA fingerprinting techniques on isolates obtained from outbreaks that have occurred in Canada over the last 10 years.

EPIDEMIC MORTALITY IN DOUBLE-CRESTED CORMORANTS AND THE “REVENGE OF THE TREES” HYPOTHESIS

Frederick A. Leighton1, Ian Shirley1, Thijs Kuiken2
1Canadian Cooperative Wildlife Health Centre, Saskatoon, Canada; 2Institute of Virology, Rotterdam, The Netherlands

The “revenge of the trees” hypothesis posits that, when cormorants establish new nesting colonies on forested islands, the trees are killed and the proportion of cormorant nests made on the ground versus in trees increases over time. Earlier departure of young cormorants from ground nests compared to tree nests increases the period of potential disease transmission among hatch year birds, and the probability of epidemics increases. Repeated epidemic mortality leads to colony site abandonment, and the forest regrows. Mortality was monitored from 1994 to 2006 at a colony of Double-crested Cormorants (Phalacrocorax auritus) at Doré Lake, Saskatchewan. This colony was established in 1983, when the island was forested. High mortality of hatch year birds occurred in 1990 and 1992, at which time all trees were dead and many had fallen. From 1994 to 2006, the colony was visited 2-3 times each summer, from 15 July to 25 August. Birds found sick or dead were examined for cause of death at the Western College of Veterinary Medicine. Epidemics with high mortality of fully-grown hatch year birds occurred in 9 of the 13 years of the survey: Newcastle disease in 1995, 1997, 1999 and 2003, and avian cholera in 1998, 2000, 2002, 2005 and 2006. The estimated size of the colony ranged from 4,000 to 11,000 nests, and showed no trend over time. Further testing of the hypothesis should include data on nest departure time of tree- versus-ground nesting birds, epidemic curve models, and monitoring the colony site up to abandonment.
[47] Bird Movement Predicts Buggy Creek Virus Infection in Insect Vectors

Charles R. Brown¹, Mary Bomberger Brown¹, Amy T. Moore¹, Nicholas Komar²
¹University of Tulsa, Tulsa, OK, USA; ²Centers for Disease Control & Prevention, Fort Collins, CO, USA

Predicting the spatial foci of zoonotic diseases is a major challenge for epidemiologists and disease ecologists. Migratory birds are often thought to be responsible for introducing some aviozoonotic pathogens such as West Nile and avian influenza viruses to a local area, but most information on how bird movement correlates with virus prevalence is anecdotal or indirect. We report that the prevalence of Buggy Creek virus (BCRV) infection in cimicid swallow bugs (Oeciacus vicarius), the principal invertebrate vector for this virus, was directly associated with the likelihood of movement by cliff swallows (Petrochelidon pyrrhonota), an amplifying host for the virus, between nesting colonies. The prevalence of BCRV in bugs was also directly correlated with the number of swallows immigrating into a site. Birds that move into a site are often transient individuals that may have more often encountered virus elsewhere. These results indicate that the magnitude and direction of daily bird movement in a local area can accurately predict transmission foci for this virus and provide rare quantitative evidence that birds can play a critical role in the dispersal of certain vector-borne viruses.

[48] Effects of Migratory Stress & Testosterone on the Recrudescence of Latent West Nile Virus Infections in the Gray Catbird

Jennifer C. Owen¹, Mary Garvin², Amanda Jo Williams¹, Frank R. Moore¹
¹University of Southern Mississippi, Hattiesburg, MS, USA; ²Oberlin College, Oberlin, OH, USA

West Nile virus (WNV, Flavivirdae, Flavivirus) is a pathogen of health concern to human and wildlife populations. While many aspects of the ecology of WNV are well understood, the mechanism by which its annual cycle is reinitiated each spring in temperate regions is not known. One hypotheses explaining how WNV and related viruses over-winter, is spring recrudescence of latent virus in avian reservoir hosts. Field studies can only provide circumstantial evidence for such a mechanism; therefore, controlled experiments must be conducted to demonstrate that recrudescence occurs and to identify the physiological changes that induce it. We conducted controlled laboratory experiments to examine the effects of immunosuppression through exogenous hormones and artificially induced migratory disposition on cryptic WNV infections in captive Gray Catbirds (Dumetella carolinensis). Hatching year catbirds (n=60) were inoculated with WNV in September 2006 and then held until January 2007, when birds were either induced to migrate via extended photoperiod and/or implanted with testosterone, or neither (non-migratory and placebos). Birds were then bled every two days during experimental period and tested for WNV infection via reverse transcription polymerase chain reaction (RT-PCR). We detected no active infections in any of the experimental groups. Our results suggest that the re-initiation of annual WNV transmission cycle is not due to the reactivation of chronic WNV infections in Gray Catbirds from elevated testosterone or migration.
[49] PRELIMINARY FINDINGS OF LONG-BILLED HAWK SYNDROME IN OREGON RED-TAILED HAWKS

Rob Bildfell¹, Wilson Rumbeiha², Deborah Sheaffer³, Colin Gillin⁴
¹Oregon State University, Corvallis, OR, USA; ²Michigan State University, Lansing, MI, USA; ³Audubon Society of Portland, Portland, OR, USA; ⁴Oregon Department of Fish & Wildlife, Corvallis, OR, USA

Reports of raptors, especially red-tailed hawks (*Buteo jamaicensis*), with beak abnormalities have been increasingly frequent in the Pacific Northwest during the past few years. In an effort to identify some of the factors that may be contributory to “long-billed hawk syndrome”, four Oregon red-tailed hawks with beak abnormalities and two hawks with grossly normal beaks were necropsied. A variety of histopathologic changes were observed in the beaks but the main features were epithelial hyperplasia and parakeratosis, with various degrees of inflammation and of damage to supportive collagenous and osseous tissues. A variety of potential causative factors were identified in the abnormal beaks, including *Staphylococcus* species, two species of nematode, and high levels of aluminum. However, no agent/factor was common to all birds. We will discuss these results and the current knowledge of long-billed hawk syndrome.

[50] WEST NILE VIRUS IN IDAHO: PUBLIC & GOVERNMENT RESPONSE TO MORTALITY IN WILDLIFE, HORSES & HUMANS IN 2006

Mark L. Drew¹, Leslie Tengelsen², Marilyn Simunich³
¹Idaho Department of Fish & Game, Caldwell, ID, USA; ²Idaho Department of Health & Welfare, Boise, ID, USA; ³Idaho State Department of Agriculture, Boise, ID, USA

West Nile Virus (WNV) was introduced into North America in 1999. The disease spread across the country by 2004. West Nile Virus was initially found in Idaho in 2003 in alligators and an alligator farm worker. The first confirmation of locally acquired WNV in birds, horses and humans in Idaho was in 2004. The distribution of WNV continued to expand from 11 (2004) to 15 (2005) to 38 counties (2006) and numbers of human, horse and bird cases continued to increase. In 2006, positive mosquito pools were found by 6 mosquito abatement districts conducting mosquito surveillance. A total of 490 dead birds were reported of which 236 were tested for WNV. Of these, 127 (54%) birds were positive for WNV. In addition, hundreds of fox squirrels developed hind limb paresis or died from suspected WNV. Numerous rabbits were also suspected to have been affected by WNV. A total of 338 horses were confirmed by laboratory testing to be infected with WNV in Idaho, along with numerous reports of untested sick horses. A total of 996 human cases were reported in 2006 with 23 fatalities. In response to the scale of WNV infections in Idaho, local and state government made emergency declarations and funded emergency aerial application of pesticide for mosquito control in 6 counties. Although late in the epidemic, some mosquito control was realized, but public concern remained high. Appropriate mosquito control at the residential, local and state level is needed in concert with avian and equine surveillance efforts to manage WNV in Idaho prior to emergency declarations.
**[51] PATHOGENS ASSOCIATED WITH FISHER POPULATIONS IN NORTHERN CALIFORNIA**

Richard N. Brown1,2,3, Mourad W. Gabriel2,3, Greta Wengert2,3, Sean Matthews4,5, J. Mark Higley5, Richard Callas6, Steven Self2, Janet E. Foley3

1Humboldt State University, Arcata, CA, USA; 2Integral Ecology Research Center, McKinleyville, CA, USA; 3University of California, Davis, CA, USA; 4Wildlife Conservation Society, Hoopa, CA, USA; 5Hoopa Tribal Forestry, Hoopa, CA, USA; 6California Department of Fish & Game, Redding, CA, USA; 7Sierra Pacific Industries, Redding, CA, USA

In 2004, the US Fish and Wildlife Service determined that West Coast populations of fishers (*Martes pennanti pacificus*) merited listing under the federal Endangered Species Act. Disease was noted in their determination as one of five factors potentially threatening fishers in this DPS, and our study provides information on exposures of fishers to pathogens in northern California. Our analysis includes a maximum of 101 independent samples from 76 fishers trapped between December, 2004, and March, 2007, near Hoopa, and 19 samples from individual fishers trapped between January and March, 2006, at two sites west or north of Redding, California. We report seroprevalence of 4% (5 of 120) of fishers exposed to canine distemper virus (CDV), 27% (30 of 112) to canine parvovirus (CPV), 4% (5 of 118) to canine herpes virus (CHV), 4% (5 of 119) to canine adenovirus (CAV2), 7% (6 of 78) to West Nile virus, 49% (23 of 47) to *Toxoplasma gondii*, 80% (70 of 88) to *Anaplasma phagocytophilum*, and none were seropositive for *Bartonella* spp. or *Yersinia pestis*. Seroprevalences did not differ statistically among study areas, but samples seropositive to CPV and CHV were collected only from the population near Hoopa. Eighteen (18% of 98) fecal samples were PCR-positive and product sequences matched Genbank sequences of *A. phagocytophilum*. Disinfection of equipment, including fisher handling gear, is recommended to minimize anthropogenic spread of directly transmitted pathogens.

**[52] PATHOGENS ASSOCIATED WITH MESOCARNIVORES THAT ARE SYMPATRIC TO A POPULATION OF FISHERS IN NORTHWESTERN CALIFORNIA**

Mourad W. Gabriel1,2, Richard N. Brown1,2,3, Greta M. Wengert1,2, J. Mark Higley4, Sean Matthews4,5, Janet E. Foley1

1University of California Davis, Davis, CA, USA; 2Integral Ecology Research Center, McKinleyville, CA, USA; 3Humboldt State University, Arcata, CA, USA; 4Hoopa Tribal Forestry, Hoopa, CA, USA; 5Wildlife Conservation Society, Hoopa, CA, USA

Fishers (*Martes pennanti*) in the Pacific states are a candidate for listing under the Federal Endangered Species Act and disease is cited as a potential threat. We evaluated the prevalence of exposure to pathogens in a community of mesocarnivores sympatric with a population of fishers near Hoopa, California. We collected and analyzed samples from 27 gray foxes, (*Urocyon cinereoargenteus*), 10 striped skunks (*Mephitis mephitis*), 4 spotted skunks (*Spilogale gracilis*), 16 ringtails (*Bassariscus astutus*) and 4 raccoons (*Procyon lotor*) between March, 2004 and February, 2007. We report seroprevalence of 2% (1 of 62) to canine distemper virus, 30% (19 of 45) to parvovirus, 9% (6 of 58) to canine adenovirus 2, 0% (0 of 63) to canine herpes virus, 4% (2 of 43) to West Nile virus and 50% (32 of 64) to *Anaplasma phagocytophilum*. Sixteen percent (3 of 19) of the whole blood samples were PCR-positive for and sequences matched Genbank sequences of *A. phagocytophilum*. Twenty percent (10 of 49) of the fecal samples were PCR-positive for parvovirus DNA and sequencing is currently ongoing. There was no significant difference in seroprevalence of CDV, CPV, CAV, CHV and WNV between fishers sampled in the area and their sympatric mesocarnivores. Surveillance of health in communities comprising sensitive species provides information necessary for comprehensive wildlife management and conservation.
[53] Increasing Intraspecific Aggression in an Expanding Otter Population

Vic Simpson
Wildlife Veterinary Investigation Centre, Cornwall, England

The otter (*Lutra lutra*) population of England declined dramatically in the late 1950s and 1960s. They became extinct over most of the country but a small population remained in the South West. Starting in 1988, any otters found dead in the region have been examined post-mortem in order to monitor the health status of the population. There has been strong evidence of a population recovery, with a steady increase in the numbers submitted each year and recolonisation of former haunts. Of the 598 otters examined by the end of 2006 the majority (81%) had been killed by road traffic. The deaths were strongly seasonal and there was an adult bias. However, irrespective of the cause of death, many otters had recent bite wounds. As the population increased, the proportion of otters with bites also increased, rising from 12.5% in the first few years to a peak of nearly 70% in 2004. At the same time, there were striking increases in the prevalence of other disease conditions, including dental lesions, pulmonary disease and renal calculi. Most of the bites were attributed to intraspecific aggression, with all ages classes affected and bites equally common in both sexes. The temporal pattern of bites varied according to age class. It is proposed that as the population expands there is increased competition for resources which leads to increased interactions, often violent, and this makes otters more likely to be killed on roads. These results have implications for those involved in rehabilitation and in implementing mitigation measures.

[54] Leishmania spp. in Wild Carnivores Captured in the Pantanal, Brazil

Rodrigo S. P. Jorge1,2,3, Cáris Maroni Nunes4, Cristiana de Melo Trinconi4, Henrique Borges de Paula4, Ana Karina Kerche Dias5, Fernando Ferreira1
1University of São Paulo, Brazil; 2Predator National Center, Atibaia, Brazil; 3Brazilian Institute of Conservation Medicine – Triade, São Paulo, Brazil; 4Veterinary Medicine Course, UNESP, Araçatuba, Brazil; 5Institute of Biosciences/UNESP, Botucatu, Brazil

Visceral leishmaniasis (VL) is a public health problem of major concern. In Latin America, 90% of the cases occur in Brazil, where approximately 4,000 new human cases happen every year and 5 to 10% of these people die. VL in Brazil is caused by the protozoan *Leishmania chagasi*. The main vector involved in its transmission is *Lutzomyia longipalpis* and the domestic dog is considered the main reservoir. Wild canids have also been found naturally infected. Thus, they are considered important potential reservoirs, although their role in the cycle of the disease is not well understood. From 2002 to 2006, 16 free-ranging wild carnivores were captured (including 9 crab-eating foxes *Cerdocyon thous*, 4 racoons *Procyon cancrivorous*, 2 maned wolves *Chrysocyon brachyurus* and 1 ocelot *Leopardus pardalis*) in the Pantanal and blood samples were collected and preserved. Additionally, 70 domestic dogs from the surrounding settlements were also sampled. Search for *Leishmania* spp. kDNA was performed by polymerase chain reaction (PCR). Six wild carnivores (3/9 crab-eating foxes, 1/4 racoons, 1/2 maned wolves, 1/1 ocelot) and 20 domestic dogs were positive. These results suggest the presence and natural transmission of the agent in the region, including the sylvatic environment. Differentiation between *Leishmania* species will be done in the near future, allowing elaboration of specific measures aiming to control this zoonotic disease in the region. Additionally, the potential impact of leishmaniasis on the conservation of wild carnivores should be further examined.
[55] PREVALENCE OF SELECTED INFECTIOUS DISEASES IN BLACK-FOOTED CATS & SYMPATRIC CARNIVORES IN THE NORTHERN CAPE: PRELIMINARY RESULTS

Nadine Lamberski1, Alex Sliwa2, Beryl Wilson3, Jason R. Herrick4, Edward J. Dubovi5
1San Diego Wild Animal Park, Escondido, CA, USA; 2Cologne Zoo, Köln, Germany; 3McGregor Museum, Kimberley, South Africa; 4Cincinnati Zoo & Botanical Garden, Cincinnati, OH, USA; 5Cornell University, Ithaca, NY, USA

This study is part of a larger conservation initiative to determine the ecology, reproductive biology, genetics, and health of the black-footed cat (Felis nigripes) in the Northern Cape Province of the Republic of South Africa. It is based on the hypothesis that an assessment of distribution, genetic diversity, disease exposure, and reproductive fitness in free-ranging black-footed cats will allow for better characterization of the species’ conservation status and provide comparative data that can be used to monitor the health of in situ and ex situ populations over time. As natural habitat disappears or becomes fragmented, populations of black-footed cats may become genetically isolated, which could result in reduced reproductive fitness and increased susceptibility to disease. Further consequences include increased contact with other carnivores and the pathogens they carry including domestic dogs and cats. Black-footed cats share their territory, prey base, and infectious disease susceptibility with many small carnivores including genets, caracals, African wildcats, yellow mongoose, suricates, Cape fox, bat-eared fox, black-backed jackals, and striped polecats providing numerous opportunities for disease transmission. If wild populations of black-footed cats are fragmented and facing disease challenges, the conservation status of this species may be more critical than currently believed. Determining the seroprevalence of diseases in black-footed cats and other small carnivores may help elucidate the infectious diseases that can place fragile populations at risk. Additionally, comparing disease prevalence among populations may help identify populations at an increased risk of catastrophic disease outbreaks.

[56] CLINICAL & PATHOLOGICAL CONSEQUENCES OF FELINE IMMUNODEFICIENCY VIRUS INFECTION IN WILD AFRICAN LIONS IN BOTSWANA

Melody E. Roelke12, Meredith Brown1, Hanlie Winterbach3, Christiaan Winterbach3, Graham Hemson4, Jennifer L. Troyer12, Dahlem Smith2, Randall C. Johnson12, Jill Pecon-Slattery1, Alfred L. Roca12, Katherine Alexander5, Stephen J. O’Brien2
1 National Cancer Institute, Frederick, MD, USA; 2SAIC-Frederick, Inc., Frederick, MD, USA; 3Tau Consultants, Maun, Botswana; 4Wildlife Conservation Research Unit, Tubney, Oxon, UK; 5Department of Wildlife & National Parks, Kasane, Botswana

Feline immunodeficiency virus (FIV) is a lentivirus related to human immunodeficiency virus (HIV) that causes feline AIDS in domestic cat (Felis catus). Lion-specific strains of FIV (FIVple) are endemic in many free-ranging populations of African lions. While long-term studies of FIV genome variation reveal patterns consistent with co-adaptation of virus and host in free-ranging African lions (Panthera leo), there still is speculation in the literature concerning the degree to which infection with these viruses impacts the health of the wild animals. Media reports in Botswana suggest that FIVple infection poses a threat to lions, while most of the published lion ecology literature supports a benign infection, despite recent finding that FIVple infection results in reduced CD4+ T-cell counts in free-ranging and captive lions. This study is the first systematic examination of clinical correlates of (FIVple) infection in wild lions. Specifically, clinical, biochemical, and serological parameters were compared between FIVple-positive (N=47) and negative (N=17) lions anesthetized and sampled multiple between 1999 and 2006 in Botswana. Significant differences (p ≤ 0.05) between infected and uninfected lions were observed in lymphadenopathy, gingivitis, tongue papillomas, dehydration, coat condition, red blood cell parameters, liver enzymes, and serum proteins. In addition, histopathologic examination of spleen and lymph node biopsies from infected lions (N=9) revealed a spectrum of changes consistent with lymphoid depletion, which is the hallmark pathology documented in immunodeficiency virus infections of humans, macaques, and domestic cats. We therefore suggest that there may be clinical consequences of concern related to FIVple infection in free-ranging lions.
[57] BIOCHEMICAL & MOLECULAR CHARACTERISTICS OF Pasteurella spp. & Mannheimia spp. ISOLATED FROM BIGHORN & DOMESTIC SHEEP IN HELLS CANYON

E. Frances Cassirer1,2, Margaret A. Davis2, Douglas R. Call2, Subramaniam Srikumaran2, Glen C. Weiser3
1Idaho Department of Fish & Game, Lewiston, ID, USA; 2Washington State University, Pullman, WA, USA; 3University of Idaho, Caldwell, ID, USA

We compared biochemical and molecular characteristics of Pasteurella spp. and Mannheimia spp. bacteria isolated from the lungs of 35 adult and juvenile bighorn sheep with pasteurellosis pneumonia to bacteria in these genera collected from healthy bighorn sheep in the same populations, and to isolates from sympatric domestic sheep (O. aries). We used pulsed-field gel electrophoresis (PFGE) to investigate the genetic profiles of Pasteurella spp. associated with disease in bighorn sheep and to assess the spatial and temporal dynamics of these bacteria in a free-ranging bighorn sheep metapopulation. We found multiple biovariants and genetic profiles associated with pneumonia, and we found that organisms with the same genetic profiles were isolated from both sick and healthy bighorn sheep within the same populations. We did not find any common genetic profiles in bighorn and domestic sheep. We also found no association of genes for known virulence factors leukotoxin (lktA gene) and superoxide dismutase (sodC gene) with pneumonia. The pattern of genetic relatedness of microorganisms across the landscape appeared to be consistent with the known structure of the Hells Canyon bighorn sheep metapopulation. As expected, organisms with identical genetic profiles were most frequently found within a sheep population. However, we also found some bacteria with identical genetic profiles in several different, often geographically clustered populations, suggesting possible transmission across populations. While pasteurellosis is an important cause of mortality in this bighorn sheep metapopulation, we found no evidence for the presence of pathogenic epidemic strains responsible for pneumonia outbreaks. The results of this study suggest that the Pasteurella spp. and Mannheimia spp. isolated from these animals were opportunistic secondary pulmonary invaders.

[58] SCRAPIE GENETIC FINDINGS IN A HERD OF DESERT BIGHORN SHEEP

Scott C. Bender1, Katherine O’Rourke2
1Navajo Nation Veterinary Program, Navajo Nation, Window Rock, AZ; 2US Department of Agriculture-Agricultural Research Service, Pullman, WA, USA

DNA samples were collected from a closed herd of Desert Bighorn Sheep (Ovis canadensis nelsoni) in a remote area of the Navajo Nation, over a span of 8 years, for eventual used in determining the degree and risk of in-breeding in this herd, with regard to population maintenance, of this herd. Blood samples were collected, split for future use and then a portion submitted to look at the codon 171 and later codon 136 of the PrP-sc gene, which is involved in the susceptibility of sheep to Scrapie, to see if either of these two codons showed any diversity, like that found in domestic sheep. The finding of these results will be presented and reviewed with thoughts toward all the North American wild sheep and the risk, if any, Scrapie may pose to these populations.
[59] FERAL SWINE CONTACT WITH DOMESTIC SWINE: POTENTIAL FOR DISEASE TRANSMISSION

A. Christy Wyckoff1, Scott E. Henke1,4, Tyler A. Campbell2, David G. Hewitt1, Kurt C. VerCauteren3
1Texas A&M University-Kingsville, Kingsville, Texas USA; 2US Department of Agriculture-Wildlife Services, Kingsville, Texas, USA; 3US Department of Agriculture-Wildlife Services, Fort Collins, Colorado, USA

Feral swine (Sus scrofa) are present in 38 of the 50 United States, and their populations continue to expand. Backyard and other transitional domestic swine are widely regarded as vulnerable to diseases harbored by feral swine. Our objectives were to determine seroprevalence of selected diseases in Texas feral swine populations, and identify contact events between feral and domestic swine. The serosurvey included pseudorabies virus (PRV), swine brucellosis (Brucella spp.), porcine reproductive and respiratory syndrome (PPRS), and classical swine fever (CSF). Overall prevalence of antibodies against brucellosis and PRV were 11% and 30%, respectively. Feral swine from southern Texas were 7.2 times more likely to have been exposed to PRV than brucellosis; whereas, feral swine from eastern Texas were 1.3 times more likely to have been exposed to brucellosis than PRV. Seroprevalence of PRRS antibodies was low at 3% of feral swine from southern Texas. All samples tested negative for antibodies to CSF. To determine the frequency of contact events between feral swine and neighboring domestic swine we analyzed movement data from 37 adult feral swine that were trapped ≤10 km from neighboring domestic swine and collared with GPS collars. Seven of the 37 feral swine had contact (relocated within 100 meters of) with domestic swine. Additionally, we analyzed 60 consecutive days of experimental track plots around control pens and domestic sow pens, and found greater visitation to the domestic swine pen than to the control pen. Our data demonstrate that seropositive feral swine have direct contact with domestic swine presenting opportunity for disease transmission.

[60] BOVINE TUBERCULOSIS ECOLOGY IN DOÑANA NATIONAL PARK, SPAIN: THE ROLE OF WILD UNGULATES AS DISEASE RESERVOIRS IN THE LAST IBERIAN LYNX STRONGHOLDS

Christian Gortazar1, Manuel Reglero1, Maria Paz Martín-Hernando1, Maria Jose Torres Sánchez2, Joaquin Vicente1, Juan J. Negro3, Javier Aznar Martín4
1IREC National Wildlife Research Institute (CSIC-UCLM-JCCM), Ciudad Real, Spain; 2Universidad de Sevilla, Spain; 3Estacion Biológica Doñana CSIC, Sevilla, Spain. 4Servicio de Microbiología, HH UU Virgen del Rocío, Sevilla, Spain

Tuberculosis (TB) due to Mycobacterium tuberculosis complex, mainly involving Mycobacterium bovis, is a worldwide disease that affects a wide range of domestic and wild animals and humans. The existence of wildlife reservoirs limits the effectiveness of eradication schemes, largely based on testing and culling of TB-positive cattle. In Spain, an increase in TB prevalence in wild ungulates has been reported. We studied the particular situation of TB in Doñana National Park (southern Spain), one of the two last strongholds for the Iberian lynx (Lynx pardinus), a highly endangered felid that is susceptible to TB. In contrast to most other Spanish wild ungulate populations, no commercial hunting and no artificial feeding takes place in Doñana, and traditional cattle breeding still exists. This, along with lynx presence, makes Doñana an ideal study area for TB ecology. In 2006, compulsory skin testing revealed 7% reactors among cattle from the study area (data from Veterinary Services). From April 2006 to April 2007, 124 European wild boar (Sus scrofa), 95 red deer (Cervus elaphus), and 100 fallow deer (Dama dama) were sampled within the park, necropsied, and examined by histopathology and microbiology. Mycobacterium bovis was isolated from tonsil and lymph node samples of 50% wild boar, 15% red deer, and 10% fallow deer. A north-south gradient in TB prevalence was observed. The presentation will focus on the comparative study of TB in these three wild ungulates, discussing the possible reasons for the observed spatial and inter-specific differences.
[61] DESCRIPTION OF AN OUTBREAK OF TUBERCULOSIS & SUBSEQUENT EPIDEMIOLOGICAL INVESTIGATION IN A CAPTIVE BREEDING HERD OF WOOD BISON

Brett T. Elkin¹, John S. Nishi¹,²
¹ Department of Environment and Natural Resources, Yellowknife, NT, Canada; ²ALCES© – Landscape Ecology Group, Millarville, AB, Canada

Two major issues facing recovery of the threatened wood bison (Bison bison athabascae) in Canada include conservation of genetic diversity and the presence of bovine tuberculosis (Mycobacterium bovis) and brucellosis (Brucella abortus) in the greater Wood Buffalo National Park metapopulation. The Hook Lake Wood Bison Recovery Project (HLWBRP) was a long-term wildlife co-management conservation project that was initiated to assess possible techniques to salvage healthy bison calves from an infected free-roaming population. A captive breeding herd was established from wild-caught newborn calves, using a combination of techniques to attempt disease elimination and an intensive testing regime to monitor herd health status. In spring 2005, a single case of tuberculosis was confirmed in a clinically normal 2.5 yr old captive-born male culled for management reasons. Herd testing and epidemiological investigation were conducted, including both live animal testing (intradermal tuberculin skin test; blood tests) and postmortem evaluation (necropsy, histology, culture) during depopulation. Tuberculosis was found in 12 animals, but there was no evidence of brucellosis. Our investigations revealed the source of the infection, route and pattern of transmission within the herd, and risk factors that facilitated disease entry and spread. We present a history of the disease control and testing protocols for this herd, describe the outbreak and live animal and postmortem results, and offer a preliminary assessment of why and how the outbreak occurred. We suggest that these findings have broader implication for developing feasible salvage techniques from wildlife populations that are infected with bovine tuberculosis and brucellosis.

[62] LESSONS LEARNED FROM THE HOOK LAKE WOOD BISON RECOVERY PROJECT: RELEVANCE & APPLICATION TO THE LARGER ISSUE OF NORTHERN DISEASED BISON IN CANADA

John S. Nishi¹,², Brett T. Elkin¹
¹ Department of Environment and Natural Resources, Yellowknife, NT, Canada; ²ALCES© – Landscape Ecology Group, Millarville, AB, Canada

The Hook Lake Wood Bison Recovery Project (HLWBRP) was initiated by the community of Fort Resolution and the Government of the Northwest Territories to salvage disease-free bison calves from a wild herd of wood bison (Bison bison athabascae) in the Slave River Lowlands – a subpopulation of the greater Wood Buffalo National Park metapopulation that is known to be infected with Mycobacterium bovis) and Brucella abortus. This captive breeding herd was a pilot project to evaluate possible approaches to genetic salvage and disease eradication for recovery of this threatened species. A combination of techniques was used including the capture, isolation and hand-rearing of 58 wild-caught neonates. All wild-caught calves were treated with a multi-drug antibiotic therapy during their first 5 mo of captivity, combined with biannual live animal disease testing, pre-partum isolation and post-partum brucellosis testing for first-time dams and offspring, and genetic management of captive breeding. Unfortunately, in spring 2005, we found a case of tuberculosis. This initial discovery was followed up by an intensive epidemiological investigation, additional testing, selective culling, and eventually destruction of the entire herd in spring 2006. We provide a follow-up assessment and outline the lessons learned from this wildlife management project. We cover issues including genetic management and conservation, wildlife disease risk assessment methods, disease test performance, advanced reproductive technologies, and the dynamic political challenges of addressing local community/stakeholder concerns. We outline practical suggestions for how wildlife management agencies may move forward on the northern diseased bison issue and its political and epidemiological challenges.
[63] EPIZOOTIOLOGY OF GENERALIZED DEMODICOSIS IN A FLORIDA BLACK BEAR POPULATION

Mark W. Cunningham¹, Scott Terrell², Bambi Ferree¹, Linda M. Penfold³
¹Florida Fish & Wildlife Conservation Commission, Gainesville, FL, USA; ²Disney’s Animal Kingdom, Bay Lake, FL, USA; ³White Oak Conservation Center, Yulee, FL, USA

Generalized demodicosis is rare in free-ranging carnivores and has been described in only one black bear outside of Florida. However, since 1990, 36 bears have been diagnosed with generalized demodicosis with the majority located in the Ocala population. Clinical signs vary by gender, age, reproductive status, and season, and range from mild periocular alopecia to generalized alopecia. Histopathologic changes are also variable but may include mild to severe perifollicular fibrosis, periadnexal inflammation (with occasional furunculosis), and dermal perivascular infiltrates of lymphocytes, plasma cells, and eosinophils. All cubs of affected sows go on to develop high numbers of mites in their first year. However, most males begin to recover from the infestation by their second year while most females progress to chronic generalized demodicosis. Females with chronic generalized demodicosis have significantly higher serum progesterone concentrations compared to normal females. The etiology for this condition in Florida black bears is unknown.

[64] UNUSUALLY HIGH PREVALENCE OF CERUMINOUS GLAND CARCINOMAS IN CHANNEL ISLAND FOXES ON SANTA CATALINA ISLAND, CALIFORNIA

T. Winston Vickers¹, Linda Munson², David K. Garcelon³
¹Institute for Wildlife Studies, Long Beach, CA, USA; ²University of California, Davis, CA, USA; ³Institute for Wildlife Studies, Arcata, CA, USA

During health surveillance following the precipitous decline of island foxes (Urocyon littoralis) on four of six Channel Islands, an unusually high number of ceruminous gland carcinomas were detected in foxes from Santa Catalina Island (SCA). Most carcinomas were confined to the ear canal, but others had extensive local invasion and metastasis leading to death. No carcinomas were detected in foxes from other islands. To determine the prevalence in the SCA wild population, ears were examined and proliferative lesions were biopsied on foxes trapped for population surveillance. In 2004, random foxes ≥1 year old were examined, in 2005 37% of animals estimated to be 1 – 3 years old and 78% of foxes estimated to be > 3 years old were randomly selected for exams, and in 2006 surveillance focused on foxes with ear lesions. In 2004, 10 of 111 foxes (9%) ≥1 year old had carcinoma confirmed by histopathology, and prevalence was 30 % (9 of 30) in foxes > 3 years old. In 2005, 18 of 47 (38%) foxes > 3 years old had carcinoma. In 2006, 20 of 45 (44%) foxes > 3 years old had carcinoma. Among foxes 1 – 3 years old, carcinoma was detected in 1% (1 of 81) in 2004, 2% (1 of 46) in 2005, and 3% (1 of 35) in 2006. This prevalence of cancer is a cause for concern in a recovering population that now has only approximately 500 foxes. An epidemiological investigation to determine true prevalence and evaluate possible risk factors is ongoing.
[65] EVALUATION OF SCIURIDS AS ECOLOGICALLY SIGNIFICANT HOSTS FOR ANAPLASMA PHAGOCYTOPHILUM IN CALIFORNIA

Nathan C. Nieto, Janet E. Foley
University of California, Davis, CA, USA

Granulocytic anaplasmosis (GA), caused by Anaplasma phagocytophilum, is a potentially fatal, emerging rickettsial disease of humans, domestic animals, and wildlife. The reservoir for GA in the western US was hypothesized to be the dusky-footed woodrat (Neotoma fuscipes), because experimental infection in woodrats can last from 1-3 months, and surveillance identifies repeatedly-infected individuals. However, many locations in northern California with numerous equine and canine GA cases have abundant woodrats with little to no evidence of exposure. This was parallel with the ecology of Lyme borreliosis (LB), in which the reservoir had been thought to be woodrats. However, recent LB evidence suggests that woodrats often are infected with B. bissetii, which is not a human pathogen, while grey squirrels (Sciurus griseus) are consistently infected with B. burgdorferi ss. The purpose of this study was to determine whether sciurids from multiple areas of northern California were exposed to or infected with A. phagocytophilum. Sciurids of 10 different species were either live-trapped or retrieved as road-kill and tested for A. phagocytophilum by PCR and serology. Arboreal squirrels (Glaucomys sabrinus, S. griseus, S. carolinensis, and Tamiasciurus douglasii) had greater evidence of exposure and active infection than sciurids that tend to be less arboreal or ground dwelling (Spermophilus beecheyi, Sp. lateralis, and Tamias sp.). In addition, tree squirrels also had much higher prevalence estimates than woodrats from many of the same areas. Such extensive exposure suggests that tree squirrels may be important in the maintenance of GA in California.

[66] THE DYNAMICS OF HEALTH IN FIELD VOLE POPULATIONS: A HAEMATOLOGICAL PERSPECTIVE

Pablo M. Beldomenico, Sandra Telfer, Stephanie Gebert, Lukasz Lukomski, Malcolm Bennett, Michael Begon
University of Liverpool, Liverpool, UK

The periodic fluctuations of cyclic small mammal populations have puzzled biologists for decades. Pathogens have been suggested to be important drivers of population dynamics, but, although some studies investigated the impact of specific etiologic agents, those using generic indices of health to assess condition in an integrative manner have been rare. Hematological dynamics in natural populations of field voles were investigated to determine environmental and host factors associated with infection, immunocompetence and general condition. Three field vole populations were monthly sampled for two years, and on each trapping session, a blood specimen from every individual was processed to obtain a complete blood cell count. Also, samples from an experimental colony were analyzed, to reinforce the results and allow sounder conclusions. Sets of mixed effects models were developed for each main cell type to separately evaluate the effects of various factors on blood parameters of juveniles, post-juveniles, and mature breeding females. Season was the main driver of the dynamics of all cell types examined. In winter, voles appear vulnerable but infections do not occur. Spring, however, seems to be when voles are most at risk of disease, particularly at high past population densities.
[67] SIN NOMBRE VIRUS (SNV) & DEER MICE DYNAMICS IN A PAIRED SYLVAN & PERIDOMESTIC POPULATION IN MONTANA

Amy J. Kuenzi, Richard J. Douglass
Montana Tech, Butte, MT, USA

Most human cases of hantavirus pulmonary syndrome in the United States are caused by Sin Nombre virus acquired in a peridomestic setting, yet studies of the ecology and infection dynamics in the reservoir host, the deer mouse (Peromyscus maniculatus), have focused on sylvan populations. Although the dynamics of natural sylvan populations may influence the numbers and behavior of peridomestic deer mice, the specific human and rodent behaviors that lead to peridomestic exposure can be elucidated only through studies in the specific environment of exposure. Since 1995, we have collected monthly demographic, ecological, and epidemiological data from both a sylvan and a peridomestic population of deer mice in western Montana. Population size in the peridomestic population has tracked that of the sylvan population, but declines in population size begin sooner in peridomestic populations possibly indicating a space constraint in this habitat. Prevalence of antibodies to SNV has been consistently higher in the peridomestic population compared to the sylvan population.

[68] REGULATORY T CELL-LIKE RESPONSES IN DEER MICE PERSISTENTLY-INFECTED WITH SIN NOMBRE VIRUS

Tony Schountz¹, Joseph Prescott², Lauren Oko¹, Katy-Marie Mirowsky², Ann Cogswell¹, Alejandra Galvez Fuenzalida³, Brian Hjelle²
¹University of Northern Colorado, Greeley, CO, USA; ²University of New Mexico School of Medicine, Albuquerque, NM, USA

Hantavirus cardiopulmonary syndrome is a zoonotic illness associated with a systemic inflammatory immune response, capillary leak, noncardiogenic pulmonary edema and shock. Cytokines, including tumor necrosis factor (TNF), interferon-γ (IFNγ) and lymphotoxin (LT), are thought to contribute to its pathogenesis. In contrast, infected rodent reservoirs of hantaviruses experience few or no pathologic changes and the host rodent can remain persistently infected for life. Generally, it is unknown why such dichotomous immune responses occur between humans and reservoir hosts. Thus, we examined CD4+ T cell responses from one such reservoir, the deer mouse (Peromyscus maniculatus), infected with Sin Nombre virus. Proliferation responses to viral nucleocapsid antigen were relatively weak in T cells isolated from deer mice, regardless of acute or persistent infection. The T cells from acutely-infected deer mice synthesized a broad spectrum of cytokines, including IFNγ, IL-4, IL-5, and transforming growth factor-β1 (TGFβ1), but not TNF or LT. However, in T cells from persistently-infected deer mice only TGFβ1 was expressed by all lines while some expressed IFNγ or IL-5. The Fox-p3 transcription factor, a marker of regulatory T cells, was expressed by most of these cells. Collectively, these data suggest that TGFβ1-expressing regulatory T cells may play an important role in limiting immunopathology in the natural reservoir host, but this response likely interferes with viral clearance. Such a response may have arisen as a mutually-beneficial coadaptive evolutionary event between hantaviruses and their rodent reservoirs so as to limit disease while also allowing the virus to persist.
[69] NATURAL & EXPERIMENTAL INFECTION OF WHITE-TAILED DEER WITH AN EHRlichia SP. FROM THE UNITED STATES CLOSELY RELATED TO EHRlichia Ruminantium

Michael J. Yabsley¹, Amanda D. Loftis², Susan E. Little³
¹Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA; ²Centers for Disease Control & Prevention, Atlanta, GA, USA; ³Oklahoma State University, Stillwater, OK, USA

An Ehrlichia sp. (PM Ehrlichia sp.) closely related to Ehrlichia ruminantium was recently detected in a domestic goat experimentally infested with lone star ticks (LST, Amblyomma americanum) collected from Georgia, USA. The infected goat exhibited pyrexia and mild clinical pathologic abnormalities consistent with ehrlichiosis. At least two other Ehrlichia species (E. chaffeensis and E. ewingii) are maintained in nature by a cycle involving LST as the primary vector and white-tailed deer (Odocoileus virginanus) as a known or suspected reservoir. To investigate the possibility that white-tailed deer are potential hosts of the PM Ehrlichia sp., whole blood samples collected from 87 wild deer were screened with a species-specific nested PCR assay targeting the citrate synthase gene. In addition, two laboratory-raised white-tailed deer fawns were each infested with 120 wild-caught LST adults from Missouri, and blood samples were periodically collected and tested for the PM Ehrlichia sp. Of 87 deer tested from 20 locations in the southeastern United States, 3 (3.2%) deer from KY, NC, and VA were positive for the PM Ehrlichia sp. Wild-caught ticks transmitted the PM Ehrlichia sp. to one of two deer fawns, and colony-reared nymphal LST acquired the organism from the deer, maintained it transstadially as they molted to adults, and transmitted the PM Ehrlichia sp. to two naïve fawns. These findings indicate that white-tailed deer are naturally and experimentally susceptible to infection with an Ehrlichia sp. closely related to E. ruminantium and are able to serve as a source of infection to lone star ticks.

[70] DETECTING TICK-BORNE PATHOGENS IN AUSTRALIAN TICKS

I-M. Vilcins¹, J. Old², E. Deane¹
¹Macquarie University, NSW, Australia; ²University of Western Sydney, NSW, Australia

Over 50 species of tick have been described in Australia since 1970, including three introduced species. To date, little is known of the role these ticks play in the transmission of tick-borne disease. Past research has focused on species that harbor pathogens which affect humans or domestic and agricultural animals. However, the majority of Australian ticks parasitise native species and have been little studied. Because ticks are known for transmitting the broadest array of pathogens of all arthropod vectors, this study was aimed at detecting and characterizing genera of known virulence in Australian ticks. Since November 2004, close to 2000 tick samples have been collected opportunistically from a wide range of host animals and geographical regions in Australia. Ticks collected from native marsupial and reptile host species were targeted for molecular screening. Primers amplifying several key genes for the genera Coxiella, Rickettsia, Bartonella, Borrelia, Hepatozoon and Ehrlichia were used to identify novel and previously identified species in extracted tick DNA, each representing new tick host and geographical records. Uncharacterized Rickettsia and Hepatozoon species were identified in the common marsupial tick Ixodes tasmani collected from Tasmanian devils (Sarcophilus harrisii) and koalas (Phascolarctos cinereus). Phylogenetic analysis of several sequences obtained for conserved and variable genes reflected a high level of bacterial and protozoal species diversity in Australian ticks.
[71] GIARDIA ASSEMBLAGE A: HUMAN GENOTYPE IN MUSKOXEN IN THE CANADIAN ARCTIC

Susan Kutz1, Andrew Thompson2, Kami Kandola3, John Nagy4, Caroline Wielinga2, Lydden Polley5, Brett Elkin4
1University of Calgary, Calgary, AB, Canada; 2Murdoch University, Murdoch, WA, Australia; 3Stanton Territorial Health Authority, Yellowknife, NT, Canada; 4Government of the Northwest Territories, Yellowknife, NT, Canada; 5University of Saskatchewan, Saskatoon, SK, Canada

As part of an ongoing program for assessing the biodiversity and impacts of parasites in Arctic ungulates we examined 72 muskox fecal samples from Banks Island, Northwest Territories, Canada for Giardia and Cryptosporidium. Cryptosporidium spp. was not detected, but 15 of 72 samples were positive for Giardia. Genetic sequencing of five isolates of Giardia demonstrated G. duodenalis, Assemblage A, the zoonotic genotype. The evidence suggests that this is an example of ‘spill-over’ of Giardia from people to wildlife in a remote arctic region. The epidemiology of this parasite in muskoxen, the health implications, and the parasite flow among various wildlife species and people are discussed.


Jonas Malmsten1, Bjørnar Ytrehus2, Erik Ågren1, Jan Chirico1
1National Veterinary Institute, Uppsala, Sweden; 2National Veterinary Institute, Oslo, Norway

In the winter of 2006-2007, several reports of hair loss in free-ranging Scandinavian moose (Alces alces) have been reported to the National Veterinary Institutes of Norway and Sweden. Several moose with hair loss were shot during the regular hunting season, which ended January 31st, 2007, and others were found dead in the forests of Mid-western Sweden, and Mid-Eastern Norway. The moose found dead were in poor body condition and the hair loss affected up to 90 per cent of the body surface. In addition, during the spring of 2007, several reports of live moose with alopecia affecting 30-80 per cent of the body were observed in Mid-western Sweden, Mid-eastern Norway, and Southern Sweden. The majority of these moose were reported to be in good body condition. In one area, between 10-20 per cent of the population is believed to suffer from this hair loss syndrome. The population density in that area is estimated to be 45-50 moose per 10 000 acres in the wintertime. No definitive cause has been identified, but the deer ked (Lipoptena cervi), is believed to play a major role. Up to 16,000 deer keds have been counted in one moose necropsied at Norway’s National Veterinary Institute (Ytrehus, unpubl. data), and 150 deer keds in 15 square inches of skin. This type of hair loss syndrome in moose has not been described previously. A joint research project between the National Veterinary Institutes of Norway and Sweden has been initiated.
AN INVESTIGATION ON THE PARASITES OF OSTRICH BY SCREENING EGGS IN FECES, ISFAHAN, IRAN

Soraya Naem, Navid Rafeei
Urmia University, Urmia, Iran

Ostriches are the largest living birds in the world and are already farmed in over 100 countries, from the cold winter climates of Alaska, Norway and Sweden, all the way south to the equatorial countries of Zaire, Brazil and Indonesia. Markets for ostriches are currently breeder markets with value determined as much by nostalgia as the value of products provided by the ostriches. In the long term, if the ostrich industry is to thrive, the birds will have to generate revenue sufficient to cover their costs of production. The main products from ostrich are 1) a red meat which is lower in fat and cholesterol than turkey, 2) leather which is extremely durable with unique markings and 3) decorative by-products, namely, feathers and eggs. In this survey which was carried out in 2006, a total number of 300 fecal samples from different ostrich farms of Isfahan, Iran were collected and fixed in 10% formaldehyde. A complete record was kept for each ostrich, including age, sex, clinical history and demographic data. Floatation technique using zinc sulfate solution was done on fecal samples for screening eggs. The results were indicated that 14 examined ostriches (4.6%) were infected with Codiostomum struthionis. This nematode occurs in the large intestine of the ostrich and is in addition a non-pathogen parasite. Furthermore, 6% of examined birds (30 ostriches) showed mild infection with Eimeria spp.

ELECTROLYTE DEPLETION & OSMOTIC IMBALANCE IN AMPHIBIANS WITH CHYTRIDIOMYCOSIS

Jamie Voyles, Lee Berger, Sam Young, Rick Speare, Rebecca Webb, Jeffrey Warner, Donna Rudd, Ruth Campbell, Lee F. Skerratt
James Cook University, Townsville, Queensland, Australia

Mounting evidence implicates the disease chytridiomycosis, caused by the fungus Batrachochytrium dendrobatidis, in global amphibian declines and extinctions. While the virulence of this disease has been clearly demonstrated, there is, as yet, no mechanistic explanation for how B. dendrobatidis kills amphibians. To investigate the pathology of chytridiomycosis blood samples were collected from uninfected, aclinically infected and clinically diseased amphibians and analyzed for a wide range of biochemical and hematological parameters. Here we show that green tree frogs (Litoria caerulea) with severe chytridiomycosis had reduced plasma osmolality, and reduced plasma sodium, potassium, magnesium and chloride concentrations. Stable plasma albumin, hematocrit and urea levels indicated that hydration status was unaffected, signifying depletion of electrolytes from circulation rather than dilution due to increased water uptake. These results suggest that B. dendrobatidis kills amphibians by disrupting normal epidermal functioning leading to osmotic imbalance through loss of electrolytes. Determining how B. dendrobatidis kills amphibians is fundamental to understanding the host-pathogen relationship and thus the population declines attributed to B. dendrobatidis. Understanding the mechanisms of mortality may also explain interspecific variability in susceptibility to the disease.
[75] Pathology of Young Captive Crocodiles

Philip Ladds¹, Ian Jerrett², Cathy Shilton², Lorna Melville²
¹Southern Cross University, Lismore, NSW, Australia; ²Berrimah Veterinary Laboratory, Darwin, NT, Australia

Failure to thrive, illness and mortality are significant problems in young crocodiles in captivity. Causes are many and varied with several diseases often being present concurrently. Illustrated in this overview is the pathology of some of these diseases, the causes of which – confirmed or suspected – include viruses (poxvirus, adenovirus, herpesvirus, possible arbovirus); bacteria – especially if Gram-negative; Chlamydophila sp., Dermatophilus sp.; fungi causing cutaneous or systemic disease; protozoa such as Goussia-like organisms and hemoproteozoa – possibly hemogregarines; nematodes within the abdominal cavity or associated with gastric ulcers; trematodes in blood vessels, intestine and kidney; pentastomes in the lung; nutritional diseases such as gout, osteomalacia caused by calcium-vitamin D deficiency, encephalomalacia associated with thiamine deficiency, and squamous metaplasia caused by avitaminosis A. In addition, in hatchlings, a sometimes fatal ‘bubble foot’ syndrome, characterized by digital subcutaneous emphysema is of unknown cause but may be due to gas supersaturated pond water.

[76] Aspects of the Epizootiology of Acropora White Syndrome on Reefs Across the Indo-Pacific Ocean

Greta S. Aeby¹, Thierry M. Work²
¹Hawaii Institute of Marine Biology, Kaneohe, HI, USA; ²National Wildlife Health Center, Honolulu, HI, USA

Acropora white syndrome (AWS) is a disease affecting reef corals within the Indo-Pacific, which results in progressive tissue loss from the coral colony. AWS first emerged on the Great Barrier Reef in 1999 and has since been discovered on coral reefs in numerous locations across the Indo-Pacific. We conducted disease surveys in three regions of the Indo-Pacific (American Samoa, Johnston Atoll, Northwestern Hawaiian Islands) to determine prevalence and frequency of occurrence of AWS. We also marked individual infected Acropora colonies within the NWHI to determine the lethality of the disease. AWS was found in all three regions documenting that the disease occurs across the entire Indo-Pacific region from Australia up to the NWHI, which is one of the northernmost reefs in the Pacific. Frequency of disease occurrence (FDO) was high in all three regions. America Samoa had three out of seven sites (FDO=42.9%) with corals having signs of the disease, Johnston Atoll had eight of 12 sites with disease (FDO=66.7%) and the NWHI revealed AWS at seven of nine sites (66.7%). Overall disease prevalence was highest at Johnston Atoll (4.5 %) as compared to American Samoa (0.18%) and NWHI (1.2%). Within the NWHI, 97.6% of the marked colonies with AWS suffered partial to total mortality within one year with a case fatality rate of 46%.
[77] DISTRIBUTION & MORPHOLOGY OF GROWTH ANOMALIES IN ACROPORA FROM THE INDO-PACIFIC

Thierry M. Work¹, Greta S. Aeby², Steve L. Coles³
¹National Wildlife Health Center, Honolulu, HI, USA; ²University of Hawaii, Kaneohe, HI USA; ³Bishop Museum, Honolulu, HI, USA

We assessed the distribution and prevalence of growth anomalies (GA’s) in Acropora from French Frigate Shoals (Hawaii), Johnston Atoll, and Tutuila (American Samoa), developed a nomenclature for gross morphology, characterized GA’s at the cellular level, and obtained preliminary indices of their spatial patterns and progression within coral colonies. Acropora GA’s were found in all three regions, but the distribution and prevalence of Acropora GA’s was highest in American Samoa. GA’s were grouped into 7 gross morphologies (exophytic, bosselated, crateriform, nodular, vermiform, fimbriate, or annular). On histology, GA’s consisted of proliferating basal body wall (calicodermis, mesoglea, and gastrodermis apposed to skeleton) with three distinct patterns of necrosis. There was no evidence of anaplasia or mitotic figures (common but not necessarily required morphologic indicators of neoplasia). Compared to normal tissues, GA’s had significantly fewer polyps, zooxanthellae within the gastrodermis of the coenenchyme, mesenterial filaments, and gonads but significantly more necrosis. On two colonies with GA’s monitored at two points over 11 months, numbers of GA’s per colony increased from 90 to 300%, and significant clustering of GA’s occurred within colonies. The evidence of GA’s being true neoplasias (tumors) is mixed, so a cautionary approach is urged in use of morphologic terminology.

[78] SAXITOXIN POISONING AS A CAUSE OF MORTALITY IN COMMON TERNS DURING THE 2005 SEVERE HARMFUL ALGAL BLOOM OFF THE SOUTHERN NEW ENGLAND COAST

Valerie Shearn-Bochsler¹, Rebecca J. Harris², Lee Bar-Sagi³, Anna Ludi³, Michael Brady⁴, Monica Williams⁴, Tod Leighfield⁵
¹National Wildlife Health Center, Madison, WI, USA; ²Massachusetts Audubon Society, Cummaquid, MA, USA; ³Tufts University, North Grafton, MA, USA; ⁴Monomoy Island National Wildlife Refuge, Chatham, MA, USA; ⁵NOAA National Ocean Service, Charleston, SC, USA

From May to July 2005, a massive bloom of the toxic dinoflagellate species Alexandrium fundyense occurred off the coast of southern New England. A. fundyense produces a potent neurotoxin, saxitoxin (STX), which accumulates in filter-feeders and produces paralytic shellfish poisoning (PSP) in humans eating contaminated bivalves. Over the course of several days in early June 2005, more than 40 common terns (Sterna hirundo) were found sick or dead at Monomoy Island National Wildlife Refuge in southern Massachusetts. Sick birds exhibited lethargy, torticollis and an inability to fly straight. Many dead terns were found adjacent to piles of vomited ingesta, composed mainly of small fish (sand launce, Ammodytes americanus). Most of the dead terns were gravid breeding females, and many were found with rubbery or broken eggs protruding from the cloaca or lying on the sand nearby. Domoic acid and saxitoxin levels in vomited fish, gizzard content (when present), and liver from dead terns were measured, and compared with control levels from terns from the same and nearby locations, collected when no red tide was present. 29/31 samples of vomitus and 9/16 samples of gizzard content contained saxitoxin at 2-123 μg STX equiv/100 g, and 6/34 liver samples from dead birds collected during the red tide were positive at 2-7 μg STX equiv/100g. In contrast, saxitoxin was not detected in any of the gizzard content and liver samples from 18 control birds. None of the samples tested contained domoic acid. This mortality event is very similar to that described at the same location by Nesbit et. al. in 1978; our control data provide additional evidence that both die-offs were likely due to saxitoxin poisoning.
[79] **METASTATIC CARCINOID IN A WILD MOUNTAIN GORILLA**

Christopher A. Whitter, Jacques Iyanya, Michael R. Cranfield, Jennifer A. Luft, Linda J. Lowenstein

1Mountain Gorilla Veterinary Project, Ruhengeri, Rwanda; 2 North Carolina State University, Raleigh, NC, USA; 3Maryland Zoo in Baltimore, Baltimore, MD, USA; 4University of California, Davis, CA, USA

A geriatric female mountain gorilla (*Gorilla beringei beringei*) in the Virunga National Park, Democratic Republic of Congo, was reported to Mountain Gorilla Veterinary Project for progressive decline culminating in immobility and abandonment by her group. She was found moribund and suffering from severe muscle atrophy, moderate louse infestation, severe dental attrition, and wrinkling, pitting and bleeding of palmar aspects of feet and hands. After extensive deliberation, the gorilla was anesthetized for examination, samples were taken and ultimately euthanasia performed with authorization of government authorities. The field necropsy procedure was severely constrained, but a firm fibrous circumferential mass was identified at the level of the pylorus along with marked gastric and colonic distension, and a moderate amount of abdominal effusion. The liver was diffusely marbled with thin white-tan linear streaks throughout and two small, white-tan nodules that raised the capsular surface and extended into the underlying hepatic parenchyma. The gorilla was emaciated. The mass was a pyloric/duodenal carcinoid that was metastatic to liver and regional lymph nodes. Diagnosis was confirmed by positive immunohistochemical staining with chromogranin A and electron microscopy. Additional significant histological lesions included: gastric mucosal atrophy; periportal bridging fibrosis and granulomatous hepatitis with intraleisonal nematode eggs (*Capillaria hepatica*); and moderate AV valve endocardiosis and aortic outflow tract atherosclerosis. To our knowledge this is the first described malignancy in free-ranging mountain gorillas and the first carcinoid described in any gorilla. This case also highlights wildlife management issues relating to field euthanasia of high-profile, endangered species.

[80] **PASTEURELLOSIS IN A GREAT ANTEATER**

Maria C. Tosta, Abelardo Morales, Antmar Henríquez, Héctor Conde, Víctor Bermúdez

1Central University of Venezuela; 2Zoological “Las Delicias,” Maracay, Venezuela; 3Zoological Park “El Pinar,” Caracas, Venezuela

Bacteremic pasteurellosis is an uncommon form of *Pasteurella multocida* infection, usually involved in local infections. This systemic infection often occurs in immunocompromised patients, especially when defense mechanisms have been impaired by viral or mycoplasmal infections or following stress associated with poor management practices. *Pasteurella multocida* is member of the respiratory complex that can affect domestic and wild animals. Pasteurellosis is well-described in domestic animals, but is less well-documented in wildlife. We describe a case of pasteurellosis in great anteater (*Myrmecophaga tridactyla*). A 4-yr-old male great anteater died after prolonged anorexia, nasal discharge and weight loss in the Zoological “Las Delicias”, Maracay, Venezuela. On necropsy, the lungs showed interstitial pneumonia and bilateral lung consolidation. Other organs did not reveal any significant alteration. Microscopically, there was suppurrative bronchopneumonia with lymphohaplasmatocytic infiltrate; meningitis, endocarditis, and multifocal hepatic necrosis also were seen. Coagulation of the intravascular system was observed in the rest of the tissue. *Pasteurella multocida* was cultured from blood, as well as from lung, liver, spleen and kidney tissue. Our investigation suggests that *P. multocida* infection in this anteater may have come from aerosol or contact with birds, or possibly from rodents or others animals in the zoo.
GASTRITIS ULCERATION SYNDROME IN PTERONURA BRASILIENSIS ASSOCIATED WITH HELICOBACTER PYLORI

Abelardo Morales1, Maria C. Tosta1, Antmar Henríquez3, Héctor Conde2, Víctor Bermúdez1
1Central University of Venezuela; 2Zoological “Las Delicias”, Maracay, Venezuela; 3Zoological Park “El Pinar,” Caracas-Venezuela

Gastritis ulceration syndrome is a common pathology in domestic animals and in man. Infection with Helicobacter pylori plays a predominant role in this syndrome, although this syndrome has received little study in wild animals under captive conditions. We describe a multidisciplinary study of gastritis syndrome and ulceration in Pteronura brasiliensis associated with Helicobacter pylori. A 10-year-old male Pteronura brasiliensis died after prolonged anorexia, chronic emesis and weight loss in the Zoological Park “El Pinar”, Caracas, Venezuela, and a 4-year-old male Pteronura brasiliensis died after prolonged anorexia, emesis and weight loss in the Zoological “Las Delicias”, Maracay, Venezuela. On necropsy, the stomachs of both animals showed gastric and duodenal ulcerations. Others organs did not have any significant alterations. Microscopically, there was gastritis and ulcerative gastric and duodenal enteritis with plasma cells and severe lymphocyte infiltration. The stomach samples were positive for Warthing-starry stain, and Helicobacter pylori was confirmed in formalin fixed paraffin embedded gastric section by PCR. Our results show that Helicobacter pylori can cause infection in wild species in captivity, although it is possible that the infection was accidental in this case. This is the first report on Helicobacter pylori infection in Pteronura brasiliensis in Venezuela.

SHEEP-ASSOCIATED MALIGNANT CATARRHAL FEVER IN FREE-RANGING MOOSE IN SASKATCHEWAN, CANADA

Aleksija Neimanis1, Claire Jardine2, Janet Hill3, Trent Bollinger1,3
1Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada; 2Ontario Veterinary College, Guelph, ON, Canada; 3Western College of Veterinary Medicine, Saskatoon, SK, Canada

Malignant catarrhal fever (MCF) is a sporadic disease of artiodactyls caused by various gamma herpesviruses. Both ovine herpes virus-2 (OHV-2) and caprine herpes virus-2 (CpHV-2) have been associated with MCF in free-ranging moose (Alces alces) in Scandinavia, but similar cases have not been documented in North America. On August 21, 2006, an adult bull moose found in sternal recumbency was euthanized near Brownlee, SK, Canada (N50°46’, W106°2’). It was severely dehydrated and thin, and the small intestine and bladder multifocally were eroded and ulcerated. Microscopically, there was fibrinoid necrosis and lymphoplasmacytic vasculitis and perivasculitis of omental and adrenal arteries and arterioles. No pathogenic bacteria were cultured and immunohistochemistry for bovine viral diarrhea virus did not detect viral antigen. Polymerase chain reaction (PCR) amplified OHV-2 virus from the small intestine and bladder. To confirm the PCR result, a consensus primer PCR method was used to amplify a segment of the herpesviral DNA polymerase gene for sequencing. The 414 bp product was 99% identical to published OHV-2 sequences, 78% identical to CpHV-2, and 83% identical to white-tailed deer-associated MCF. In a retrospective survey, OHV-2 virus was amplified from a second adult moose with lymphoplasmacytic meningoencephalitis collected near Kinley, SK (N52°2’, W107°22’) in 2003, but attempts to sequence this material were unsuccessful. We believe this is the first description of MCF in free-ranging moose in North America. Disease requires contact with infected sheep or goats, and MCF in moose may become more prevalent as moose distribution continues to expand into agricultural prairie.
[83] THE ROLE OF THE BIOTOXIN DOMOIC ACID IN REPRODUCTIVE FAILURE IN CALIFORNIA SEA LIONS ON SAN MIGUEL ISLAND

Tracey Goldstein1, Tanja S. Zabka1, Robert DeLong2, Elizabeth A. Wheeler1, Donald P. King3, Scott Reid3, Gina Ylitalo4, Sibel Bargu5, Tod Leighfield6, Frances Van Dolah6, Frances M. D. Gulland1
1The Marine Mammal Center, Sausalito, CA, USA; 2The National Marine Mammal Laboratory, Seattle, WA, USA; 3Institute of Animal Health, Pirbright Laboratory, Woking, Surrey, UK; 4Northwest Fisheries Science Center, Seattle, WA, USA,
5University of California, Santa Cruz, CA USA, 6National Ocean Services Laboratory, Charleston, SC, USA

Domoic acid is a neurotoxin produced by marine algae including *Pseudo-nitzschia australis* that binds to glutamate receptors. California sea lions (*Zalophus californianus*) ingest the toxin when foraging on schooling planktivorous fish. Adult females comprise 60% of stranded animals affected with neurological signs and almost one third had reproductive failure including abortions, premature live births and dead *in utero* pups. Domoic acid was detected in maternal urine and in fetal fluids demonstrating that it crosses the placenta exposing the fetus to the toxin. To determine whether domoic acid was playing a role on sea lion rookeries, 67 premature pups were sampled on San Miguel Island in 2005 and 2006 to investigate the causes for reproductive failure. Analyses included domoic acid, contaminant and infectious disease testing and histologic examination. Domoic acid was detected in 20% of samples, potential pathogens cultured included *Salmonella enteriditis* and *Streptococcus phocae* and caliciviral RNA was detected in the umbilical cord in five cases. Histopathologic findings included placent al abruption, brain edema and systemic and localized bacterial infections of amnion origin. The only brain lesion seen in six animals with domoic acid concentrations was brain edema (a common finding, and in some cases the only lesion in premature pups born to domoic acid affected females in rehabilitation). Summed PCB’s and DDT’s were lower than those measured previously in premature sea lion pups. While the etiology of premature parturition was varied, these results suggest that domoic acid plays a contributory role in reproductive failure on sea lion rookeries.

[84] ISOLATION & PRELIMINARY CHARACTERISATION OF A MORBILLIVIRUS RESPONSIBLE FOR AN OUTBREAK OF DISTEMPER IN SEALS FROM MAINE

Ole Nielsen1, Keith Matassa2, Allison MacHutchon1, Shannon Prendiville2, Greg Smith3, Hana Weingartl1, Lynn Burton3
1Department of Fisheries and Oceans, Winnipeg, MB, Canada; 2University of New England, Biddeford, ME, USA; 3Canadian Food Inspection Agency, Winnipeg, MB, Canada

Commencing in the spring of 2006 an increase in grey (*Halichoerus grypus*) and harbor seal (*Phoca vitulina*) strandings was noted at a marine mammal rehabilitation center in Maine. The index case, a male grey seal pup exhibited neurological signs (seizures) consistent with distemper. At necropsy significant findings included non-suppurative meningoencephalitis and a positive immunohistochemistry result (brain) for canine distemper virus (CDV). Bronchointerstitial pneumonia had been observed in stranded harbor seals (*Phoca vitulina*); seroconversion and positive polymerase chain (PCR) reaction to morbillivirus was also detected subsequently in stranded animals of both species. The present study was undertaken to isolate and identify the virus responsible for these mortalities. Tissues harvested from 18 harbor seals, one grey seal and one hooded seal (*Cystophora cristata*) were submitted for viral isolation using a transfected Vero cell line expressing the universal morbillivirus cell receptor “signaling lymphocyte activation molecules” or SLAM. After five days incubation, a single sample from a stranded/dead harbor seal showed evidence of cytopathic effect (CPE) consist with morbillivirus infection and upon electron microscopy examination revealed particles with the size and morphology of a morbillivirus species. The isolate was neutralized by anti-CDV antiserum and reacted positively in a PCR test specific for the genus morbillivirus. Sequencing of the PCR product conclusively identified the isolate as phocine distemper virus (PDV). These results further supports the theory that PDV is circulating in North American seal populations and that cell lines possessing SLAM receptors are useful in the isolation of marine mammal morbillviruses from stranded animals.
[85] UPDATE ON NORTHERN FUR SEAL STRANDINGS ALONG THE CENTRAL CALIFORNIA COAST SINCE 1975

Felicia B. Nutter, Tracey Goldstein, Frances Gulland
The Marine Mammal Center, Sausalito, CA, USA

Northern fur seals (Callorhinus ursinus) are mainly pelagic and strand infrequently along the central California coast. From January 1975 through April 2007, 204 northern fur seals stranded alive and were admitted to the Marine Mammal Center, accounting for fewer than 2% of the total admissions. Of those cases, 202 records were available for review. Pups < 1 year stranded most commonly (n=143), followed by juveniles (1-4 years, n=25) and adults (>4 years, n=31). Sex ratio was fairly even, with 110 females and 90 males (sex not recorded, n=2), however adult females (n=34) stranded more often than adult males (n=2). Most animals were admitted between August and January (n=167), from Marin (n= 13), San Mateo (n=15), Santa Cruz (n=47), Monterey (n=29), and San Luis Obispo (n=68) counties. Annual admissions were highest during El Nino conditions in 1992 (n=21), 1997 (n=32), 1998 (n=10), 2005 (n=17), and 2006 (n=32). Emaciation was the most common clinical sign for both pups and adults. Successfully rehabilitated animals were released (n=85), 97 died during treatment, 14 were euthanized due to poor prognosis, 2 were transferred to other facilities, the outcome was not recorded for 2 animals, and 2 were undergoing treatment at the time of writing. Domoic acid intoxication was documented in 2005 by both toxicologic analysis and histopathology, showing that species normally feeding in offshore waters are also at risk. Clinical signs consistent with domoic acid intoxication, including abortions and seizures, are recorded for stranded fur seals as early as 1978.

[86] INFECTION OF BEEF CATTLE WITH MYCOBACTERIUM PINNIPEDII DUE TO CATTLE GRAZING IN COASTAL AREAS IN CLOSE CONTACT WITH THE NEW ZEALAND FUR SEAL – TWO CASE STUDIES

Scott H. Loeffler1, Geoffrey W. de Lisle2, Desmond M. Collins2, Kevin B. Crews1
1Animal Health Board, Riccarton, Christchurch, New Zealand; 2Wallaceville Animal Research Centre, Upper Hutt, New Zealand

A novel species of the Mycobacterium tuberculosis complex, M. pinnipedii, has been shown previously to be endemic in the New Zealand Fur Seal population. Although this mycobacterium has been implicated in transmission of tuberculosis to man, there has been no documented scientific report of M. pinnipedii causing disease or diagnostic problems for M. bovis eradication programs in domestic cattle. This paper describes two case studies of beef cattle that became infected with M. pinnipedii by cohabitating coastal pastures with wild seal colonies. In each of two M. bovis-free areas of New Zealand that were geographically separate, a single animal in a cattle herd was found to be infected. In neither case was there any evidence of cow to cow transmission of M. pinnipedii. The strain typing methodology used and how this was essential for ruling out an infection of cattle originating from terrestrial wildlife is described.
Identifying factors influencing the spatial spread of disease is critical to predicting populations at highest risk, designing surveillance efforts, and developing effective control programs. Prevalence of chronic wasting disease (CWD) in free-ranging white-tailed deer in south-central Wisconsin is spatially heterogeneous suggesting there is heterogeneity in the spatial diffusion of the disease. We used deer population genetic structure to identify features of the landscape associated with genetic differentiation between selected study areas and a core-area where CWD originated in Wisconsin. The degree of genetic differentiation of study area deer from core-area deer was highly correlated with observed CWD prevalence. Deer in study areas separated from the core-area by the Wisconsin River were the most genetically different from deer in the core-area and had the lowest CWD prevalence, suggesting this river limits dispersal of deer and the spread of disease. Our results suggest that spatial genetic structure of host populations can be used to identify features of the landscape that influence gene flow (i.e., dispersal) and predict the spread of infectious disease into new areas. This landscape genetics approach may be used proactively to identify high risk populations based on their genetic connection to infected populations to facilitate effective disease surveillance and preventative actions.
[89] DEVELOPMENT OF DIAGNOSTIC TESTS FOR *OTOSTRONGYLUS CIRCUMLITUS* INFECTION IN NORTHERN ELEPHANT SEALS

Jocelyn G. Elson-Riggins¹,³, Frances M. Gulland², Brian M. Aldridge¹
¹The University of London, North Mymms, Hertfordshire, UK; ²The Marine Mammal Center, Sausalito, CA, USA; ³Montana State University-Billings, Billings, MT, USA

The lungworm *Otostrongylus circumlitus* (Nematoda: Metastrongyloidea) is the most significant pathogen-specific cause of northern elephant seal (*Mirounga angustirostris*) morbidity and mortality along the central California coast. This parasite accounted for over 12% of elephant seal admissions to The Marine Mammal Center (TMMC), Sausalito, California, between 1992 and 2001. In juvenile elephant seals, the clinical signs are non-specific, and mortality often occurs with low intensity infections during the pre-patent period of the nematode life cycle. There is a need for reliable diagnostic tests for detecting infection that will assist veterinarians in case management, but are independent of fecal examination for larvae. We have developed an enzyme-linked immunosorbent assay (ELISA), using whole nematode extracts, for the detection of anti-*O. circumlitus* antibodies in elephant seals. In preliminary validation studies, sensitivity, specificity, positive and negative predictive values of 100% were observed. An additional quantitative real time polymerase chain reaction (q-PCR) based test for detecting nematode nucleic acid in blood is under development. It is anticipated that the application of these two assays together will be useful for the diagnosis and management of *O. circumlitus* infections, as well as for additional studies on the natural history and pathophysiology of this important parasite.

[90] INFECTED *LITORIA RHEOCOLA* PRESENTING CLINICAL SIGNS OF AMPHIBIAN CHYTRIDIOMYCOSIS HAVE COMPARABLE DETECTABLE QPCR VALUES TO INFECTED, ACLINICAL FROGS

Andrea D. Phillott¹, Lee F. Skerratt¹, Keith R. McDonald², Ruth G. Campbell¹
¹James Cook University, Townsville, QLD, Australia; ²Queensland Parks & Wildlife Service, Atherton, QLD, Australia

Amphibian chytridiomycosis is the first disease believed to have caused the extinction of many wild animal species globally. The etiological agent is *Batrachochytrium dendrobatidis*, a chytrid fungus. Clinical signs of infection include erythema of the abdomen, limbs and digits, lack of righting response, lethargy and tetany. Signs of disease may appear suddenly and death often occurs within days. The quantitative, real-time Taqman PCR (qPCR) assay is the most sensitive, least invasive, and only quantitative diagnostic test for amphibian chytridiomycosis. Common mist frogs, *Litoria rheocola*, presented with clinical signs of amphibian chytridiomycosis during routine frog monitoring of the Wet Tropics in north-eastern Queensland, Australia. qPCR values for clinical frogs did not differ significantly from adjacent infected but aclinical *L. rheocola*. Aclinical, infected frogs physically appear unaffected and behave in the same manner as uninfected frogs, despite their similar qPCR values to moribund animals. Some infected, aclinical animals were recaptured in the following 6 month period, indicating sub-lethal infection is possible. This study highlights the necessity for caution in interpreting qPCR results in terms of the severity of the disease in individuals.
[91] APPLICATION OF A NOVEL VIRUS DETECTION SYSTEM IN ROCKY MOUNTAIN BIGHORN SHEEP IN MONTANA

Mark W. Atkinson¹, Neil J. Anderson¹, David Wick²
¹Montana Fish, Wildlife & Parks, Bozeman, MT, USA; ²BVS-Inc., Stevensville, MT, USA

Respiratory viruses have been implicated as primary pathogens or as co-factors in the development of respiratory disease in bighorn sheep (Ovis canadensis) since 1966. Nevertheless, due to difficulties in the interpretation of serologic results and technical limitations associated with traditional virus isolation techniques, our understanding of the true role of viruses in the pathogenesis of respiratory disease in free-ranging wild sheep remains limited. With a goal of better understanding the factors influencing population health, we utilized a newly available technology, the Integrated Virus Detection System (IVDS), to demonstrate a reliable, consistent and economically feasible method to detect respiratory and other viruses in free-ranging bighorn sheep. IVDS is a reagent-less, non-gene based method that can identify all viruses in a sample by utilizing physical properties for discrimination and characterization through comparison with known virus families. In 2007, as a component of statewide management activities in Montana, 220 Rocky Mountain bighorn sheep were captured and handled. Duplicate nasal, oropharyngeal and rectal dry rayon swabs were collected from individual sheep and subsequently shipped in phosphate buffered saline and water to the IVDS instrument for screening. Initial analysis compared specimens obtained from field samples to four viruses known to occur in bighorn sheep: Bovine Virus Diarrhea (BVD), Infectious Bovine Rhinotracheitis (IBR), Bovine Respiratory Syncytial Virus (BRSV) and Parainfluenza-3 (PI-3). Results demonstrate the ability of IVDS to detect the presence of viruses from field samples. We discuss these results and the implications of this technology for future disease surveillance programs in wildlife.

[92] THE USE OF MICROSEATLITES TO INFORM FUTURE MANAGEMENT OF A DEADLY FLY PARASITISING DARWIN’S FINCHES, GALAPÁGOS ISLANDS

Rachael Y. Dudaniec¹, Sonia Kleindorfer¹, Mike G. Gardner¹,²
¹Flinders University, South Australia; ²Adelaide University, South Australia

The blood-sucking ectoparasitic fly, Philornis downsi, is the only pathogen of Darwin’s finches known to cause high fitness impacts, including reduced weight gain in nestlings, anemia, and reduced hemoglobin level. Mortality is also severe, with 19-62% brood loss across years. The parasite is found on 11 of 13 Galapágos Islands and is considered a serious threat to Darwin finch species. Genetic markers like microsatellites can elucidate core biological aspects of mobile insect parasites, including mating behavior and population genetic differentiation. This information is necessary for controlling invasive flies using the Sterile Insect Technique (SIT), which involves the targeted release of laboratory-reared sterile male flies to reduce, and eventually negate, population growth. Here, results are presented for 9 P. downsi microsatellite loci screened across ~600 parasitic fly larvae collected from 45 nests of Darwin’s finches across islands of the Galapágos. We addressed two core questions essential for managing P. downsi: (1) Do flies reinfest nests and do females mate multiply to produce their offspring?; and (2) Does P. downsi show genetic variation across island populations, indicating population divergence? We found low relatedness between parasite offspring collected from individual bird nests, indicating polyandry among female flies. P. downsi populations also showed some genetic variation across islands. SIT programs work most efficiently when remating frequency among female flies is low, and genetic variation is relevant for optimizing SIT effectiveness on individual fly species or strains. Thus, our findings have application in the context of assessing SIT viability and managing P. downsi on Galapágos.
[93] PRELIMINARY EVALUATION OF BLOOD-BASED ASSAYS FOR THE DIAGNOSIS OF BOVINE TUBERCULOSIS IN ELK FROM THE RIDING MOUNTAIN NATIONAL PARK REGION

Todd K. Shury¹, Konstantin P. Lyashchenko², Doug Bergeson³, Om P. Surujballi⁴, Cyril Lutze-Wallace⁴
¹ Parks Canada Agency, Saskatoon, SK, Canada; ² Chembio Diagnostic Systems, Inc., Medford, NY, USA; ³ Parks Canada Agency, Wasagaming, MB, Canada; ⁴ Canadian Food Inspection Agency, Fallowfield, ON, Canada

An outbreak of bovine tuberculosis (Mycobacterium bovis) has been investigated in elk (Cervus elaphus), white-tailed deer (Odocoileus virginianus) and cattle (Bos taurus) in and around Riding Mountain National Park (RMNP) in south-western Manitoba, Canada since 1991. Four blood tests to detect M. bovis in naturally infected free-ranging elk in and around RMNP were evaluated between 2002 and 2006. These tests included a Fluorescence Polarization Assay (FPA), Lymphocyte Stimulation Test (LST), Lateral Flow Immunoassay (CervidTB STAT-PAK®, or Rapid Test – RT) and Multi-Antigen Print Immunoassay (MAPIA™). Test sensitivity based on M. bovis culture or tissue-based PCR for confirmatory testing from tissues collected at necropsy (N = 74) was highest for the LST (85.7%) and lowest for FPA (47.6%) while MAPIA (61.9%) and RT were intermediate (57.1%). Positive predictive values ranged from 24.4% to 76.5%. The LST also had the greatest agreement with culture results (kappa = 0.68), while the MAPIA™ and RT showed somewhat less agreement (kappa = 0.61, 0.45 respectively) and the FPA showed none (kappa = -0.07). Although the LST shows great promise as a sensitive diagnostic test for bovine tuberculosis in elk, it suffers from logistic constraints that may limit its use with free-ranging cervids. While the RT is not as sensitive, it can use whole blood samples, in addition to serum or plasma, and it has the potential as a simple and valuable field test for detecting M. bovis in free-ranging cervids. These tests have proven valuable for determining the geographic range of bovine tuberculosis in this area.

[94] SENTINEL-BASED SURVEILLANCE OF COYOTES TO DETECT BOVINE TUBERCULOSIS IN MICHIGAN

Kurt C. VerCauteren¹, Todd C. Atwood¹, Thomas J. DeLiberto¹, Holly J. Smith¹, Justin S. Stevenson¹, Bruce V. Thomsen², Thomas Gidlewski², Janet Payeur²
¹ US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; ² US Department of Agriculture-National Veterinary Services Laboratories, Ames, IA, USA

Mycobacterium bovis, the etiologic agent that causes bovine tuberculosis, was found to be endemic in free-ranging white-tailed deer (Odocoileus virginianus) in the northeastern Lower Peninsula of Michigan in 1995. The presence of tuberculosis in a wildlife reservoir and the concurrent incidence in cattle resulted in Michigan losing its bovine tuberculosis accredited-free status. Subsequent wildlife surveillance programs identified coyotes (Canis latrans) as potential bio-accumulators of M. bovis, generating interest in their potential to serve as cost- and labor-effective sentinels for monitoring disease risk. Our goal was to evaluate the efficacy of using coyotes as sentinels to detect M. bovis presence in an agro-forested landscape. From November 2003 to September 2005, we captured and sampled 175 coyotes for M. bovis in the endemic area of Michigan. Fifty-eight coyotes tested positive for M. bovis, and infection prevalence by county ranged from 19-52% (X̄ = 33%, SE = 0.07). By contrast, prevalence of M. bovis in white-tailed deer was significantly lower (i.e., 0.66%; Mann-Whitney U4,4 = 16, P <0.001). By focusing on coyotes as opposed to deer, we sampled 97% fewer animals and increased the likelihood of detecting M. bovis by 40%. Our work shows that sentinel coyote surveys have potential to be effective cost- and labor-sensitive indicators of M. bovis presence in sympatric wildlife and domestic livestock.
[95] DEVELOPMENT OF RECOMBINANT RABIES VIRUSES FOR ORAL WILDLIFE VACCINATION

Marty K. Soehnlen1, Xianfu Wu1, Kayla I. Bean1, Richard Franka1, Denis Bankovskiy2, Charles E. Rupprecht1
1Centers for Disease Control & Prevention, Atlanta, GA, USA; 2Pokrov Plant of Biologics, Volginskii, Vladimir Region, Russia

Rabies is a fatal, but preventable viral encephalitis caused by viruses in the genus Lyssavirus. The WHO estimates that more than 55,000 people die annually from rabies. In the USA, wildlife rabies accounts for over 90% of the cases reported to the CDC each year. This burden is due in part to the diversity of wildlife reservoirs and the difficulties in design of broadly cross-reactive vaccines. Currently, the only licensed oral wildlife rabies vaccine in the USA is a vaccinia-rabies glycoprotein (V-RG) virus. The V-RG vaccine is efficacious in coyotes, foxes, and raccoons, but its effectiveness is limited in other major reservoirs. With the intent of designing additional wildlife biologicals, we have developed a murine model to test the safety and efficacy of newly created attenuated recombinant rabies virus vaccines, constructed using a fixed ERA rabies virus strain, via reverse genetics and site directed mutagenesis. We compared 10 different viral constructs administered intracranially, intramuscularly, and orally in ICR mice. One month after vaccination, animals were challenged with a coyote street rabies virus variant. Animal survival and induction of virus-neutralizing antibodies were measured. These new biologicals were not only safe when inoculated in the brain, but also efficacious in disease prevention after experimental challenge. Preliminary studies have shown the efficacy and immunogenicity of a glycoprotein-modified ERA recombinant virus vaccine in captive red foxes. Such research offers novel opportunities for the design of attenuated rabies viruses to serve as gene delivery vectors in future wildlife disease management.

[96] IMMUNOLOGIC RESPONSES & PROTECTION IN ELK VACCINATED WITH BRUCELLA ABORTUS STRAIN RB51 OVER-EXPRESSING SOD & WBOA & CHALLENGED WITH VIRULENT BRUCELLA ABORTUS

Pauline Nol1, Steven C. Olsen2, William S. Stoffregen2, Jack C. Rhyan1, Steven M. Boyle3, Gerhardt G. Schurig2, Nammalwar Sirranganathan2
1US Department of Agriculture-Veterinary Services, Fort Collins, CO, USA; 2 US Department of Agriculture-Agricultural Research Service, Ames, IA, USA; 3Virginia Polytechnic Institute & State University, Blacksburg, VA, USA

The infection of elk with brucellosis in the Greater Yellowstone Area (GYA) has led to transmission of brucellosis to a number of cattle herds in the GYA and the consequent loss of brucellosis-free status for Wyoming. Currently available brucellosis vaccines provide either minimal or no protection in elk against experimental Brucella challenge. The purpose of the pilot study reported here was to evaluate a new brucellosis vaccine that has been shown to have enhanced protection in a murine model of brucellosis. Elk were randomly assigned to intramuscular (IM) vaccination with 1010 CFU B. abortus strain RB51 over-expressing both SOD (superoxide dismutase encoded by sodC) and wboA (mannosyltransferase encoded by wboA) or IM vaccination with an oral boost of 1011 CFU. Additional elk were injected IM with saline (control). Vaccinates demonstrated transient responses on conventional brucellosis serologic tests after inoculation. Elk were experimentally challenged in mid-gestation with 107 CFU of B. abortus strain 2308. Although sample sizes were small and the two vaccine treatments did not appear different, there was a trend for vaccinated elk to have reduced incidence of abortion, uterine/mammary infection, or maternal infection as compared to control elk. Our data suggest that further studies of this vaccine in elk are warranted.
[97] COMPARISON OF DIFFERENT METHODS OF ADMINISTRATION OF CANINE DISTEMPER VACCINE TO AFRICAN WILD DOGS

Bonnie L. Raphael, Patrick Thomas, Rosie Woodroffe  
Wildlife Conservation Society, Bronx, NY, USA

The African wild dog (*Lycaon pictus*) is one of the world’s most endangered predators. Formerly widespread throughout sub-Saharan Africa, today just 3-6,000 wild dogs remain in the wild, with many populations still declining. The wild dogs’ decline reflects the expansion of human populations and the consequent fragmentation of habitat available to wildlife. Wild dogs fare poorly in human-dominated landscapes, partly because people perceive them as a threat to livestock and kill them, and partly because the domestic dogs that inevitably live alongside people carry diseases that can devastate wild dog populations. The diseases that threaten wild dogs – particularly rabies and distemper – are shared with a wide array of other host species. For this reason, disease control measures could take several forms. Previous attempts to protect wild dogs by direct vaccination have met with considerable problems. Newly developed recombinant vaccines against rabies and canine distemper may offer solutions to problems encountered with inactivated or modified live vaccines. They are immunogenic in both domestic dogs and wild canids. And, cannot revert to virulence and cause disease. And, finally, these vaccines can be administered orally, potentially improving vaccine coverage in wildlife. Evaluation of the efficacy of recombinant distemper vaccine to produce antibodies has been carried out on wild dogs at the Bronx Zoo. Immune responses to distemper vaccines administered orally or by injection were compared. Canine distemper titers were determined via serum neutralization testing at the New York State Diagnostic Laboratory at Cornell.

[98] DEVELOPING A SURGICAL TECHNIQUE FOR IMPLANTING TRANSMITTERS IN WESTERN GREBES

Joseph K. Gaydos¹, J. Gregory Massey², Lori A. Gaskins², Paul Siegel³, David Nysewander⁴, Joseph Evenson⁴, Michael Ziccardi²  
¹University of California, Eastsound, WA, USA; ²University of California, Davis, CA, USA; ³Virginia Polytechnic & State University, Blacksburg, VA, USA; ⁴Washington Department of Fish & Wildlife, Olympia, WA, USA

Western grebes (*Aechmophorus occidentalis*), one of two endemic grebe species in North America, are in decline on the west coast of the United States. The absence of a safe and effective technique for implanting satellite or radio transmitters however, has prevented linking important western grebe winter (marine) and summer (freshwater) habitat. Also, western grebes are one of the marine bird species most impacted by oil spills on the west coast; however the absence of a technique for implanting transmitters prevents monitoring them post-release after rehabilitation from oiling. Twenty-one western grebes were captured and utilized in a study to determine why a surgical technique standard for implanting intra-celomic transmitters in other marine bird species failed in this species and if minor surgical modifications improved transmitter implantation success. Seven birds were implanted with 30 gram VHF transmitters using a modified surgical technique for implanting intra-celomic transmitters with a percutaneous antenna. Using the same approach and closure, seven birds had a celiotomy with disruption of the air sac and seven control birds underwent anesthesia only. Stress related changes in immune function, waterproofing, behavior, and a suite of hematologic and biochemical parameters were measured. Six transmitter, six celiotomy and seven control birds survived to the study duration at nine days post-surgery. Results of this in-depth study on the physiological and behavioral effects of transmitter implantation are helping to develop a safe and effective surgical procedure for implanting transmitters in western grebes.
There can be many definitions for the term, *Informatics*, but the concept that will be used here is a discipline that is an integration of subject knowledge, information management, and information technology. Informaticians may ask the questions, what data and information are needed to answer scientific questions, as well as how might these best be collected, stored, retrieved and displayed. Medical informatics is one of the best known sub-fields, with electronic medical records and management of digital diagnostic and monitoring data as examples of common applications. Logically, veterinary informatics would be a further sub-class, with wildlife disease informatics included here. This presentation will cover the foundations of a few important components in this area, such as the development of surveillance systems, and the communication and exchange of information within the wildlife health community. It will provide an overview and introduction to the special session on this topic.
The Wildlife Disease Association Conference Program and Abstracts booklet is distributed to all meeting attendees. Abstracts were lightly edited to comply with formatting and space limits, but otherwise were printed as submitted. The Wildlife Disease Association does not regard this Conference Program and Abstracts booklet as a publication, and abstracts included herein should not be cited in scientific literature.
PRESENTATION SCHEDULE FOR POSTERS

GENERAL POSTER SESSION ONE
ECOLOGY, MANAGEMENT, & SOCIOPOLITICAL CHALLENGES OF WILDLIFE DISEASE MANAGEMENT
MONDAY 2:45P – 3:45P

Arlene Alvarado  [100]  THE RELATIONSHIP BETWEEN POPULATION SIZE, AGGRESSION & INFECTION WITH SIN NOMBRE VIRUS (SNV) IN ADULT FEMALE DEER MICE

Todd C. Atwood  [101]  ASSESSING THE POTENTIAL FOR TRANSMISSION OF MYCOBACTERIUM BOVIS FROM RACCOONS TO CATTLE IN MICHIGAN

Kimberlee Beckmen  [102]  INVESTIGATION OF TRACE MINERAL DEFICIENCIES IN AN ALASKAN DALL SHEEP POPULATION

E. Frances Cassirer  [103]  SELENIUM SUPPLEMENTATION OF FREE-RANGING BIGHORN SHEEP IN HILLS CANYON

Randy W. DeYoung  [104]  LANDSCAPE-GENETIC ANALYSIS OF POPULATION STRUCTURE IN GRAY FOX: IMPLICATIONS FOR ORAL RABIES VACCINE PROGRAMS

Cindy Driscoll  [105]  A WHALE OF A STORY – DOCUMENTING EVIDENCE OF SHIPSTRIKE & ENTANGLEMENT IN A SEI WHALE IN MARYLAND WATERS

J. Paul Duff  [106]  WILDLIFE DISEASE SURVEILLANCE IN BRITAIN, AN OFFICIAL SCHEME

Alan M. Fedynich  [107]  SURVEY FOR BLOOD PARASITES IN THE ENDANGERED WOOD STORK FROM SOUTHEASTERN UNITED STATES

D. Gavier-Widén  [108]  INFECTIOUS & PARASITIC DISEASES IN ENDANGERED FENNOSCANDIAN ARCTIC FOXES

Ben Gonzales  [109]  RESPIRATORY DISEASE IN MOUNTAIN SHEEP: KNOWLEDGE GAPS & FUTURE RESEARCH WORKSHOP RESULTS

J.S. Hall  [110]  AVIAN INFLUENZA IN WILD RACCOON POPULATIONS: CAN PERIDOMESTIC WILD MAMMALS SERVE AS BRIDGES BETWEEN WATERFOWL AND HUMANS?

Kathryn P. Huyvaert  [111]  BIVALVE MOLLUSKS AS BIOACCUMULATORS OF INFLUENZA A VIRUSES: IMPLICATIONS FOR MONITORING AVIAN INFLUENZA IN THE WILD

Scott Hygnstrom  [112]  SURVEILLANCE OF HANTA VIRUS (SN NOMBRE) IN NEBRASKA RODENTS, 1994-2004

Philip H. Jones  [113]  PREDICTING PLAGUE EPIZOOTICS IN BLACK-TAILED PRAIRIE DOG COLONIES WITH A SENSITIVE PCR-BASED PROTOCOL

Kevin Keel  [114]  SEVERE, SOFT-TISSUE MINERALIZATION IN BULLFROG LARVAE FROM WASTEWATER TREATMENT WETLANDS
Mark D. Kellogg  [115] **SURVEILLANCE FOR *Francisella tularensis* in Muskrat of the Slave River Delta, Northwest Territory of Canada Using Several Different Diagnostic Methods**

Roni King  [116] **Oral Rabies Vaccination in Israel**


Michael Lynch  [118] **Seasonal Variation in Blood Parameters & Characterization of Physiological Responses to Population Management Operations in Koalas**

Carolina A. Marull  [119] **Live Shearing of Free-Ranging Guanaco (*Lama guanicoe*) in Argentina: A Possible Management Tool for Conservation**

Amy T. Moore  [120] **Dispersing Cimicid Vectors Have Low Buggy Creek Virus Infection Rates**

Soraya Naem  [121] **A Survey on Hydatid Cyst of Liver & Lung of Camels in Sabzevar, Iran**


Pauline Nol  [123] **Susceptibility of Richardson’s Ground Squirrels to Attenuated & Virulent Strains of *Brucella abortus***

Valerie A. O’Brien  [124] **Invasive House Sparrows as Alternative Hosts for Buggy Creek Virus**

R. Orusa  [125] **Wild Animal Diseases: The Italian Surveillance Net**

Eran Raizman  [126] **The Role of Raccoons in the Epidemiology of Leptospirosis**

Anna M. Schotthoefer  [127] **Wetland Characteristics Associated with Trematode Infections in Amphibians: Implications for Conservation and Restoration**

Tony Schountz  [128] **A Rapid Field Immunoassay for Identifying Sin Nombre Hantavirus-Infected Deer Mice**

Daniel M. Tompkins  [129] **Johne’s Disease in New Zealand Wildlife**

Eric Vander Wal  [130] **Estimating Interaction Rates with Proximity Collars as a Means to Quantify Disease Transmission Among Elk**
[100] The relationship between population size, aggression & infection with Sin Nombre virus (SNV) in adult female deer mice

Arlene Alvarado, Amy Kuenzi
Montana Tech, Butte, MT, USA

We examined the relationship between behavioral interactions and potential infection with Sin Nombre virus (SNV) in deer mice (Peromyscus maniculatus), the primary reservoir for SNV. SNV is shed from infected individuals in their urine, feces and saliva. One mode of horizontal transmission of SNV infection occurs by biting during intraspecific aggressive encounters. Previous studies indicate more adult males are seropositive for SNV, possibly because they engage in more intraspecific aggressive interactions as evident by a higher proportion of adult males with wounds or scars (used as an index of aggressive encounters). Since aggression typically increases as population size increases due to increased encounters and conflicts over limited resources, we hypothesize that aggressive encounters involving females will increase during times of higher population numbers. Thus, we should see a positive correlation between the frequency of scarring in females and population size. Consequently, the number of females with antibodies to SNV should also increase during these times. We examined these relationships using long term data collected from two field sites in Montana.

[101] Assessing the potential for transmission of Mycobacterium bovis from raccoons to cattle in Michigan

Kurt C. VerCauteren, Todd C. Atwood, Thomas J. DeLiberto, Holly J. Smith, Justin S. Stevenson
US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA

In 1995 Mycobacterium bovis, the causative agent of bovine tuberculosis (bTB), was found to be endemic in free-ranging white-tailed deer (Odocoileus virginianus) in a 4-county area in northcentral Michigan. Shortly thereafter, bTB was detected in local beef cattle operations and the United States Department of Agriculture revoked Michigan's bTB accredited-free status, resulting in immense economic consequences. A subsequent multi-species surveillance program identified raccoons (Procyon lotor) as a spill-over host for Mycobacterium bovis, and it was posited that spatial interaction with raccoons may facilitate transmission of M. bovis to cattle. To that end, we assessed the extent to which raccoons exploited space used by livestock to better understand the potential for horizontal disease transmission between free-ranging wildlife and domestic animals. Raccoons often configured home ranges to overlap adjacent ranches, and resource selection functions indicated raccoons intensively utilized space concurrent with livestock and configured the arrangement of core utilization areas to include livestock food sources. Furthermore, there was a direct relationship between raccoon-cattle interaction probabilities and the spatial juxtaposition of livestock food sources. Our results provide useful metrics to incorporate into future efforts to develop spatially explicit models of bTB dynamics. Modeling efforts can then be used as a foundation to predict the epidemiological ramifications of interactions between wildlife and domestic livestock in agrarian landscapes.
[102] INVESTIGATION OF TRACE MINERAL DEFICIENCIES IN AN ALASKAN DALL SHEEP POPULATION

Kimberlee Beckmen1, Jim Herriges2, Jim Lawler3, Mark Bertram4
1Alaska Department of Fish & Game, Fairbanks AK, USA; 2Bureau of Land Management, Fairbanks, AK, USA; 3Gates of the Arctic National Park & Preserve, Fairbanks AK, USA; 4Yukon Flats National Wildlife Refuge, Fairbanks AK, USA

A study of trace mineral status in Dall Sheep (*Ovis dalli dalli*) from the White Mountains of Alaska was undertaken to discover if the occurrence of ‘stump headed” horn abnormalities was related to deficiencies of minerals. Two spinal fracture/capture myopathy deaths occurred in vitamin E and selenium deficient adult females occurred and 3-week post-capture mortality rates were significantly higher than in other regions of Alaska (11.2% vs. 2.7%). The two spinal fractured sheep had osteoporosis and osteopenia, however serum and liver calcium levels were not correlated with horn abnormalities or fractures in captured sheep. Serum, blood and hair samples from 48 sheep were analyzed for trace minerals. White Mountains (WM) sheep samples had marginal levels of selenium and were significantly lower than sheep from Lake Clark National Park (LK). Copper concentrations in WM sheep hair samples were marginal to deficient. However, in serum, LC sheep had significantly lower mean copper concentrations than WM. Compared to domestic sheep, 80% of LC and 31% of WM sheep were copper deficient. Mean serum zinc from WM sheep was significantly lower than LK sheep and 81% vs. 57%, respectively, were marginal or deficient compared to domestic sheep. Hair was also marginal to deficient in zinc compared to domestic sheep. The addition of vitamin E/selenium injections at capture, intranasal xylazine injections and conducting net-gun capture operations mainly in the fall, significantly reduced capture mortality rate and decreased the incidence of capture myopathy. The proximate cause of horn abnormalities remains to be elucidated.

[103] SELENIUM SUPPLEMENTATION OF FREE-RANGING BIGHORN SHEEP IN HELLS CANYON

Crystal A. Strobl1, Victor L. Coggins1, E. Frances Cassirer2
1Oregon Department of Fish & Wildlife, Enterprise, OR, USA; 2Idaho Department of Fish & Game, Lewiston, ID, USA

Selenium deficiency may play a role in predisposing animals to disease, and consequently, selenium supplementation could potentially increase the ability of animals to mount an effective immune response to pathogenic organisms. Between 1997 and 2006, we provided commercially available salt blocks supplemented with 90 mg/kg of selenium and six other trace minerals (Zn, Fe, Mn, Cu, I, Co) to bighorn sheep (*Ovis canadensis canadensis*) in selected populations in the Hells Canyon metapopulation, and in 2000 and 2001 we also provided these populations with high selenium (120 mg/kg) and Vitamin E (600 IU/lb) fiber blocks. We analyzed selenium levels from whole blood collected at capture and found that levels were adequate (>0.05 ppm) based on standards in domestic sheep. Bighorn sheep were observed using supplemental blocks in all populations where available, however, whole blood selenium levels in two of the supplemented populations (average blood selenium = 0.12 ppm) did not differ from populations that were not supplemented (average selenium levels in 3 unsupplemented populations 0.12 – 0.21 ppm, p > 0.05). Average selenium level in the third supplemented population was twice that of all other populations (0.42 ppm, p <0.001). Two months after we removed mineral blocks from this population, blood selenium had declined to levels observed in the unsupplemented populations (x = 0.22, p = 0.23). However, despite the success of supplementation at elevating blood selenium levels, this population continued to experience pneumonia-caused mortality in adults and lambs. We discuss possible reasons for the success or failure of supplementation to increase blood selenium in this study and the failure of supplementation to significantly improve the health of bighorn sheep in Hells Canyon.
[104] LANDSCAPE-GENETIC ANALYSIS OF POPULATION STRUCTURE IN GRAY FOX: IMPLICATIONS FOR ORAL RABIES VACCINE PROGRAMS

Angeline Zamorano1, Randy W. DeYoung1, J. Jeffrey Root2, Tyler A. Campbell3, Brian T. Mesenbrink4, Guy Moore5, Bruce Leland6
1Texas A&M University-Kingsville, Kingsville, TX, USA; 2US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 3US Department of Agriculture-Wildlife Services, Kingsville, TX, USA; 4US Department of Agriculture-Wildlife Services, Kerrville, TX, USA; 5Texas Department of State Health Services, Austin, TX, USA; 6US Department of Agriculture-Wildlife Services, San Antonio, TX, USA

Gray foxes (Urocyon cinereoargenteus) in central Texas carry a distinct strain of rabies. Because of the health risks threatening wildlife, domestic animals and humans, oral vaccinations in the form of aerially broadcast baits have been dispensed over a broad region of central Texas. Management of this oral rabies vaccination (ORV) zone is difficult considering the large geographic scale and minimal knowledge of gray fox movements and dispersal. Knowledge of population structure within the ORV zone would be valuable for effective bait delivery and could increase the efficiency of rabies control. We genotyped 470 foxes from 33 counties at 5 microsatellite loci and sequenced 400 bp of the mtDNA control region for 42 foxes. Foxes had a high level of genetic diversity (heterozygosity = 0.81 and 0.6 for microsatellite and mtDNA, respectively). Microsatellite data revealed low but statistically significant genetic structure (Fst = 0.007) over the entire data set. However, only 1 of 14 pairwise Fst tests among sample locations was significant and there was no geographic pattern to the distribution of mtDNA haplotypes. Spatial autocorrelation analysis of microsatellite genotypes indicated that individuals within 75 km were more genetically similar than expected. The autocorrelation correlogram suggested a stabilizing profile, containing a mixture of high and low genetic similarity at larger spatial distance classes (>100 km). Fox populations appear genetically similar across a broad geographic extent, possibly due to high rates of dispersal. The effective control of rabies in Texas may require a spatially extensive ORV zone.

[105] A WHALE OF A STORY – DOCUMENTING EVIDENCE OF SHIPSTRIKE & ENTANGLEMENT IN A SEI WHALE IN MARYLAND WATERS

Cindy Driscoll1, Tricia Kimmel1, Charley Potter2, Dave Rotstein3
1Maryland Department of Natural Resources, Oxford, MD, USA; 2Smithsonian Institution, Washington, DC, USA; 3University of Tennessee, Knoxville, TN, USA

On April 17, 2006 at 1600 hours the Maryland Department of Natural Resources (MD DNR) received a call reporting a dead whale on the bow of an 800-foot long container ship in the Chesapeake Bay near Annapolis, MD. The carcass was determined to be a Sei whale (Balaena borealis). Once the ship docked in Curtis Bay, Baltimore, MD, the whale was successfully removed from the bow by tugboats and secured to the dock overnight. The following day it was lifted out of the water, weighed and transported on a 40-foot flatbed trailer to a nearby landfill and examined. A complete necropsy was performed on the 36-foot, 8.5-ton male whale and samples were collected by a team of biologists and veterinarians from the MD DNR and the Smithsonian Institution. The gross necropsy revealed a thin animal with numerous fractures and associated hemorrhaging. These findings suggested that the animal was alive when struck and died as the result of physical trauma and shock. Histopathological analysis at the University of Tennessee supported these findings. Additionally, lesions were observed in the mouth and palate that suggested a prior entanglement. Microscopic tissue examination confirmed that the lesions were relatively recent (weeks to months). The combination of gross and microscopic findings suggests that this whale was likely compromised as the result of a prior entanglement and thus more vulnerable to a ship strike. This case – a collaborative effort with many organizations - highlights the importance of conducting a thorough necropsy and collecting appropriate diagnostic samples to gain a full understanding of the circumstances surrounding the death of an animal.
WILDLIFE DISEASE SURVEILLANCE IN BRITAIN, AN OFFICIAL SCHEME

J. Paul Duff, Paul J. Holmes, Matt Hartley
1Veterinary Laboratories Agency (VLA), UK; 2Department of Environment, Food and Rural Affairs (DEFRA), UK

Investigation of wildlife disease by the British government veterinary laboratory network has occurred for several decades, and an officially supported scheme was first set up in 1998 - the Veterinary Laboratories Agency, Diseases of Wildlife Scheme (VLADoWs). In addition, the government is also developing a Wildlife Health Strategy and this should be released for public consultation in the near future. This presentation will describe how the Diseases of Wildlife Scheme works and how it is based on surveillance through a well developed regional laboratory network in England and Wales. The important categories of work undertaken will be summarized and how the results are reported and disseminated will be described. The Diseases of Wildlife Scheme, and its antecedents, produced the first reports of several emerging wildlife diseases, or the first isolations of the causative agents of these diseases in Britain. Examples which will be listed and they include Bovine tuberculosis in badgers (Meles meles), rabbit hemorrhagic disease, European brown hare syndrome, squirrel pox disease and frog ranavirus infection.

SURVEY FOR BLOOD PARASITES IN THE ENDANGERED WOOD STORK FROM SOUTHEASTERN UNITED STATES

1Texas A&M University-Kingsville, TX, USA; 2Mississippi State University, Mississippi State, MS, USA; 3Savannah River Ecology Laboratory, Aiken, SC, USA

The wood stork (Mycteria americana) is a threatened or endangered species in several states in the U.S. Because of the wood stork’s status, studies have examined the general ecology of wood storks. However, studies focusing on endoparasites have been mainly limited to examinations of wood storks found dead. Consequently, little information exists regarding endoparasites within the continental wood stork population. The blood protozoan Haemoproteus crumenium has been identified from several populations of wood storks in North America. However, there have been no reports of wood storks being infected with species of Plasmodium or Leucocytozoon. During 2003, 71 wood storks were captured and aged at nesting sites in Georgia and from dispersal sites in Mississippi and Louisiana. Two thin blood smears were made on microscope slides from each bird. Smears were air-dried, preserved in methanol, stained with Diff-Quik®, and examined for parasites. Smear examination time included 5 minutes at 400x magnification and 10 minutes at 1,000x magnification. Haemoproteus crumenium was found in 5 (7% prevalence) birds, whereas, Leucocytozoon sp., Plasmodium sp., and microfilarids were not observed. Mean intensity of H. crumenium was 4.4 ± 0.7 (SE) per 2,000 erythrocytes counted. All infected birds were aged as subadults or adults and were sampled in Mississippi. This study advances our knowledge about blood parasites in wood storks and helps biologists better understand possible limiting factors, such as parasite infections that may be influencing wood stork populations in North America.
INFECTIOUS & PARASITIC DISEASES IN ENDANGERED FENNOSCANDIAN ARCTIC FOXES

D. Gavier-Widén1, F. Widén1, M. Berg2, A-L Berg3, C. Bröjer1, E. Ågren1, K. Bernodt1, H. Uhlhorn1, T. Mörner1, A. Angerbjörn4
1National Veterinary Institute (SVA), Uppsala, Sweden; 2Swedish University of Agricultural Sciences, Sweden; 3AstraZeneca, Södertälje, Sweden; 4Stockholm University, Sweden

The arctic fox (Alopex lagopus) in Fennoscandia is threatened with extinction, and only approximately 150 adults remain in the wild. A conservation program was initiated in 1991. Wild-caught foxes were kept at a Swedish breeding centre. Arctic foxes from the breeding center and from the wild were examined post-mortem at SVA as part of the health-monitoring program. Data was collected from approximately 50 foxes. The most frequent disease in the breeding colony was severe, fatal, often necrotizing, encephalitis. The first case occurred in 1991, with several episodes of disease until 2004, when the last remaining fox in captivity was affected and the colony was terminated. Results of PCR analysis indicated that the encephalitis was apparently caused by a Herpesvirus. Presently, farmed blue foxes (Alopex lagopus), replacing arctic foxes for exhibition purposes in zoos have also been affected by necrotizing encephalitis. None of the wild foxes has shown encephalitis.

Other diseases affecting free-ranging arctic foxes were hemorrhagic enteritis, sarcoptic mange and pneumonia caused by Pasteurella multocida. The following parasites were identified in the gastrointestinal tract and lungs of either wild or captive foxes: Mesocestoides lineatus, Toxocara leonina, Toxocara canis, Strongyloides stercoralis, Taenia sp, Uncinaria stenocephala and Alaria alata, Crenosoma vulpis, Capillaria aerophila and Capillaria sp. Parasitic pneumonia was a frequent finding. Two foxes showed cystitis associated with the presence of numerous nematodes (Capillaria plica). A few foxes had antibodies against Toxoplasma gondii and/or parvovirus.

RESPIRATORY DISEASE IN MOUNTAIN SHEEP: KNOWLEDGE GAPS & FUTURE RESEARCH WORKSHOP RESULTS

Ben Gonzales1, Elena Garde2, Dave Jessup3, Frances Cassirer4
1California Department of Fish & Game, Rancho Cordova, CA, USA; 2British Columbia Ministry of Environment, Victoria, BC, Canada; 3California Department of Fish & Game, Santa Cruz, CA USA; 4Idaho Department of Fish & Game, Lewiston, ID, USA

We held a two-day workshop on respiratory disease in bighorn sheep (Ovis canadensis) in April 2007 to review current knowledge and to discuss priorities for future research. Objectives of the workshop were to: 1) Promote and foster interdisciplinary consultation and collaboration among laboratory researchers, diagnosticians, epidemiologists, and disease specialists and managers, 2) Provide an overview of recent and ongoing research on respiratory disease in domestic ruminants and wild sheep, and 3) Identify knowledge gaps and future research needs and provide recommendations for research priorities to funding organizations. Thirty-two participants were provided with relevant literature prior to the workshop and two keynote speakers and seven researchers and diagnosticians gave presentations on the first day. Breakout groups on the second day addressed research priorities, disease outbreak investigation, and risk assessment. Workshop participants concluded that research priorities include the identification, characterization, ecology, and epidemiology associated with the introduction of novel and/or virulent microorganisms into free-ranging bighorn sheep populations; investigation of social factors impeding acceptance and implementation of current research findings; and development of quantitative risk assessments for bighorn and domestic sheep management. Recommendations for sample collection and analysis for disease outbreak investigation were also developed. More information on this workshop is posted on the American Association of Wildlife Veterinarians website http://www.aawv.net/. A follow-up workshop scheduled for the Fall of 2007 for wildlife and wildland managers, grazers and conservationists will provide a summary of the respiratory disease workshop, summarize current “best management practices” for domestic and bighorn sheep management, review methods for resolving conflicts between domestic and bighorn sheep, and emphasize the use of risk assessment.
AVIAN INFLUENZA IN WILD RACCOON POPULATIONS: CAN PERIDOMESTIC WILD MAMMALS SERVE AS BRIDGES BETWEEN WATERFOWL AND HUMANS?

J.S. Hall1, K. Bentler1, G. Landolt2, J. Root1, R. Minnis3, T. Campbell4, S. Barras5, S. Elmore1 J. Pilon1, K. Pabilonia2, H. Sullivan1, C. Driscoll6, D. Slate7, L. Clark1, R. McLean1
1US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 2Colorado State University, Fort Collins, CO, USA; 3Mississippi State University, Starkville, MS, USA; 4US Department of Agriculture-Wildlife Services, Kingsville, TX, USA; 5US Department of Agriculture-Wildlife Services, Concord, NH, USA; 6US Department of Agriculture-Wildlife Services, Starkville, MS, USA; 7Maryland Department of Natural Resources, Oxford, MD, USA

Raccoons (Procyon lotor) are widespread, mobile, and frequently come into contact with wild waterfowl, agricultural operations, and humans. Serosurvey results showed that raccoons are exposed to avian influenza virus and develop antibodies based on that exposure. We found antibodies to AI subtypes H10N7, H4N6, H4N2, H3, and H1. Seroprevalences ranged from 0% in LA, TX, CA, and GA, 2.4% in MD, 15.6% in CO, to 25% in WY. Experimental infection studies showed that raccoons become infected with avian influenza virus, shed infectious virus, and can transmit virus to naïve raccoons. Analyses of the cellular receptors for influenza virus revealed that raccoons have both avian and human type receptors. Human-type receptors are predominant in the upper respiratory tract with both types present in the lungs. The potential exists for co-infection of multiple subtypes of influenza virus with genetic reassortment and the creation of novel strains of influenza. Experimental infection of raccoons with a human-adapted strain of influenza virus confirmed that these animals may play an important role in influenza disease ecology and pose undetermined risks to agriculture and humans.

BIVALVE MOLLUSKS AS BIOACCUMULATORS OF INFLUENZA A VIRUSES: IMPLICATIONS FOR MONITORING AVIAN INFLUENZA IN THE WILD

Kathryn P. Huyvaert1,2, Alan B. Franklin1, Jenny S. Carlson1, Kevin T. Bentler1, Kacy Cobble1, Dale L. Nolte1
1US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 2Colorado State University, Fort Collins, CO, USA

Avian influenza viruses naturally infect a diversity of wild bird species, primarily waterfowl, shorebirds, and other waterbirds. Recent rapid spread of highly pathogenic H5N1 avian influenza virus to new locations and species, however, has necessitated development of early detection and monitoring strategies for birds as well as their aquatic habitats. Avian influenza viruses can persist for extended periods in water, but the potential for dilution and patchy distributions of the virus in water raise concerns about direct water sampling. A novel solution to these problems of virus detectability is to use bioaccumulators, aquatic organisms that naturally filter and concentrate viruses from surrounding water. In controlled laboratory experiments, we evaluated whether Asian clams (Corbicula fluminea) could effectively bioaccumulate influenza A viruses H3N2, infecting humans, and H4N8, an avian influenza virus. We used real time RT-PCR technologies to quantify virus accumulations in clam tissues from groups exposed to different concentrations of virus in water over time. Clams accumulated virus to higher concentrations than the surrounding water from 6 to 100 hours after initial exposure. The degree and duration of accumulation depended on the initial concentration of virus in the water. Thus, our experimental data support the general hypothesis that influenza A viruses are detectable in the tissues of freshwater mollusks exposed to water treated with viable virus and that mollusks may effectively accumulate low concentration of influenza A virus from surrounding water. Here, we also discuss the utility of bioaccumulators in surveillance and monitoring efforts for avian influenza viruses in the wild.
[112] SURVEILLANCE OF HANTAVIRUS (SIN NOMBRE) IN NEBRASKA RODENTS, 1994-2004

Scott Hygnstrom¹, Christina Kocher¹, Wayne Kramer²
¹University of Nebraska, Lincoln, NE, USA; ²Nebraska Health and Human Services System, Lincoln, NE, USA

We conducted serosurveys of small rodents in Nebraska for the Sin Nombre strain of hantavirus during the late fall and early winter of 1994, 1996, 1997, 1998, 2002, and 2004. Our objectives were to determine the 1) geographic distribution of Sin Nombre in Nebraska and 2) changes in prevalence of the virus across a 10-year period. In 1994 through 2004, we collected and tested 1,965 individuals of 15 species of small rodents and 1 shrew. Sixty percent of the capture consisted of deer mice (Peromyscus maniculatus). The species with the highest seroprevalence of Sin Nombre included the deer mouse (55%), Western harvest mouse (Reithrodontomys megalotis, 29%), and prairie vole (Microtus ochrogaster, 15%). The prevalence of Sin Nombre in the samples across years was 4.1%, 10.1%, 5.3%, 11.1%, 7.1%, and 3.7% in 1994, 1996, 1997, 1998, 2002, and 2004, respectively. Prevalence in Nebraska counties that were surveyed across the state ranged from 0% to 21.5%. Sin Nombre was observed in samples throughout Nebraska during the 10-year period and no geographic or temporal patterns were discernable.

[113] PREDICTING PLAGUE EPIZOOTICS IN BLACK-TAILED PRAIRIE DOG COLONIES WITH A SENSITIVE PCR-BASED PROTOCOL

Philip H. Jones, Hugh B. Britten, David A. Hanson, Leigh R. Washburn
University of South Dakota, Vermillion, SD, USA

Within the United States, sylvatic plague has extirpated a significant number of Black-tailed prairie dog (Cynomys ludovicianus) populations. One major factor is the flea vectors that transmit plague from host to host. Oropsylla hirsuta and O. tuberculata cynomuris comprise the majority of fleas that infest black-tailed prairie dogs colonies which suggests that a small number of flea species are likely to be responsible for carrying the plague among and between colonies. There are opposing views about whether prairie dogs act as reservoirs for the plague. The current predominant model states that prairie dogs are highly susceptible epizootic hosts. However, our findings suggest that there may be a threshold prevalence of plague-positive fleas below which epizootics do not occur. Our data on plague prevalence in burrow-collected fleas suggests that prairie dog colonies begin to show widespread outbreaks once a certain percentage of infected fleas have been reached on a colony. We developed a method for detecting plague-infected fleas with the amplification of the Y. pestis pla gene using a PCR-based assay. Fleas were collected from fourteen colonies from Fort Belknap Indian Reservation (FBIR) from 2002, 2003, and 2005. Plague prevalence had increased from 16.5% plague-positive burrows in 2002 to 27.1% plague-positive burrows in 2003 to 36.3% plague-positive burrows in 2005. A plague epizootic began on eight of the 14 sampled colonies in the FBIR complex in early summer 2005. These data suggest that prairie dogs themselves may act as reservoirs and epizootic hosts for plague.
[114] **SEVERE, SOFT-TISSUE MINERALIZATION IN BULLFROG LARVAE FROM WASTEWATER TREATMENT WETLANDS**

*Kevin Keel*¹, *Alena Ruiz*², *Aaron Fisk*³, *John Maerz*²

¹Southeastern Cooperative Wildlife Disease Study–University of Georgia, Athens, GA, USA; ²University of Georgia, Athens, GA, USA; ³University of Windsor, Windsor, Ontario, Canada

Constructed and naturally occurring wetlands are increasingly used for tertiary treatment of wastewater ultimately reclaimed for distribution through municipal water supplies. A perceived added benefit of such facilities is the production or preservation of wildlife habitat. Wastewater treatment wetlands at one site in Georgia were surveyed to determine relative abundance and health of tadpoles. Effluent from this wastewater treatment facility is divided into three streams, each passing through a separate series of wetlands. Tadpoles were abundant but many bullfrog larvae (*Rana catesbeiana*) had severe lesions consisting of large (up to 1-cm-diameter), mineralized nodules protruding from the tail or gular region. The prevalence of lesions was inversely correlated with increased distance from the wastewater discharge site. Sectioning of formalin-fixed specimens revealed more extensive mineralization involving the vertebrae or muscles of the head and tail. Nodules examined microscopically were not associated with parasitic or infectious agents, and individual connective-tissue fibers and muscle cells were also mineralized. The nodules consisted entirely of calcium phosphate. Total, serum-calcium concentrations of tadpoles, and calcium concentrations in water samples did not differ significantly in wetlands with increasing distance from the discharge site. The only significant finding to date is elevated vitamin D levels in tadpoles with calcifications. At this time, the primary cause of elevated vitamin D levels is undetermined but it appears to be remediated by passage of water through the wetlands. However, based on reduced fitness of affected tadpoles, the argument for wastewater treatment wetlands as habitat beneficial for wildlife may be inappropriate.

[115] **SURVEILLANCE FOR FRANCISELLA TULARENSIS IN MUSKRAT OF THE SLAVE RIVER DELTA, NORTHWEST TERRITORY OF CANADA USING SEVERAL DIFFERENT DIAGNOSTIC METHODS**

*Mark D. Kellogg*¹, *Wes Carter*¹, *Edward Stevens*¹, *Mark Wolcott*¹, *Fred Mandeville Jr.*², *Brett Elkin*³

¹US Army Medical Research Institute of Infectious Diseases, Fort Detrick, MD, USA; ²Northwest Territory Environment & Natural Resources Wildlife Division, Fort Resolution, NT, Canada; ³Northwest Territory Environment & Natural Resources Wildlife Division, Yellowknife, NT, Canada

Tularemia is an infectious disease caused by the bacterium, *Francisella tularensis*. It is endemic throughout Canada as a water-borne disease of muskrats, beaver, and rodents living in aquatic habitats. Transmission is tick-borne in rodents, rabbits, and hares. *F. tularensis* does not grow well on standard microbiological media and detection has relied upon combinations of immunofluorescence staining of tissue samples or blood, and serological detection of antibodies. Local trappers provided 718 carcasses collected in the Slave River delta in the Northwest Territory of Canada in the spring and fall of 2005. Liver, kidney, spleen, lymph node, lung, and skeletal muscle were removed at necropsy. Samples were tested for the presence of *F. tularensis* DNA using two real-time PCR-based targets, an outer membrane-associated protein using an electrochemiluminescence immunoassay, culture on *F. tularensis* selective medium, and with an immunohistochemistry alkaline phosphatase assay, using a mouse monoclonal anti-tularensis antibody. In addition to tissues, water, and soil samples were collected from “push-ups” at several sites where trapping was conducted. Environmental samples were tested using culture and molecular diagnostic techniques. None of the methods utilized detected the presence of DNA, antibodies or antigens indicating *F. tularensis*. Histopathology of the tissues revealed schistosomiasis in most animals, with accompanying subacute multifocal hepatitis and perivasculitis. The majority of the histopathologic findings were considered to be incidental and clinically insignificant. In conclusion, prevalence of *F. tularensis* as detected by several immunologic and molecular techniques is very low in muskrats of the Slave River delta.
[116] ORAL RABIES VACCINATION IN ISRAEL

Roni King1, Boris A. Yakobson2, N. Devers2, Zvia Mildenberg2, Shmuel Amir1, Dan David2
1Israel Nature & Parks Authority, Jerusalem, Israel; 2 Kimron Veterinary Institute, Bet Dagan, Israel

Since 1998, Oral Rabies Vaccination (ORV) has been used as the main method to control wildlife rabies in Israel. The target species of the project are the red fox (Vulpes vulpes) that serves as the main vector of the virus, and the golden jackal (Canis aureus). The decline in the abundance of the disease, as shown in the numbers of wildlife that were diagnosed at the Israeli Veterinary Institute, justifies the continued use of this method. From a small-scaled field trial of about 500 km², the project has expanded to > 20,000 km². A spatial analysis of rabies incidence sites showed a significant correlation with the extent of ORV distribution. During 2005/6, an outbreak of rabies in the vaccinated Golan Heights in northern Israel was observed in feral/stray dogs probably coming across the border from Syria, with no positive cases in foxes or jackals. A phylogenic analysis of the isolated viruses supports this hypothesis, showing that there are not originating from the same group of isolates that were found in this area in the past. This incident points to the possibility of these feral dogs as the possible reservoir of the virus, and the potential source of future outbreaks in Israel.

[117] USE OF A NOVEL “EQUIVALENCE TESTING” PROGRAM FOR MONITORING FREEDOM OF MYCOBACTERIUM BOVIS INFECTION IN DEER GAME ESTATES IN NEW ZEALAND

Scott Loeffler1, Graham Nugent2, Dave Ramsey3, Andrea Byrom2
1 Animal Health Board, Riccarton, Christchurch, New Zealand; 2 Landcare Research, Lincoln, New Zealand; 3 Rylah Institute for Environmental Research, Heidelberg, Victoria, Australia

In New Zealand, there are approximately 5000 herds of farmed deer, of which 29 are currently known to be infected with Mycobacterium bovis. All herds of farmed deer are required to be skin tested on an annual, biennial or triennial basis, depending on the area disease risk. In addition, New Zealand has a large feral deer population of unknown TB status that run wild on land owned by the New Zealand Department of Conservation. Thirdly, some farmers living adjacent to these areas, have created game estates on their properties for the purpose of hunting trophy stags. These stags are usually released from accredited TB free farms to run with the feral hinds on the game estates. Intradermal skin TB testing of the hinds and stags on the Game Estates is not feasible due to their feral nature. However, these animals could pose a substantial disease risk to adjacent farmed. This paper describes an how an equivalence testing program was developed for Game Estates based on the post-mortem examination of a portion of the culled hinds and an equivalence testing where one possum equals one deer and one ferret or pig equals 10 deer. These “equivalences,” based on spatial calculations of species-specific probabilities of contracting tuberculosis and roaming areas, are described. The program has been well-received by game estate managers and is audited by third parties.
[118] SEASONAL VARIATION IN BLOOD PARAMETERS & CHARACTERIZATION OF PHYSIOLOGICAL RESPONSES TO POPULATION MANAGEMENT OPERATIONS IN KOALAS

Michael Lynch1, Allen McIlwee2, John Reece3
1Melbourne Zoo, Parkville, VIC, Australia; 2Department for Environment and Heritage, Mount Gambier, SA, Australia; 3Royal Melbourne Institute of Technology, Bundoora, VIC, Australia

Seasonal differences for selected blood parameters were investigated in an over-abundant koala population. Mean values for PCV, hemoglobin, total lymphocytes, total protein, albumin, urea and cholesterol were all significantly higher in samples taken in spring compared with fall. Seasonal differences in blood parameters were presumed to reflect an increased quantity and quality of Eucalypt sp. leaf available to animals in the spring as compared to the end of summer. Variations in the same parameters were measured over time in animals translocated to two different locations and a control group returned to the site of capture. Selected blood parameters were measured at the time of first capture, again at approximately two weeks post-treatment, then monthly for up to six months. A high mortality rate and significant weight losses in occurred at one translocation site within the first 30 days after treatment. It is highly likely that most trees at this translocation site were unpalatable to the animals although Eucalypt species eaten by koalas in other locations were present. Surviving animals had significantly higher initial serum albumin at initial capture than those that died suggesting the animal’s nutritional status when they entered the trial influenced survival. Animals that died or were removed to care within the first 30 days showed significantly reduced body mass at the first recapture. In contrast, body mass did not significantly alter at any stage of the trial for animals known to be alive at Day 30. Changes in blood parameters of surviving animals mirrored seasonal differences.

[119] LIVE SHEARING OF FREE-RANGING GUANACO (LAMA GUANICOE) IN ARGENTINA: A POSSIBLE MANAGEMENT TOOL FOR CONSERVATION

Carolina A. Marull1, Carmanchahi Pablo2, Lager Irene3, Samartino Luis3, Marticorena Damián4, Rago Virginia1, Fortuny M. Laura1, Marcoppido Gisela3, Novaro Andrés5 Uhart Marcela1
1Field Veterinary Program, Wildlife Conservation Society, Argentina; 2UNCOMA, National Research Council, Neuquén, Argentina; 3INTA Castelar, Buenos Aires, Argentina; 4University of Buenos Aires, Argentina; 5Wildlife Conservation Society, Neuquén, Argentina

Guanaco are the most abundant wild ungulates of arid environments in South America. However, their populations have declined dramatically since European colonization due to habitat degradation, competition with introduced domestic sheep, overhunting and lack of management plans. More recently, the high commercial value of fine wool fibers has favored an explosion of private initiatives to shear free-ranging guanaco in Argentina Patagonia, which could lead to further reductions of their populations if not properly controlled. In an effort to obtain critically needed information and experience to prepare guidelines for the rational management of this emerging resource we began a community cooperative guanaco shearing project with the inhabitants of La Payunia Wildlife Reserve and the financial support of the government of Mendoza in 2005. By means of this initiative we expect to create a sustainable alternative for rural development in the region, focusing on the conservation of guanaco and its environment. One of our roles in these pilot experiences has been to train community members in animal wellbeing practices, proper handling of wild animals, and monitoring of shearing effects on free-ranging guanaco populations. On the other hand, because the main source of income for these communities comes from farming of small ruminants that are raised in areas where guanaco roam free, we are evaluating the presence of pathogens and evaluating transmission risks between both groups. We will discuss the management and conservation results of the initial phase of the project and disease exposure results to date.
[120] **Dispersing Cimicid Vectors Have Low Buggy Creek Virus Infection Rates**

Amy T. Moore¹, Valerie A. O'Brien¹, Allison Johnson², Mary Bomberger Brown¹, Charles R. Brown¹

¹University of Tulsa, Tulsa, OK, USA; ²Saint Olaf College, Saint Olaf, MN, USA

Arthropod-borne viruses are often not distributed homogenously among potential vectors, with infection rates potentially varying with vector age, spatial location, or behavioral characteristics. Buggy Creek virus (BCRV) is an alphavirus in the western equine encephalomyelitis virus complex and has an unusual ecology, being vectored principally by the cimicid swallow bug (*Oeciacus vicarius*) and amplifying in the colonially nesting cliff swallow (*Petrochelidon pyrrhonota*) and the introduced house sparrow (*Passer domesticus*) that sometimes nests in swallow colonies. Swallow bugs are sedentary and disperse rarely by clinging to the feet and legs of swallows moving between colonies. We examined BCRV infection rates in dispersing bugs by comparing virus prevalence in newly established colonies and in immigrant bugs brought into sites at periodic intervals. New colonies averaged 9.3% of bug pools positive, compared to 33.7% in established colonies. Immigrant bugs at two sites had relatively little virus (8.6% pools positive), compared to overall infection rates (33.2%). These data indicate that dispersing swallow bugs are less likely to be infected with BCRV than sedentary individuals at colony sites and that infection status may correlate with bug movement behavior.

[121] **A Survey on Hydatid Cyst of Liver & Lung of Camels in Sabzehvar, Iran**

Soraya Naem, Abazar Jafari

Urmia University, Urmia, Iran

The camel is a large, strong desert animal and can travel great distances across hot, dry deserts with little food and water. There are two kinds of camels; the Arabian camel, also called dromedary, which has one hump and the Bactrian camel, which has two humps. Camel milk is a staple food of desert nomad tribes and is richer in fat and protein than cow’s milk. Camel meat has been eaten for centuries. It is reported that camel meat tastes like coarse beef, but older camels can prove to be tough and not too flavorful. Not just the meat, but also blood is consumable item as is the case in northern Kenya where camel blood is a source of iron, vitamin D, salts and minerals, although Muslims do not drink or consume blood products. In this study which was carried out on camels in 2006, a total number of 52 camels were examined in a slaughterhouse in Sabzehvar City, Iran. The Iranian camel has one hump and is used by people in some areas, especially in border cities. A complete record was kept for each camel, including age, sex, clinical history and demographic data. The results were indicated that only 2% of examined camels were infected with hydatid cysts. Both infected cases were female and hydatid cysts were removed from their livers. No infection was seen in the lung of examined camels.
[122] WILDLIFE HEALTH MANAGEMENT CHALLENGES IN JAPAN: PAST, PRESENT, & FUTURE

Yasuko Neagari¹, Michael D. Samuel²
¹University of Wisconsin, Madison, WI, USA; ²Wisconsin Cooperative Wildlife Research Unit-University of Wisconsin, Madison, WI, USA

The recent emergence of zoonotic diseases such as West Nile Virus and HPAI have created worldwide concern about the importance of wildlife health and the potential interface with human and domestic animal systems. Wildlife health issues are an ongoing concern in Japan where Avian Botulism, Lyme disease, Sarcoptic mange, Toxoplasmosis, and lead poisoning have been reported sporadically. In addition, HPAI has recently been found in domestic poultry, but the source of infection has not been determined. Furthermore, there are a number of ecological (e.g., migratory birds); geographical (e.g., high densities of domestic animals, human, and wildlife); and social/economic factors (e.g., large scale livestock production, feeding wildlife, tourism, and pet trade) that increase the potential risk of the introduction and spread of diseases in Japan. In spite of these potential health and economic threats of emerging wildlife disease problems, Japan does not have a public system to monitor, control, or provide advice for wildlife health issues. It is crucial to establish comprehensive and interdisciplinary wildlife health research/management programs to maintain healthy ecosystem in Japan. Therefore, I consider the historical, ecological, social, legal, and economic reasons why wildlife health systems have not developed in Japan. I propose appropriate systems for Japan considering the following questions: how do we form the collaboration to deal with wildlife/ecosystem health among agencies and organizations that have different values? What kinds of functions do we need for management of wildlife health? Who has authorities and/or expertise? From where can we get the funding?

[123] SUSCEPTIBILITY OF RICHARDSON’S GROUND SQUIRRELS TO ATTENUATED & VIRULENT STRAINS OF BRUCELLA ABORTUS

Pauline Nol¹, Steven C. Olsen², Jack C. Rhyann¹, Sarah M. Coburn¹
¹US Department of Agriculture-Veterinary Services; Fort Collins, CO, USA; ²US Department of Agriculture-Agricultural Research Service, Ames, IA, USA

Wild elk and bison populations in the Greater Yellowstone Area serve as reservoirs for brucellosis and have been implicated in transmitting disease to domestic cattle. Considerable effort has been devoted to investigating the efficacy and safety of Brucella abortus strain RB51 (sRB51) and other attenuated vaccine strains of B. abortus in elk and bison. A previous investigation of the safety of sRB51 in various non-target species revealed that Richardson’s ground squirrels (Spermophilus richardsonii) develop persistent infections when orally inoculated with the vaccine. The present study was to establish whether oral inoculation with sRB51, B. abortus strain 19 (s19), or virulent B. abortus produces disease in this species. Six groups of non-gravid ground squirrels were orally inoculated with 6 x 10⁸ cfu sRB51 (n=10), 2.5 x 10⁴ cfu s19 (n=10), 2.5 x 10⁷ cfu s19 (n=7), 1.3 x 10⁶ cfu B. abortus strain 1687 (s1687) (n=5), 2.1 x 10⁸ cfu s1687 (n=5), or vaccine diluent (control) (n=4). Although 2 animals in the higher dose s19 group and 1 animal in each of the other inoculated groups showed persistence of bacteria in various tissues 14 to 18 weeks post inoculation, we found no evidence of disease caused by B. abortus in non-pregnant Richardson’s ground squirrels based on clinical signs, gross lesions, and histopathology.

Poster
[124] INVASIVE HOUSE SPARROWS AS ALTERNATIVE HOSTS FOR BUGGY CREEK VIRUS

Valerie A. O'Brien, Abinash Padhi, Amy T. Moore, Stephanie A. Strickler, Charles R. Brown
University of Tulsa, Tulsa, OK, USA

Invasive wildlife species can sometimes impact disease dynamics profoundly, causing epizootics and emerging epidemics. We investigated the potential role of the introduced house sparrow (*Passer domesticus*), a common human commensal in North America, as an amplifying host for the poorly known Buggy Creek virus, an alphavirus in the western equine encephalomyelitis virus complex. This virus is vectored primarily by the cimicid swallow bug (*Oeciacus vicarius*) and presumably amplified mostly in the colonially nesting cliff swallow (*Petrochelidon pyrrhonota*), the principal host of the swallow bug. Because house sparrows use cliff swallow nests at many colonies and are also parasitized by the swallow bug, they represent recent additions to the cliff swallow/swallow bug ecosystem. Using RT-PCR to identify viral RNA in sera, we found little evidence of any amplification by either adult or nestling cliff swallows. In contrast, 46% of nesting house sparrows 5-17 days of age had detectable virus. Phylogenetic analysis of virus isolates from swallow bugs taken from nests containing house sparrows vs. cliff swallows at two sites showed no strong evidence of sequence differences among isolates from the two species, suggesting that the higher rates of virus amplification in house sparrows are not related to evolutionary differences among viruses in the different species. Why house sparrows appear to amplify Buggy Creek virus more frequently than cliff swallows is unclear.

[125] WILD ANIMAL DISEASES: THE ITALIAN SURVEILLANCE NET

R. Orusa¹, S. Robetto¹, A. Gaffuri³, S. Gavaudan⁴, V. Ferrantelli⁵, C. Pasolli⁶, A. Petrella⁷, A. Pintore⁸, M. Di Ventura⁹, A. Battisti¹⁰, S. Sandulli¹¹, U. Santucci², T. Lo Valvo¹

¹CeRMAS Centro di Referenza Nazionale per le Malattie degli Animali Selvatici, IZS Piemonte, Liguria e Valle d’Aosta, Area Sanitaria della Valle d’Aosta, Italy; ²Ministero della Salute, Italy; ³IZS Lombardia-Emilia Romagna, Italy; ⁴IZS Sicilia, Italy; ⁵IZS Venezie, Italy; ⁶IZS Puglia-Basilicata, Italy; ⁷IZS Sardegna, Italy; ⁸IZS Abruzzo-Molise, Italy; ⁹IZS Lazio-Toscana, Italy; ¹⁰IZS Mezzogiorno, Italy

Every year, the National Reference Centre for Wild Animal Diseases on behalf of the Ministry of Health collects and organizes data about the presence of wild animal diseases from each Italian region. There is a referent for wild animal diseases in each Istituto Zooprofilattico Sperimentale, who has to monitor sanitary situations in the territory. After elaboration, the aggregate data from Italy are then sent to the OIE Working Group on wildlife diseases. Infectious diseases in wildlife can interfere in the health of domestic animals, of humans and also damage wild populations. It is then of great importance to have a good knowledge regarding the diseases present in wild populations and their effects on wildlife, domestic animals and humans. Two kinds of data are received by the National Reference Centre for Wild Animals Diseases from Italian territories. For some diseases, there are scientific projects that investigate the presence of select pathogens in a wild population; these data are the most meaningful and they also can be used to monitor the prevalence or to exclude the presence of the pathogen in the territory. For many other diseases, data are from isolated findings of positive cases discovered by acquiring diagnostic suspects; the only information received from these data is the presence of a disease in a territory. Understanding this distinction is important in analyzing and interpreting wildlife disease surveillance data.
[126] **THE ROLE OF RACCOONS IN THE EPIDEMIOLOGY OF LEPTOSPIROSIS**

**Eran Raizman**, Olin Rhodes Jr., Wu Ching Ching, Roman Pogranichniy, Guha Dharmarajan, James Beasley  
Purdue University, West Lafayette, IN, USA

Increases in raccoon (*Procyon lotor*) abundance in fragmented agricultural regions are alarming for a number of reasons, including increased prevalence of diseases transmissible to humans and domesticated species. The potential risks associated with rapidly increasing raccoon populations in agricultural landscapes have not been well characterized for raccoon borne diseases that threaten livestock health such as Leptospirosis. The objective of this ongoing study in Northcentral Indiana is to assess the role of raccoons in the wildlife-livestock-bacteria triangle. As a part of a larger study on the ecology of raccoons, blood samples were obtained from approximately 700 raccoon and tested for *Leptospira interrogans* serovars. In addition, with the aim to assess active bacterial shedding into the environment, samples of bladder, kidney, urine, and liver have been obtained from more than 150 animals euthanized in this study up-to-date. Preliminary results indicate that of a 200 samples 45 (23%) were positive to at least one of the following serovars: *L. pomona* (5%), *L. hardjo* (15%), *L. grippotyphosa* (12%), *L. bratislava* (7%), and *L. autumnalis* (12%). The assessment of Leptospira serovar shedding by raccoons into the environment of domestic animals will add an important facet to the control and prevention of several important livestock diseases among them Leptospirosis and Bovine Viral Diarrhea (BVD).

[127] **WETLAND CHARACTERISTICS ASSOCIATED WITH TREMATODE INFECTIONS IN AMPHIBIANS: IMPLICATIONS FOR CONSERVATION AND RESTORATION**

**Anna M. Schotthoefer**, Jason R. Rohr, Rebecca A. Cole, Catherine M. Johnson, Lucinda B. Johnson, Val R. Beasley  
1University of Illinois at Urbana-Champaign, Urbana, IL, USA; 2Pennsylvania State University, University Park, PA, USA; 3National Wildlife Health Center, Madison, WI, USA; 4Monongahela National Forest, Elkins, WV, USA; 5University of Minnesota Duluth, Duluth, MN, USA

Infection by larval trematodes has been implicated in causing limb deformities, behavioral changes, and mortality in amphibians. The consequences of such effects are likely to impair the sustainability of amphibian populations. Therefore, effective amphibian conservation and restoration plans, should include strategies to alleviate the intensities of larval trematode infections. Unfortunately, little is known about the wetland characteristics that promote larval trematode transmission. To address this lack of knowledge, we applied multivariate techniques to evaluate the characteristics of wetlands that were positively associated with larval trematode infections in amphibian populations of the Midwestern US. Exposure to contaminants (particularly atrazine), snail species richness, and composition of wetland vegetation were identified as important determinants of larval trematode abundances in recently metamorphosed frogs. Landscape context of wetlands also strongly influenced abundances, suggesting disease management plans will have to consider the surrounding terrestrial habitats. Time of year, climatic conditions, amphibian stage structure, and invertebrate and vertebrate communities at wetlands may also be important. Collectively, our results indicate the need for experimental research to identify the wetland characteristics that may be manipulated to reduce larval trematode infections in amphibians.
[128] A RAPID FIELD IMMUNOASSAY FOR IDENTIFYING SIN NOMBRE HANTAVIRUS-INFECTED DEER MICE

Tony Schountz¹, Charles H. Calisher², Tiffany R. Richens², Audrey A. Rich¹, Jeffrey B. Doty², Mark Hughes², Barry J. Beaty²
¹University of Northern Colorado, Greeley, CO, USA; ²Colorado State University, Fort Collins, CO, USA

Identification of hantavirus-infected rodents has relied on detection of viral RNA, virus, or antibody, in field-collected samples shipped to a laboratory. Usually, the rodents are killed and frozen for further testing. This obviates the use of live rodents or requires costly, time-consuming, and usually unsuccessful recapture efforts. We developed a protein-A/G enzyme immunoassay (PAGEIA) for antibody to Sin Nombre hantavirus (SNV) that requires about an hour to complete under field conditions. Deer mice (Peromyscus maniculatus) were trapped at a site in southwestern Colorado and tested for antibodies to SNV. The specificity of the PAGEIA was comparable to standard EIA; its sensitivity was 97.1%. Its use provides investigators with a means of rapidly identifying infected rodents without having to euthanize them. Given that protein-A/G binds to IgG from many mammals, it is likely the test can be adapted for use in tests of other mammals and for other antigens.

[129] JOHNE’S DISEASE IN NEW ZEALAND WILDLIFE

Graham Nugent, Jackie Whitford, Jamie Glossop, Daniel M. Tompkins
Landcare Research, Lincoln, New Zealand

Johne’s disease caused by Mycobacterium paratuberculosis has emerged as a major cause of premature death among young farmed deer in New Zealand, and has long been a widespread and difficult-to-control chronic wasting disease in sheep and cattle herds. We surveyed small mammals and birds on three Johne’s-infected deer farms in New Zealand to determine whether wildlife were potentially important as reservoirs of infection. Although only three animals had visible signs of infection, M. paratuberculosis was detected from mycobacterial culture of mesenteric lymph nodes in six mammal species, and the alimentary tract of two bird species. Prevalences were often high, with infection found in 36% of 42 hedgehogs (Erinaceus europaeus), 26% of 113 rabbits (Oryctolagus cuniculus), and 25% of 73 possums (Trichosurus vulpecula). Prevalence also varied between farms, but the differences between farms were not the same for each species. Fecal cultures were positive for 13% of the infected mammals, indicating they were shedding bacilli when killed. The results suggest that M. paratuberculosis infection is likely to be common in small mammals on New Zealand farms infected with Johne’s disease. The high prevalences, and the presence of M. paratuberculosis in wildlife feces, obviously creates potential for transmission from wild animals to livestock. Also, the wide-ranging bird species in particular could conceivably play a role in disease spread between otherwise unconnected farms. Infected wildlife may therefore contribute to the difficulty of controlling Johne’s disease in livestock, but their importance will depend on whether they can sustain the disease independently and/or the relative frequency with which they infect susceptible livestock.
Bovine tuberculosis (Tb; *Mycobacterium bovis*) was first discovered in cattle adjacent to Riding Mountain National Park (RMNP; MB, CAN) in 1991. Elk (*Cervus elaphus*) has been determined to be the primary reservoir species for Tb. Managing, or eradicating, disease in wildlife reservoirs is arguably more difficult than within strictly agricultural settings; largely due to the obfuscating nature of ecologically complex behaviours (e.g., driven by habitat selection and predator avoidance) in heterogeneous environments. One of the most fundamental variables for understanding disease transmission is contact-rate. We present preliminary results of a telemetry collaring effort on female and male elk employing SirTrack Proximity Collars©. Proximity collars collect data on interaction time and duration of interaction among collared individuals. The animals are subsequently tracked through space to determine spatially explicit contact-rates. This information is augmented with interaction data collected from a controlled herd of elk.
## PRESENTATION SCHEDULE FOR POSTERS

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[131] SCREENING WILD ASIAN ELEPHANTS IN SOUTHERN INDIA FOR HUMAN STRAIN OF TUBERCULOSIS

David Abraham
Wildlife Conservation Society, National Centre for Biological Sciences, Bangalore, India

India has the largest population of Asian elephants (Elephas maximus), both in captivity and in the wild. India also has the largest incidence of tuberculosis in human population, and elephants in captivity are susceptible to human strain of tuberculosis (Mycobacterium tuberculosis). Emerging infectious diseases are known to cause population declines and significantly affect the distribution and abundance of animal populations world over. In the human dominated landscape in southern India, transmission of tuberculosis from humans to captive elephants, and then to wild elephants can have serious implications in conservation of this endangered species. This study tried to ascertain the prevalence of tuberculosis in wild elephants using a non-invasive technique for detecting M. tuberculosis DNA in dung samples in wild elephants. It was hypothesised that based on the level of interaction with humans, the populations of elephants studied might have varying chances of getting tuberculosis. Amplification of insertion element IS6110 of M. tuberculosis DNA in the dung samples of wild elephant by polymerase chain reaction (PCR) was evaluated in the diagnosis of tuberculosis. Dung samples of 226 wild Asian elephants collected from seven protected areas in southern India were analysed. The technique used, heat and detergent lysis without DNA extraction, followed by PCR amplification of the 123-bp fragment of IS6110 insertion element, and detection of products by agarose gel electrophoresis along with positive and negative controls. PCR amplification of IS6110 was not observed in the 226 samples analysed. This study reveals that the non-invasive techniques, when standardised will be the best tools for monitoring wildlife health in future.

[132] SEROPREVALENCE OF Trypanosoma cruzi FROM RACCOONS AND OPOSSUMS FROM GEORGIA

Emily L. Brown, Dawn M. Roellig, and Michael J. Yabsley
Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA

Trypanosoma cruzi, the causative agent of American trypanosomiasis (Chagas’ disease) is a substantial public health problem in Latin America. In the US, several species of wildlife are the primary hosts, although some domestic animal and human cases have been reported. A wide range of mammals are naturally infected with T. cruzi, but the two primary reservoirs in the US are believed to be raccoons (Procyon lotor) and opossums (Didelphis virginiana). Raccoon and opossum serum samples from Georgia were tested for anti-T. cruzi antibodies using the indirect immunofluorescent antibody test. Twenty-one of 59 (36%) raccoons and 21 of 71 (30%) opossums were seropositive for T. cruzi at a 1:40 titer cutoff. The comparable prevalence suggests that the exposure level of raccoons and opossums is similar. However, these data are in contrast to previous studies based on culture, which indicated that the T. cruzi prevalence was lower in opossums compared with raccoons. This is the first study to investigate the seroprevalence of T. cruzi in Virginia opossums. Once complete, this study will bring insight into the seroprevalence in these and additional hosts from multiple states in the US, potential temporal changes in seroprevalence, and differences in seroprevalence between urban and rural mammal populations.
[133] FECAL PARASITES OF WOLVES SYMPATRIC & ALLOPATRIC TO DOGS IN COASTAL BRITISH COLUMBIA

Heather M. Bryan1, Paul. C. Paquet1,2, Chris T. Darimont2,3, Judit E. Smits1
1University of Saskatchewan, Saskatoon, SK, Canada; 2Raincoast Conservation Foundation, Bella Bella, BC, Canada; 3University of Victoria, Victoria, BC, Canada

On the remote and sparsely populated central and north coasts of British Columbia (BC), little is known about fecal parasites in wild or domestic animals, yet the potential for parasite transfer and exposure to similar parasites exists among populations of unique coastal wolves and free-ranging dogs. Accordingly, we are undertaking a multi-year study that will provide baseline data on parasites in wolves and dogs across this mainland and archipelago area. We hypothesize that parasite intensity and prevalence will be similar between sympatric wolves and dogs, whereas wolves allopatric with dogs will harbor different parasite communities. Based on standard coprological techniques, our preliminary results have shown that dogs and wolves in the study area host at least nine parasite genera. In 17 dog feces, prevalence was highest for Sarcocystis (29%), followed by Toxocara (12%), Tanaiids (6%), Trichuris (6%) and Giardia (6%). In 53 wolf feces, prevalence was highest for Tanaiids (36%), followed by Sarcocystis (19%), Giardia (11%), Diphyllobothrium (9%), Toxascaris (4%), Trichuris (2%), Alaria (2%), and Demodex (2%). These results will be augmented by data from the 2007 field season including at least 200 fecal samples from wolves and 70 fecal samples from dogs.

[134] USING PROTEIN MICROARRAY TECHNOLOGY TO MONITOR LONG-TERM STRESS IN GRIZZLY BEARS

Ruth I. Carlson1, Marc R. L. Catter2, Gordon B. Stenhouse3, David M. Janz1
1University of Saskatchewan, Saskatoon, SK, Canada; 2Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada; 3Foothills Model Forest & Alberta Sustainable Resource Development, Hinton, AB, Canada

Grizzly bear (Ursus arctos) populations in Alberta, Canada, are potentially threatened by human activities, particularly increased access into grizzly bear habitat as a result of resource extraction activities (mining, oil and gas, and forestry), municipal development, and recreation. We hypothesize these activities are causing long-term stress in some grizzly bears. Although short-term stress can be beneficial to animals in coping with immediate stressors such as predator avoidance, long-term stress can have negative effects on an individual’s health status, including immune function, reproduction and growth. Our primary research objective is to evaluate effects of landscape structure and change on the health of resident grizzly bears. As one component of our research initiative, we are developing an antibody-based protein microarray to detect long-term stress in grizzly bears. Specifically, the microarray will detect increased or decreased expression of a suite of stress-activated proteins. We are collecting skin and muscle samples from grizzly bears, determining stress protein patterns in these samples, and integrating these results with other health data, such as measures of growth, and immune and reproductive functions to provide an overall health index. After corroboration using field data, this proteomic technique will provide an essential tool for early warning of potential health problems in grizzly bears that may arise as a result of human activities. Further, as this technique is based on evolutionary conserved stress proteins, the microarray may potentially be used to evaluate long-term stress in other wildlife.
[135] ECOLOGICAL FACTORS AFFECTING THE PREVALENCE OF SIN NOMBRE VIRUS IN FORESTED ECOSYSTEMS

Laurie J. Dizney¹, Philip D. Jones¹ and Luis A. Ruedas¹,²
¹Department of Biology, Portland State University, Portland, OR, USA; ²Museum of Vertebrate Biology, Portland State University, Portland, OR, USA

Zoonoses are diseases carried by wildlife that can affect human populations; their control and prevention often remain intractable problems in public health. For example, Ebola, Avian Influenza, SARS, West Nile Virus and the New World Hantaviruses are all recently discovered zoonoses. The goal of this study was to investigate ecological factors, particularly biodiversity, and their effects on the incidence of zoonotic disease. We hypothesize that as biodiversity of the mammal community increases, the prevalence of Sin Nombre virus, a Hantavirus, in the ecosystem decreases. To test this hypothesis, a web-sampling grid was placed in five natural areas in and around Portland, Oregon. In order to trap as many different species as possible, 352 live-traps of four different trap types were placed on a web for four consecutive nights and checked daily. Each park was trapped nineteen times over the course of three years. Biodiversity was calculated with a Simpson's Index. Blood samples from captured animals were tested for hantaviral antibodies using ELISA. We captured 5058 specimens and found Sin Nombre virus–positive deer mice (Peromyscus maniculatus), the natural host, in all parks. Using a regression, we found a strong significant negative relationship between site biodiversity and percent infection rate: more precisely, as biodiversity decreased, the prevalence of Sin Nombre virus in the ecosystem increased, exponentially so when diversity became very low, a phenomenon we describe as a zoonotic release. Biodiversity therefore appears to control this zoonotic disease, further supporting the need for conservation of biodiverse ecosystems.

[136] ECTOPARASITE INTENSITY DIFFERS WITH SOCIAL NESTING PATTERN & NEST SIZE IN DARWIN’S TREE FINCHES

Rachael Y. Dudaniec, Sonia Kleindorfer
Flinders University, South Australia, Australia

Social nesting behaviour in is known to often entail costs associated with increased parasite numbers in hosts. Avian parasite intensity is often found to increase with the level of nest aggregation in intraspecific comparisons (e.g. colonial nesting species), though little is known about the effect of interspecific host breeding density for parasite intensity in generalist host-parasite systems. Darwin’s tree finches show heterospecific nesting aggregations and solitary nesting at a spatial scale of 22 m. Nestlings are parasitised by larvae of the mobile blood-sucking fly Philornis downsi, which shows 100% prevalence in finch nests and causes 19-62 % total brood loss on Santa Cruz Island, Galapagos Archipelago. We document significantly higher P. downsi total intensity (the number of parasites per nest for tree finch nests with many close neighbours (defined as having ≥2 active nests within 22 m of the focal nest), than at solitary nests (defined as having 0-1 active nests within 22 m of the focal nest). An increase in P. downsi intensity with host body size has been previously shown. Therefore, the relation between host body mass, nest size, and P. downsi total intensity is also examined within and across finch species. Parasite intensity is found to be significantly higher in large nests (even within species). These findings lend insight into the dispersal behaviour and host preference of P. downsi ectoparasites, which are important components to understand within this system for developing an effective control strategy.
[137] HELMINTH BURDENS OF DOUBLE-CRESTED CORMORANTS IN SASKATCHEWAN: LINKS TO DIET COMPOSITION & POPULATION TRENDS

Heather Fenton1, Christopher Somers2, Catherine Soos1,3, Emily Jenkins1,3, Frederick Leighton3,4, Lydden Polley1, Brent Wagner1
1University of Saskatchewan, Saskatoon, SK, Canada; 2University of Regina, Regina, SK, Canada; 3Environment Canada, Saskatoon, SK, Canada; 4Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada

In the summer of 2006, we investigated parasites in double-crested cormorants (Phalacrocorax auritus) at four lakes in Saskatchewan, Canada. This complemented ongoing investigation of food habits, behavior, and population trends of colony-nesting birds at these sites (two in the boreal region, two in the prairie region). We examined carcasses of 49 apparently healthy adult cormorants that had been shot by cooperating local hunters. Helminth intensities in stomach and small intestinal contents were compared among sites. There were significant differences in both stomach nematode counts (F = 10.31, P < 0.001) and small intestinal cestode and trematode counts (F = 3.67, P = 0.022) among sites. Differences in parasite community and intensity among the sites may have resulted from differences in diet (based on prey species identification in regurgitation samples from juvenile cormorants) and population size (based on number of nests per colony in aerial photographs). Cormorants at Reed Lake had the lowest cestode counts, as well as the lowest proportion of fish forming their diet. Cormorants at Dore Lake, where the highest number of nesting birds was observed, had the highest intensity of proventricular nematodes (primarily Contracaecum spp.). Parasite intensity was not correlated with body mass index (BMI), suggesting that BMI may not be a sensitive measure of sublethal parasitism effects in this case. This project demonstrates the value of complementary investigations of disease ecology and wildlife population biology, and the value of involvement of wildlife stakeholders in such studies. Similar work is ongoing in the summer of 2007.


Pamela J. Ferro1, John El-Attrache1,2, Xingwang Fang2, Markus J. Peterson1, Todd Merendino3, Blanca Lupiani1
1Texas A&M University, College Station, TX, USA; 2Ambion Inc., Austin, TX, USA; 3Texas Parks & Wildlife, Bay City, TX, USA

Waterfowl are known reservoirs for avian influenza (AI) viruses; however, little is known regarding the prevalence or persistence of these viruses in nature, particularly the Gulf Coast of Texas, an important waterfowl wintering area. The objectives of this study were to determine what subtypes persist in this geographical location and identify waterfowl species that may serve as reservoirs in wintering areas. Cloacal swabs were collected from hunter-harvested waterfowl during the 2005–2006 hunting season at state owned wildlife management areas along the coast of Texas. Samples were screened for AI using real-time reverse transcriptase polymerase chain reaction (rRT-PCR) and virus isolation was attempted on all rRT-PCR positive samples. A total of 1465 samples were collected and tested for AI by rRT-PCR; 86 were positive for AI (5.7% prevalence). AI viruses were isolated from 7 of the 86 rRT-PCR positive samples (sensitivity and specificity of rRT-PCR compared to virus isolation was 100 and 94.6%, respectively). AI subtypes identified (H1N2, H1N4, H4N6, H6N2, and H10N7) are common in North America. All isolates were from dabbling ducks (green-winged teal, blue-winged teal, mottled duck, and northern shoveler); none were from diving ducks. Our data support previous reports that dabbling ducks have a higher prevalence of AI infection than diving ducks. These results are from the first year of a multi-year project. By sampling waterfowl in the same locations over time, we hope to generate valuable information on the prevalence and persistence of AI along the Gulf Coast of Texas.
[139] IMMUNOHISTOCHEMICAL, MICROBIOLOGICAL, & MOLECULAR EPIDEMIOLOGICAL TESTS FOR BRUCELLOSIS IN ROCKY MOUNTAIN ELK

Amanda M. Fluegel¹, Todd Cornish¹, William Edwards², Ken Mills¹
¹University of Wyoming, Laramie, WY, USA; ²Wyoming Game & Fish Department, Laramie, WY, USA

Brucellosis, caused by the bacterium Brucella abortus, is endemic in bison (Bison bison) and Rocky Mountain elk (Cervus elaphus nelsoni) in the Greater Yellowstone Area of Wyoming, Montana, and Idaho. Current diagnostic methods used to identify infection in elk include serological testing and bacterial culture, but the correlation between serology and culture results is poor, bacterial culture is slow and likely to be positive only later in gestation or following abortion or parturition, and isolates cannot be sufficiently characterized to trace outbreaks. There is a need for more informative, sensitive, and rapid diagnostic tests to detect brucellosis in elk. As part of the Wyoming Game and Fish Department’s brucellosis surveillance program, elk were trapped using corral traps and serologically tested for brucellosis on the Grey’s River and Dell Creek feedgrounds in the winters of 2005 and 2006. Twenty-two seropositive cow elk aged ≥ 1.5 years were killed and necropsied. Paired tissue samples were collected and processed for bacterial culture, PCR, histopathology and immunohistochemistry (IHC). Tissue sections were stained with an anti-B. abortus polyclonal antibody for IHC. Brucella abortus was isolated from 47.4% (9/19) of the seropositive cow elk and 5% (1/19) of the fetuses. Tissues were evaluated by PCR to identify the presence of B. abortus in fresh tissue. PCR and immunohistochemistry results will be compared to culture (gold-standard test) results to determine the sensitivity and specificity of each assay. A multiple locus variable number tandem repeats analysis (MLVA) capable of strain typing will be used to characterize Brucella isolates.

[140] IMMUNITY TO OVINE HERPESVIRUS 2 INDUCED MALIGNANT CATARRHAL FEVER IN AMERICAN BISON

Katherine L. Gailbreath¹, ², J. Lindsay Oaks², Christopher J. Davies¹, Donal O’Toole³, Hong Li²
¹Washington State University, Pullman, WA, USA; ²US Department of Agriculture-Agricultural Research Service, Pullman, WA, USA; ³University of Wyoming, Laramie, WY, USA

Ovine herpesvirus-2 (OvHV-2) is carried subclinically by sheep and is the major cause of malignant catarrhal fever (MCF) in North America. The disease occurs sporadically in cattle (Bos taurus) and a variety of captive wild and exotic ruminants but can be devastating in American bison (Bison bison). While the majority of clinically ill animals succumb to disease, a significant number of healthy cattle and bison are subclinically infected as indicated by detection of antibody against MCF group viruses and OvHV-2 DNA in peripheral blood. The virus has never been propagated in vitro and experimental infection involves nebulization with nasal secretions from shedding sheep. In dose response nebulization experiments with cattle and bison we found that a high dose of virus is required to establish infection in cattle and few succumb to disease. In contrast, a relatively low dose results in infection and disease in bison making them the preferred experimental host. We have sequenced bison MHC class I alleles and are in the process of developing a microarray for bison MHC class I haplotyping. This technology will allow us to specifically evaluate the cell-mediated immune response which is critical for development of vaccines. To begin, we will identify potentially protective OvHV-2 antigens by determining bison MHC class I allele-specific peptide motifs which will be used to search the OvHV-2 genome for candidate peptides. Synthetic peptides will be tested for MHC class I binding and will be used as antigen in cell-mediated immunoassays such as IFNγ ELISPOT and cytotoxicity assays.
[141] **MODELING EFFECTS OF MAMMAL COMMUNITY STRUCTURE & LAND USE CHANGE ON A MULTI-HOST PATHOGEN: THE CASE OF *TRYPANOSOMA CRUZI* IN THE PANAMA CANAL ZONE**

Nicole L. Gottdenker, C.R. Carroll
University of Georgia, Athens, GA, USA

Anthropogenic land use change (e.g., deforestation, habitat fragmentation) can alter host-parasite relationships and affect disease transmission. In this study, we modify an SI (susceptible-infected) compartment model to evaluate infection dynamics of a multi-host, vector borne parasite. Our study system, located in the Panama Canal Zone, consists of the protozoan parasite *Trypanosoma cruzi*, the triatomine vector *Rhodnius pallescens*, the palm *Attalea butyracea* (important vector habitat), and wild and domestic mammal reservoirs, in particular the common opossum *Didelphis marsupialis*. We evaluate how different habitat types (contiguous forest, forest edge habitat, pasture, and peridomiciliary areas) and resulting changes in mammal community composition have the potential to alter *T. cruzi* infection dynamics in the vector *R. pallescens* and compare model results to existing data.

[142] **PRELIMINARY FINDINGS OF VIRAL ANTIGEN DETECTION FOR WNV, EEE, SLE & AI IN TISSUES FROM WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN SOUTH GEORGIA**

Dallas R. Ingram, Debra L. Miller, Charles A. Baldwin and J. Mitchell Lockhart
1. University of Georgia, Tifton, GA, USA; 2. Valdosta State University, Valdosta, GA, USA

Antibodies to West Nile virus (WNV), Eastern equine encephalitis virus (EEE), St. Louis encephalitis virus (SLE) and Avian influenza virus (AI) have been documented in the serum of wild turkeys (*Meleagris gallopavo*), but few studies have looked for the presence of viral antigen in tissues. Tissues, including blood, internal organs and other tissues when available, were opportunistically collected from wild turkeys (*N* = 19) in South Georgia during the 2005 and 2006 hunting seasons. The RNA was extracted from the fresh tissues including heart, lung, spleen, liver and brain. Samples were then tested for WNV, SLE, EEE and AI using rt-PCR. Results showed that 63% (12) of the 19 turkeys were positive for WNV, 33% (4) of 12 were positive for SLE, and 0% (0) were positive for EEE or AI. Three of the birds were positive for both WNV and SLE. SLE was only detected in the brain. None of the heart samples were positive for any of the viruses. Corresponding clinical disease was not observed in any of the tested turkeys. These findings suggest that wild turkeys may be subclinically infected with WNV and SLE. It remains unclear if wild turkeys can serve as reservoirs of these pathogens. It is possible that these birds may succumb to these viruses when stressed but this remains to be tested.
[143] Evidence of Exposure of Wild Carnivores Captured in the Pantanal (Brazil) to Canine Distemper Virus

Rodrigo S. P. Jorge1,2,3, Fernando Ferreira1
1University of São Paulo, Brazil; 2National Research Center for the Conservation of Natural Predators, Atibaia, Brazil; 3Brazilian Institute of Conservation Medicine – Triade, São Paulo, Brazil

In the last two decades, infectious diseases have emerged as an important issue when dealing with conservation of wildlife. During that period canine distemper virus (CDV) has been connected with the mortality of several species of free-ranging wild carnivores. CDV is very common in domestic dogs and, thus, they have often been implicated as the source of the virus in wildlife epizootics. From 2002 to 2006, 75 free-ranging wild carnivores were captured in the Pantanal and serum samples were collected. 79 domestic dogs from the surrounding settlements were also sampled. They were all tested for antibodies against CDV with a microscopic serum-neutralization test. 21 wild carnivores were considered positive, with a titer ≥ 8, resulting in a total frequency of 28% [0.182405<CI 95%<0.395630], including crab-eating foxes Cerdocyon thous (12/43), racoons Procyon cancrivorous (2/13), maned wolves Chrysocyon brachyurus (3/8), ocelots Leopardus pardalis (3/4) and a puma Puma concolor (1/7). Among domestic dogs 65 (82.28%) were positive [0.720575< CI 95%<0.899587]. These results show that the wild carnivores have been exposed to CDV and, thus, the virus is present in that region. Domestic dogs may have been the source of CDV to the wild carnivores. The higher frequency of positive animals among the domestic dogs reinforces that possibility. CDV may cause a negative impact in the population of wild carnivores in the region increasing the mortality of adults in reproductive age and the mortality of pups during the period of decrease of maternal antibodies.

[144] Rabies Antibodies in a Bush Dog Captured in the Pantanal, Brazil

Rodrigo S. P. Jorge1,2,3, Ronaldo G. Morato2, Monique Pereira2, Edson S. Lima3, Karin Scheffer4, Pedro Carniel Jr.4, Ivanete Kotait4, Fernando Ferreira1
1 University of São Paulo, Brazil; 2Predator National Center, IBAMA, Atibaia, Brazil; 3Brazilian Institute of Conservation Medicine – Triade, São Paulo, Brazil; 4Instituto Pasteur, São Paulo, Brazil

Rabies is an important issue for public health throughout the world. Although it has been controlled in developed countries, most of the developing regions of the world, including Latin America, still have high rates of occurrence. In Brazil, where efforts to control the incidence of rabies in humans have been focused in controlling the disease in dogs and cats through vaccination, it is likely that the sylvatic cycle may increase its importance. The disease also represents a threat to wildlife, especially carnivores. From 2002 to 2006, 76 free-ranging wild carnivores were captured in the Pantanal and serum samples were collected, including 43 crab-eating foxes Cerdocyon thous, 13 racoons Procyon cancrivorous, 8 maned wolves Chrysocyon brachyurus, 7 pumas Puma concolor, 4 ocelots Leopardus pardalis and 1 bush dog Speothos venaticus. Additionally, 102 domestic dogs from the surrounding settlements were also sampled. They were all tested for the presence of rabies neutralizing antibodies with a simplified fluorescence inhibition microtest (SFIMT). One bush dog and 14 domestic dogs presented a titer > 0.50 IU/mL, which demonstrates exposure to the virus or vaccination. The diagnosis of a wild non-vaccinated positive animal shows the presence of the virus in the region. Among the positive domestic dogs, 12 were vaccinated and the information given by their owners that the other 2 positive animals had not been vaccinated should be seen with caution. Based on these results, we discuss the possibilities of exposure of the non-vaccinated animals to the virus.
PREVALENCE OFECTOPARASITES IN OAHU’SFOREST BIRDS

Kira L. Krend1, Samuel A. Bader1, Matthew C. Medeiros2
1University of Hawaii at Manoa, Honolulu, HI, USA; 2University of Missouri St. Louis, St. Louis, MO, USA

The survival of Hawaii’s native birds is currently threatened by many factors, including infection by parasites and pathogens. Detailed investigation of ectoparasites on Hawaiian forest birds has not been conducted previously. *Ischnocera* feather chewing lice raise the metabolic rate of their host and reduce survival of both nestlings and adults. In addition, blood feeding *Amblycera* lice and mites may vector avian pox virus. Native and introduced forest birds at on the island of Oahu were mist netted and visually inspected for presence of eggs and adult stage ectoparasites. The overall infestation rate for the avian community was 62% (95% CI 55-68%, N=203). Native birds have 39% higher prevalence of ectoparasites than introduced species (95% CI 27-50%). Of 21 native birds captured, all were found positive for ectoparasites. In a logistic regression where species, locality, and their interaction were added to a model in respective order, only the effects of species and locality were significant (p<0.001). The effect of locality was driven primarily by one locality with relatively low ectoparasite prevalence. The higher prevalence in native species may be associated with a tightly coevolved system with indigenous parasites, or with the introduction of a novel parasite exploiting naïve native hosts. Genus and species level identification of the ectoparasites must be performed to determine host specificity. Challenge experiments may be conducted to determine the effect of infestation on host fitness. Site variability in prevalence may be due to environmental factors; further study of ectoparasite ecology will be required.

EVALUATION OF GRIZZLY BEAR HEALTH IN WESTERN ALBERTA

Johan Lindsjö1, Marc Cattet2, and Gordon Stenhouse3
1University of Saskatchewan, Saskatoon, SK, Canada; 2Canadian Cooperative Wildlife Health Centre, Saskatoon, SK, Canada; 3Foothills Model Forest & Alberta Sustainable Resource Development, Hinton, AB, Canada

Human activities that result in landscape change have potential to adversely affect the health of wildlife populations, particularly those of species at risk, such as grizzly bears (*Ursus arctos*). A working hypothesis of the Foothills Model Forest Grizzly Bear Research Program is landscape change caused by human activities causes long-term physiologic stress in grizzly bears which eventually results in decreased health at the individual level, e.g., reduced growth, diminished reproductive function, and poor performance at the population level, e.g., reduced reproductive and survival rates. A primary objective of this research is to link measures of health with long-term stress in grizzly bears and with human-caused change in the physical structure of their habitat. As one component of the research program, we are developing a health function score system based on grizzly bear biological data collected from 1999 to 2006. This scoring system will enable us to compress complex information from many measured variables into several values that reflect accurately growth, reproduction, immunity, and longevity. Health function scores for individual grizzly bears with known home range will be examined to determine differences in relative health among grizzly bear populations in Alberta, and to locate areas in the province where grizzly bear health appears compromised. This information will provide resource managers with necessary knowledge to ensure the long-term conservation of grizzly bears in Alberta.
[147] EVALUATION OF THE ELK BRUCELLOSIS TEST-AND SLAUGHTER PROGRAM AND CONTINUED STUDIES ON THE EPIDEMIOLOGY OF BRUCELLOSIS IN FEEDGROUND ELK

Laura L. Linn¹, William Edwards², Terry Kreeger³, Cynthia Tate², and Todd Cornish¹
¹University of Wyoming, Laramie, WY, USA; ²Wyoming Game & Fish Department, Laramie, WY, USA; ³Wyoming Game & Fish Department, Wheatland, WY, USA

*Brucella abortus*, the causative agent of brucellosis, has been largely eliminated from cattle in the United States through a federal/state eradication program that began in 1930s. The disease remains endemic in free-ranging elk and bison in the Greater Yellowstone Area. Winter feedgrounds in this area indirectly concentrate animals during the peak period of transmission of brucellosis thus presenting a significant risk to cattle in the proximity. In an attempt to reduce brucellosis seroprevalence in elk, the Wyoming Game & Fish Department implemented a five-year pilot test-and-slaughter program in 2006. During the initial year of trapping, 157 adult female elk were sampled and 58/157 (36%) were found to be seropositive for brucellosis and removed from the population. Preliminary results indicated 17/58 (29.3%) were culture positive for *B. abortus*. During the 2007 trapping season, 79 animals were sampled and 13/79 (16.5%) seropositives were removed. Preliminary results indicate 8/13 (62%) were culture positive for the bacteria. We intend to continue this evaluation of the success of the test-and-slaughter program, and also continue general studies on the epidemiology of brucellosis in feedground elk. These studies focus on the host factors that influence the decision to remove individual elk including the correlation of culture status to serological test results, the probability of abortion, potential of live birth to play a role in transmission, and the geographic ranges of both abortions and live births. Such information will be decisive to state agencies and private citizens charged with minimizing risks of brucellosis transmission between wildlife and livestock.

[148] AVIAN INFLUENZA VIRUSES IN SHOREBIRDS AT THE DELAWARE BAY MIGRATORY STOPOVER SITE

Angela M. Maxted, David E. Stallknecht, M. Page Luttrell, Ginger Goekjian
Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA

Annual epizootics of low pathogenic avian influenza (LPAI) are well documented in arctic-breeding shorebirds during their four to six week spring migratory stopover at Delaware Bay, Delaware and New Jersey, USA. In 2006, as in previous years, Ruddy Turnstones were disproportionately infected, accounting for 86% of avian influenza (AIV) isolations. Species-specific prevalence was 16% on the New Jersey shore, and 24% on the Delaware shore. In contrast, prevalence in sympatric shorebird and gull species was 0-2%. The H7 subtype accounted for at least 78% of 63 AIV infections, with the H7N3 subtype predominating. The predominance of one viral subtype suggests local infection and clonal viral expansion. H7N2, H7N4, H7N7, H6N7, and H9N2 viral subtypes were also isolated; this variety of subtypes present suggests reassortment of virus and/or multiple introduction sources. None of the H7 viruses had amino acid sequences compatible with highly pathogenic avian influenza (HPAI). Further study is needed to understand the transmission dynamics of avian influenza among birds at Delaware Bay.
Bird feeders are a source of enjoyment for many wildlife watchers. However, they have also been implicated as reservoirs for many avian diseases which can be detrimental to wildlife health. Aggregations of birds at a single location increase the chances of disease transmission, and outbreaks have been linked to contaminated feeders or transmission from bird to bird contact while visiting feeders. While research on *Salmonella* spp. has largely focused on birds and fomites in poultry and livestock farms, there is little information about bird feeder contamination. Avian salmonella causes severe disease, with clinical signs ranging from mild, including depression, ruffled feathers, weight loss and discolored droppings, to severe, including blindness and sudden death. This project aimed to survey feeders in Clarke County, Georgia for *Salmonella* spp. by culture analysis. Seventeen feeders were swabbed from eight locations in Clarke County using cotton swabs that were subsequently incubated for 16-18 hours in *Salmonella* selective broth. Media was spread onto XLT-4 agar plates, incubated for 24 hrs, and any bacterial colonies were characterized. One feeder out of 17 (5.9%) showed growth consistent with *Salmonella*, while 9 out of 17 (52.9%) showed other bacterial colonies. These results indicate that bacterial growth on feeders can be highly prevalent in localized areas, and remains a valid concern for transmission to wild populations. The isolation of *Salmonella* on surfaces where birds aggregate further bolsters the concern that contaminated feeders are adequate fomites for avian salmonella transmission. Future work includes additional sampling and isolating colonies for identification using PCR.

Bovine viral diarrhea virus (BVDV) is a significant pestivirus of domestic and wild ruminants. Vertical transmission can produce persistently infected (PI) animals that are immunotolerant and shed virus throughout their lives. Acutely and persistently infected animals are significant reservoirs for viral transmission. There is serologic evidence of pestiviral infection in more than 40 species of free-ranging and captive mammals. Isolation of BVDV from wild ruminants is rare, and when sequenced these isolates are usually BVDV type 1. Only four species (cattle, white-tailed deer, mouse deer, and eland) have been identified as persistently infected with BVDV. This study provides serological, molecular, immunohistochemical, and histological evidence for BVDV infection in two captive mountain goats (*Oreamnos americanus*) in the same zoological park in Idaho. The study was triggered by isolation of BVDV from tissues and immunohistochemical identification of viral antigen within lesions of a 7-month old male mountain goat (case 1). Sequencing and phylogenetic analysis identified the isolate as BVDV type 2. Blood was collected from other mountain goats and white-tailed and mule deer on the premises for BVDV serum neutralization, viral isolation, and PCR. One 3-month old mountain goat (case 2) was antibody negative and BVDV positive. Three months later this goat died, and though still antibody negative, BVDV was isolated from tissues and identified by immunohistochemistry within lesions. These findings provide evidence of persistent infection in a mountain goat, underscoring the need for pestiviral control strategies for wild ruminants in zoological collections.
[151] DURATION OF PROTECTIVE WEST NILE VIRUS IMMUNITY IN HOUSE SPARROWS (Passer domesticus)

Nicole Nemeth, Richard Bowen
Colorado State University, Fort Collins, CO, USA

The study objectives were to characterize the duration of protective immunity to West Nile virus (WNV) and look for persistent infectious virus in house sparrows (Passer domesticus). Seronegative sparrows (n=114) were experimentally inoculated to induce WNV immunity, and housed with seronegative controls (n=20). All were bled at 1-, 6-, 12-, 18-, and 24-months post-infection (PI) for determination of antibody titers. At 6-, 12-, and 24-month PI, ten immune sparrows and two seronegative controls were challenged with WNV and subsequent viremia levels assessed. At 1-, 6-, 12-, 18- and 24-months PI, oral swabs from inoculates were evaluated for persistent infectious viral shedding, and three birds were sacrificed for tissue testing, which also occurred for sparrows that died naturally. Antibody titers were determined by plaque reduction neutralization test and viral titers by Vero cell plaque assay. Thus far, antibodies persist and are protective for ≥24-months PI. One individual challenged at 6-months PI had low level viremia of three days' duration. No bird-bird transmission occurred. Of inoculated sparrows caged for 1-7 day PI bleedings, mortality rates were 27.3% (3/11) versus 8.4% (9/107) for free-flight birds not handled following inoculation. Persistent virus was not detected in oral swabs or tissues through 24-months PI except for low levels in the oral swab of one sparrow at 1-month PI, and from the spleen of the same bird on 43 days PI. Long-term maintenance of antibodies in birds allows them to resist disease and viremia upon subsequent re-infection, potentially decreasing annual WNV transmission and increasing herd immunity.

[152] CLIFF SWALLOWS & SWALLOW BUGS: DO THEY PLAY A ROLE IN WEST NILE VIRUS TRANSMISSION?

Paul T. Oesterle, Jeffrey S. Hall, James Carlson, Nicole Mooers, Robert G. McLean, Larry Clark
US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA

Cliff swallows (Petrochelidon pyrrhonata) nest synchronously in large colonies. These colonies are frequently in close proximity to mosquito breeding habitat, leading to potentially high rates of exposure to West Nile virus (WNV). As insectivores, cliff swallows are also potentially exposed to WNV through ingestion of infectious mosquitoes. In addition, mud nests of cliff swallows are co-inhabited by a hematophagous parasite, the swallow bug (Oeciacus vicarius), the primary vector of an alphavirus, Buggy Creek virus. Cliff swallows are not adversely affected by WNV, but develop viremia levels sufficient to infect mosquitoes. The breeding ecology cliff swallows and their symbiotic relationship with swallow bugs suggest a potential additional mechanism in the transmission of WNV. To investigate the potential involvement of swallows and swallow bugs in WNV transmission, we sampled nestlings and bugs from 2003-06. Blood and oral swabs from swallows, and swallow bug individuals and pools, were tested for the presence of WNV RNA by RT-PCR. In 2003, 22.4% (30/137) of nestlings and 1.9% (13/704) of individual bugs tested positive, while 18.9% (7/37) of nests contained at least one WNV positive bug. Since then, WNV transmission in northern Colorado has been low and cliff swallow and swallow bug data have reflected these lower levels. Experimental studies are planned to more closely evaluate swallow bugs as potential vectors of WNV.
[153] PREVALENCE & FITNESS COSTS OF *IXODES HIRSTI* IN AUSTRALIAN BIRDS

**Margot Oorebeek, Sonia Kleindorfer**
Flinders University, Adelaide, South Australia, Australia

Birds in Australia have been found to have a higher ectoparasite prevalence than birds in the northern hemisphere. Ticks are one of the ectoparasites that are commonly found on birds. However, no extensive studies investigating prevalence and fitness costs of avian ticks have been reported in Australia. This research investigates the distribution of avian ticks in South Australia and the costs they impose on their hosts. Wide-spread mist netting was performed across several parks. A total of 1104 birds (representing 30 species) were captured from 2004 till 2006. We recorded the immature stages of two species of ticks on the birds; *Ixodes hirsti* and a currently unidentified *Ixodes* sp. Thirty percent (326/1104) of the birds were infested with at least one tick, with infestation intensities ranging from 1 to 48 ticks per bird. The prevalence of ticks fluctuated within a year, with a peak in June and a total absence of ticks from December till March. The fitness costs the ticks impose on their hosts, expressed in condition measurements and reproductive success, will be discussed using the New Holland Honeyeater (*Phylidonyris novaehollandiae*) as a model species.

[154] IMPLICATIONS OF MESOMAMMAL SCAVENGING BEHAVIOR ON THE HORIZONTAL TRANSMISSION OF *TRYPANOSOMA CRUZI* IN NORTH AMERICA

**Dawn M. Roellig, Michael J. Yabsley**
Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA

*Trypanosoma cruzi*, the causative agent of Chagas disease in humans, has become a parasite of increasing interest in the United States following the diagnosis of two human autochthonous cases within the last year. The maintenance of *T. cruzi* in native US wildlife populations increases the potential for zoonotic transmission in North America. While considerable research has been conducted on *T. cruzi* isolates from South America, studies on North American isolates are imperative to understanding its transmission and pathogenicity within the United States. In the Southeastern US, only two vectors (*Triatoma* spp.) are present; however, the prevalence of *T. cruzi* in raccoons (*Procyon lotor*) and opossums (*Didelphis virginiana*) can be high. To investigate an alternative, non-vector-based transmission method, we tested the hypothesis that raccoons scavenging infected hosts can result in infection. Macerated tissue from selected organs infected with the amastigote stage of *T. cruzi* was orally administered to experimental groups of raccoons (n=2/group) at 0, 24, or 48 hours after tissue sample collection. Serology, polymerase chain reactions, and parasite counts were performed with blood and sera collected every 3 days until humane euthanasia on day 45 post-inoculation. Histology of major organs collected at necropsy was conducted to identify pseudocysts of amastigotes in tissue. We propose the biological significance of orally ingesting intracellular *T. cruzi* in the maintenance of the parasite in the sylvatic environment.
[155] HELMINTH ASSEMBLAGES IN COMMON GROUND DOVES & INCA DOVES FROM SOUTH TEXAS

Autumn J. Smith, Alan M. Fedynich
Caesar Kleberg Research Institute-Texas A&M University, Kingsville, TX, USA

One hundred eight doves representing two columbid congeners, the common ground dove (*Columbina passerina*) and the Inca dove (*Columbina inca*), were examined for helminths to assess species richness, prevalence, patterns of species co-occurrence, and relative abundance. Sixty common ground doves (a species that predominately occurs in rural habitats) and 48 Inca doves (a species that predominately occurs in urban habitats) were collected in Kleberg Co., Texas during summer 2006. One hundred sixty three worms were recovered from the common ground doves, representing 9 helminth species. Sixty percent of the common ground doves were infected with 1 to 4 helminth species. One nematode, *Ornithostrongylus minutus*, was the most frequently occurring species (30% prevalence) in common ground doves and numerically dominated (58% of worms recovered) the component community. *Ascaridia columbae* was the only helminth recovered from Inca doves, in which only 2 (4%) doves were infected with 7 individuals (1 and 6 worms, each). *Ascaridia columbae* was also found in common ground doves. All helminth species identified herein represent new host records for common ground doves and Inca doves. Although common ground doves and Inca doves co-occur regionally, local habitat partitioning (rural and urban) and differences in food habits may be important determinates in explaining differences in helminth community structure.

[156] COMPARISON OF PREVALENCE OF *TRICHOMONAS GALLINAE* BETWEEN THE MOURNING DOVE & WHITE-WINGED DOVE IN SOUTH TEXAS

Autumn J. Smith, Alan M. Fedynich
Caesar Kleberg Research Institute-Texas A&M University, Kingsville, TX, USA

There is concern that exotic hosts bring with them parasites that may not be harmful to themselves, but may negatively affect closely related native hosts. This could provide a selective advantage to the invading host species by negatively impacting potential native competitors. *Trichomonas gallinae* is a directly transmitted protozoan introduced into North America with infected rock doves. Several species of columbids reside in South Texas, two of which (mourning dove and white-winged dove) overlap in distribution. This provides a suitable model to identify and compare *T. gallinae* prevalence values within a co-occurring dove community. The white-winged dove is a semitropical urban dweller endemic to southern U.S. and Mexico. The mourning dove has an abundant distribution to include North and Middle America, and is considered a suburban species. The objectives of this study were to (1) determine the prevalence of *T. gallinae* in mourning doves and white-winged doves, and (2) determine if prevalence varies between species, sex, and age. Sixty doves of each species were collected in the summer of 2006. Prevalence of *T. gallinae* varied between species (*P*=0.046). However, there was no significant difference in prevalence between age (*P*=0.07) or sex (*P*=0.441) in mourning doves, and no significant difference in prevalence between age (*P*=0.781) and sex (*P*=0.931) in white-winged doves.
SYNDROMIC SURVEILLANCE AT WILDLIFE HOSPITALS: DETECTING WEST NILE VIRUS IN ARDEIDAE BIRDS IN THE SAN FRANCISCO BAY AREA OF CALIFORNIA IN 2005

Tamara Vodovoz1, Christine Kreuder-Johnson1, Leslie W. Woods2, William Reisen1, Ying Fang1, Barbara Calhoon-Young3, Ryan Carney4, Walter Boyce1, Jonna K. Mazet1
1University of California, Davis, CA, USA; 2University of Wyoming, Laramie, WY, USA; 3Placer County Health & Human Services, Auburn, CA, USA; 4California Department of Health Services, Richmond, CA, USA

Syndromic surveillance for West Nile Virus (WNV) was conducted in wading birds, family Ardeidae, at a wildlife hospital in California between May and September 2005. West Nile virus RNA was detected in dead birds by RT-PCR tests of kidney tissue. The proportionate mortality due to WNV infection was 6.5% (2/31), and severe neurologic signs were observed in an infected Snowy egret (Egretta thula). Previous exposure to WNV was detected by serologic testing in 2 (1.4%) of 139 live birds, one Black-crowned night heron (Nycticorax nycticorax) without clinical signs, and one Great blue heron (Ardea herodias) with severe trauma. Syndromic surveillance for WNV in Ardeidae birds arriving to a wildlife hospital in the summer provided detection results similar to those conducted throughout the year by the comprehensive California Department of Health Services’ (CDHS) surveillance of dead birds in the San Francisco Bay area. Surveillance for emerging infectious disease at wildlife hospitals is a useful real time source of information, which has the advantage of identifying the clinical and pathologic features of disease, and allowing the evaluation and optimization of diagnostic tests.

USE OF THE NORTHERN FULMAR (FULMARUS GLACIALIS) AS A SENTINEL FOR HUMAN CONTAMINATION OF THE ENVIRONMENT IN THE NORTHWESTERN ATLANTIC

Ines Walther1, Pierre-Yves Daoust1, Zoe Lucas2, Neil Burgess3, Greg Dobbin1
1Canadian Cooperative Wildlife Health Centre, Charlottetown, PE, Canada; 2Halifax, NS, Canada; 3Canadian Wildlife Service, Mont Pearl, NL, Canada

Seabirds represent 3% of the world’s avian species, and over 10 million of them inhabit the Canadian Arctic region. Monitoring the population dynamics and health parameters of these birds is an important tool to assess the quality of their marine environment and, particularly, the alterations that it is undergoing as a result of global climate change and other anthropogenic processes. The northern fulmar (Fulmarus glacialis) is a pelagic bird of the family Procellariidae. For many years, the propensity of birds of this species to ingest foreign material has been used to monitor levels of marine litter in the North Sea. A similar project was initiated in northwestern Atlantic waters through the examination of northern fulmars collected on Sable Island, an isolated island east of Nova Scotia, Canada. A total of 50 northern fulmars, collected between 2003 and 2005 as part of a beached bird survey, were examined through a combination of necropsy, histology, bacteriology, parasitology and toxicology. Findings of particular interest included ingestion of plastic material, muscular sarcocystosis, multicentric fibromas, mild multifocal myocarditis, and high levels of mercury and organochlorine contaminants in some birds. The significance of the high prevalence of plastic material in the stomach of these birds remains uncertain. The remote natural habitat of the northern fulmar does not lend itself easily to a study of health parameters in this species. This study hopes to add to the current information available on these parameters.
PREVALENCE OF LIVER FLUKE (*FASCIOLOIDES MAGNA*) EGGS IN FECES FROM ELK (*CERVUS ELAPHUS*) IN NORTHERN WISCONSIN

**Trina M. Weiland, Shelli A. Dubay, Todd C. Huspeni, Timothy M. Ginnett**  
University of Wisconsin-Stevens Point, Stevens Point, WI, USA

Elk (*Cervus elaphus*) were once common throughout Wisconsin but were extirpated in the late 1800’s. In 1995, the Wisconsin Department of Natural Resources (WDNR) acquired 25 elk from Michigan and reintroduced them in the Chequamegon National Forest in northern Wisconsin. The herd has been closely monitored since that time. From 1997 to 2003, survival was extremely high, but increased mortality has led to recent decreased population growth. Most mortalities have been attributed to predation and vehicle collisions, but liver flukes (*Fascioloides magna*) have been directly or indirectly involved in several recent mortalities. In winter 2006-2007, the herd estimate was 110 animals. Our goal was to determine minimum prevalence of infection for liver flukes in the Clam Lake elk herd. We collected fecal samples from known groups of radio-collared animals and from individual female elk during the calving season. Samples were collected during March, May-June (calving), July, and November in 2006 and in March, May-June, and July in 2007. We processed fecal samples in the laboratory using the formalin–ethyl acetate sedimentation technique and identified fluke eggs by microscopic characteristics. In 2006, we collected 47 fecal samples from 2 elk groups in March, 18 samples from 2 groups in May, 51 samples from 3 groups in July, and 21 samples from 2 groups in November. In addition, we collected 21 samples from individual females during calving season. We will present data on prevalence of liver fluke eggs in fecal samples from 2006 and 2007 and discuss management implications of infection.
### PRESENTATION SCHEDULE FOR POSTERS

**General Poster Session Two**

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[160] SEROLOGICAL EPIDEMIOLOGY OF HAWAIIAN MONK SEALS: THE ROLE OF INFECTIOUS DISEASE MONITORING IN CONSERVATION

A. Alonso Aguirre1, Thomas J. Keefe2, John S. Reif2, Lizabeth Kashinsky3, Pamela Yochem4, Jeremiah T. Saliki5, Jeffrey L. Stott6, Tracey Goldstein7, J. P. Dubey7, Robert Braun8, George Antonelis8
1Columbia University, New York, NY, USA; 2Colorado State University, Fort Collins, CO, USA; 3JIMAR, Honolulu, HI, USA; 4Hubbs-Sea World Research Institute, San Diego, CA, USA; 5Oklahoma State University, Stillwater, OK, USA; 6University of California, Davis, CA, USA; 7USDA/ARS/ANRI/PBESL, Beltsville, MD, USA; 8National Marine Fisheries Service, Honolulu, HI, USA

Serum specimens were obtained from 332 Hawaiian monk seals (Monachus schauinslandi) captured at six sites in the Northwestern Hawaiian Islands between 1997 and 2001. Specimens were tested for antibodies to several potential pathogenic viruses, bacteria, and parasites known to cause morbidity and mortality in other marine mammal species. Antibody titers were found to phocine herpesvirus 1, Chlamydophila abortus, Leptospira bratislava, L. hardjo, L. icterohaemorrhagica, and L. pomona. Depending on which of the 10 different serologic tests was employed, prevalence of antibody to Brucella spp. ranged from 1% to 50% in all populations except Kure Atoll where no seropositives were identified. Based on the inconsistencies among multiple tests and laboratories used and the lack of validation by isolation of organism or relevant clinical signs, the Brucella findings in monk seals are inconclusive. This survey is linked to conservation efforts of this endangered species. Serology and surveillance are the most effective tools available to avoid the introduction of emerging infectious diseases into a population. The need for more sensitive and specific diagnostic tools must be addressed as new technologies become available. It is recommended that evaluation of health becomes a standard procedure in future conservation efforts of Hawaiian monk seals.

[161] A CALL TO AUTHORS FOR STANDARDIZATION OF DATA COLLECTION & REPORTING RESULTS FOR STUDIES & CASE PRESENTATIONS INVOLVING CHEMICAL IMMOBILIZATION & REMOTELY DELIVERED ANESTHETIC AGENTS

Keith Amass1, Mark Drew1,2, Julie Smith3
1Safe-Capture International, Inc., Mount Horeb, WI, USA; 2Idaho Department of Fish & Game, Wildlife Health Laboratory, Caldwell, ID, USA; 3Iams Pet Imaging Center, Vienna, VA, USA

Authors of investigative studies or case presentations describing chemical immobilization techniques begin their discussions defining the measurement intervals or observation parameters used for data collection in their study. A literature review finds data collection and reporting to lack standardization between authors. Similar terms often have different definitions. The term, “Induction Time” has been defined as the period from injection of the immobilizing drugs until the animal is (a) immobile (either standing or recumbent), (b) recumbent (position unspecified), (c) in lateral recumbency, (d) head down (e) safe to handle or (f) reaches an anesthetic plane. Similarly, “Down Time” has multiple definitions in the literature: (a) time from recumbency to standing, (b) time from induction to antagonist administration, (c) time from injection of the immobilizing drug until the animal becomes recumbent. We propose adoption of standardized data collection and reporting techniques to afford more meaningful comparison between techniques and information involving chemical immobilization and remotely delivered anesthetic agents. A checklist of suggested definitions, measurement intervals, and observational parameters is provided as a standardized framework of reference. We developed this checklist using models presented in the published literature by various individuals, working with a variety of species, in multiple countries. Capture, immobilization, and anesthetic procedures in nondomestic animals have the potential for injury and mortality to animals and staff. It is our duty as practitioners to maximize the amount of information gathered and shared from these procedures, so that techniques can be fully emulated or undesirable impacts defined and avoided.
[162] ELECTRIC BURN INJURY IN THE ORAL CAVITY IN A NILGIRI LANGUR (PRESBYTIS JOHNI): A CASE REPORT

S. Anoop, S. Ajith Kumar, P. Reshmi
College of Veterinary and Animal Sciences, Pookot, Wayanad, Lakkidi, Kerala, South India

Wild animals are exposed to various physical injuries like burns due to fire, electrocution, etc. Electrocution to wild animals can occur due to protective electric wire fencing or while entering human habitat for food. An acute case of electric burn injury of the oral cavity, tongue and face in a nilgiri langur and its successful treatment has been discussed. A 15 year old male nilgiri langur weighing 10.5 Kg was brought to the teaching veterinary college hospital, Wayanad, by the forest officials with the history that the animal has been electrocuted and was found lying nearby a transformer. The animal was found to be dehydrated and was keeping its mouth open and there was drooling of saliva. The eyes were tightly closed and there was edema and alopecia in the periorbital region and face. General anesthesia was affected with 150 mg of ketamine hydrochloride intramuscularly after premedicating with diazepam 2 ml intramuscularly. The animal was administered with electrolytes, antibiotics, anti-inflammatory agents and topical and intraoral medication after anesthesia. The animal made an uneventful recovery after five days of treatment and was released back to the wild.

[163] WILDLIFE MIDDLE EAST NEWS: A NEW INITIATIVE TO RAISE THE AWARENESS OF ENVIRONMENTAL & CONSERVATION ISSUES AFFECTING WILDLIFE IN THE MIDDLE EAST

Tom Bailey1, Declan O’Donovan2, Chris Lloyd3, Theri Bailey4
1Dubai Falcon Hospital, Dubai, United Arab Emirates; 2Wadi Al Safa Wildlife Centre, Dubai, United Arab Emirates; 3Nad Al Shiba Vet Hospital, Dubai, United Arab Emirates; 4Zayed University, Dubai, United Arab Emirates

There are great pressures on the environment and wildlife throughout the Middle East. The rapid pace of economic development, the fragility of the natural ecosystems and low population densities are factors making many indigenous species vulnerable to extinction. The expansion of human populations and the increasing contact between domestic and wild animals has also increased disease transmission between wild and domestic species, including humans. Some governments have recognized the need to tackle these conservation issues and over the last 10-15 years a number of projects working with both captive and free-living wildlife have been established in the region. The Middle East is an important migration route and wintering area for a large proportion of northern Palearctic birds. In this sensitive area, habitat degradation, oil spills, pesticide use, and infectious disease outbreaks have the potential to cause immense impacts on free-living and captive wildlife populations. In some cases wildlife species, e.g. waterfowl, may carry diseases such as the highly pathogenic avian influenza virus that can cause great economic impact to domestic poultry industries, cause disease in other birds such as falcons, as well as being highly dangerous to humans. The factors hindering the ability of the veterinarians, biologists and wildlife managers to work in the region are discussed. The objectives and a review of the first year of operation of Wildlife Middle East News will be presented.
SEROPREVALENCE OF H5 AVIAN INFLUENZA VIRUS ANTIBODIES IN BIRDS FROM UNITED ARAB EMIRATES


1Dubai Falcon Hospital, Dubai; 2Wadi Al Safa Wildlife Centre, Dubai; 3H.E. Sheikh Butti Maktoum's Wildlife Center, Dubai; 4Central Veterinary Research Laboratory, Dubai, United Arab Emirates

Many serotypes of avian influenza virus (AI), including HPAI serotypes (H5 and H7), have been isolated in birds from the Middle East region. Little is known on the prevalence of AI in UAE, as there have been only some sporadic isolates (MANVELL et al., 2000; KENT et al., 2006). In order to gain knowledge on the epidemiology of AI in UAE, a serological study was performed between September 2005 and March 2006. Overall, 443 serum samples obtained from apparently healthy wild and captive birds, representing 7 orders and 38 species, were assayed for antibodies to the antigen H5N2 of AI using the haemagglutination inhibition test. Only birds that were not vaccinated against AI were included in the study. An overall seroprevalence of 13% was found. The orders that had higher seropositive proportion were Ciconiformes (18/60; 30%), Anseriformes (15/76; 20%), Galliformes (10/76; 13%) and Falconiformes (10/130; 7.7%).

EFFECTS OF CAPTURE METHOD ON BLOOD PARAMETERS IN CARIBOU: EVALUATION OF PHYSICAL & CHEMICAL IMMOBILIZATION TECHNIQUES

Kimberlee Beckmen1, Jennifer Schmidt2, Mark Keech1, Bruce Dale3

1Alaska Department of Fish & Game, Fairbanks AK USA; 2University of Alaska Fairbanks, Fairbanks AK, USA; 3Alaska Dept of Fish & Game, Palmer AK, USA

The adverse effects of capture stress and potential for mortalities are a concern when capturing cervids. In this study we evaluated the effects of different capture protocols, 2 physical and 2 chemical, on various blood parameters related to capture stress. The physical capture methods were net-gunning from a helicopter (n=16) and hand-capture with manual restraint from boats during a river crossing (n=20). Chemical combinations evaluated were carfentanil/xylazine (n=54) and ketamine/medetomidine (n=9). Drugs were administered via helicopter darting. Blood parameters used to quantify stress and risk of capture myopathy included lactate and creatinine phosphate (CPK). Use of a hand-held lactate monitor was validated for field use in caribou with a significant correlation to laboratory serum lactate (p<0.0001). Mean serum CPK concentrations were significantly higher in hand-captured caribou than in chemically-immobilized caribou. Caribou darted with a ketamine/medetomidine had the lowest mean CPK and lactate concentrations but only the latter was significantly different from other capture methods. Increased lactate was significantly correlated with increasing chase time (r=0.46, p<0.0001). Mean lactate levels in physically captured caribou were nearly three times that of chemically immobilized caribou. These data indicate that physical capture methods appear to be more ‘stressful’ for caribou than helicopter darting and thus may pose a higher risk for capture myopathy. Furthermore, the drug combination of ketamine/medetomidine appears to at least as safe as carfentanil/xylazine and eliminates the need for the controlled narcotic. Body condition, season, and reproductive state also need to be considering how and when to capture caribou.
[166] HIGHLY PATHOGENIC H5N1 AVIAN INFLUENZA SURVEILLANCE IN TEXAS FERAL SWINE

Tyler A. Campbell¹, Randy W. DeYoung², Jeffrey S. Hall³, Erin M. Wehland², Lon I. Grassman², David B. Long¹
¹US Department of Agriculture-Wildlife Services, Kingsville, TX, USA; ²Caesar Kleberg Wildlife Research Institute-Texas A&M University, Kingsville, TX, USA; ³US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA

An influenza pandemic is currently regarded by many public health officials as a significant threat to global public health. The next influenza pandemic will likely be caused by a virus that possesses surface proteins to which humans have no immunity. Previous influenza pandemics occurred via genetic reassortment in an animal co-infected by avian and human influenza virus strains. One likely candidate for such an intermediate host or “mixing vessel” is feral swine (Sus scrofa). The invasive feral swine occur across North America, and large populations inhabit locales frequented by bird species that serve as documented AI reservoirs and where swine can contact humans frequently. We conducted surveillance on feral swine for the presence of avian-origin influenza viruses (including the highly pathogenic H5N1) in Texas, a state where millions of migratory and resident waterfowl and shorebirds winter among a large population (ca. 2 million) of feral swine. We obtained nasal swabs and blood serum from hunter-harvested animals and nuisance animals removed by Texas Wildlife Services during May 2006–Feb 2007. We screened samples for all 16 hemagglutinin (H) and 9 neuraminidase (N) subtypes of the influenza virus. To date, we have not detected avian-origin influenza viruses in >400 samples. We will continue surveillance efforts through September 2007. Early detection is critical for disease management strategies to be successful. This study is an important step in better understanding the dynamics of this highly-publicized zoonotic disease and to understand potential routes of human exposure.

[167] MYCOBACTERIUM TUBERCULOSIS INFECTION IN AN ORANGUTAN

Sungwon Chae, Yooncheol Ha, Yonghoon Lee, Duyeol Kim, Chanhee Chae
Seoul National University, Seoul, Republic of Korea

A respiratory disorder was noted in a 5-year-old female orangutan (Pongo pygmaeus) kept in the Yongin Farmland. Radiographically, multiple radiodense foci ranging from 2 to 6 mm diameter were seen throughout the lung lobes. Grossly, the thoracic cavity revealed a firm texture and grayish-pink discoloration of the left apical lung lobe. Histopathologically, multifocal areas of granulomatous pneumonia present the right and left apical lung lobes. Both primers from IS1081 and IS6110 targeting 196 bp and 245 bp respectively were used in polymerase chain reaction. Mycobacterium tuberculosis was isolated from liver and confirmed by polymerase chain reaction.
[168] BLOOD SERUM CHEMISTRY & HEMATOLOGY IN FIELD-FRESH OPOSSUMS IN NORTHWEST MISSOURI

Steven Hellstrom, Cary D. Chevalier
Missouri Western State University, Saint Joseph, MO, USA

Standard serum chemistry and hematological values were measured on 14 field-fresh Virginia opossums (Didelphis virginiana) (8 males, 6 females) from the natural areas on campus. The purpose of this study was to establish reference standards of serum chemistry and hematology of this population of opossums under chemical restraint. Individuals were chemically restrained with a ketamine-acepromazine-atropine drug cocktail. The following serum components were measured: glucose, sodium, potassium, chloride, blood urea nitrogen (BUN), creatinine, BUN/creatinine ratio, calcium, phosphorus, alkaline phosphatase, GGTP, magnesium, total bilirubin, aspartate transferase, alanine transferase, cholesterol, triglyceride, CPK, total protein, albumin, globulin, lipase, and amylase. Hematological values measured included: leukocytes, erythrocytes, hemoglobin, hematocrit, mean cellular volume, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, platelet count, neutrophils, lymphocytes, monocytes, eosinophils, basophils, and banded neutrophils. There were gender differences for only three serum chemistry values (P < 0.05): glucose (males higher than females), ALT (SGPT; females higher than males), and BUN/creatinine ratio (females higher than males). No significant gender differences (P > 0.05) were observed among hematological values. Blood chemistry and hematology profiles are important for establishing normal health profiles which, in turn, are essential for monitoring population health. Drugs used for chemical restraint often impact “normal” blood chemistry profiles. Normal reference profiles of animals under chemical restraint should be established and would be useful to anyone involved with wildlife health.

[169] AVIAN INFLUENZA VIRUS SURVEILLANCE IN OHIO ZOOLOGICAL INSTITUTIONS

Patricia M. Dennis1,2, Lindsey J. Long1, Jacqueline M. Nolting1, Dennis A. Senne3, William Saville1, Richard D. Slemons1
1Ohio State University, Columbus, OH, USA; 2Cleveland Metroparks Zoo, Cleveland, OH, USA; 3US Department of Agriculture-National Veterinary Services Laboratory, Ames, IA, USA

Avian collections in zoological institutions accredited by the Association of Zoos and Aquariums (AZA) serve as unique sentinels for emerging infectious diseases in North America. Found in urban and rural settings across the United States, AZA institutions quarantine all animals entering their collections, house individually identified animals which receive regular health examinations, and veterinarians perform complete necropsies on collection animals that die. During 2006 and 2007, AZA avian collections in Ohio were incorporated into our ongoing avian influenza virus (AIV) surveillance efforts. The outdoor environment of the zoo is often utilized by both zoo birds and wild bird populations from late spring through early fall and the zoo collections include exotic avian species, bringing additional host factors into play. Cloacal and oropharyngeal swabs and blood samples were taken from birds as they were moved to their outdoor pens in the spring and back into indoor enclosures in the fall. During summer environmental samples were collected on the grounds of five AZA institutions. No AIVs were recovered from the spring and fall of 2006 cloacal swabs, four type A influenza isolates were recovered from 2006 environmental samples and results of spring 2007 are pending. To date, no antibodies have been detected to the type specific antigen of AIVs. By initiating AIV surveillance measures, these institutions have provided additional information toward understanding the disease ecology of avian influenza viruses and have taken a proactive stance in protecting the health of their avian collections, personnel and visitors to their respective zoos.
[170] AN UPDATE ON AVIAN INFLUENZA IN WILDLIFE & RESULTS OF MONITORING AND SURVEILLANCE IN MARYLAND 2006-2007

Cindy P. Driscoll1, Larry J. Hindman1, Richard D. Slemons2, Dennis A. Senne3
1Maryland Department of Natural Resources; 2Ohio State University; 3US Department of Agriculture-National Veterinary Services Laboratory, Ames, IA, USA

The Maryland Department of Natural Resources (MD DNR), in conjunction with the Ohio State University (OSU) began collaborative monitoring of wild birds for Avian Influenza (AI) in 1999. In 1999 OSU began surveillance of mallard ducks on Maryland Regulated Shooting Areas (RSA). In 2005 MD DNR began sampling of other avian species being handled by wildlife state and federal biologists in banding and monitoring efforts around the state. Samples are initially processed at OSU and sub-typed at the US Department of Agriculture National Veterinary Services Laboratory, Ames, Iowa. Low Path AI is routinely found in health and disease surveillance of wild birds of North America and around the world. While Type A influenza viruses may be transmissible to other species of animals it does not move between species readily. Aquatic birds (shorebirds and waterfowl) are considered to be the natural reservoir of this virus. Occasionally, LPAI is detected in US poultry – such as the LPAI outbreaks in Delaware and Maryland poultry farms in 2004. MD DNR works closely with the poultry industry on the Eastern Shore of MD and has developed an excellent working relationship to further the understanding of the role of wild birds and poultry in Avian Influenza. To date, several novel AI subtypes have been detected in MD to date and will be reported in this poster.

[171] POTENTIAL TRICHOMONAS GALLINAE INFECTION IN RED-SHOULDERED HAWK NESTLINGS IN NORTHEASTERN WISCONSIN

Shelli A. Dubay1, Janet King1, Richard W. Gerhold2
1University of Wisconsin-Stevens Point, Stevens Point, WI, USA; 2Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA

Trichomonas gallinae is a protozoan parasite that can cause significant mortality in nesting hawks. Nestlings are exposed to T. gallinae by consuming infected avian prey. In Wisconsin, red-shouldered hawks (Buteo lineatus) are listed as threatened species, and nestling survival has been lower than that documented in other parts of their range. Causes for low productivity have not been determined. In 2006, we documented bird remains around red-shouldered hawk nests in northeastern Wisconsin, providing evidence of a mechanism for transmission of T. gallinae to nestlings. Our objective was to determine if T. gallinae infection possibly contributes to low nest productivity for red-shouldered hawks in Wisconsin. In March and April 2007, red-shouldered hawk nests were located using broadcast calling and nest searching techniques. We evaluated status of nests several times from April to June but climbed nests and handled nestlings in June when nestlings were 80% to fledging. At that time, we evaluated nest productivity and sampled nestlings for T. gallinae. We used the InPouch™ system to evaluate nestlings for T. gallinae infection by swabbing the mouth and upper crop of birds with a cotton swab and inoculating the swabs into liquid medium provided with the InPouch™ system. Media were monitored for presence of T. gallinae for several days after sampling. Results from these analyses will be used to determine if T. gallinae infection could contribute to low nest productivity in red-shouldered hawk nestlings in Wisconsin.
[172] EFFICACY OF RHODAMINE B AS A BIOMARKER FOR RACCOONS

Tricia L. Fry, Mike R. Dunbar
US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA

The Oral Rabies Vaccination (ORV) program, administered by Wildlife Services, has long desired an effective, easy to use biomarker that would allow for non-invasive identification of animals that have been exposed to the ORV baits. Presently, the ORV program uses tetracycline, an antibiotic deposited in growing bone and teeth; tetracycline has proven to be reliable, but finding this biomarker is invasive and expensive. Our research examines rhodamine B as a possible alternative biomarker for the ORV program. Rhodamine B is a chemical dye that when ingested, stains the oral cavity and is absorbed systemically in growing tissues such as hair and vibrissae producing fluorescent orange bands under UV light. We fed 18 raccoons rhodamine B and monitored their whiskers and fur for fluorescence for 15 weeks using three methods to observe fluorescence. All raccoons exhibited fluorescence in their whiskers. An average of 55% of whiskers sampled from each individual on each sampling day exhibited fluorescence. Evaluation of whiskers using a UV equipped microscope and hand held UV lights will be compared to determine if evaluation of whiskers can reliably be done in the field. At the conclusion of the study, we conducted necropsies on all raccoons to look at the systemic effects of the dye. Gross and histopathologic examination of tissues revealed only subtle lesions consistent with those previously reported in wild raccoons. Rhodamine B appears to be a safe and effective biomarker that may reduce the need for invasive sampling techniques to assess the success of the ORV program.

[173] VERMINOUS MENINGOENCEPHALITIS IN A Sika deer (Cervus nippon): An apparent case of Parelaphostrongylosis

Richard W. Gerhold¹, M. Kevin Keel¹, Kim Arnold², Doug Hotton³
¹Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA; ²Maryland Department of Agriculture, Salisbury, MD, USA; ³Maryland Department of Natural Resources, Salisbury, MD, USA

An adult, female, free-ranging, Sika deer (Cervus nippon yakushimae) from Wicomico County, Maryland was submitted for postmortem examination. The animal was circling and had no fear of humans when it was euthanized by personnel of the Maryland Department of Natural Resources. There were no gross lesions and the deer was negative for rabies. Microscopic examination revealed lymphoplasmacytic, neutrophilic, and eosinophilic meningoencephalitis with intraleisonal, adult nematodes, larvae, and eggs. The nematodes were characterized by a thin cuticle, polymyarian coelomyarian musculature, accessory hypodermal chords, and large multinucleate intestinal cells with a low microvillus border and no more than 2 cells per cross section. These features are consistent with Parelaphostrongylus tenuis and related nematodes in the family Protostrongylidae. Inflammation was also present in the optic nerves, pituitary glands, and surrounding connective tissue which contained emboli of larvated and embryonated eggs. To our knowledge, this is the first report of protostrongyle-induced encephalitis in a Sika deer.
Swine play an important role in the disease ecology of influenza. Having cellular receptors in common with birds and humans, swine provide opportunities for mixed infections and potential for genetic reassortment between avian, human, and porcine influenza. Feral swine populations are rapidly expanding both in numbers and range and thus are increasingly coming into contact with waterfowl, humans, and agricultural operations. In this study, over 875 feral pigs were sampled from six states across the United States for serological evidence of exposure to influenza. In Oklahoma, Florida, and Missouri no seropositive feral swine were detected. Seropositive swine were detected in California, Mississippi, and Texas. Seroprevalences in these states ranged from 1.1% in MS, 5.3% in CA, and 14.4% in TX. All positive swine were exposed to H3N2 subtype, the predominant subtype currently circulating in domestic swine. The only exceptions were in San Saba County, TX where of the 15 seropositive samples, four were positive for H1N1 and seven for H1N1 and H3N2. In Texas, there was large geographical and temporal variation in seroprevalence and no obvious connection to domestic swine operations. From these results, it is apparent that influenza in feral swine poses a risk primarily to swine production operations. However because feral swine share habitat with waterfowl, prey on and scavenge dead and dying birds, are highly mobile, and increasingly are coming into contact with humans, the potential for these animals to become infected with avian or human influenza in addition to swine influenza is a distinct possibility.

Rodent populations of the southwest United States exhibit periodic plague outbreaks called enzootic plague. These outbreaks result in a high death rate and infected fleas then look for new sources of blood, increasing the risk of human infection. Surveillance of animal populations to identify high rates of plague can be used to predict disease in humans. Data on background levels of infection are also useful in differentiating natural outbreaks from bioterrorism events. Sixty-five carcasses were obtained from several areas of Colorado in August 2006. Animals were trapped and euthanized near prairie dog colonies in the USDA Central Plains Experimental Range, Fort Carson, and the Colorado Springs area. Samples of blood were obtained using Nubuto strips. Liver, lung, kidney, spleen, lymph nodes, and heart tissues were collected by necrospy. Ectoparasites were obtained from the carcasses and burrow swabs. Samples were analyzed for *Yersinia pestis* DNA using two real-time PCR-based targets, a mass-spectrometric method (Ibis T5000 system), antigens using an electrochemiluminescence immunoassay (ECL), immunohistochemistry, and culture. Three of 18 prairie dogs were positive for *Y. pestis* by all methods of analysis. Seven animals were positive by immunohistochemistry, ECL, PCR, and mass spectrometry. Five of 20 ground squirrels were positive for *Y. pestis* by PCR and mass spectrometry, but all were culture, IHC, and ECL negative. One rabbit tested positive by ECL, IHC, PCR, and mass spectrometry. Disconcordant results appeared to result from differing limits of detection, but emphasize the importance of using multiple orthogonal methods to confirm the presence of *Y. pestis* in environmental testing.
MASSACHUSETTS WILDLIFE DISEASE SURVEILLANCE PROGRAM: THE ROLE OF WILDLIFE AS SENTINELS OF DISEASES OF PUBLIC HEALTH IMPORTANCE

Janet Martin, Alison Robbins
Tufts University Cummings School of Veterinary Medicine, North Grafton, MA, USA

The link between animal and human health is undeniable and we must begin to take a more holistic view of health and disease. The majority of new emerging diseases are zoonotic, and many involve a wildlife connection. New projects such as the Wildlife Disease Surveillance Program at TCSVM that coordinate projects within existing human and veterinary health monitoring frameworks to form mutually beneficial collaborations between both public and private agencies and organizations, will be on the forefront of protecting the public health.

This program provides an infrastructure enabling the detection of unusual disease events affecting wild animals in the state of Massachusetts, thereby acting as an advanced warning of the presence of infectious disease that could threaten human or domestic animal health. The “canary in the coalmine” analogy reflects the benefits of sensitive animal indicators as early warning systems to detect and prevent human health problems. Baseline levels of endemic diseases affecting wildlife health must be initially established, followed by monitoring for disease events that fall outside the established normal pattern. This information will be vital as part of an overall health surveillance system which will provide an early response to disease events. The hallmark of this program is the creative linking of existing infrastructures, both within the state and nationally, to develop cooperative networks that enhance pre-existing program capabilities. By taking full advantage of resources that already exist this program will act to decrease the burden on each individual organization while increasing the overall level of health protection statewide.

WILDLIFE SANITARY SURVEILLANCE IN CATALONIA, NE SPAIN: FINDINGS, ACTUAL ORGANIZATION & FUTURE PERSPECTIVES

Gregorio Mentaberre, Ricardo Casanovas, Encarna Casas-Díaz, Jorge R. López-Olvera, Francesc Closa, Ignasi Marco, Santiago Lavin
1Servei d'Ecopatologia de Fauna Salvatge, Facultad de Veterinaria, UAB, Cerdanyola V., Barcelona, Spain; 2Departament de Medi Ambient i Habitatge de la Generalitat de Catalunya, Barcelona, Spain; 3Universidad CEU Cardenal Herrera, Valencia, Spain

Public administrations have ignored wildlife health for long time and have focused diseases control and eradication programmes in domestic animals. Because of this attitude, many of these programmes have failed to attainment of their objectives, making wildlife role as reservoirs or transmitters clear and showing the need for considering wild species in control and eradication programmes. Besides, disease’s outbreaks in wildlife populations caused by domestic livestock have appeared. Therefore, in the last few years, “only or global animal health” concept and initiatives to coordinate sections involved in the study and control of domestic and wild animal’s health are emerging. In Spain, Catalonia has been a region at the forefront of the study of wildlife diseases, thanks to creation of the Wildlife Ecopathology Research Group (SEFaS) of the Veterinary Faculty of Barcelona Autonomous University, in 1991. Since then, the SEFaS has developed an intense work specially focused on indigenous wild artiodactyls, in agreement with the Environment Department of the Catalonian administration. As a result of its activity, it has been possible to detect and study numerous diseases in wildlife populations in Catalonia and other Spanish regions, and management and control measures have been proposed. Some examples are presented. Also, since time ago, we aim to extend collaboration to Agriculture, Livestock Farming and Fishing, and Public Health Departments, since we have demonstrated transmission of diseases between wild and domestic animals and presence of zoonoses (emerging and re-emerging diseases) in our geographical context. Measures to improve detection and prevent spreading of diseases are proposed.
[178] **NEUROAXONAL DEGENERATION SYNDROME IN AN ELEPHANT (Elephas maximus)**

Abelardo Morales¹, Maria C. Tosta¹, Antmar Henríquez², Víctor Bermúdez¹

¹Central University of Venezuela; ²Zoological “Las Delicias”, Zoological “Caricuao”, Caracas, Venezuela

The elephant (Elephas maximus) is an endangered species with low fecundity and premature death in the wild. We report a multidisciplinary study of neuroaxonal degeneration syndrome in an elephant (Elephas maximus). A 36-year-old female captive elephant (Elephas maximus), with a history of chronic claudication, died after prolonged anorexia and weight loss at the Zoological Park “Caricuao” in Caracas, Venezuela. On necropsy, the liver was found to be swollen and friable, and the kidneys were found to be swollen with fibroplastic pattern in cortical region and adherence of the renal capsule. Others organs did not reveal any significant alterations. Microscopically, there was degenerating myelin, focal Wallerian degeneration of axons in the white matter, some cells bodies with central chromatolysis, atrophy and apoptosis. These results suggest neuroaxonal degeneration syndrome in the elephant. Given the occurrence of this condition associated at this geographic location, factors others than age (genetic, nutritional, and/or environmental) may influence this degenerative process in peripheral nervous system in captive elephants in Venezuela.

[179] **AVIAN INFLUENZA SURVEILLANCE IN WILD BIRDS: AN EARLY DETECTION SYSTEM**

R. Orusa², S. Ghiggia², E. Barcucci¹, S. Salvati¹, S. Robetto², A. Peracino², M.L. Mandola¹

¹Laboratorio di Virologia e Sierologia Virologica, Italy; ²Centro di Referenza Nazionale per le Malattie degli Animali Selvatici Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle D’Aosta, Turin, Italy

The European Community since 2005 has required to the member states the preparation of avian influenza surveillance plans on wild birds in order to verify the circulation of the viral strains. Viral strains belonging to all subtypes HA could determinate low pathogenicity avian influenza viruses (LPAI) while up to the present (except for two cases) only the subtype H5 and H7 has been causing High Pathogenicity Avian Influenza (HPAI). Low pathogenic viruses can undergo mutations or reassort with viruses in the domestic and possibly resident bird populations until an HPAI virus arises. Wild birds have been shown to introduce novel influenza gene segments into a population that when reassorted with existing viruses can generate a new virus strain with different antigenic and other biological characteristics. Data collection and reporting are important to prevent further spreading of H5N1. Continue surveillance and testing of poultry and captive wild birds, included domestic ducks that are able to carry the virus asymptomatically, are crucial to understand the general patterns in outbreaks, possible routes of transmission and the potential impacts on migratory bird populations. Better surveillance of wild birds and more research on the behavior of the virus in wild bird populations is important to predict future outbreaks. In this work, the collected Avian Influenza diagnostic tests on wild bird data carried out by the Laboratorio di Virologia e Sierologia virologica of the Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d’Aosta since September 2005 are presented.
[180] A PRELIMINARY STUDY TO ASSESS HEALTH STATUS IN WILDLIFE POPULATION BY THERMAL IMAGING

R. Orusa\textsuperscript{1}, M. Zanolla\textsuperscript{2}, S. Robetto\textsuperscript{1}, A. Peracino\textsuperscript{1}, C. Stelletta \textsuperscript{2}, M. Morgante\textsuperscript{2}
\textsuperscript{1}CeRMAAS Centro di Referenza Nazionale per le Malattie degli Animali Selvatici IZS Piemonte, Liguria e Valle d’Aosta, Area Sanitaria della Valle d’Aosta, Italy; \textsuperscript{2}Dipartimento di Scienze Cliniche Veterinarie, Facoltà di Medicina Veterinaria, Università degli studi di Padova, Italy

Using infrared thermography (IRT) it is possible to measure and visualize the body surface temperature of animals by detecting the thermal radiation that they emit. The main advantages of using IRT are that it is non-invasive and fast, so it can be used at a distance and/or in dynamic conditions. The aim of this study was to show some potential future applications of thermography on wild ungulates. Images were gathered on non-captive ibexes and chamois living in the National Park of Gran Paradiso in Valle d’Aosta, Italy. The ability of IRT to detect animals at various distances was evaluated and the influences of factors such as coat characteristics and environmental conditions were considered. Qualities and limits of the technique were analyzed and possible solutions for a reliable result were suggested. The objectivity of thermal imaging might be limited by intraspecific social behavior, fear of humans and external factors. With close-up images it was possible to measure the temperature in the eye region and at the base of the horn. Infrared thermography could be used to calculate density of an animal population during night surveys or to detect animals hidden in the vegetation. The ability to detect animals in darkness could be useful to study the nocturnal behavior of these animals. The potential uses of this technique include also monitoring health status to control the spread of transmissible diseases like foot-and-mouth disease and mange, studying the activity of the rumen, evaluating the level of hair insulation, and diagnosing pregnancy.

[181] EFFECTS OF GNRH IMMUNIZATION ON REPRODUCTION & BEHAVIOR IN FEMALE ROCKY MOUNTAIN ELK

Jenny G. Powers\textsuperscript{1}, Dan L. Baker\textsuperscript{1}, Mary M. Conner\textsuperscript{2}, Anneke H. Lothridge\textsuperscript{1}, Tracy L. Davis\textsuperscript{1}, Terry M. Nett\textsuperscript{1}
\textsuperscript{1}Colorado State University, Fort Collins, CO, USA; \textsuperscript{2}Utah State University, Logan, UT, USA

There is an increasing need in protected environments, for non-lethal methods of managing overabundant wild ungulates. Immunocontraception using gonadotropin releasing hormone (GnRH) vaccination is one approach. This study evaluated the safety and efficacy of GnRH immunization in captive female elk (Cervus elaphus nelsoni). We investigated the effects of active GnRH vaccination on; maintenance of pregnancy, neonatal survival, dam health, reproductive behaviors, and subsequent pregnancy rates. Seventeen captive pregnant elk, in mid-gestation, were immunized with either a GnRH vaccine (GonaCon\textsuperscript{TM}) (n = 10) or control vaccine (n = 7). Throughout the remainder of gestation we found no differences in serum progesterone concentrations or calving rates. Likewise, there were no differences in neonatal survival or growth rates. Vaccine injection sites showed little evidence of swelling, pain, or abscesses. All control females became pregnant while only 10% of GnRH immunized females were pregnant. Reproductive behavior measurements, revealed no differences in general breeding/herding behaviors. Male pre-copulatory behaviors directed towards treated females were nearly twice those directed towards control females, while differences in female pre-copulatory behavior rates were not significant. Copulatory behaviors were too infrequent to detect a difference between treatment groups. We concluded that active immunization of female elk during mid-gestation using a single dose of GonaCon\textsuperscript{TM} does not affect success of the current pregnancy, results in 90% reduction in pregnancy rates the following breeding season, and induces minimal changes in social breeding behaviors. Ongoing studies are investigating the duration of vaccine efficacy in treated females and potential long-term reproductive effects in developing calves.
[182] SURVEILLANCE FOR TYPE A INFLUENZA VIRUS IN CANADA GEESE (Branta canadensis) IN FAIRFIELD COUNTY, CONNECTICUT, 2005

K. Quesenberry1,2, S. Tirrel1, C Lyons1, P. Rabinowitz1, D Fish1
1Yale University, New Haven, CT, USA; 2The Animal Medical Center, New York, NY, USA

Canada geese have established resident populations in many sections of New England and are ubiquitous in public recreation areas. In many areas along the migratory flyways, Canada geese are in contact with migrating ducks, which are reservoir hosts of low pathogenic avian influenza viruses. To determine the prevalence of avian influenza virus in Canada geese and to determine if geese can act as a surveillance species for influenza viruses circulating in migratory ducks, fecal samples were collected from Canada geese at 10 recreation areas and public parks in Fairfield County, CT. Samples were tested for type A influenza virus by real-time reverse transcriptase polymerase chain reaction (RRT-PCR). Of the 410 samples tested, none were positive for type A influenza virus. The results of this study indicate that influenza A virus is not prevalent in Canada geese in Fairfield County, CT and that geese do not appear useful as a sentinel species for influenza virus in migratory ducks.

[183] PREVALENCE & CHARACTERIZATION OF BOVINE VIRAL DIARRHEA VIRUS IN WHITE-TAILED DEER POPULATION IN INDIANA

Roman M. Pogranichniy, Eran Raizman, Leon Thacker, Greg Stevenson
Purdue University, West Lafayette, IN, USA

Bovine viral diarrhea (BVD) is one of the economically important diseases of production animals. For many years, different types of vaccines have been available in the market, yet this disease is hard to control in high density population areas. Detection and isolation of BVD virus (BVDV) from any potential reservoir is very important. One potential source is wild ruminants. Ear notches and lymph nodes were collected during deer hunting season in Indiana. Two cytopathic BVD viruses were isolated from the wild population of white-tailed deer (Odocoileus virginianus) from 745 collected samples. These were genotyped as type 1a and 1b by comparing nucleotide sequence at the 5’ UTR regions of these isolates and reference viruses. Infection prevalence detected in the 745 samples tested for BVDV was 0.03%. Wild ruminants infected and shedding BVD virus should be taken into consideration during an eradication program of BVDV from the livestock population.
SKUNK RABIES EPIZOOTIC IN NORTHWESTERN WYOMING

Craig A. Ramey¹, Jean Bourassa¹, Marshall Robin³, Kenneth H. Mills⁴
¹US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; ²US Department of Agriculture-Wildlife Services, Powell, WY, USA; ³University of Wyoming, Laramie, WY, USA

Striped skunks (Mephitis mephitis) are the most important reservoir for rabies epizootics on the Great Plains. In February 1989, an index case occurred near Cowley, WY, along a tributary of the Shoshone River system previously rabies free. USDA's Wildlife Services (WS) cooperated with state and local officials in a monitoring and control program starting in 1990 and ending in 1992. Its primary goal was to address the public's concerns about human and domestic animal's health and safety. The epizootic was monitored by WS personnel using live traps along the Shoshone River system. Less than 10% of the sample was composed of traditional surveillance data - public referrals of suspiciously acting wildlife and road kills. All skunks (>300) were shipped to the Wyoming State Veterinary Laboratory for confirmation of rabies using immuno-fluorescent testing of brain tissues. Analysis of capture locations and dates indicated a tsunami wave-like pattern of spread reaching nearly all areas of the river system by November 1991 from its headwaters near Cody downstream to the Bighorn Canyon/Reservoir. This epizootic was limited by many factors including the availability of habitat, skunk depopulation by WS, and the public’s increased surveillance. Positive outcomes included: (1) no human sicknesses or deaths, (2) synergism among public and local, state, and federal agencies, (3) increasing our knowledge of skunk rabies epizootics, and (4) post hoc evaluation of the results for planning future surveillance and/or eradication programs. Finally, the need for a skunk rabies vaccine that could have limited the epizootic by producing a manmade barrier utilized in association with the natural barriers.

EFFECTS OF RACCOONPOX VIRUS ANTIBODIES ON RABORAL V-RG® VACCINATION IN RACCOONS

J. Jeffrey Root¹, Robert G. McLean¹, Jorge E. Osorio²
¹US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; ²University of Wisconsin, Madison, WI, USA

The USDA, Wildlife Services oral rabies vaccination program uses a live vaccinia-vectored vaccine (Raboral V-RG®) to vaccinate select terrestrial wildlife species against rabies virus in several regions in the eastern and southern U.S. Several naturally occurring orthopoxviruses have been found in North America. The effects of antibodies to these orthopoxviruses on successful V-RG vaccination in raccoons (Procyon lotor) and other terrestrial wildlife species are largely unknown. This question is the subject of this study. To accomplish this, ten raccoons were pre-immunized with a recombinant raccoon-pox virus vaccine (RCN-F1). At later dates, the ten per-immunized and an additional 10 control raccoons were vaccinated with V-RG on two occasions. The rabies virus neutralizing antibody (VNA) titers of the two groups were compared from serum samples collected at subsequent time points. These results and ensuing recommendations will be the focus of this presentation.
PARASITIC & VIRAL DISEASES OF DOGS IN TWO NORTHERN CANADIAN COMMUNITIES & IMPLICATIONS FOR WILDLIFE & HUMAN HEALTH

Amanda L. Salb¹, Herman W. Barkema², Brett T. Elkin²³, RC Andrew Thompson⁴, Douglas P. Whiteside¹², Sandie R. Black¹², J. P. Dubey⁵, John A. Ellis⁶, Steven Krakowka⁷, Susan J. Kutz²
¹Calgary Zoo Animal Health Centre, Calgary, AB, Canada; ²University of Calgary, Calgary, AB, Canada; ³Government of the Northwest Territories Wildlife and Fisheries Division, Yellowknife, NT, Canada; ⁴Murdoch University, Murdoch, WA, Australia; ⁵US Department of Agriculture, Beltsville, MD, USA; ⁶University of Saskatchewan, Saskatoon, SK, Canada; ⁷The Ohio State University, Columbus, OH, USA

In northern Canadian communities there are close interactions between people, dogs, and wildlife. Residents of these communities frequently practice subsistence hunting and fishing and also feed game and fish to their dogs, which is sometimes the main component of their diet. Sled dogs also are used for transportation out on the land for subsistence and sport hunting and are typically housed outdoors. Consequently, dogs and people can be exposed to diseases from wildlife, and dogs may contribute to the spread of disease within wildlife ecosystems and human areas. Dogs living in these remote communities have limited access to veterinary care, which includes health checks, routine vaccinations and fecal examinations with targeted antiparasitic treatment protocols. In August 2006, fecal and serum samples were collected from 132 dogs presented at sponsored canine health clinics held in Fort Chipewyan, Alberta, and Fort Resolution, Northwest Territories. Detailed histories regarding diet, husbandry and previous veterinary care were also collected. Fecal parasites (Alaria, Diphyllobothrium, cestodes, Giardia, Isospora, Sarcocystis, Toxascaris, Toxocara, and Uncinaria) were identified using the Modified Wisconsin method and ELISA. Serology was used to identify dogs exposed to Neospora, Toxoplasma, Brucella, Bordetella, Canine Distemper Virus, Canine Parvovirus, and Canine Respiratory Coronavirus. This study found that through diet and husbandry, northern dogs may be exposed to a variety of diseases of importance to their health as well as to the health of wildlife and people. In this respect, dogs may serve as sentinels for disease present in wildlife and a potential “disease-bridge” between wildlife and people.

MORTALITIES IN CAPTIVE RAISED STRIPED BASS (Morone saxatilis) ASSOCIATED WITH INTRACOELOMIC INFECTIONS WITH THE NEMATODE PHILOMETRA SPECIES

Guylaine Séguin¹, Francis Bouchard², F. Carl Uhland¹, Stéphane Lair¹
¹Canadian Cooperative Wildlife Health Centre, St. Hyacinthe, Québec, Canada; ²Ministère des Ressources naturelles et de la Faune du Québec, Québec, Canada

The striped bass (Morone saxatilis) was once an important resource both for commercial and recreational fisheries in the St. Lawrence River (Quebec, Canada). This population, which was known as the northernmost indigenous population of striped bass, started to decline in the mid-1950s, disappeared in the late 1960’s and was officially designated extirpated in 1996. A multi-agency restoration program, involving the captive propagation of fingerlings collected in the Miramichi River (New Brunswick, Canada), was implemented in 2002. The goal of this program is to produce breeding groups which will yield fingerlings to restock this depleted population. An unusually high mortality rate (reaching 20% /month) was observed during the winter of 2006 in captive fish from the 2005 cohort. Postmortem examinations revealed marked coelomic distensions associated with the presence of extremely numerous nematodes of the genera Philometra sp. These parasites induce an extensive, multifocal to coalescing granulomatous and hyperplasic coelomitis. Given the intensity of the lesions, heavy infection by Philometra sp. was presumed to be the driving factor of the unusual mortality rate observed in the 2005 cohort. No evidence of transmission from wild collected bass to hatchery raised fish could be documented, and examination of 2 and 3 years old fish failed to reveal infective parasite. Even if these observations suggest that this species of Philometra sp. cannot be established in this captive environment, infections by this nematode can represent a significant cause of mortality during the first year of life of these fish under this hatchery setting.
Although dysfunction anywhere in the hypothalamic-pituitary-thyroidal axis may result in thyroid hormone deficiency, greater than 95% per cent of clinical cases of hypothyroidism result from destruction of the thyroid gland itself (primary hypothyroidism). The two most common causes in domestic animals adult-onset primary hypothyroidism are lymphocytic thyroiditis and idiopathic atrophy of the thyroid gland, each accounting for about one-half of the cases of hypothyroidism. Other rare forms of hypothyroidism include iatrogenic conditions, neoplastic destruction of thyroid tissue and congenital (or juvenile-onset) hypothyroidism (cretinism). Hypothyroidism in the great anteater is poorly documented. A 7 year-old female great anteater (*Myrmecophaga tridactyla*) presented with a history of symmetrical alopecia, leukoderma and progressive chronic dermatitis at the Zoological “El Pinar,” Caracas, Venezuela. Alopecia was confluent around periocular regions, cervical and inguinal. Clinical examinations were followed by serial biopsies of the skin, as well hematology, profile biochemical and hormonal profile. Microscopically, lesions were characterized by symmetrical alopecia and orthokeratotic hyperkeratosis with secondary pyoderma with myxedema and accumulation of mucins in the dermis and subcutis, and atrophy of the piloerector muscle. The hematological test revealed nonresponsive anemia. The profile endocrine results were T4 0.35 µg/dL and T3 0.48 ng/dL and the serum cholesterol concentration was 116 mg/dL, CK 26 UI/L. These results support hypothyroidism syndrome in this captive great anteater.

The clinical manifestations and lesions associated with the syndrome of hyperadrenocorticism primary result from over production of cortisol by hyperactive cells of the adrenal cortices. In domestic animals, Cushing’s diseases has long been identified, nevertheless in wildlife it is poorly documented. Tumors of the adrenal gland, specifically pheochromocytoma related to this pathology, have been reported in *Nasua nasua*. A 9-year-old male *Nasua nasua* with a history of symmetrical patchy alopecia, easily epilated hair, dry seborrhea with dull hair and increased fragility of the skin, leukoderma and progressive chronic dermatitis presented at the Zoological “Las Delicias” Maracay, Venezuela. Alopecia was confluent in the axillary and inguinal regions. Polyuria, polydipsia, polyphagia, weight loss and lethargy were noted. Clinical examinations were followed by serial biopsies of the skin, as well hematology, profile biochemical and hormonal profile. Microscopically, lesions were characterized by symmetrical alopecia and follicular atrophy, follicles dilated with keratin and calcinosis cutis and secondary pyoderma. Endocrinological evaluations were: cortisol 26.29 ug/dL; ACTH 22.68 ug/dL. Biochemical results included high serum alkaline phosphatase activity (120 U/L), hypercholesterolaemia (220 mg/dL), hyperglycaemia (190 mg/dL), and BUN (45mg/dL). These results support a diagnosis of Cushing’s disease in *Nasua nasua*. Probably this syndrome associated with a pituitary adenoma and or adrenocortical tumor primary and the patient’s clinical condition is a paraneoplastic syndrome.
[190] EOSINOPHILIC GRANULOMA COMPLEX IN A Felis pardalis

Maria C. Tosta1, Abelardo Morales1, Nicolas Chiachio2, Víctor Bermúdez1
1Central University of Venezuela; 2Zoological “El Pinar,” Caracas, Venezuela

Feline eosinophilic granuloma complex (FECG) is a common inflammatory skin disease of cats, which consists of a group of lesions that affect the skin, mucocutaneous junctions, and oral cavity. EGC is not specific disease but simply several cutaneous reaction patterns in cats. Classically, three lesions have been characterized in feline EGC: indolent ulcers, eosinophilic plaque, and eosinophilic granuloma. A 9-year-old male Felis pardalis presented with a history of alopecia, leukoderma and progressive chronic dermatitis non-responsive to glucocorticoid and antibiotic therapy at the Zoological “El Pinar,” Caracas, Venezuela. Clinical examinations were followed by serial biopsies of the skin, as well hematology, profile biochemical and hormonal profile. Microscopically, there were hyperplastic, ulcerated, superficial perivascular to interstitial dermatitis neutrophils, eosinophilic with lymphoplasmyocytic infiltrate and secondary pyoderma. Fibrosis and fragmented degenerate collagen fibers bordered by degranulated eosinophils, mast cells, multinucleated giant cells and macrophages. Endocrinological and biochemical evaluation did not reveal any significant alterations. Eosinophilia in the blood was moderated. Feline Eosinophilic Granuloma Complex is an uncommon syndrome of unknown cause that affects the skin of cats; however, in wild cats it is unusual to see FEGC.

[191] OPTIMIZATION OF RECOVERY & CRYOPRESERVATION TECHNIQUES FOR EPIDIDYMAL SPERMATOZOA FROM PLAINS BISON

Lisa C. Aurini1, Douglas P. Whiteside1,2, Brett Elkin1,3, Jacob C. Thundathil1
1University of Calgary, Calgary, AB, Canada; 2Calgary Zoo Animal Health Centre, Calgary, AB, Canada; 3GNWT Environment & Natural Resources, Yellowknife, NWT, Canada

With diseases such as bovine tuberculosis and brucellosis threatening the long-term viability of free-ranging populations of threatened wood bison (Bison bison athabascae) in Canada, there is a critical need to optimize salvage techniques to preserve genetic diversity. The objective of this study was to develop an optimal method for the recovery and cryopreservation of epididymal spermatozoa from plains bison as a potential model for wood bison. Cauda epididymides recovered from bison (Bison bison bison) at slaughter (n = 19) were minced and incubated in TALPH buffer for 3 h at 36 °C. After centrifugation, the resulting sperm pellet was diluted in semen extender and frozen-stored using a bovine semen cryopreservation procedure. The mean (± SEM) percentage of morphologically normal spermatozoa present in raw (immediately after releasing spermatozoa to the TALPH), initial (20 min in extender), chilled (12-18 h) and frozen-thawed samples were 52.5 ± 4.3, 68.5 ± 2.6, 66.0 ± 2.4, and 58.0 ± 2.2 respectively. Motility (70.0, 70.0 and 60.0; median %), mean percentage (± SEM) of viability (66.2 ± 2.2, 63.7 ± 2.5, and 38.7 ± 2.8) and acrosomal integrity (92.4 ± 0.9, 90.0 ± 1.0, and 85.2 ± 1.1) of spermatozoa at initial, chilled, and frozen-thawed samples were evaluated, respectively. Two commercially available extenders (Triladyl® and AndroMed®) were equally efficacious. When used for in-vitro fertilization of plains bison oocytes, mean percentages of cleavage for chilled vs. post-thaw samples were 71.2 ± 4.8 and 73.1 ± 5.6, respectively. Although cryopreservation was detrimental, by using this methodology, epididymal spermatozoa retained acceptable post-thaw sperm characteristics and fertility.
Hepatic Lipidosis & Other Pathological Findings in Two Captive Adult Porcupines Dying from a ‘Sudden Death Syndrome’

Robert Barigye, Ev Schamber, Teresa K. Newell, Neil W. Dyer
North Dakota State University, Fargo, ND, USA

Routine necropsy examination and histologic evaluation of tissue sections demonstrated severe hepatic lipidosis (HL) in two adult captive porcupines (Erethizon dorsatum) and pulmonary adiaspiromycosis in one of the two animals. The male porcupine had a markedly enlarged pale liver that microscopically showed large unilocular vacuoles within hepatocellular cytoplasm. In addition to the hepatic lesions, the lung section from the female porcupine had numerous intraalveolar fungal spherules that were variably associated with a mixed cell inflammatory response, barely encapsulated and morphologically consistent with Emmonsia crescens. These results suggest that HL may be an important differential of sudden death in captive porcupines, and that porcupines may harbor unusual infectious pathogens. The authors of this report hypothesize that HL may be associated with the feeding of improvised commercial diets in captive porcupines. The possible association of the condition with dietary and/or host factors in porcupines needs to be thoroughly investigated.

The Suitability of Dried Blood on Filter Paper for the Detection of Trypanosoma sp. in Northern Caribou & Reindeer

Beth Martin1, Greg Appleyard2, Perry Barboza3, Michelle Oakley4, Kimberlee Beckmen5, Alasdair Veitch6, Susan Kutz7
1 University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; 2Alberta Provincial Laboratory for Public Health, Calgary, Alberta, Canada; 3University of Alaska Fairbanks, Fairbanks, AK, U.S.A.; 4Department of Environment, Yukon Government, Yukon, Canada; 5Alaska Department of Fish & Game, Fairbanks, AK, USA; 6Environment & Natural Resources, Government of the NWT, Norman Wells, NWT, Canada; 7University of Calgary, Calgary, Alberta, Canada

The health and sustainability of wildlife populations is important for residents of northern Canada who rely on wildlife, including caribou, for subsistence and income. Since 2003, residents in the Sahtu Settlement region of the NWT have participated in a community-based wildlife health monitoring project to acquire baseline information and monitor trends in caribou health. Select hunters collect a variety of samples, including blood on Nobuto filter paper strips, from caribou harvested for subsistence. Collecting blood using filter paper strips is easy, quick, and transportable in a field situation, however, the suitability of this technique for detecting blood-borne parasites in caribou has not previously been determined. We compared detection of DNA from Trypanosoma sp. on filter paper to detection in whole blood. Blood was collected from 2 caribou and 16 reindeer. Nobuto filter paper strips were immediately saturated with blood, dried overnight and then stored at room temperature until they were frozen one month later. Whole blood also was collected in EDTA tubes, aliquoted to 1.8 ml cryovials, refrigerated overnight and then stored frozen until analysis. Samples were tested 13 months after collection. DNA was extracted, and nested PCR, using primers specific for Trypanosoma sp., was completed on paired whole blood and filter paper samples from all animals. We detected Trypanosoma sp. in 11 filter paper samples but only 5 whole blood samples (2 being only weak positives). Our results indicate that Trypanosoma sp. can be detected by PCR from dried blood collected on filter paper strips, and that this may be superior to PCR analysis of frozen whole blood.
## FRIDAY WORKSHOPS

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The Wildlife Disease Association *Conference Program and Abstracts* booklet is distributed to all meeting attendees. Abstracts were lightly edited to comply with formatting and space limits, but otherwise were printed as submitted. The Wildlife Disease Association does not regard this *Conference Program and Abstracts* booklet as a publication, and abstracts included herein should not be cited in scientific literature.
WORKSHOP – SPATIAL EPIDEMIOLOGY: TECHNIQUES & APPLICATIONS

Chairs: Jerome Freier & Matthew Farnsworth
US Department of Agriculture-Centers for Epidemiology and Animal Health, Fort Collins, CO, USA

This workshop will provide an overview and some in-depth discussion of spatial epidemiology techniques and applications, with special emphasis on approaches that may be useful in the study and control of wildlife diseases. The workshop will cover: 1) data acquisition, processing, and visualization, 2) pattern analysis and quantifying spatial structure, and 3) a discussion, with examples, of spatial analysis and modeling approaches in disease systems. The following broad subject areas will underpin specific topics that will be addressed:

COURSE OUTLINE
Basic epidemiology – Concepts & definitions
• Basic statistics – Define common metrics used to summarize epidemiological data.
• Disease data quality issues – Sensitivity & specificity, location uncertainty, sampling bias.
• Describe common data structures used in epidemiological studies.
• Describe ecologic considerations in epidemiological investigations.

Geospatial processing of data for analysis - Methods for structuring data prior to spatial analysis.
Discussion will focus on various methods used to represent spatial analysis units for epidemiological investigations.

Health & population data – Data quality issues to be considered prior to analysis, such as bias in the population tested for a disease.

Spatial analysis techniques and examples – visualization, exploration, and modeling spatially referenced disease data.
• Exploring spatial relationships – Exploratory Data Analysis approaches with an emphasis on getting to know your data.
• Identifying general patterns – Global measures of spatial structure
• Identifying clusters – Statistics for locating clusters and pattern analysis
• Model based approaches to disease mapping for epidemiological inference

Wrap-up & Discussion
WORKSHOP – WILDLIFE FORENSICS

Chair: Richard K. Stroud
US Fish & Wildlife Service, Ashland, OR, USA.

FORENSIC PATHOLOGY FOR THE WILDLIFE INVESTIGATOR

The medical examiner is a well recognized part of teams for human death investigations. The wildlife investigator, trained in pathology and other biological sciences, can fulfill a key role on the forensic team. Recognizing lesions of forensic importance and interpreting those lesions along with proper protection, handling, and presentation of evidence is essential to forensic investigation of wildlife criminal activity. Taking part in legal cases obligates the wildlife pathologist to certain responsibilities. The most obvious objective for a pathological evaluation of a carcass of an animal is to determine cause of death. Other objectives that must be considered in a forensic evaluation include recovery of trace evidence, reconstruction and documentation of the sequence of events where possible, and estimation of time of death. Most illegal killing of wildlife includes gunshot, poisoning, and certain types of trauma including electrocution of birds. This course discusses lesions and investigative priorities for forensic necropsy investigations.

Forensic investigation gunshot cases requires that the pathologist attempt to answer certain questions including: type of weapon used, number of times shot, trajectory of wound path, lethality or incapacitation caused by the wound, and duration of the wound. In addition, recovery and proper preservation of the projectile for evaluation by the firearms examiner is a part of the pathologist’s responsibility. Trauma wounds are also important for the wildlife pathologist to document because the pattern of the wounds often tells a story of what has happened to the animal. Several types of trauma injuries are encountered in wildlife forensic investigations. These include patterned, blunt force, and sharp force injuries. In addition, predator and scavenger injury must be considered and differentiated from possible injury related to illegal activities. Recognizing electrical contact injury, which has forensic implications, also is important for large birds of prey.

Intentional poisoning of wildlife is widespread in the US and constitutes a major area of wildlife forensic pathology investigation. The objectives of forensic examination of a suspected poisoning case are to identify and quantify the presence of a toxic substance, determine the source of the toxic material, and determine if the victim was the primary target or if it was a secondary (perhaps accidental) poisoning. The pathology exam must eliminate other causes of death, establish presence of a toxic substance in significant quantities, and document a possible exposure route or source. Laws protecting wildlife may include provision for liability for losses through industrial toxic waste spills, oil spills, obstructing structures, and attractive nuisances that kill wildlife. The wildlife forensic pathologist may be asked to participate in forensic cases that document mortalities of wildlife that are due to corporate negligence. Wildlife mortality due to oil spills, oil tank entrapment, cattle carbohydrate (molasses) supplement entrapment, power pole electrocution, stationary towers in flyways, and cyanide leach mining operations are only a few of the examples of wildlife mortality cases that require documentation of cause of death using a forensic format. Such cases may be a greater challenge for the wildlife forensic pathologist than the usual poaching or poisoning case because large companies have the resources to challenge findings and conclusions of the pathologist and other forensic scientists involved in the case.
WORKSHOP – NEW FIELD ANESTHESIA TECHNIQUES & DRUGS
Organized by the American Association of Wildlife Veterinarians

Chair: Lisa L. Wolfe
Colorado Division of Wildlife, Fort Collins, CO, USA

This workshop will provide a forum for presenting and discussing information on new drugs, drug combinations, equipment, and techniques that may be useful in anesthetizing wildlife under field conditions.

8:30a INTRODUCTORY REMARKS & WORKSHOP FORMAT

8:40a R. Bruce Heath [194] ANESTHESIA & MONITORING EQUIPMENT – GETTING IT THERE & MAKING IT WORK

9:00a Ben J. Gonzales [195] CHEMICAL RESTRAINT OF ROOSEVELT ELK USING MEDETOMIDINE AND TELAZOL®

9:20a Gregorio Mentaberre [196] ASSESSING USEFULNESS OF AZAPERONE TO REDUCE CAPTURE STRESS IN WILD UNGULATES

9:40a Michele Miller [197] FIELD ANESTHETIC TECHNIQUES FOR CAPTURE & TRANSLOCATION OF PENINSULAR PRONGHORN

10:00a BREAK

10:10a Bonnie L. Raphael [198] RESTRAINT & REGIONAL ANESTHESIA IN CHINESE ALLIGATORS

10:30a William R. Lance USE OF BUTORPHANOL, AZAPERONE, & MEDETOMIDINE AS AN EFFECTIVE SCHEDULE IV ANESTHETIC COMBINATION IN WILDLIFE

10:50a David L. Hunter A REVIEW & COMPARISON OF OPIOID OPTIONS FOR WILD UNGULATE ANESTHESIA

11:10a Panel Discussion NEW FIELD ANESTHESIA TECHNIQUES & DRUGS FOR WILDLIFE
[194] ANESTHESIA & MONITORING EQUIPMENT – GETTING IT THERE & MAKING IT WORK

R. Bruce Heath  
Colorado State University (Emeritus), Fort Collins, Colorado, USA

I have established beach anesthesia throughout the Pacific Rim, mostly for marine mammals. Extreme packing is the key step, using a variety of totes and pelican cases. California beaches can be easy however the Aleutians are stark and challenging in transportation alone. Commercial air must get you to the helicopter or research vessel which in turn is or goes to base camp. Monitoring equipment minimums are temp probes and pulse oximetry, with capnograph next. Even new ambulatory multiple channel EKG units are heavy and don’t add that much diagnostic information. Infrared equipment performs erratically in sunlight and must be shielded. Simple zip-loc bags can be utilized along with plastic tarps for equipment and patient protection. Anesthesia equipment has evolved for me down to very simple tripod mounted units that set up anywhere. Weather must be considered and planned for and patient safety must be provided for. I insist on knowledgeable anesthesia personnel and find many techs perform as well or better than we do!!?? Biologists seem to like funny cliffs, coastal winter storms, extreme boat rides and long waits for opportunity.

[195] CHEMICAL RESTRAINT OF ROOSEVELT ELK USING MEDETOMIDINE AND TELAZOL®

Robert J. Schaefer¹ and Ben J. Gonzales²  
¹California Department of Fish and Game, Redding CA., USA; ²California Department of Fish and Game, Rancho Cordova, CA., USA

During January through February 2007, we trapped and chemically immobilized 8 adult Roosevelt elk (Cervus elaphus roosevelti) using medetomidine (20 mg) and Telazol® (500 mg). Atipamezole (100 mg) IM was used to antagonize medetomidine effects. Elk weights based on girth measurements ranged from 550-610 lbs and all elk were estimated to be >3yrs old. Mean (±SD) induction and anesthesia (to administration of reversal) times were 7.25 ± 2.7 and 70 ± 13.8 min., respectively. Recovery times after reversal were 6 ± 2.7 min. Heart rates averaged 61.3 and ranged from 43-96 bpm. Mean (±SD) pulse oximeter O₂ saturation was 70.2 ± 7.2%, with all but one elk’s % O₂ saturation increasing during anesthesia. All but 2 elk had no corneal, palpebral, swallow or ear reflex during anesthesia. Physiologic parameters indicate a very deep plane of anesthesia; however, all inductions and reversals were smooth and unremarkable and all elk were alive at > 3 months. Two additional free ranging elk have been immobilized successfully using an identical protocol. With refinement of dosages and under similar conditions, this combination shows promise as a reversible, non-opiate alternative for immobilizing trapped and free ranging Roosevelt elk.
[196] ASSESSING USEFULNESS OF AZAPERONE TO REDUCE CAPTURE STRESS IN WILD UNGULATES

Gregorio Mentaberre¹, Encarna Casas-Díaz¹, Jorge R. López-Olvera², Roser Velarde¹, Ignasi Marco¹, Francesc Closa¹, Oscar Cabezón¹ Santiago Lavin¹
¹Servei d’Ecopatologia de Fauna Salvatge, Facultad de Veterinaria, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain; ²Universidad CEU Cardenal Herrera, Valencia, Spain

Obtaining biological samples to study wildlife diseases can be performed, sometimes, from game animals. Nevertheless, when working with endangered, not hunted species, the only way to get samples is capturing live animals. In these cases, we face up to capture stress derived problems, which can be fateful. Therefore, studies aimed to assess usefulness of different available tranquilizers to control and minimize damaging effects of stress are needed. We must take into account that tranquilizers do not work in the same way in all species and that some of them can cause adverse effects with worse consequences than those we want prevent. In this sense, it is important to spread the results of these studies, not only when positive, but also when negative. In this way, we would avoid repetition of studies already done by other research groups with bad results and/or tragic consequences. We captured and treated with azaperone 16 Pyrenean chamois (Rupicapra pyrenaica pyrenaica) and 11 roe deer (Capreolus capreolus). Eight Pyrenean chamois died acutely after been captured and treated. All roe deer were restrained during 3 hours without showing any problem. Further studies point azaperone out as the most probable cause of the mortality. These results advise not to use azaperone in the Pyrenean chamois, and recommend its use in the roe deer.

[197] FIELD ANESTHETIC TECHNIQUES FOR CAPTURE & TRANSLOCATION OF PENINSULAR PRONGHORN

Michele Miller¹, Don Neiffer¹, Kevin Leiske², Ramon Castellanos³, Jeff Holland⁴, and Joe Kalla¹
¹Disney’s Animal Programs, Lake Buena Vista, FL, USA; ²Living Desert, Palm Desert, CA, USA; ³Vizcaino Desert Biosphere Reserve, Baja California Sur, Mexico; ⁴Los Angeles Zoo, Los Angeles, CA, USA

The Peninsular pronghorn ((Antilocapra americana peninsularis) is one of the most endangered large mammals in North America. Only one remnant population existed in 1994, estimated at less than 200 individuals. A semi-captive breeding population was established in situ in 1998 as part of the Peninsular Pronghorn Conservation Recovery Program. With the success of the program, capture for health assessment, radio collar placement, and translocation became a necessity. Several anesthetic regimens were tested on adult males between 2003 and 2005 during initial field immobilizations. In December 2005, twenty-six pronghorn were captured using a modified boma technique and translocated individually under general anesthesia. Complete physical exams, sample collection, treatments, and measurements were accomplished prior to transport. Several induction and maintenance combinations of injectable drugs were compared using tiletamine-zolazepam, ketamine, detomidine, and propofol. Subjectively, induction using 100 mg tiletamine-zolazepam + 250 mg ketamine + 1 mg detomidine IV total dose for an adult pronghorn (approximate dosages: 2.2-2.8 mg/kg tiletamin-zolazepam, 5.5-6.9 mg/kg ketamine, 0.02-0.03 mg/kg detomidine IV), supplemented with small boluses of propofol (usually 25-50 mg IV total dose; dosages: 0.36-1.1 mg/kg IV), resulted in the best muscle relaxation, respiratory rates, and recoveries. All anesthetic procedures that included detomidine were reversed with atipamezole at a dosage of 5:1. Only two mortalities resulted: one associated with human error (hemorrhage due to venipuncture) and one due to regurgitation/aspiration. This technique can be modified for net gun capture as well as provide an alternative to dart capture in this species.
Chinese alligators (*Alligator sinensis*) are the most endangered of the 23 crocodilian extant species, with fewer than an estimated 130 left in the wild. The Wildlife Conservation Society has been involved in conservation of the species for over 50 years. As part of a long-term recovery program, WCS has been working with the China State Forestry Administration, Anhui Forestry Bureau, and the East China Normal University to repatriate captive bred alligators, from US institutions and Chinese breeding facilities, to the wild. An integral part of the releases involves radio tracking individual alligators. Radio transmitters are sutured to their tails after drilling through dorsal lateral osteoderms. In order to assure humane handling of the animals, a restraint box which allowed the animals head, legs and tail to be unrestrained was developed and used. Anesthetic regimens including epidural lidocaine, local lidocaine and local articaine were tested. The most reliable and field applicable method of regional anesthesia was found to be administration of 2% lidocaine directly under osteoderms.
Effective wildlife disease management (WDM) requires knowledge of disease and animal ecology, but also an understanding of the broader system in which WDM occurs. The Learning Lab uses systems simulation models to improve insights into the complexity of WDM, and to build capacity among managers to weigh trade-offs of resources used in WDM. Participants will balance management actions against budgetary considerations and expected effect on the disease population(s). Emphasis is on human dimensions of WDM that contribute to perceived impacts of wildlife disease and management efforts, including: tolerance thresholds for perceived disease risks to wildlife, domestic animals, and humans; social acceptability of management options; and the effect of information and communication efforts. The model portrays effects of CWD on two adjacent deer populations, as well as the effect of hunting, culling, or other population management actions. After completion of this session, participants should have greater insight into how to tackle the question, “When a wildlife disease issue arises or is anticipated, what suite of factors needs consideration and how do these play into the approaches taken?” Participants will also gain an understanding of the use of simulation models in an educational setting.
WORKSHOP – CHRONIC WASTING DISEASE

Chairs: Laurie Baeten, Mary Kay Watry
Colorado Division of Wildlife, Fort Collins, CO, USA; Rocky Mountain National Park, Estes Park, CO, USA

This workshop will provide a forum for presenting and discussing new information on chronic wasting disease (CWD), a naturally-occurring prion disease of North American deer (*Odocoileus* spp.), wapiti (*Cervus elaphus nelsoni*), and moose (*Alces alces*).

12:00p Ian K. Barker [199] A 30-YEAR RETROSPECTIVE INVESTIGATION OF CHRONIC WASTING DISEASE IN CERVIDS AT THE TORONTO ZOO

12:15p Riccardo Orusa [200] FIRST CHRONIC WASTING DISEASE EPIDEMIOSURVEILLANCE OF ROE DEER IN NORTH-WESTERN ITALY

12:30p Mary Kay Watry [201] GENETIC RELATEDNESS OF MULE DEER WITH CHRONIC WASTING DISEASE IN NORTH-CENTRAL COLORADO

12:45p Amy C. Dechen [202] MOVEMENT PATTERNS AMONG GPS-COLLARED WHITE-TAILED DEER IN CENTRAL NEW YORK: EVALUATING THE PARAMETERS THAT INFLUENCE THE SPREAD OF CHRONIC WASTING DISEASE

1:00p Candace Mathiason [203] BIOASSAY FOR INFECTIOUS PRIONS IN SALIVA, BLOOD, OR EXCRETA FROM CWD+ DEER

1:15p Terry R. Spraker [204] DETECTION OF PRP$_{CWD}$ IN RETINA TISSUES IN WHITE-TAILED DEER & ROCKY MOUNTAIN ELK WITH CWD

1:30p BREAK

1:45p Terry R. Spraker [205] DETECTION OF PRP$_{CWD}$ IN RECTAL LYMPHOID TISSUES IN POSTMORTEM & LIVE ROCKY MOUNTAIN ELK AS A POSSIBLE PRECLINICAL TEST FOR CWD

2:00p Erik E. Osnas [206] TRANSMISSION OF CHRONIC WASTING DISEASE IN WISCONSIN WHITE-TAILED DEER: IMPLICATIONS FOR CONTROL

2:15p J.L. Pilon [207] DEVELOPMENT OF A CHRONIC WASTING DISEASE VACCINE: PROGRESS & PROMISE

2:30p DISCUSSION & OTHER INFORMATION SHARING ON CHRONIC WASTING DISEASE
A 30-YEAR RETROSPECTIVE INVESTIGATION OF CHRONIC WASTING DISEASE IN CERVIDS AT THE TORONTO ZOO

Caroline Dubé, Kay G. Mehren, Ian K. Barker, Brian L. Peart, Aru Balachandran

1Canadian Food Inspection Agency, Ottawa, ON, Canada; 2Toronto Zoo, Toronto, ON, Canada; 3University of Guelph, Guelph, ON, Canada; 4Canadian Food Inspection Agency, Nepean, ON, Canada

“Spongiform encephalopathy” was diagnosed in a wasting mule deer (Odocoileus hemionus hemionus) with neurological signs that died at the Toronto Zoo in 1978. The case was retrospectively assigned to the syndrome chronic wasting disease (CWD) when it was described by Williams & Young in 1980. Subsequent to CWD becoming reportable to the Canadian Food Inspection Agency, the status of the zoo with respect to this disease became of regulatory concern. Retrospectively, records of animal movements, clinical signs, and post mortem findings were examined for all North American cervids that died 1973-2003, and clinically-suspect animals were identified. All available samples of fixed, wax-embedded lymphoid or central nervous system tissue from cervids aged >12 months of age that died at the Toronto Zoo over the period of interest were tested using prion protein immunostaining. Chronic wasting disease prion antigen was detected in 8 animals among the 105 of 7 species/subspecies tested: 7/9 clinically-suspect mule deer and 1/13 clinically-suspect black-tailed deer. The disease was probably introduced by infected mule deer obtained from Denver Zoo in 1973. Animal-to-animal contact and environmental contamination were the most likely methods of spread at the zoo. No mule deer left the Toronto Zoo site, and the last animal with confirmed CWD, a black-tailed deer, died in 1981. Historic findings and ongoing testing of cervids indicate that the Toronto Zoo collection has a very low risk of currently being infected with CWD. (Canadian Veterinary Journal 47: 1185-1193, 2006.)

FIRST CHRONIC WASTING DISEASE (CWD) EPIDEMIOSURVEILLANCE OF ROE DEER IN NORTH-WESTERN ITALY

Daniela Meloni, Riccardo Orusa, Luca Rossi, Serena Robetto, Tatiana Lo Valvo, Francesco Marucci, Luca Nocilla, Daniela Gastaldi, Elena Bozzetta

1CEA, Istituto Zooprofilattico Sperimentale del Piemonte Liguria e Valle d’Aosta, Turin, Italy; 2CERMAS, Istituto Zooprofilattico Sperimentale del Piemonte Liguria e Valle d’Aosta, Italy; 3Dipartimento di Patologia Animale, Facoltà di Medicina Veterinaria, Turin, Italy; 4Azienda Sanitaria Locale n. 5 Collegno, Turin, Italy

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy (TSE) which has been identified in captive and free-ranging cervids for >20 years in North America, where it is currently enzootic. Circulation of TSEs in European population of wild ungulates has not been documented, but the high prevalence of scrapie infection in Italy and the synchronous or alternate use of common grazing areas by domestic and wild ruminants may present the possibility of spread to the latter. Furthermore, due to the strong similarities between CWD and scrapie (clinical signs, lesions, horizontal transmission), scrapie has been proposed as a possible origin of CWD. TSE surveillance in deer has recently become necessary in Italy according to EU regulation. Data available to date are the results of voluntary plans. The aim of this study was to define maximum prevalence of TSE infection in roe deer (Capreolus capreolus) culled or found dead in North-Western Italy. Brain stems from animals (>1 year old) were collected and screened by a USDA-approved CWD rapid test (Idexx Herdchek CWD Antigen Kit) and a TSE rapid test approved according to 260/2006 EC Regulation (Bio-rad TeSeE). In case of positivity to one rapid test, the sample was submitted for immunohistochemistry and Western blotting. Preliminary results on 300 samples did not reveal the presence of TSE. Much wider sampling will verify the endemic presence of TSE among free-ranging roe deer in our study area or, alternatively (in the case of negative results), will define the expected maximum prevalence of TSE in the studied population.
[201] Genetic Relatedness of Mule Deer with Chronic Wasting Disease in North-Central Colorado

Mary Kay Watry1, 2, Lisa L. Wolfe3, Bruce Wunder1
1Colorado State University, Fort Collins, CO, USA; 2Rocky Mountain National Park, Estes Park, CO, USA; 3Colorado Division of Wildlife, Fort Collins, CO, USA

Chronic wasting disease (CWD) has been recognized in mule deer populations in north-central Colorado for over 20 years. Mechanisms of spread include animal to animal contact, exposure to carcasses and exposure to habitat that CWD positive individuals have previously used. Mule deer offspring stay with their mother for the first year and related females typically form groups that forage and migrate together. Related individuals, therefore, may have similar exposures to both CWD positive deer and environmental sources of CWD. In order to examine whether CWD positive mule deer were more closely related to one another than would be expected we examined the genotypes of 250 mule deer in north-central Colorado. Pairwise relatedness values were calculated for all individuals, all males, all females, all CWD positive individuals, CWD positive males, and CWD positive females. We then compared the values in each category to determine whether CWD positive mule deer were more closely related to each other than would be expected given the relatedness values for the larger population.

[202] Movement Patterns Among GPS-Collared White-Tailed Deer in Central New York: Evaluating the Parameters That Influence the Spread of Chronic Wasting Disease

Amy C. Dechen, David M. Williams, William F. Porter
State University of New York, Syracuse, NY, USA

Chronic wasting disease, a highly contagious, fatal prion disease found in North American cervids, was discovered in Central New York in 2005. To effectively manage CWD, as any disease, it is important to understand how the disease is transmitted from one individual to another, and how far and how fast an infected individual can spread the disease. Rate of spread is largely dependent on the social behavior and movements of deer. Our objective was to create a Risk Assessment Mapping Program (RAMP) designed to incorporate behavioral, spatial, and climatic parameters to predict direction and magnitude of disease spread from a point of first occurrence. We deployed 89 GPS collars on white-tailed deer (Odocoileus virginianus) in 2 study areas in Central New York to evaluate the behavioral parameters associated with potential disease spread at multiple spatial scales. Here, we present one component of the RAMP that evaluates the spatial distribution and habitat utilization of collared animals. Investigation of multiple core areas across sex and age classes of our study animals revealed distinct landcover preferences with respect to agricultural and forested habitat matrices, elevational gradients, and closer proximity to roads. Additionally, life history characteristics including seasonal migration, site fidelity, and dispersal were identified and quantified based on observed variation in habitat use over time. These analyses provide essential fine-scale estimates of the behavioral factors that are likely to contribute to disease spread in various landscape matrices, and when incorporated in the RAMP model, will provide managers with tools to predict isopleths of potential disease risk in the environment.
BIOASSAY FOR INFECTIOUS PRIONS IN SALIVA, BLOOD, OR EXCRETA FROM CWD+ DEER

Candace Mathiason1, Jenny Powers2, Sallie Dahmes3, David Osborn4, Karl Miller4, Robert Warren4, Gary Mason1, Sheila Hays1, Jeanette Hayes-Klug1, Davis Seelig1, Margaret Wild5, Lisa Wolfe5, Terry Spraker1, Michael Miller5, Christina Sigurdson1, Glenn Telling6, Edward Hoover1.
1Colorado State University, Fort Collins, CO, USA; 2US National Parks Service, Fort Collins, CO, USA; 3Wasco Inc., Monroe, GA, USA; 4University of Georgia, Athens, Athens GA, USA; 5Colorado Division of Wildlife, Fort Collins, CO, USA; 6University of Kentucky, Lexington, KY, USA

Chronic wasting disease (CWD) - a transmissible spongiform encephalopathy (TSE) of deer, elk and moose - is known for its facile transmission in nature. A critical concern of this TSE, as well as all prion diseases, is the potential presence of infectious prions in body fluids of infected individuals. To address this question directly we experimentally exposed cohorts of CWD-naïve hand-raised deer to saliva, blood or urine and feces from CWD positive deer. The recipient deer were monitored by serial tonsil biopsy while under strict indoor housing conditions to exclude potential adventitious prion exposure. We report the presence of infectious prions capable of transmission in saliva and blood of CWD positive deer. To our surprise we were unable to detect the aberrant form of CWD prion (PrPCWD) in recipient deer orally fed urine and feces from CWD-positive donor deer, despite multiple exposures. A second bioassay study using source materials from the first study produced identical results. The presence of infectious CWD in the saliva of CWD-positive deer helps explain the efficient transmission of this disease in nature, while its presence in blood provides a foundation for antemortem assay development.

DETECTION OF PRPCWD IN RETINA TISSUES IN WHITE-TAILED DEER & ROCKY MOUNTAIN ELK WITH CWD

Terry R. Spraker1, Thomas L. Gidlewski2, Justin J. Greenlee3, Delwin Keel4, Amir N. Hamir5, Katherine O’Rourke6
1Colorado State University, Fort Collins, CO, USA; 2US Department of Agriculture-Veterinary Services, Fort Collins, CO, USA; 3US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 4Wisconsin Diagnostic Laboratory, Madison, WI, USA; 5US Department of Agriculture-Agricultural Research Service, Ames, IA, USA; 6US Department of Agriculture-Agricultural Research Service, Pullman, WA, USA

Eyes from 80 captive white-tailed deer (Odocoileus virginianus) that were killed during a depopulation program were collected and placed in 10% neutral buffered formalin. None of these 80 white-tailed deer showed any clinical signs suggestive of CWD prior to euthanasia (gunshot); however 79% were positive for CWD by using immunohistochemical staining of the brain stem and head lymphoid tissues. Eyes from seven captive and two research elk (Cervus elaphus nelsoni) were collected and placed in Davison’s fixative. Clinical signs typical of CWD were observed in five elk (three with M/M genotype, one M/L and one L/L). The other four were non-clinical (three with genotype M/M and one L/L), but did have a previous positive rectal biopsy. The globe from each animal was trimmed and embedded in a single paraffin block and sectioned at 5 µm. Tissue sections were stained with H&E and immunostained with Anti-Prion 99 and P4 for the detection of PrP CWD. Examination of the eyes from the white-tailed deer revealed four to have detectable PrP CWD within the retina. Sections from all nine elk had PrP CWD in eight of the ten retinal layers. The most prominent features were heavy PrP CWD staining in the inner and outer plexiform layers with minimal intracytoplasmic staining in ganglia cells in the M/M and M/L elk. The two L/L elk had minimal PrP CWD staining in the plexiform layers, but relatively heavy staining in the cytoplasm of ganglia cells. An occasional ganglion cell within the ganglion cell layer contained an intracytoplasmic vacuole in the M/M elk.
Preclinical diagnostic tests for transmissible spongiform encephalopathies have been described for mule deer (Odocoileus hemionus), using biopsy tissues of palatine tonsil; for sheep, using lymphoid tissues from palatine tonsil, third eyelid and rectal mucosa. The utility of examination of the rectal mucosal lymphoid tissues for detecting chronic wasting disease (CWD) was investigated in Rocky Mountain elk (Cervus elaphus nelsoni), a species for which there is not a live-animal diagnostic test. Postmortem rectal mucosal sections were examined from 308 elk from two privately-owned herds that were depopulated. The results of the postmortem rectal mucosal sections were compared to immunohistochemical (IHC) staining of the brain stem, retropharyngeal lymph nodes and palatine tonsil. Seven elk were found positive using the brain stem (dorsal motor nucleus of the vagus nerve), retropharyngeal lymph nodes and palatine tonsil. Six of these elk were positive in postmortem rectal mucosal sections. The remaining 301 elk in which PrP\textsuperscript{CWD} was not detected in the brain stem and cranial lymphoid tissues also were free of PrP\textsuperscript{CWD} in the postmortem rectal mucosal sections. Approximately 450 live elk from 3 CWD infected farms were biopsied over a two year period. Most elk were biopsied twice over this two year period. Seven infected elk with no or minimal clinical signs were found. The use of rectal mucosal lymphoid tissues may be suitable for a live animal diagnostic test as part of an integrated management strategy to limit CWD in elk.

Chronic wasting disease (CWD) is an emerging infectious disease affecting North American deer and elk populations. The disease has currently been found in 13 states and provinces in the United States and Canada. Understanding rate of disease transmission (force of infection) and estimating prevalence within the current CWD distribution is important for the management of the disease. However, heterogeneities in disease transmission among host classes due to age, sex, or other risk factors can bias population prevalence and force of infection estimates. We use statistical models that include individual-level effects of age and sex to estimate the force of infection, population prevalence, and temporal changes in prevalence for CWD in white-tailed deer in southern Wisconsin. We found that older males were more likely to be infected than older females and that infection rates accelerated with age for males but not females. We also found that prevalence was slowly increasing during the four years since disease management began. There was also significant heterogeneity in the rate of prevalence change at smaller scales, which were similar to patterns expected from simple spatial models of an invasive disease. While the increased prevalence in males suggests that selective culling of males would decrease prevalence and density of infected animals, long-term disease dynamics are more sensitive to the future number of susceptibles; therefore, female culling is necessary.
Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy (TSE) of domestic and wild cervids in North America. To address possible prevention regimens for CWD, we have taken an active vaccination approach using prion derived-peptide sequences, a carrier protein, and an adjuvant to overcome self-tolerance. Twenty CL57/BL6 mice per group were vaccinated and boosted with 50 μg of the carrier protein-peptide conjugate; all vaccines produced a humoral immune response as measured by ELISA. After vaccination, mice were challenged with the Rocky Mountain Laboratory (RML) mouse-adapted scrapie strain. The mouse-model results demonstrated that our method could generate titers toward the prion protein peptides and most importantly, improve the life span of RML mouse adapted scrapie challenged mice. Using the insights gained from this initial mouse-model study we have recently begun evaluating a vaccine candidate in the target species, mule deer (Odocoileus hemionus).
WORKSHOP – AVIAN INFLUENZA

Chairs: Emily Jenkins¹ & Alan B. Franklin²
¹Environment Canada, Saskatoon, SK, Canada; ²US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA

This workshop will provide a forum for presenting and discussing new information on endemic and emerging strains of avian influenza (AI), including surveillance and control strategies, as well as implications for wildlife, domestic animal, and human health.

12:00p D. O. Joly [208] HIGH PATHOGENIC AVIAN INFLUENZA (H5N1) IN MONGOLIAN WILD BIRDS


12:30p Philippe Berny [210] THE AVIAN INFLUENZA CRISIS IN FRANCE IN 2006: UNEXPECTED MORTALITIES IN WILD BIRDS

12:45p Dolores Gavier-Widén [211] NATURAL HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 INFECTION IN WILD BIRDS: CHARACTERIZATION OF THE ROUTES OF VIRAL SHEDDING

1:00p E. Jane Parmley [212] CANADA’S NATIONAL WILD BIRD AVIAN INFLUENZA SURVEY: WHAT ARE WE DOING, WHAT HAVE WE FOUND, AND WHERE ARE WE GOING?


1:30p Alan B. Franklin [214] DISTRIBUTION OF AVIAN INFLUENZA IN THE UNITED STATES BASED ON AVIAN FECAL SAMPLES UNDER THE WILD BIRD AVIAN INFLUENZA EARLY DETECTION SYSTEM

1:45p BREAK

2:00p Justin D. Brown [215] SUSCEPTIBILITY OF WOOD DUCKS TO H5N1 HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS

2:15p Thijs Kuiken [216] HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS (H5N1) DOES NOT TARGET INTESTINAL EPITHELIUM OF WILD DUCKS

2:30p Richard D. Slemons [217] TEMPORAL & SPATIAL DYNAMICS OF AVIAN INFLUENZA VIRUS INFECTIONS IN MIGRANT & RESIDENT FREE-FLYING WILD DUCKS

2:45p DISCUSSION & OTHER INFORMATION SHARING ON AVIAN INFLUENZA
[208] HIGH PATHOGENIC AVIAN INFLUENZA (H5N1) IN MONGOLIAN WILD BIRDS

Martin Gilbert, D. O. Joly, W. B. Karesh
Wildlife Conservation Society, Bronx, NY, USA

Outbreaks of H5N1 high pathogenicity avian influenza (HPAI) have occurred in poultry over the past 10 years in Southeast Asia and subsequently spread throughout Eurasia and North and West Africa by 2005–2007. The mechanism of geographic spread was unknown. We identified western Mongolia as an ideal region for testing the hypothesis that wild birds could introduce H5N1 HPAI into a new area as there are very few domestic poultry in that region, and thus presence of HPAI would most likely be from introduction by wild birds during migration. Faecal samples were obtained from 862 live birds of five species across nine geographically isolated sites. During the survey, a bird die-off (n = 116, 9 species) was reported at Erhel Lake. During a subsequent investigation we isolated HPAI H5N1 from one of four carcasses suitable for necropsy (a whooper swan); in addition, the Mongolian government reported isolates from three whooper swans and one bar-headed goose. Isolation of H5N1 in wild birds in an area where there were no domestic birds strongly suggests that at least one species of migratory bird can carry the virus over long distances and introduce it to new waterfowl populations; this species remains unidentified. This is the strongest evidence to date that migratory birds cannot be excluded as a mechanism for the subsequent spread of HPAI H5N1 throughout Eurasia and into Africa during 2005–2007 in addition to other known routes. Given uncertainty about the role of wild birds in the spread of HPAI H5N1, we recommend that biosecurity surrounding domestic bird production is the most effective way to reduce spillover to and spillback from wild bird populations.

[209] GAINING INSIGHT INTO THE ROLE WILD BIRDS PLAY IN THE SPREAD OF HPAI H5N1 VIRUS THROUGH PARTNERSHIPS: DID HITCHCOCK’S THE BIRDS HAVE IT RIGHT?

Scott H. Newman1,2, Juan Lubroth2, William B. Karesh1, Martin Gilbert1, Nicolas Gaidet3, Ward Hagemeijer1, Tim Dodman4, John Y. Takekawa3, Diann Prosser5, Stephanie Desvaux3, Damien Joly1, Marcela Uhart1, Kristine Smith1, Sergei Khomenko4, Julien Cappelle3, Baz Hughes6, Ruth Cromie6, and Richard Hearn6

1Wildlife Conservation Society, Bronx, NY, USA; 2Food & Agriculture Organization of the United Nations, Rome, Italy; 3CIRAD, Montpellier, France; 4Wetlands International, Wageningen, The Netherlands; 5US Geological Survey, Vallejo, CA, USA, and Beltsville, MD, USA; 6Wildfowl & Wetlands Trust, Slimbridge, Gloucestershire, United Kingdom

The Food & Agriculture Organization of the United Nations, through its Emergency Prevention System for transboundary animal diseases has been involved in prevention, control and eradication of livestock and poultry diseases since 1994. With the large number of wild bird mortalities and overwhelming geographical expansion of H5N1 highly pathogenic avian influenza (HPAI) in 2003, FAO extended this program to address the role that wild birds may play in the epidemiology and spread of the H5N1 strain. Activities included; 1) wildlife disease, avian ecology, and capture technique training; 2) global wild bird surveillance; 3) disease ecology and migration studies; and 4) information dissemination through meetings, publications, and web-based mechanisms. Collaborations with national governments, CIRAD, WI, WCS, WWT, and local NGOs have enabled wild bird surveillance to be conducted on thousands of wild birds in wetlands, markets, and near outbreak farms in Africa, South America, Eastern Europe, and Asia. Additional partnerships with USGS have facilitated migration and disease ecology studies with satellite telemetry based in Mongolia, China, Malawi, Mali, and Nigeria. An important element of all activities has been training through partnerships in the field and through specific courses, contributing to enhanced global capacity for future surveillance. International meetings and workshops provide further opportunity for insight through information exchange. Since 2005, FAO, traditionally an agriculture-based organization, has contributed over $2.5 million towards wildlife activities and restructured its animal disease program in an effort to improve understanding of disease ecology and transmission between wildlife and livestock, clearly an important aspect of many transboundary diseases.
[210] THE AVIAN INFLUENZA CRISIS IN FRANCE IN 2006: UNEXPECTED MORTALITIES IN WILD BIRDS

Philippe Berny
Université de Lyon, Marcy l’étoile, France

During the fall of 2005 and early winter 2006, avian influenza (AI) reached the EU, and some cases were detected in France (Ain). As a member of the wildlife disease surveillance system, the laboratory received, as usual, suspected poisoning cases. A retrospective survey of all poisoning cases detected in France during the past 5 years clearly point out a « strange » epidemics of poisoning in birds in 2006. In the French system, wild animals are necropsied by local vet laboratories and only when poisoning is suspected are samples submitted to the tox laboratory, together with information on the circumstances of exposure and, whenever possible, the products suspected. This presentation focuses on the differences observed between 2006 and the previous years of surveillance. Unusually frequent cases of poisoning were recorded in mallards (Anas platyrhynchos) and pigeons (Columba livia and Columba palumbus) with products like alpha-chloralose or insecticides. The distribution of cases was not strictly related to the areas with AI. Most cases occurred within a few days or weeks of the AI case in February. Circumstances of exposure included illicit poisoning and misuse of chemicals. This epidemic ended as it had started: abruptly. Considering the media impact of this AI crisis, it is hypothesized that many people tried to kill birds considered as a threat.

[211] NATURAL HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 INFECTION IN WILD BIRDS: CHARACTERIZATION OF THE ROUTES OF VIRAL SHEDDING

Caroline Bröjer, Erik Ågren, Henrik Uhlhorn, Jonas Malmsten, Karin Bernodt, Torsten Mörner, Dolores Gavier-Widén
Department of Wildlife, Fish and Environment. National Veterinary Institute (SVA), Uppsala, Sweden

Highly pathogenic avian influenza (HPAI)-H5N1 is an infectious systemic viral disease that results in high morbidity and mortality in poultry, affects a wide range of wild bird species and is also a potential zoonosis. An outbreak of HPAI-H5N1 occurred in wild birds in Sweden in 2006. The affected species included ducks, geese, swans, gulls and raptors. Encephalitis and pancreatitis were the most frequently observed lesions, followed by pneumonia. Little information is available on the pathobiology of natural infection, the tissue distribution of virus and the routes of viral shedding in wild birds. Initially, the diagnostic testing of dead birds at SVA was based on PCR analysis of oropharyngeal and cloacal swabs, and was shortly after replaced by testing of tracheal swabs. PCR of tracheal swabs gave false negative results in a significant proportion of the affected birds, mostly those with encephalitic forms of disease. The virus was subsequently demonstrated in these cases by PCR, viral isolation and immunohistochemistry of brain tissue. The aim of the present investigation was to obtain more clear information on the viral tissue-targeting and replication sites and its relation to shedding by the natural routes. The study utilized immunohistochemistry with emphasis on the mucosae of the respiratory (nasal, tracheal, bronchial), digestive (intestine at various levels) and urinary tracts. Variability related to the species of bird, organ involvement, severity and estimated time-course of the disease was observed. The diagnostic and epidemiological implications of the described natural viral shedding are discussed.
Beginning in the summer of 2005, a survey was undertaken to document the presence and distribution of influenza A viruses in Canadian wild birds. That year, cloacal swabs were collected from live, healthy ducks from across Canada. In 2006, the survey was greatly expanded to include a wider variety of wild bird species across more of the country. In addition, the method of sample collection was changed such that both a cloacal and an oropharyngeal swab were obtained from each bird and placed together in a single vial. A total of 4405 samples were collected during the first year of the survey and 4268 samples were successfully linked with field data. Of these, 37% (1572/4268) tested positive for the presence of influenza A virus by RRT-PCR. In 2006, samples were collected from 10411 birds and 9986 were tested for the presence of avian influenza by RRT-PCR. Overall, 33% (1279/3842) of live wild ducks, 3% (152/5044) of other live waterfowl and shorebird species, and 16% (176/1101) of hunter-killed geese tested positive. All virus subtypes detected to date have been of low pathogenicity and of North American lineage. As well as the live bird survey, wild birds found dead that are submitted to a primary diagnostic lab for post-mortem examination are also tested for avian influenza. The dead bird survey was initiated late in 2005 and is ongoing. To date, 2863 birds have been submitted and tested for avian influenza by RRT-PCR; 4% (105/2863) have tested positive.
[214] DISTRIBUTION OF AVIAN INFLUENZA IN THE UNITED STATES BASED ON AVIAN FECAL SAMPLES UNDER THE WILD BIRD AVIAN INFLUENZA EARLY DETECTION SYSTEM

Alan B. Franklin1, Robert G. Mclean1, Jeffrey S. Hall1, Heather Sullivan1, Kaci VanDalen1, Matthew L. Farnsworth1,2, Susan A. Shriner1, Ginger R. Young1, Kevin T. Bentler1, Paul T. Oesterle1, Jenny S. Carlson1, Kacy R. Cobble1, Stacey A. Elmore1, James C. Carlson1, Nicole L. Mooers1, Sean Hauser1, Theodore D. Anderson1, Katheryn P. Huyvaert1,3, Ryan S. Miller2, Thomas J. DeLiberto1, Seth Swafford1

1US Department of Agriculture-Wildlife Services, Fort Collins, CO, USA; 2US Department of Agriculture-Veterinary Services, Fort Collins, CO, USA; 3Colorado State University, Fort Collins, CO, USA

As part of the U.S. Interagency Strategic Plan for an Early Detection System for Highly Pathogenic H5N1 Avian Influenza in Wild Migratory Birds, we analyzed 50,184 fecal samples from multiple avian species collected in 2006 from waterbird habitat in all 50 states in the U.S. and Pacific Islands. An average of 1,004 samples were collected per state (range = 114 – 1,505). Samples were pooled (up to 5 samples/pool) in the laboratory and screened for avian influenza (AI) by RT-PCR. We tested a total of 10,259 pools, which were considered the unit of analysis. Overall, AI was detected in 4.1% of the sample pools and H5/H7 subtypes were detected in 0.21% of the sample pools. We used logistic regression in an information-theoretic model selection approach to examine factors affecting prevalence patterns of sample pools in the conterminous 48 states in the U.S. Prevalence in sample pools varied by state (range = 0.0 – 10.5% for AI and 0.0 – 1.5% for H5/H7 subtypes) and by migratory waterfowl flyway. The Central flyway had the highest prevalence of AI in sample pools (5.9%), followed by the Pacific (4.8%), Mississippi (3.7%), and the Atlantic (3.0%). We also analyzed patterns in AI prevalence in sample pools based on species composition at sampled sites, time when samples were taken during migratory movements and band recovery locations of waterfowl from potential sources of origin. These analyses will help to elucidate preliminary patterns for further analysis of potential routes of first introduction of highly-pathogenic Asian H5N1 into the U.S.

[215] SUSCEPTIBILITY OF WOOD DUCKS TO H5N1 HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS

Justin D. Brown1, David E. Swayne2, David E. Stallknecht1

1Southeastern Cooperative Wildlife Disease Study-University of Georgia, Athens, GA, USA; 2US Department of Agriculture-Agricultural Research Service, Athens, GA, USA

Since 2002, H5N1 highly pathogenic avian influenza (HPAI) viruses have caused mortality in numerous species of wild birds. Although these infections document the susceptibility of wild birds to H5N1 HPAI viruses and the spillover of these viruses from infected domestic birds to wild birds, it is unknown if these viruses can persist in free-living avian populations. Wood ducks (Aix sponsa) are highly susceptible to infection with H5N1 HPAI viruses. In order to quantify this susceptibility and further evaluate the likelihood of H5N1 HPAI viral maintenance in a wild bird population, we determined the minimal concentration of virus required to produce infection in wood ducks. To accomplish this, 25 wood ducks were inoculated intranasally with decreasing concentrations of a H5N1 HPAI virus. The minimal infectious dose and lethal dose of H5N1 HPAI virus in wood ducks were very low (10^{0.75} and 10^{1.35} 50% mean tissue culture infectious dose (TCID_{50})/ml, respectively) and less than that of chickens (10^{2.80} and 10^{2.80} TCID_{50}/ml). These results confirm that wood ducks are highly susceptible to infection with H5N1 HPAI virus. The data from this study, combined with what is known experimentally about H5N1 HPAI virus infection in wood ducks and viral persistence in aquatic environments, suggest that the wood duck would represent a sensitive indicator species for H5N1 HPAI. Results also suggest that the potential for decreased transmission efficiency associated with reduced viral shedding (especially from the cloaca) and a loss of environmental fitness (in water), may be offset by the ability of this virus to be transmitted through a very low infectious dose.
HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS (H5N1) DOES NOT TARGET INTESTINAL EPITHELIUM OF WILD DUCKS

Juthatip Keawcharoen, Debby van Riel, Theo M. Bestebroer, Geert van Amerongen, Rob van Lavieren, Albert D.M.E. Osterhaus, Ron A.M. Fouchier, Thijs Kuiken
Institute of Virology, Erasmus Medical Centre, Rotterdam, The Netherlands

Low pathogenic avian influenza viruses (LPAIV) replicate mainly in the intestinal epithelium of ducks. This corresponds with the presence on the intestinal epithelium of sialic acid-alpha-2,3-galactose terminated sialosaccharides, the preferred receptor of avian influenza viruses. Although free-living ducks may play a role in the epidemiology of highly pathogenic avian influenza virus (HPAIV) infection of the subtype H5N1, its pathogenesis in these species is poorly understood. Therefore, we inoculated HPAIV A/turkey/Turkey/1/05 (H5N1) into the trachea and esophagus of eight individuals of each of six duck species: mallard (Anas platyrhynchos), common teal (Anas crecca), Eurasian wigeon (Anas penelope), gadwall (Anas strepera), Eurasian pochard (Aythya ferina), and tufted duck (Aythya fuligula). Pharyngeal and cloacal samples for virological examination were collected daily, and four individuals from each species were necropsied at four days after inoculation for pathological and virological examination. More virus was excreted from the pharynx than from the cloaca in all species. Based on virus isolation and immunohistochemistry, pharyngeally excreted virus probably originated from air sac and lung, while cloacally excreted virus probably originated from pancreas and liver. Gadwalls, plochars, and tufted ducks showed evidence of HPAIV (H5N1) replication in multiple tissues, but not in intestinal epithelium. The observed differences in tissue tropism between HPAIV (H5N1) and LPAIV in wild ducks may largely explain the disparity in pattern of virus excretion.

TEMPORAL & SPATIAL DYNAMICS OF AVIAN INFLUENZA VIRUS INFECTIONS IN MIGRANT & RESIDENT FREE-FLYING WILD DUCKS

Richard D. Slemons¹, Jacqueline M. Nolting¹, Vernon D. Stotts², H. Lloyd Alexander³, Roy Kroll⁴, Mark Shieldcastle⁵, Dennis A. Senne⁶, Max Brugh⁷
¹Ohio State University, Columbus, OH, USA; ²Easton, MD, USA; ³Camden, DE, USA; ⁴Port Clinton, OH, USA; ⁵Ohio Division of Natural Resources, Crane Creek Experiment Station, OH, USA; ⁶US Department of Agriculture-National Veterinary Services Laboratory, Ames, IA, USA; ⁷Athens, GA

Over the last 25 years recommendations from numerous type A influenza virus symposia have stressed the need to further define the natural history of type A influenza viruses in wild birds. The focus of this presentation is to define the local dynamics of AIV infections in free-flying waterfowl populations in an effort to better interpret larger data sets. In 2005 and 2006, two pairs of study sites were established. Each pair of study sites was located in a different state and the two sites of each pair were located approximately 18 miles from each other. Resident, wild mallards were the primary populations at one set of sites and migratory, dabbling ducks were the primary populations at the other paired sites. Virus isolation attempts in embryonating-chicken-eggs were conducted on either cloacal swabs or very fresh fecal samples. Sequential sampling was conducted at each site over 2-3 months each year. The frequency of AIV recovery and distribution of HA-NA combinations recovered varied markedly by time, by state, by paired sites and even by individual sites. Consolidating the data from this project by year and by state provides user friendly and easy to present information but, at the same time obscured the dynamic nature of the type A influenza virus infections in these populations. This local dynamics must be taken into consideration when developing policy and drawing conclusions from AIV surveillance data in wild birds.
WORKSHOP – WILDLIFE DISEASE INFORMATICS
Organized by the American Association of Wildlife Veterinarians

Chair: F. Joshua Dein
NBII Wildlife Disease Information Node, Madison, WI, USA

There can be many definitions for the term, Informatics, but the concept that will be used here is a discipline that is an integration of subject knowledge, information management, and information technology. Informaticians may ask the questions, what data and information are needed to answer scientific questions, as well as how might these best be collected, stored, retrieved and displayed? Medical informatics is one of the best known sub-fields, with electronic medical records and management of digital diagnostic and monitoring data as examples of common applications. Logically, veterinary informatics would be a further sub-class, with wildlife disease informatics included here. This workshop will explore the foundations of a few important components in this area, such as the development of surveillance systems, and the communication and exchange of information within the wildlife health community.

[218] THE CASE FOR SHARING CRITICAL WILDLIFE HEALTH DATA ON A GLOBAL SCALE

Damien O. Joly, William B. Karesh, Robert A. Cook
Wildlife Conservation Society, Bronx, NY, USA

There is great need to share wildlife disease data to aid in the protection of wildlife, domestic animal, and human health. There are no accepted international standards for identifying and communicating information on diseases of any type of wild animals, even if the infectious disease is a known threat to livestock or human health. Humanity is of course concerned about the health of people and by extension the health of its food supply, and has invested tremendous resources to combat disease threats over time. Only recently has there been a growing awareness in the livestock and public health sectors and by extension, the public policy community, that the health of wildlife plays a critical role in a holistic approach to controlling disease threats. Sharing data allows integrated analyses and provides data to be applied to problems other than that originally intended at collection. Lessons from other disciplines, including software development and genetics have taught us that free access to the intellectual products of others leads to rapid advances in any particular discipline. However, achieving a “wildlife disease data commons” is difficult, with many obstacles to be overcome. We discuss some of these difficulties, including perceived loss of control, uncertainty about “duplicate publication”, data integration, and the technology associated with sharing data. We discuss possible solutions to these problems, and outline some critical aspects of a data sharing system.
WORKSHOP – PLAGUE ECOLOGY

Chairs: Tonie E. Rocke, Jack Cully
National Wildlife Health Center, Madison, WI, USA; Kansas Cooperative Fish & Wildlife Research Unit-Kansas State University, Manhattan, KS, USA

This workshop will provide a forum for presenting and discussing new information on plague in North American and other ecosystems, including ecology, impacts on species and ecosystems, and surveillance and control strategies.

[219] REAL-TIME MONITORING OF PLAGUE INFECTIONS IN RODENT HOSTS

Tonie E. Rocke¹, Sandra Dawe¹,², Jorge Osorio²
¹National Wildlife Health Center, Madison, WI, USA; ²University of Wisconsin, Madison, WI, USA

Traditional approaches to track disease progression typically require large numbers of animals and the time-consuming tasks associated with quantifying pathogen load over time in various tissues and organs ex vivo. As an alternative technique, bioluminescent imaging may be used to determine the kinetics of disease progression in vivo, reducing the number of animals required and the animal-to-animal variability. In order to test hypotheses regarding the pathogenesis of plague in both laboratory and natural rodent hosts, we engineered *Yersinia pestis* strain CO92 to express the bacterial luciferase operon, *Photorhabdus luminescens luxCDABE*. The resulting lux*+* *Y. pestis* was confirmed to be as virulent as its parent strain, and standard protocols were then established for monitoring and quantifying bioluminescent *Y. pestis* using a photon-counting, intensified charge-coupled device camera. We determined the spatiotemporal distribution of infection in mice exposed to the organism via different routes of inoculation, establishing models for bubonic, septicemic and pneumonic plague. We also confirmed that the levels of detectable bioluminescence correlated to bacterial load in specific tissues within the infected host. Similar studies will be completed with natural rodent hosts, such as ground squirrels and prairie dogs. With these baseline studies completed, the role of certain virulence genes in the pathogenesis of disease can be studied, as well as the effectiveness of potential disease interventions, such as vaccines and other therapeutic agents.

[220] PLAGUE IN MOUNTAIN LIONS FROM THE GREATER YELLOWSTONE AREA OF WYOMING

Cynthia Tate¹, Todd Cornish², Rosemary Jaffe³, Toni Ruth⁴, Ken Mills², Amy Boerger-Fields², Brian Parrie⁴, Terry Kreeger¹, Howard Quigley⁵
¹Wyoming Game & Fish Department, Laramie, WY, USA; ²Wyoming State Veterinary Laboratory, Laramie, WY, USA; ³Montana Fish, Wildlife & Parks, Bozeman, MT, USA; ⁴Wildlife Conservation Society, Gardiner, MT, USA; ⁵Beringia South, Kelly, WY, USA

Plague (*Yersinia pestis* infection) was diagnosed in four radio-collared mountain lions (*Puma concolor*) that died in the summer and fall of 2005 and 2006 in the Greater Yellowstone Area. The four cases, submitted to the Wyoming State Veterinary Diagnostic Laboratory, included a female lion and one of her cubs. A second cub was found alive and never developed clinical signs of disease, although it had a plague titer of 1:512 via fluorescent antibody test. The other two cases were a 10-year-old female pregnant with near-term triplets, and a young adult male. The three adult lions were in fair to good nutritional condition, suggesting that the course of disease was rapid. Gross lesions included pneumonia in all cases with lung available, and cervical lymphadenitis in all cases with lymph nodes available. Microscopically affected mountain lions had corresponding supplicative to necrotizing bronchointerstitial pneumonia and/or supplicative and necrotizing lymphadenitis with abundant intralesion coccobacilli. The diagnosis was confirmed in all animals by bacterial culture and identification and either by fluorescent antibody test or immunohistochemistry for *Y. pestis*. These four cases contradict the general impression that mountain lions are relatively resistant to plague, and suggest that plague may be a more common cause of mortality in this species than previously recognized. These cases also highlight the need for appropriate personal hygiene measures for wildlife professionals and hunters when handling mountain lion carcasses in the field or laboratory.
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WDA Buildings of Interest (In grey on map)
Please note: Sweet, Hobbs, & Bilheimer/Dodge are rooms in the Walter G. Reusch Auditorium