

ABSTRACTS

[1] WILDLIFE AND PUBLIC HEALTH IN THE ARCTIC

Eric Dewailly

Centre de Recherche du CHUQ, Université Laval et Institut National de Santé Publique du Québec, Québec, Québec, Canada

Presenting author: Dewailly, Eric (Eric.Dewailly@crchul.ulaval.ca)

Until recently, the Inuit could be considered both geographically and genetically isolated. With a traditional diet rich in lipids and proteins, Inuit are probably the most important existing human group with a typical hunter-gatherer diet. Living exclusively from the land and the sea can provide all necessary nutrients. Even today, Inuit still have the highest blood concentration of omega-3 fatty acids and selenium which is probably responsible for their relative protection against cancer and heart disease. But wildlife is also a source of zoonoses and seroprevalence studies in Nunavik show, for example, a north-south trend for toxoplasmosis which has a probable marine origin. Other important zoonoses include trichinellosis and indirectly botulism. Industrial development has led to long range transport of contaminants such as persistent organic pollutants (POPs) and mercury in the Arctic. Today, Inuit are among the highest exposed humans to these toxic compounds. Health effects on the developing child and in adults have been demonstrated. Hunting was also the source of high lead exposure and isotope studies in the late 90's provided support for a restriction in use of lead ammunition in Nunavik which was followed by a drastic decrease in newborn lead exposure. For more than 10 years, the Nunavik Nutrition and Health Committee is a central forum including Inuit representatives, veterinarians, nutritionists and medical doctors. It has been an exceptional tool to inform populations and take action about risks and benefits related to the use of wildlife resources.



[2] THE NUNAVIK TRICHINELLOSIS PREVENTION PROGRAM: COMBINING SCIENCE WITH TRADITIONAL INUIT PRACTICES

Manon Simard,¹ Sylvain Larrat,² Stéphane Lair,² Denise Bélanger,³ and Jean-François Proulx⁴

¹Nunavik Research Centre, Makivik Corporation, Kuujuaq, Québec, Canada; ²Centre québécois sur la santé des animaux sauvages / Canadian Cooperative Wildlife Health Center, Faculté de médecine vétérinaire, Université de Montréal, St. Hyacinthe, Québec, Canada; ³International Veterinary Group, Faculté de médecine vétérinaire, Université de Montréal, St. Hyacinthe, Québec, Canada; ⁴Department of Public Health, Nunavik Regional Board of Health and Social Services, Kuujuaq, Québec, Canada.

Presenting author: Simard, Manon (m_simard@makivik.org)

The Nunavik Trichinellosis Prevention Program (NTPP) is an initiative combining modern science with lay knowledge on access to safe local food. For Inuit, eating walrus raw or fermented (igunaq) is a delicacy. During the mid-80's, numerous outbreaks of trichinellosis in Nunavik were documented by public health authorities. Recommendations were to have walrus meat tested for *Trichinella nativa* at the nursing station before consumption. Low level compliance and lack of sensitivity of direct trichinoscopy forced authorities to send samples for testing to a southern laboratory. Despite all efforts, receipt of results was lengthy. Walrus harvest dropped significantly and access to high quality country food became a concern. In 1992, a local pilot project on trichinellosis prevention started in Salluit, after local and regional stakeholders decided to develop a plan to remedy the situation. Integration of the 14 Nunavik communities in the NTPP occurred in 1996. This presentation will describe the evolution of the screening test to its present state, implementation and evaluation of the program, update on human and walrus passive surveillance data, other scientific information collected between 1992 and 2009, and a discussion of the influence of scientific results on harvest practices. Success of this program led to multiple benefits... It directly affected the walrus hunt, and contributed to its economic, social and cultural renewal. The early identification of regional hosts of *T. nativa*, development of a simple, inexpensive and rapid diagnostic test and adapted communication strategies all contributed to the success of this ongoing public health intervention.



[3] THE CANADIAN SEAL HUNT

Lena Measures

Fisheries and Oceans Canada, Maurice Lamontagne Institute, Mont-Joli, Québec, Canada.

Presenting author: Measures, Lena (Lena.Measures@dfo-mpo.gc.ca)

In Canada seals are hunted for subsistence and commercial purposes. Subsistence hunts are primarily for ringed seals which are an important source of food and income for northern aboriginal peoples. In Atlantic Canada there is a commercial seal hunt on harp, hooded and grey seals, whose populations are estimated at 9 million, 600,000 and 330,000, respectively. Current Marine Mammal Regulations do not allow hunting of harbour seals in Atlantic Canada. The Atlantic seal hunt is directed primarily at harp seals and is the largest marine mammal hunt in the world. Of those harvested annually, greater than 95% are young-of-the-year (it is illegal to kill whitecoats). Seal products consist of oil, fur and meat for domestic and international consumption. Controversy has surrounded the harp seal hunt for many years. A Canadian Veterinary Medical Association report indicated that 98% of seals harvested during the hunt were killed in an acceptably humane manner. An independent veterinarians' working group on the Canadian harp seal hunt in 2005 recommended changes to improve management of the harvest. The most significant pathogen of Canadian seals is phocine distemper virus (PDV) which is enzootic in the harp seal population and considered a reservoir for PDV. No epizootic due to PDV, as reported in Europe, has been documented in Canadian seals. Poor ice conditions cause increased mortality of pups. Seal hunting poses various occupational hazards including zoonotic diseases such as seal finger, sealpox, *Brucella* sp., *Leptospira interrogans*, *Giardia duodenalis*, *Toxoplasma gondii* and Vesivirus.



[4] NON-CONSUMPTIVE USE OF WILDLIFE IN A MARINE PROTECTED AREA CONTEXT

Nadia Ménard

Parks Canada, Saguenay-St. Lawrence Marine Park, Tadoussac, Québec, Canada.

Presenting author: Ménard, Nadia (nadia.menard@pc.gc.ca)

The establishment in 1998 of the Saguenay-St. Lawrence Marine Park, one of Canada's first marine protected areas, is the result of twenty years of studies, public support and negotiations. Its establishment is a significant event in the field of marine conservation in Canada. Ensuring sustainability, preserving biodiversity and ecological processes, enhancing awareness and visitor experiences as well as increasing knowledge are all ongoing goals of the Marine Park. The area covered by the Marine Park is recognized for many reasons, namely for exceptional whale-watching, an isolated population of St. Lawrence Estuary beluga as well as the majestic Saguenay Fjord. Seabirds, seals, and whales are the most conspicuous wildlife, and their great numbers are an indication of the exceptional conditions in this area. The estuarine ecosystems found here are very rich biologically but are also under many types of pressure. Life abounds here, yet, as in other parts of the Great Lakes — St. Lawrence watershed, human activities exert pressure such as pollution, coastal development, intensive marine traffic, and fishing. The multiplicity of activities occurring in such an exceptional area makes the Marine Park a valuable case study for how to address a variety of issues in a marine protected area context. This presentation will focus on issues and innovative solutions put in place with respect to managing non-consumptive use of marine wildlife in the Marine Park, namely, wildlife viewing.



[5] POLAR BEARS IN A CHANGING ARCTIC

Andrew E. Derocher

Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada.

Presenting author: Derocher, Andrew E. (derocher@ualberta.ca)

Polar bears (*Ursus maritimus*) are the poster species for global warming yet the challenges facing this species go far beyond this issue. As the Arctic's top marine predator, polar bears are also vulnerable to a variety of effects including human-caused mortality, industrial development, novel pathogens and parasites, and persistent organic pollutants. Throughout much of their range, polar bear harvest plays an important social, cultural, and economic role in northern communities. While harvest is usually well managed, changing sea ice conditions are increasing human-bear interactions that often result in additional polar bear mortality. Industrial developments in polar bear habitat and increased marine traffic have been identified as important risk factors as the Arctic changes. The diversity of diseases and parasites is limited in polar bears compared to their terrestrial ancestors but the risk of new vectors and novel infections increases as temperate species expand northward. Polar bears have some of the highest levels of persistent organic pollutants in the Arctic. While individual effects are partially understood, the impact pollution has on reproduction and survival remains unclear. The interactions of increased nutritional stress caused by habitat loss, diseases and parasites, pollution and other stressors are poorly understood. Models of habitat and energetics, however, predict that polar bears will decline markedly in the coming decades. Monitoring of polar bears in a changing Arctic is currently inadequate to understand the effects of rapid change and national and international research and management is needed to coordinate an effective multi-disciplinary early detection and response system.



[6] WILDLIFE DISEASE: A PUBLIC HEALTH PRIORITY IN A CHANGING WORLD

Nick H. Ogden

Centre for Food-borne, Environmental & Zoonotic Infectious Diseases, Public Health Agency of Canada, Ottawa, Ontario, Canada.

Presenting author: Ogden, Nick H. (Nicholas_Ogden@phac-aspc.gc.ca)

Not so long ago infectious diseases were considered by ecologists as the unimportant 'coup de grâce' for wildlife whose survival has been affected by nutritional and other stressors. It is now recognised that infectious diseases are a key component of wildlife ecology and as important in regulating wildlife populations as competition, resource supply and predators. Following HIV, SARS, West Nile virus and avian influenza, it is also now recognised that zoonotic wildlife diseases are a key source of emerging infectious diseases of global public health significance. Furthermore, the opportunities for emergence and spread of zoonoses may be increasing due to coincident global changes in climate, land use and human population growth. In this presentation I review the risks to public health from wildlife diseases, how global changes may be driving their emergence and re-emergence as risks to public health by affecting their ecology. I also review, using local and global examples, how understanding the ecology of these diseases may assist us to predict, respond to and manage them, via multidisciplinary approaches and modelling tools.



[7] INTERACTIONS BETWEEN PARASITES AND IMPLICATIONS FOR HOST-PARASITE DYNAMICS

Sandra Telfer

Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen, UK.

Presenting author: Telfer, Sandra (s.telfer@abdn.ac.uk)

Although studies usually focus on single parasite systems, most individuals in wild populations probably spend the majority of their lives coinfecting with more than one parasite species. Parasites can interact directly by competing for resources or indirectly via the host immune system. Antagonistic interaction may arise due to resource shortages or cross-effective immune responses, whilst interactions beneficial to one or both parasites can result from down-regulation of all or part of the immune system. I will use a 6 year time-series from individually tagged field voles (*Microtus agrestis*) to examine interactions in a microparasite community. Analyses demonstrate strong effects of co-infection on host susceptibility, with large positive and negative effects. Indeed, effects are typically of greater magnitude, and explain more variation in infection risk, than effects more commonly considered in disease studies, such as age, sex or season. Interactions between parasite species also affect infection length. Such findings highlight that parasite interactions may be critical to host-pathogen dynamics, with potential effects on disease transmission and spread, as well as host fitness and demographic rates.



[8] EPIDEMIOLOGY AND DISTRIBUTION OF BOVINE TB IN ELK AND WHITE-TAILED DEER IN THE RIDING MOUNTAIN NATIONAL PARK REGION

Todd K. Shury,¹ and Doug Bergeson²

¹Parks Canada Agency, Saskatoon, Saskatchewan, Canada; ²Parks Canada Agency, Riding Mtn. National Park, Manitoba, Canada.

Presenting author: Shury, Todd (todd.shury@pc.gc.ca)

Surveillance for *Mycobacterium bovis* in free-ranging elk (*Cervus elaphus canadensis*) and white-tailed deer (*Odocoileus virginianus*) from south-western Manitoba was carried out from 1997 to 2010 to describe lesions, epidemiology and geographic distribution of tuberculosis (TB). Tissues were cultured from elk and deer killed by hunters, culled for management, removed as part of a blood-testing program or found opportunistically. Period prevalence in elk was approximately six times higher than deer, suggesting a significantly larger reservoir role for elk compared to deer. Prevalence was consistently higher in elk compared to deer in an area where TB has consistently been found since 1997, called the western control zone. Since 2003 there has been a decline in prevalence which is likely due to a combination of management factors. Older age classes of deer were much more likely to be culture positive compared to the youngest age classes for both deer and elk. Elk and deer sampled from the western control zone were 21 ($\chi^2 = 67.7$, $p < 0.001$) and 49 ($\chi^2 = 56.4$, $p < 0.001$) times as likely to be culture positive, respectively, compared to elk and deer tested outside this zone. Culture positive elk and white-tailed deer were much more likely to be found through blood testing, opportunistic surveillance and culling compared to hunting. No non-lesioned, culture-positive elk were detected in this study, unlike previous studies in red deer from other countries. While progress in managing *M. bovis* in these cervid populations is being realized, many challenges to eradicating the disease remain.



[9] ANTHRAX IN WOOD BISON: WHAT WE KNOW, WHAT WE DON'T KNOW, AND IMPLICATIONS FOR MANAGEMENT OF A THREATENED SPECIES

Brett Elkin,¹ Terry Armstrong,² and Amanda Salb³

¹Environment and Natural Resources, Government of the Northwest Territories, Yellowknife, Northwest Territories, Canada; ²Environment and Natural Resources, Government of the Northwest Territories, Fort Smith, Northwest Territories, Canada; ³University of Calgary, Calgary, Alberta, Canada.

Presenting author: Elkin, Brett (brett_elkin@gov.nt.ca)

Anthrax is endemic in wood bison (*Bison bison athabasca*) in northern Canada, and outbreaks occurred in three separate herds in 2010. First documented in 1962, anthrax involving a unique bison strain of *Bacillus anthracis* has caused outbreaks in Wood Buffalo National Park, the Slave River Lowlands, and the Mackenzie Bison Sanctuary. Anthrax has been detected in 14 separate years between 1962 and 2010, resulting in at least 1756 documented bison cases (ranging from 1 to 363 dead bison per outbreak). Anthrax outbreaks typically occur between June and August, and are thought to happen in hot dry summers that follow wet springs. The disease primarily affects bison, with a strong sex and age bias towards adult males. Anthrax outbreaks in northern wood bison populations have implications for ongoing national recovery efforts for this threatened species, and may pose health risks to humans, other wildlife, and domestic livestock. Federal and territorial agencies have historically implemented anthrax surveillance and control measures aimed at reducing environmental spore contamination. In order to assess the effectiveness of these disease management actions a number of key research and monitoring initiatives have been proposed. These include a retrospective descriptive analysis of past outbreaks, an investigation of the relationship between weather variables and outbreak initiation/prediction, the use of serology to better understand spatial and temporal anthrax exposure patterns, an assessment of the effectiveness of surveillance and carcass disposal techniques, and modelling the potential effect of control measures on environmental spore loading and future outbreaks.



[10] CONTINUED POPULATION DECLINE OF BRITISH GREENFINCHES DUE TO TRICHOMONOSIS

Becki Lawson,¹ Robert A. Robinson,² Katie Colvile,¹ Mike P. Toms,² Kirsi M. Peck,³ James K. Kirkwood,⁴ Julian Chantrey,⁵ Laura A. Hughes,⁵ Shinto K. John,¹ Tom W. Pennycott,⁶ Vic R. Simpson,⁷ Kevin M. Tyler,⁸ and Andrew A. Cunningham¹

¹Institute of Zoology, Zoological Society of London, London, UK; ²British Trust for Ornithology, The Nunnery, Thetford, Norfolk, UK; ³The Royal Society for the Protection of Birds, The Lodge, Sandy, Bedfordshire, UK; ⁴Universities Federation for Animal Welfare, The Old School, Brewhouse Hill, Wheathampstead, Hertfordshire, UK; ⁵Department of Veterinary Pathology, University of Liverpool, Leahurst Campus Neston, South Wirral, UK; ⁶Disease Surveillance Centre, Scottish Agricultural College, Auchincruive, Ayr, UK; ⁷Wildlife Veterinary Investigation Centre, Jollys Bottom Farm, Chacewater, Truro, Cornwall, UK; ⁸Biomedical Research Centre, School of Medicine, Health Policy and Practice, University of East Anglia, Norwich, UK.

Presenting author: Lawson, Becki (becki.lawson@ioz.ac.uk)

Finch trichomonosis was recognized as an emerging infectious disease (EID) in Great Britain in 2005. Epidemic mortality due to this parasitic infection occurred in the summer of 2006, which led to a decline of 35% of the breeding greenfinch (*Carduelis chloris*) and 21% of the chaffinch (*Fringilla coelebs*) populations in the region of the disease outbreak in central and western England that year. Opportunistic and systematic national surveillance schemes were used to investigate the causes of garden bird mortality in Great Britain. Post mortem examinations were performed on birds submitted from a subset of incidents. Sequencing of multiple loci and random amplified polymorphic DNA studies were performed on *Trichomonas gallinae* isolates from multiple bird species. Widespread seasonal disease outbreaks occurred each subsequent year, 2007-2010, with a shifting distribution. Relative abundance estimates indicate that the greenfinch population has declined across the UK by 28% since 2005, which equates to an overall mortality estimate in the order of a million birds due to this EID. No similar population decline was observed in the dunnoek (*Prunella modularis*), another common passerine within garden habitats, which was used as a control for confounding variables such as climatic variation, which might also influence population dynamics. Molecular analyses indicate that a clonal strain of *T. gallinae* is responsible for the finch epidemic. Trichomonosis was also diagnosed in a range of threatened passerine species. This EID appears to be the most significant wild bird mortality in a non-columbiform host caused by *T. gallinae* worldwide.



[11] DETERMINING CAUSES OF MORTALITY IN A DECLINING MOOSE POPULATION IN NORTHEAST MINNESOTA

Erika Butler,¹ Michelle Carstensen,¹ Glenn DelGiudice,² and Mike Schrage³

¹MN Department of Natural Resources, Forest Lake, Minnesota, USA; ²MN Department of Natural Resources, St. Paul, Minnesota, USA; ³Fond du Lac Band of Lake Superior Chippewa, Cloquet, Minnesota, USA.

Presenting author: Butler, Erika (erika.butler@state.mn.us)

Minnesota's (MN) moose are dying at rates much higher than elsewhere in North America. Moose numbers in northwestern (NW) MN plummeted from over 4,000 to fewer than 100 animals in the past 2 decades and recent studies of moose in the northeast (NE) suggest this population is also declining, albeit at a less precipitous rate. A recent study of the NE moose herd reported non-hunting mortality rates of 15-26% per year, which was significantly higher than other northern moose populations (8–12% per year) outside of MN. The specific causes of non-hunting mortality remain unknown. The MN Department of Natural Resources (DNR) began a hunter harvested herd health assessment project in 2007, from which serology identified antibodies to a variety of infectious agents (e.g. West Nile Virus, eastern equine encephalitis, leptospirosis). Anecdotal reports of sick and dead moose have most commonly identified *Parelaphostrongylus tenuis* as the cause of death, though this sampling method is biased. In January of 2012, the MN DNR will begin a moose mortality project. Global Positioning System collars will be deployed on 100 moose in NE Minnesota and an extensive network of responders highly trained in conducting field necropsies will be organized. Moose mortalities will be thoroughly investigated within 24 hours of death to identify the proximate cause of mortality and to examine the influence of potential contributing factors, such as nutritional stress.



[12] THE POWER OF GOOD GENES: RAPID HOST EVOLUTION DRIVEN BY AN EMERGING PRION DISEASE

Stacie J. Robinson,¹ Michael D. Samuel,² Chad J. Johnson,³ Marie Adams,⁴ and Debbie I. McKenzie⁵

¹Dept. of Forest & Wildlife Ecology, University of Wisconsin, Madison, Wisconsin, USA; ²U.S. Geological Survey, WI Cooperative Wildlife Research Unit, Madison, Wisconsin, USA; ³Dept. of Soil Science, University of Wisconsin, Madison, Wisconsin, USA; ⁴Biotechnology Center, University of Wisconsin, Madison, Wisconsin, USA; ⁵Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada.

Presenting author: Robinson, Stacie J. (stacie.j.robinson@gmail.com)

Infectious diseases are increasingly recognized as an important force driving population dynamics, conservation biology and natural selection in wildlife populations. Infectious agents have been implicated in the decline of small or endangered populations and may act to constrain population size, distribution, or growth rates. Further, diseases may provide selective pressures that determine the genetic diversity of populations or species. Thus understanding disease dynamics and selective pressure is crucial to understanding population processes, managing wildlife populations, and conserving biological diversity. Here we link genetic variation with differential susceptibility of white-tailed deer (*Odocoileus virginianus*) to chronic wasting disease (CWD) which influences fitness and disease-driven genetic selection. Our study found that the more susceptible genotype had over 4 times greater risk of CWD infection and, once infected, deer with the resistant genotype survived 49% longer (8.3 more months). We used these epidemiological parameters in a multi-stage population matrix model to evaluate genotype-specific population growth. The differences in disease infection and mortality rates allowed genetically resistant deer to achieve higher population growth and obtain a long-term fitness advantage. This fitness differential translated into a selection coefficient of over 1% favoring the heterozygous CWD-resistant genotype. Such strong selective pressure suggests that the resistant allele could become dominant in the population within just a few hundred years, extremely rapid in terms of evolutionary time scales. Our results will inform predictions about epidemiology, dynamics, and future trends in CWD transmission and spread, and demonstrate the potential impact of epidemics on host population genetics.



[13] PREVALENCE AND INTENSITY OF *HEPATOZOOM* SP. INFECTION IN GREEN FROGS (*LITHOBATES (RANA) CLAMITANS*) OF PRINCE EDWARD ISLAND, CANADA

Jessicca Mitchell, María Forzán, and Raphael Vanderstichel

Canadian Cooperative Wildlife Health Center, Department of Pathology and Microbiology, Atlantic Veterinary College, Charlottetown, Prince Edward Island, Canada.

Presenting author: Mitchell, Jessicca (jlmitchell@upei.ca)

The apicomplexan protozoan parasites *Hepatozoon clamatae* and *H. catesbiana* are known to infect frogs native to north-eastern North America. Prince Edward Island (PEI), one of the eastern provinces of Canada, harbours the definitive host for the parasite, *Culex territans*, and one of the susceptible hosts. To determine presence, prevalence and intensity of infection, 61 green frogs, *Lithobates (Rana) clamitans*, were sampled from four ponds on PEI. Blood was collected with a capillary tube via puncture of the maxillary vein using a 25-30 gauge needle; thin blood smears were prepared on glass microscopic slides and stained with Wright-Giemsa. Packed cell volumes (PCVs) were also measured in 19 of the frogs. Infection with *H. clamatae* and *H. catesbiana* was distinguished based on presence or absence of nuclear fragmentation, respectively, in the infected erythrocyte. The prevalence (number of infected frogsx100/total of frogs examined) and intensity (number of erythrocytes infectedx100/total erythrocytes examined per frog) of *H. clamatae* and *H. catesbiana* infections were determined by systematically scanning each blood smear and examining 2000 erythrocytes. It was found that 50-75% of PEI frogs were infected with one or both *Hepatozoon* spp., infected frogs had an average intensity of 1.1% (0.05-9.8%). Frogs infected with *H. catesbiana* were 3.2 times more likely to have a hemolysed sample ($P = 0.012$). For each parasite counted, the PCV dropped by 1.3 (~0.3%, $P = 0.001$). Results suggest that infection with *Hepatozoon* spp. may have an effect, albeit subclinical, in the haematological profile of infected green frogs.



[14] PATHOLOGY OF AVIAN KERATIN DISORDER: INVESTIGATION OF AN EMERGING DISEASE IN WILD BIRDS

Caroline Van Hemert,^{1,2} Colleen M. Handel,¹ John E. Blake,² and Todd M. O'Hara²

¹USGS Alaska Science Center, Anchorage, Alaska, USA; ²University of Alaska Fairbanks, Fairbanks, Alaska, USA.

Presenting author: Van Hemert, Caroline (cvanheme@alaska.edu)

We recently documented an epizootic of beak and other keratin abnormalities in as many as 30 wild bird species in Alaska. Additional reports from other parts of North America, Europe, and Asia suggest that “avian keratin disorder” may be an emerging disease of global significance. Prevalence of this disorder in Black-capped Chickadees (*Poecile atricapillus*) and Northwestern Crows (*Corvus caurinus*) constitute the highest rates of gross deformities ever recorded in wild bird populations. We investigated the pathology of avian keratin disorder in order to describe underlying physiological changes and to identify possible mechanisms and causative agents. In affected birds, the keratin layer of the beak becomes grossly overgrown, resulting in elongated and sometimes crossed presentation. Examination of beaks, claws, skin, and feathers using histology and scanning electron and x-ray microscopy revealed evidence of hyperkeratosis, parakeratosis, and structural defects in multiple keratinized tissues. We measured beak keratin growth in captivity and detected rates of absolute growth that were 50–100% greater in affected birds relative to controls. In addition, high, unexplained mortality rates and increased susceptibility to secondary epidermal infections suggest that this disorder occurs at a systemic level and presents severe challenges to the health and survival of affected birds. Emergence of this disorder across a growing geographic area with apparent epizootic clusters raises concern about potential etiological factors, including infectious agents and environmental contaminants. Integration of pathology results with epidemiological and ecological data offers important insights into this complex problem and will help to direct future research efforts.



[15] THE TRICH TO SAFE BIRDFEEDING: *TRICHOMONAS GALLINAE* IN CANADIAN MARITIME WILD BIRD POPULATIONS

Whitney Kelly-Clark,^{1,2} Scott McBurney,^{2,1} Spencer Greenwood,³ María Forzán,^{2,1} and Raphael Vanderstichel⁴

¹Department of Pathology & Microbiology, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada; ²Canadian Cooperative Wildlife Health Center, Atlantic Region, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada; ³Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada; ⁴Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada.

Presenting author: Kelly-Clark, Whitney (wkelly@upei.ca)

In the summer and fall of 2007–2009, trichomonosis caused mortality in purple finch (*Carpodacus purpureus*) and American goldfinch (*Carduelis tristis*) populations in the Maritime provinces of Canada. Trichomonosis, caused by *Trichomonas gallinae*, was identified at backyard feeding and watering stations, raising questions about the role of these sites in disease transmission. Columbiformes, including mourning doves (*Zenaida macroura*) and rock pigeons (*Columba livia*), are recognized reservoir hosts of *T. gallinae* and are sometimes fed by the general public at backyard feeding and watering stations with other bird species, including wild finches. The objectives of this study were to determine if *T. gallinae* was endemic in regional Columbiformes species and, if so, to examine the phylogenetic relationship between *T. gallinae* isolates recovered from Columbiformes and those causing mortality in sympatric wild finch populations. Additionally, parasite survivability in and isolation from birdfeed and water were investigated. Ten isolates were recovered from rock pigeons, of which nine were subclinical infections in individuals captured at backyard feeding and watering stations. Isolates were cultured and genotyped by PCR and DNA sequencing. At least two genotypes of *T. gallinae* (genotypes A and B) are present in Maritime bird populations. Phylogenetic analysis revealed that *T. gallinae* isolates from rock pigeons are genetically similar to those in regional wild finch populations affected by trichomonosis mortality, as well as to isolates recovered in Europe and the United States, where trichomonosis has also emerged in wild finch populations. Results from the feed and water isolation trials will also be presented.



[16] MULTIPLE *PLASMODIUM* SPECIES ASSOCIATED TO AVIAN MALARIA OUTBREAK IN MAGELLANIC PENGUINS (*SPHENISCUS MAGELLANICUS*) IN A REHABILITATION CENTER, SOUTHERN BRAZIL

Cristiane K.M. Kolesnikovas,¹ Ralph Eric Thijl Vanstreels,² Sandro Sandri,¹ Érika Martins Braga,³ Patrícia Silveira,³ Nayara de Oliveira Belo,³ Mário Steindel,⁴ Sabrina Epiphany,⁵ and José Luiz Catão-Dias⁶

¹Associação R3 Animal, Florianópolis, SC, Brazil; ²Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, Brazil; ³Departamento de Parasitologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil; ⁴Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Santa Catarina, Florianópolis, SC, Brazil; ⁵Departamento de Ciências Biológicas, Universidade Federal de São Paulo, Diadema, SP, Brazil.

Presenting author: Vanstreels, Ralph Eric Thijl (ralph_vanstreels@yahoo.com.br)

Plasmodial infections are widespread in birds throughout the world, and rarely cause severe illness. Penguins, however, are known to be exceptionally susceptible and malaria outbreaks in captive populations often lead to high mortality. In March 2009, 28 Magellanic penguins (*Spheniscus magellanicus*) were housed at the CETAS Núcleo de Fauna do IBAMA (27°S 48°W), Florianópolis, Brazil. After the sudden death of two animals, Giemsa-stained blood smears were performed for the remaining animals and revealed 19 *Plasmodium*-infected birds. All animals were treated with chloroquine (10 mg/kg hour zero; 5 mg/kg hours 6, 18 and 24; 5mg/kg SID 10 days) followed by sulfa-trimethoprim (40 mg/kg SID 10 days), and after 45 days 11 animals were dead (39.3%). Histopathology confirmed deaths resulted from avian malaria. Parasite morphology indicated the involvement of at least two *Plasmodium* subgenera, *Huffia* and *Haemamoeba*; co-infection occurred in at least two birds. Thirteen samples were submitted to PCR and gene sequencing (cyt-b mitochondrial DNA), revealing high similarity with *Plasmodium (Huffia) elongatum* and *Plasmodium (Haemamoeba) relictum*. Further studies are being conducted to clarify a possible involvement of other *Plasmodium* species. The lack of host-parasite co-evolution between malarial parasites and penguins might have led the latter to act as accidental hosts. The unusual host-parasite association might have led to an excessive pathogenicity from the parasite and/or inappropriate immune response from the host, which is supported by the histological findings of pronounced inflammation and lesions associated with tissue meronts, which are otherwise known to be relatively non-pathogenic in other avian species.



[17] ECOLOGY OF LOW PATHOGENIC AVIAN INFLUENZA VIRUSES IN A LONG DISTANCE MIGRATORY BIRD, THE BLUE-WINGED TEAL (*ANAS DISCORS*): FROM INDIVIDUALS TO POPULATIONS

Rodolfo Nallar,¹ Catherine Soos,^{1,2} Frederick A. Leighton,^{1,3} Tasha Epp,¹ and Canada's Interagency Wild Bird Influenza Survey, United States of America Early Detection System for Highly Pathogenic H5N1 Avian Influenza in Wild Migratory Birds, USFWS-Branch of Migratory Bird Surveys and the Avian Influenza Surveillance Program, and Ecuador's Wild Bird Influenza Surveillance Program

¹Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada; ²Science & Technology Branch, Environment Canada, Saskatoon, Saskatchewan, Canada; ³Canadian Cooperative Wildlife Health Centre, Saskatoon, Saskatchewan, Canada.

Presenting author: Nallar, Rodolfo (rodolfo.nallar@usask.ca)

The aim of this study is to improve our understanding of the ecology, spatiotemporal patterns and risk of avian influenza viruses (AIVs) in migratory waterfowl. Blue-winged teal (BWTE) were sampled in the Canadian prairies in 2007-2010 to examine AIV infection (determined by rRT-PCR) in relation to sex, age, nutritional condition, region, and year. Results to date indicate that, overall, 18.8% (315/1,869) of prairie BWTE were infected with AIV. When controlling for year, young birds were 1.9 times more likely to be infected compared to adults, and birds in Manitoba and Saskatchewan were 8 times more likely to be infected compared to birds in Alberta. Using data from national AIV surveillance programs in Canada, the USA, and Ecuador, we also investigated large-scale spatiotemporal trends in AIV infection across breeding and wintering ranges for BWTE. Overall proportion of BWTE infected with AIV was 18.9% in Canada (2005-10, n=3,657), 16.8% in the USA (2007-09, n=8,312), and 0% in Ecuador (2009-10, n=75). Closer examination of Canadian and USA surveillance data (n=11,969) revealed annual and seasonal variation, with peaks in late summer and fall corresponding to fall migration. As above, young birds were twice as likely to be infected compared to adults, and males were 1.2 times more likely to be infected compared to females. Spatial scan statistics revealed three areas with higher AIV infection risk in BWTE in Canada and the USA. Our preliminary results provide new insight into AIV ecology in a long-distance migratory host at individual, population, and continental scales.



[18] SEROTYPING OF *PASTEURELLA MULTOCIDA* ISOLATES FROM COMMON EIDERS (*SOMATERIA MOLLISSIMA*) IN EASTERN CANADA

Guylaine Séguin,¹ Stéphane Lair,¹ Catherine Soos,² David Blehert,³ Grant Gilchrist,⁵ Jean-François Giroux,⁴ Serge Messier,⁶ and André Dallaire¹

¹Centre québécois sur la santé des animaux sauvages / Canadian Cooperative Wildlife Health Centre, Faculté de médecine vétérinaire, Université de Montréal, St. Hyacinthe, Québec, Canada; ²Environment Canada, Saskatoon, Saskatchewan, Canada; ³USGS, National Wildlife Health Center, Madison, Wisconsin, USA; ⁴Université du Québec à Montréal, Montréal, QU, Canada; ⁵Environment Canada, Ottawa, Ontario, Canada; ⁶Faculté de médecine vétérinaire de l'Université de Montréal, St. Hyacinthe, Québec, Canada.

Presenting author: Séguin, Guylaine (guylaine.seguin@mrnf.gouv.qc.ca)

Common Eiders (*Somateria mollissima*) represent a significant resource for subsistence/recreational hunters as well as down harvesters. Although avian cholera (due to *Pasteurella multocida*) has been known for decades to cause mortality in Common Eiders, the epidemiology of the disease is still poorly understood. To assess whether asymptomatic carriers of *P. multocida* could be sources of outbreaks in breeding colonies, somatic serotyping was performed on isolates of *P. multocida* recovered from eiders that died of cholera, as well as from pharyngeal/cloacal swabs collected from clinically healthy eiders (n=2676) from 2004 to 2009 on breeding colonies located on the St. Lawrence Estuary Islands (Southern Québec), Gyr Falcon Islands (Northern Québec), and East Bay Island (Nunavut). Isolates associated with mortalities were identified as serotype 1 in Southern Québec (n=35) and as serotype 3X4 in Northern Québec (n=9). In Nunavut, mortalities were associated with multiple serotypes (1, 3X4, 3, and 4) within and among years (n=118). *Pasteurella multocida* was isolated from 0 to 5.1% of clinically healthy eiders. No association was found between serotypes recovered from dead and live birds in Québec. However, in 2008, 18 clinically healthy eiders sampled in Nunavut (shortly after outbreak onset) were infected with *P. multocida* serotype 4, the most common serotype isolated from dead birds that year. Nine of these birds were resighted in subsequent years, indicating that infected birds can survive and may serve as asymptomatic carriers. Further pathogenicity testing and genetic characterization is underway to determine whether isolates from asymptomatic birds were related to those causing outbreaks.



[19] AVIAN CHOLERA IN THE EASTERN CANADIAN ARCTIC: WHAT DO WE KNOW ABOUT RESERVOIRS?

N. Jane Harms,¹ Christina A. Allen,² David Blehert,³ Isabel Buttler,⁴ Andre Dallaire,⁵ Jeffery Foster,² Grant Gilchrist,⁴ Janet E. Hill,⁶ Samuel Iverson,^{4,7} Stephane Lair,⁵ Frederick A. Leighton,^{1,8} Scott McBurney,⁹ Guylaine Seguin,^{5,10} Josanne Verhagen,¹¹ Catherine Soos^{1,12}

¹Department of Veterinary Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada; ²Center for Microbial Genetics and Genomics, Northern Arizona University, Flagstaff, Arizona, USA; ³USGS - National Wildlife Health Center, Madison, Wisconsin, USA; ⁴Environment Canada, National Wildlife Research Centre, Ottawa, Ontario, Canada; ⁵Centre québécois sur la santé des animaux sauvages, Faculté de médecine vétérinaire de l'Université de Montréal, St. Hyacinthe, Québec, Canada; ⁶Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatchewan, Canada; ⁷Carleton University, Ottawa, Ontario, Canada; ⁸Canadian Cooperative Wildlife Health Center, Headquarters, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada; ⁹Canadian Cooperative Wildlife Health Centre, Atlantic Region, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; ¹⁰Ministère des Ressources naturelles et de la Faune du Québec, Quebec City, Québec, Canada; ¹¹Department of Virology, Erasmus MC, Rotterdam, The Netherlands; ¹²Environment Canada, Saskatoon, Saskatchewan, Canada.

Presenting author: Harms, N. Jane (naomi.harms@usask.ca)

Avian cholera has caused significant annual mortality at the largest northern Common Eider breeding colony in Canada (East Bay Island, Nunavut) since it was first detected there in 2005. Outbreaks on East Bay Island over the subsequent 5 years have been characterized by *Pasteurella multocida* isolates with different serotypes being recovered in a single season and changes in serotypes among years, raising questions about origins of these pathogens in the eastern Arctic. To characterize reservoirs, origins, and potential spread of *P. multocida* in the eastern Canadian Arctic, an international research investigation was initiated. Potentially virulent *P. multocida* isolates have been cultured from low numbers of apparently healthy Common Eiders from East Bay, many of which were resighted in subsequent years. Currently, a recently developed real-time PCR assay is being used to screen thousands of avian and environmental samples collected annually since 2007 for the presence of *P. multocida*. *Pasteurella multocida* DNA has been detected in samples from the environment and from apparently healthy birds (Common Eiders and Lesser Snow Geese) sampled before and during outbreaks on East Bay. PCR-positive samples are subsequently cultured, and all recovered *P. multocida* isolates are further examined using genotyping techniques to determine their relatedness to isolates from previous outbreaks across North America, including East Bay. Preliminary results using multi-locus sequence typing show clear differentiation among, and some variation within, serotypes. Additional genotyping techniques, including a repetitive element palindromic PCR assay, are being used to further compare isolates of the same serotype at a finer resolution.



[20] EVALUATION OF IGG RESPONSE TO *OTODECTES* SPP. IN SANTA CATALINA ISLAND FOXES DURING AN ACARICIDE TREATMENT STUDY

Megan Moriarty,¹ T. Winston Vickers,^{2,3} Kenneth Lee,⁴ Deana Clifford,^{2,5} Linda Munson,¹ and Walter Boyce²

¹University of California Davis, School of Veterinary Medicine, Davis, California, USA; ²University of California Davis, Wildlife Health Center, Davis, California, USA; ³Institute for Wildlife Studies, Arcata, California, USA; ⁴Greer Laboratories, Lenoir, North Carolina, USA; ⁵Wildlife Investigations Lab, California Department of Fish and Game, Rancho Cordova, California, USA.

Presenting author: Moriarty, Megan (memoriarty@ucdavis.edu)

Ceruminous gland carcinoma causes morbidity and mortality in Santa Catalina Island (SCA) foxes (*Urocyon littoralis catalinae*), an endangered species found only on the Channel Islands off the California coast. Researchers hypothesize that cancer development may be associated with inflammation from ear mites (*Otodectes cynotis*) found in >98% of the foxes. During 2009-2010, sera samples were repeatedly collected over a six month period from 57 SCA foxes that were treated with acaricide and 58 SCA foxes that remained untreated. The antibody response of foxes exposed to ear mites was evaluated using a mite-specific IgG ELISA. Over time there was a decrease in IgG reactivity within both treated and untreated foxes. This is a probable reflection of the sample collection timing and mite burden reduction through sampling methods, which may be overriding any difference due to treatment. Although acaricide treatment eliminated mite infestation, and IgG reactivity was consistently lower in treated foxes at each time point, the difference in IgG reactivity between treated and untreated foxes was not statistically significant. However, when compared to samples collected from Santa Cruz Island foxes, an isolated population not infested with mites, the initial antibody response was significantly higher in SCA treated, mite-free foxes. The differences in IgG levels became less evident over time and were not significantly different after six months of acaricide treatment of SCA foxes. These results demonstrate that monitoring mite specific IgG correlates with mite burden, and may be useful in future investigation of the pathogenesis of ceruminous gland carcinoma in foxes.



[21] SUSCEPTIBILITY OF WHITE-TAILED DEER AND *CULICOIDES SONORENSIS* TO AN EXOTIC EPIZOOTIC HEMORRHAGIC DISEASE VIRUS, EHDV-7 (ISRAEL)

Mark G. Ruder,¹ Andrew B. Allison,¹ Deborah L. Carter,² Sabrina N. McGraw,² Steven V. Kubiski,¹ Daniel G. Mead,¹ David E. Stallknecht,¹ and Elizabeth W. Howerth²

¹*Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA;* ²*Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA.*

Presenting author: Ruder, Mark (mgruder@uga.edu)

Epizootic hemorrhagic disease viruses (EHDV) have long been recognized as significant pathogens of white-tailed deer (WTD; *Odocoileus virginianus*), although infection of cattle has primarily been considered subclinical. However, since 2002, global reports of disease in cattle associated with certain EHDV serotypes have increased. During 2006 in Israel, an extensive EHDV-7 outbreak in cattle financially affected the Israeli dairy industry. The susceptibility of potential North American vectors and hosts to infection with EHDV-7 is unknown. Our objectives were to determine if WTD are susceptible to infection with EHDV-7 and if *Culicoides sonorensis*, the primary vector of EHDV in North America, can transmit this exotic serotype. Six WTD fawns were experimentally infected with EHDV-7 isolated from a cow during the 2006 outbreak. All six deer became infected and clinically ill, and four died or were euthanised due to severity of disease. Clinical signs, clinicopathologic abnormalities, viral dynamics, and postmortem findings were consistent with previous reports of orbiviral hemorrhagic disease in WTD. Additionally, *C. sonorensis* midges that took a blood meal from infected WTD during peak viremia transmitted the virus to a naïve WTD, as evidenced by viremia and disease. These results demonstrate that WTD are susceptible to infection with EHDV-7 and North America harbors a competent vector. The high mortality observed reaffirms the role of WTD as a sentinel species for orbiviral activity, both endemic and non-endemic. Further, the clinical similarities observed in the WTD study with disease caused by endemic EHDV serotypes highlight the importance of serotype-specific diagnostics during mortality investigations.



[22] ANAPLASMA PHAGOCYTOPHILUM IN MOOSE (*ALCES ALCES*) IN SWEDEN, AND POSSIBLE EFFECTS ON CALF HEALTH

Jonas Malmsten,¹ Lennart Söderquist,² Dolores Gavier-Widén,¹ and Anne-Marie Dalin²

¹Dept. of Clinical Sciences / Dept. of Pathology and Wildlife Diseases, Swedish University of Agricultural Sciences / National Veterinary Institute, Uppsala, Sweden; ²Dept. of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden.

Presenting author: Malmsten, Jonas (jonas.malmsten@sva.se)

Anaplasma phagocytophilum (AP) is a tick-borne, gram-negative bacterium that infects a variety of animal species. It causes tick-borne fever (TBF), a disease affecting livestock on pasture. Clinical manifestations in infected livestock and horses include pyrexia and inappetence. In sheep, abortions have been reported, as well as production losses and reduced weight gain. In wildlife, several species show presence of bacterial DNA and anti-anaplasma antibodies. Roe deer (*Capreolus capreolus*), fallow deer (*Cervus elaphus*) and other deer species can act as natural hosts for the bacterium. Moose (*Alces alces*) may harbor this pathogen, but surveys in moose are few. In our study, 51 of 216 moose (23.6%) sampled from 2007 to 2009 were positive for presence of AP-DNA. Preliminary statistical analyses show that moose from an island population (n=109) had significantly higher prevalence (31.2%) of bacterial DNA than moose sampled (n=107) on the mainland (15.9%). Calves (< 1 year, n=78) had higher prevalence of bacterial DNA (42.3%) than sub adult (1 - 2 years) and adult (> 2 years) moose (13%, n=138). To our knowledge, this is the first detailed report on PCR-detection of AP in moose. Results indicate that moose are susceptible to infection with AP, thus making them a potential natural host of the bacterium. It is unknown if the infection causes clinical disease in moose, but case reports suggest that survival of moose calves can be affected by co-infections with AP, and other bacteria. Hence, a high prevalence of AP in moose populations may affect moose calf health.



[23] DISEASE TRANSMISSION IN EXTREME ENVIRONMENTS: NEMATODE PARASITES INFECT REINDEER DURING THE ARCTIC WINTER

Anja M. Carlsson,^{1,2,5} Kenneth Wilson,¹ R. Justin Irvine,² Stuart B. Piertney,³ Odd Halvorsen,⁴ Stephen J. Coulson,⁵ Audun Stien,⁶ and Steve D. Albon²

¹Lancaster Environment Centre, Lancaster University, Lancaster, UK; ²The Macaulay Land Use Research Institute, Craigiebuckler, Aberdeen, UK; ³School of Biological Sciences, University of Aberdeen, Aberdeen, UK; ⁴Zoological Museum, University of Oslo, Blindern, Oslo, Norway; ⁵Department of Arctic Biology, University Centre in Svalbard, Longyearbyen, Norway; ⁶Norwegian institute for Nature Research (NINA), The Polar Environmental Centre, Tromsø, Norway.

Presenting author: Carlsson, Anja (a.carlsson@lancs.ac.uk)

Nematodes are found in almost all wild vertebrate populations but surprisingly few studies have investigated the host-parasite relationships in the wild. For parasites with a direct life-cycle the external environment has a major influence on their life-history parameters since development of free-living stages is highly dependent on temperature and humidity. For Arctic ungulates, such as Svalbard Reindeer (*Rangifer tarandus platyrhynchus*), parasite transmission would be expected to be focused during the short, wet summer, and this is what occurs for the nematode species *Ostertagia gruehneri*. However, the other nematode species, *Marshallagia marshalli*, appears to accumulate during winter. To experimentally test the hypothesis that *M. marshalli* is transmitted during the Arctic winter, adult reindeer caught in April were given a novel delayed-release anthelmintic bolus to remove parasites in the autumn (fall). Transmission during winter was estimated from worm burden counts in both control and treated animals sampled in October, February and April. Species composition was estimated by microscopy and molecular identification of adult and larval nematodes. Treated animals had lower adult worm burdens than controls, demonstrating the efficacy of the anthelmintic treatment. There was no change in *O. gruehneri* adult worm burdens over time but in treated animals there was a significant increase of *M. marshalli* adult worm burdens from October to April. This study confirms the contrasting life-history strategies of these two species, and is, to our knowledge, the first to experimentally demonstrate transmission during winter of a gastro-intestinal nematode in a wild mammal.



[24] USE OF ENVIRONMENTAL SITES BY MULE DEER AS A MEASURE OF RISK OF CWD TRANSMISSION IN SOUTHERN SASKATCHEWAN

María Fernanda Mejía Salazar,¹ Angeliqué Curtis,² and Trent K. Bollinger¹

¹*Department of Veterinary Pathology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada;* ²*Livermore, Colorado.*

Presenting author: Mejía Salazar, María Fernanda (mihicoltia@gmail.com)

Chronic wasting disease (CWD) is a fatal, progressive, transmissible spongiform encephalopathy (TSE), caused by prions. Routes of transmission include animal-animal and animal-environment-animal pathways. Prions deposited into the environment by infected animals are persistent and may continue to infect free-ranging cervids for years. The lack of knowledge of the transmission dynamics of CWD is hampering development of appropriate disease management responses. Since 2006, we have been studying social interactions and movement patterns from more than 400 free-ranging mule deer and 44 white-tailed deer from Southern Saskatchewan. The goal of this presentation is to show findings on the relative rates of use of environmental sites by mule deer as a measure of relative risk of CWD transmission. Twenty-two trail cameras have been used to monitor 209 different locations of 7 different site types, and to monitor 20 mule deer carcasses that died of CWD. The cameras have taken more than 60,000 photographs and over 12,000 of these contain one or more deer. We are able to determine the most frequently visited site types, as well as the characteristics of the visitors: deer age class, gender and sometimes CWD status. With data collected from the mortality sites, we can identify mammalian and avian scavengers and visitors potentially exposed to CWD prions from mule deer carcasses, and can determine the length of time CWD positive mule deer carcasses persist in the environment. Preliminary findings on how deer use anthropogenic and non-anthropogenic environmental sites and the implications for CWD transmission are discussed.



[25] PRELIMINARY FINDINGS ON REPRODUCTIVE INDICES AND FAWN SURVIVAL OF MULE DEER (*ODOCOILEUS HEMIONUS*) IN SOUTHERN SASKATCHEWAN

Asha Perera, Trent K. Bollinger

Department of Veterinary Pathology, WCVN, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.

Presenting author: Perera, Asha (asha.perera@usask.ca)

In 2010 and 2011, adult does were scanned using ultrasound to detect pregnancy status and foetal count and radio-collared. In 2009 and 2010, neonates were manually captured, measured, sampled and tagged (n=38 in 2009 and n=41 in 2010) with mortality-sensing radio-collars. Each fawn's live/mortality status was determined daily during summer and every 2-3 days during fall and winter. Whenever a mortality signal occurred, the radio-collar was located immediately to assign death to a proximate cause, using necropsy and evidence on site. In 2010 and 2011, the pregnancy rate was 100% (40/40) and the foetal rate was 2 fetuses per doe. Overall birth rate was 1.5 live fawns per doe. The overall median individual survival time was 44 days. Fawn survival rates in 2009 and 2010 were 32% and 34% respectively with no significant difference between years or sexes ($p > 0.05$). Within 30 days of birth, 46% of collared fawns died. Known causes of mortality ordered from highest to lowest were predation by coyotes, accident and hunting. The observed difference in foetal rate and birth rate may be due to foetal counting errors with ultrasound scanning, late pregnancy foetal losses, early neonatal deaths within 24 hours of birth and difficulties in locating neonates. Low first year survival rate may indicate a low annual natural recruitment rate in this chronic wasting disease (CWD) endemic, wild mule deer population. High adult mortalities due to CWD together with low juvenile recruitment may result in long term negative effects on mule deer populations.



[26] IDENTIFICATION OF THE FIRST INTERMEDIATE HOST OF *ALARIA ALATA* IN NATURAL CONDITIONS

Julien Portier,^{1,2} Damien Jouet,² Isabelle Vallée,¹ and Hubert Ferté²

¹UMR Bipar, Anses, ENVirginia, UPEC, Laboratory for Animal Health, Anses Maisons-Alfort, Maisons Alfort, France;

²JE 2533 – USC Anses « VECPAR », UFR de Pharmacie, Université de Reims Champagne – Ardenne, Reims, France.

Presenting author: Portier, Julien (julien.portier@anses.fr)

The trematode, *Alaria alata*, is a parasite of canids which needs two intermediate hosts before it proceeds to the adult stage. Very few investigations have been made on the life cycle of *A. alata*, especially for the first intermediate host, a freshwater mollusc. Only one description, made from experimental work by Ruzskowski in 1922, showed several Planorbidae species as potential hosts for *A. alata*. No descriptions exist in Western Europe where mollusc and maybe *Alaria* populations differ from those of Eastern Europe. This study was conducted in order to identify the precise species of aquatic molluscs acting as first intermediate hosts of *A. alata* in France. Eleven sampling collections were made in three different wetland areas in Eastern France. Between 2009 and 2010, more than 6000 molluscs of 7 different families were collected. All cercariae shed by these molluscs were tested by PCR with specific primers for *A. alata* and sequenced on the ITS2 ribosomal domain. When *A. alata* cercariae were identified, the shedding snail was identified using both morphology and sequencing of three different domains: the 18S and 16S ribosomal subunits and the COI mitochondrial domain. We identified 32 snails shedding *A. alata* cercariae from two different areas. Snail identification showed that two different species harbored *A. alata*: *Planorbis planorbis* and *Anisus vortex*. No cercaria shed by other snails were identified as *A. alata* cercaria.



[27] GENETIC STRUCTURE OF WHITE-TAILED DEER IN GEORGIA: A COMPARISON OF RESTOCKING HISTORY, CURRENT GENETICS, AND SUSCEPTIBILITY TO EPIZOOTIC HEMORRHAGIC DISEASE

Sabrina N. McGraw,^{1,2} Kenneth L. Jones,³ David E. Stallknecht,² Mark G. Ruder,^{1,2} and Elizabeth W. Howerth¹

¹Pathology Department, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA; ²Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, Athens, Georgia, USA; ³Department of Biochemistry and Molecular Genetics, University of Colorado School of Medicine, Denver, Colorado, USA.

Presenting author: McGraw, Sabrina N. (snmcgraw@uga.edu)

Epizootic hemorrhagic disease (EHD) can cause significant mortality in susceptible populations of white-tailed deer (WTD, *Odocoileus virginianus*). Experimental infections of deer from the northern (*O. v. borealis*) and southern United States (*O. v. texanus*) have shown markedly different susceptibility to the disease, with southern deer being more resistant. Following the near extirpation of WTD from the southeastern US by the early 1900's, restocking efforts introduced deer from distant geographic ranges. Over 20 years of surveillance data has shown a consistent pattern of morbidity and mortality due to EHD in Georgia. The aim of this study was to elucidate the genetic structure of WTD populations in Georgia to determine if 1) susceptible and resistant regions are genetically unique, 2) there are residual genetic signatures from introductions, and 3) if there are major histocompatibility complex (MHC) alleles associated with resistant populations. Population FST and AMOVA results from microsatellite and mitochondrial data suggested limited gene flow between the northern mountain and barrier island deer populations and deer in south Georgia, which form a single larger interbreeding population. Comparisons of mitochondrial DNA from sampled Wisconsin deer and barrier island source populations demonstrated residual genetics from translocated deer. A single MHC allele, at low frequencies, was observed to be associated only with resistant populations, and absent from susceptible groups. These findings suggest that susceptible deer in Georgia are within distinct populations, there are residual genetic signatures associated with restocking events, and that further work with MHC loci in association with EHD susceptibility may be warranted.



[28] PATHOGENIC VIRUSES AND THEIR POTENTIAL ROLE IN THE DECLINE AND RESTORATION OF WILD EUROPEAN EEL STOCKS

Steven van Beurden,^{1,2} Marc Engelsma,¹ and Olga Haenen¹

¹Laboratory for Fish and Shellfish Diseases, Central Veterinary Institute, part of Wageningen UR, Lelystad, The Netherlands; ²Faculty of Veterinary Medicine, Utrecht University, The Netherlands.

Presenting author: van Beurden, Steven (steven.vanbeurden@wur.nl)

The freshwater eels of the genus *Anguilla* have an extraordinary catadromic life cycle. The spawning grounds of the two North Atlantic species *Anguilla anguilla* (European eel) and *Anguilla rostrata* (American eel) are located in the Sargasso Sea, several thousand kilometers from their growth habitats in the freshwater lakes and rivers of Europe and North America, respectively. Since the 1980's North Atlantic eel stocks declined tremendously. One of the factors influencing wild freshwater eel stocks is thought to be various disease agents, including pathogenic viruses. In an extensive study from 1999 to 2007, almost 200 wild European eels from several rivers and lakes in the Netherlands were examined at necropsy and tested for the presence of viruses using cell culture, immunological assays and PCR. The observed viruses were the herpesvirus, Anguillid herpesvirus 1 (AngHV-1), and the rhabdovirus, Eel virus European X (EVEX). Both these viruses cause a hemorrhagic disease, and at eel farms, significant mortalities may result from outbreaks with these viruses. One of the means to restore wild European eel stocks is the restocking of cultured or farmed eels into the wild. Pathogenic viruses are frequently found in cultured eels, including the birnavirus, Eel virus European (EVE). Samples of cultured eels intended for restocking purposes in late spring 2011 should be tested for the presence of pathogenic viruses. Although pathogenic viruses are not considered as a major factor in the decline of wild European eel stocks, the risks and negative effects of restocking virus-infected cultured eels should be a concern.



[29] ASSOCIATION BETWEEN THE INTENSITY OF *ANISAKIS SIMPLEX* LARVAE INFECTION AND RED VENT SYNDROME IN WILD ATLANTIC SALMON IN THE PROVINCE OF QUEBEC

Sylvain Larrat,¹ Stéphane Lair,¹ and Francis Bouchard²

¹Centre québécois sur la santé des animaux sauvages / Canadian Cooperative Wildlife Health Centre, Faculté de médecine vétérinaire, Université de Montréal, St. Hyacinthe, Québec, Canada; ²Ministère des Ressources naturelles et de la Faune du Québec, Québec City, Québec, Canada.

Presenting author: Larrat, Sylvain (sylvain.larrat@umontreal.ca)

The Atlantic salmon (*Salmo salar*) is an important natural resource in the province of Quebec. Red vent syndrome (RVS), an emerging disease of Atlantic salmon in Europe, has been reported in salmon rivers of Quebec since 2008. Because RVS is associated with embedded *Anisakis simplex* larvae in the tissues surrounding the vent, it can be hypothesized that the emergence of this syndrome is a consequence of an increase in the infection intensity of this parasite. To explore this possible relationship, the intensity of infection by anisakid larvae was compared between salmon presenting macroscopic lesions of RVS (n=98) and salmon without obvious external signs (n=106). For each salmon, the numbers of anisakid larvae on the serosal aspect of the coelomic viscera, as well as in pepsin-digested standardized sections of peri-anal tissues were evaluated. A backward-stepwise logistic regression analysis was performed to evaluate the association between different variables and the presence of macroscopic lesions. The presence of lesions was significantly associated with high numbers of larvae encysted in the peri-anal region (p=0.002), but not with gender, fish length or number of coelomic larvae (p>0.05). Although the intensity of infection was significantly higher in salmon presenting with RVS, the magnitude of this relationship was moderate (odds ratio = 1.12, confidence interval: [1.04;1.22]), which suggests that, even if the number of larvae is a determinant of the pathogenesis of RVS, other factors, such as time of infection, might also play a role in the occurrence of RVS.



[30] TRACKING PATHOGEN TRANSMISSION AT THE HUMAN-WILDLIFE INTERFACE: BANDED MONGOOSE (*MUNGOS MUNGO*) AND *ESCHERICHIA COLI* AS A MODEL SYSTEM IN CHOBE, BOTSWANA

Risa Pesapane,¹ Monica Ponder,² and Kathleen Alexander¹

¹Department of Fisheries and Wildlife Science, Virginia Tech, Virginia, USA; ²Department of Food Science and Technology, Virginia Tech, Virginia, USA.

Presenting author: Pesapane, Risa (rpesapan@vt.edu)

Emerging infectious disease is on the rise, threatening both human and wildlife populations. Increasingly, human waste is identified as an attractant to wildlife and potential health threat and source of disease exposure. Exposure and invasion of specific human associated pathogens into wildlife hosts is difficult to detect in routine surveillance yet there is evidence that this is occurring however, transmission pathways remain speculative in most cases. Microbial transmission of resistant bacteria also poses a threat to global health and environmental reservoirs of resistance are a growing concern. We have a long-term study of banded mongoose (*Mungos mungo*) that live in close association with humans and their waste and therefore represent a unique sentinel of health and pathogen exposure at the human-wildlife interface. In this study, we evaluate a model organism, *Escherichia coli*, using a combined approach of bacterial culture, antibiotic susceptibility, and molecular assays. We test the hypothesis (HA) that banded mongoose utilizing human-modified environments harbor strains of *E. coli* that originate from human fecal waste. Antibiotic susceptibility results show that resistance levels range from 33.3-77.8% (5 troops, n=65) and is supported by Rep-PCR results which show significant clustering of mongoose isolates with sources of human fecal waste. This study contributes to a mechanistic understanding of pathogen transmission at the human-animal interface, providing insight into the dynamics of pathogen spillover. With human population growth expected to exceed 7 billion, overlap between humans and wildlife will only increase and along with it, the potential for pathogen spillover and emerging infectious diseases.



[31] ASSOCIATIONS BETWEEN *IXODES SCAPULARIS* TICKS AND SMALL MAMMAL HOSTS IN A NEWLY-ENDEMIC ZONE IN SOUTHEASTERN CANADA: IMPLICATIONS FOR *BORRELIA BURGDORFERI* TRANSMISSION

Catherine Bouchard,¹ Guy Beauchamp,¹ Soulyvane Nguon,² Louise Trudel,³ François Milord,⁴ Robbin Lindsay,⁵ Denise Bélanger,¹ and Nicholas Ogden⁶

¹Groupe de recherche en épidémiologie des zoonoses et santé publique, Faculté de médecine vétérinaire, Université de Montréal, Saint-Hyacinthe, Québec, Canada; ²Direction des risques biologiques et de la santé au travail, Institut national de santé publique du Québec, Québec, Canada; ³Laboratoire de santé publique du Québec, Institut national de santé publique du Québec, Ste-Anne de Bellevue, Québec, Canada; ⁴Direction des risques biologiques et de la santé au travail, Institut national de santé publique du Québec, Québec, Canada; ⁵Zoonotic Diseases and Special Pathogens, Public Health Agency of Canada, National Microbiology Laboratory, Winnipeg, Manitoba, Canada; ⁶Zoonoses Division, Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Ottawa, Ontario, Canada.

Presenting author: Bouchard, Catherine (catherine.bouchard.5@umontreal.ca)

Immature *Ixodes scapularis* infestation, and *Borrelia burgdorferi* infection, of wild small mammals were studied during May-October of 2007 and 2008 at 71 study sites in a zone where *I. scapularis* populations and Lyme disease risk are emerging in southwestern Quebec. The seasonal host-seeking activity of immature *I. scapularis* was similar to patterns reported previously in Canada and the United States of America (USA): nymphal activity peaked in spring while larval activity peaked in late summer. Synchronous activity of nymphs with some larvae was observed in late spring, which could favour establishment of *B. burgdorferi* strains that cause short-lived infections in their hosts. Of the small mammals captured, white-footed mice (*Peromyscus leucopus*), deer mice (*Peromyscus maniculatus*), chipmunks (*Tamias striatus*) and red squirrels (*Tamiasciurus hudsonicus*) carried 92.0% of the larvae and 94.2% of the nymphs collected. Adult male white-footed mice carried significantly higher numbers of both larval and nymphal *I. scapularis* than other species of small mammals and infection in this group of hosts could be expected to have the greatest effect on establishment of new endemic cycles of *B. burgdorferi* infection, and the entomological risk for Lyme disease. We conclude that seasonality and host-association were comparable to previous studies in North America, even in the context of a newly-endemic pattern for Lyme disease (i.e. low infection prevalence and low abundance of hosts and host-seeking *I. scapularis*). We speculate that the ecologic cycle of *B. burgdorferi* transmission is in a growing (versus spreading) phase in southwestern Quebec.



[32] FACTORS AFFECTING THE ABUNDANCE OF BLACKLEGGED TICKS (*IXODES SCAPULARIS*) AND THE PREVALENCE OF *BORRELIA BURGDORFERI* INFECTION IN THE THOUSAND ISLANDS REGION OF ONTARIO

Lisa Werden,¹ Amy Sharp,¹ Ian K. Barker,^{1,2} Jeff Bowman,³ Emily K. Gonzales,⁴ L. Robbin Lindsay,⁵ and Claire Jardine^{1,2}

¹Department of Pathobiology, Ontario Veterinary College, University of Guelph, Ontario, Canada; ²Canadian Cooperative Wildlife Health Centre, Guelph, Ontario, Canada; ³Ontario Ministry of Natural Resources, Peterborough, Ontario, Canada; ⁴Parks Canada Agency, Ottawa, Ontario, Canada; ⁵Public Health Agency of Canada, Winnipeg, Manitoba, Canada.

Presenting author: Werden, Lisa (lwerden@uoguelph.ca)

In 2006, endemic populations of the blacklegged tick vector *Ixodes scapularis* and *Borrelia burgdorferi*, the causative agent of Lyme disease, were first confirmed in the Thousand Islands region of Ontario. Anecdotal evidence suggested substantial differences in tick populations among islands, which have considerable biotic and abiotic variability. The objective of this study was to compare the abundance of ticks and prevalence of *B. burgdorferi* infection among islands and to assess the factors influencing transmission dynamics and the risk of human exposure to *B. burgdorferi*. Ticks were collected from small mammals and by drag sampling at 12 island and mainland sites in 2009 and 2010. Infection status of ticks based on PCR, and prevalence of antibody to *B. burgdorferi* in mammals were determined. Overall, 63% of the trapped small mammals were infested with larval ticks and 8% were seropositive in June 2009. There was dramatic inter-island variation in the abundance of ticks (0-83 nymphs per person hour dragging) and prevalence of *B. burgdorferi* infection in nymphs (0-42%). Four sites were identified as 'high risk', due to the potential for human exposure to infected ticks, based on abundance of infected ticks and intensity of human visitation. How host populations and environmental variation may contribute to the geographic differences in tick abundance and prevalence of *B. burgdorferi* infection observed in the Thousand Islands is under investigation. The results will help in devising management strategies aimed at controlling blacklegged ticks and reducing the risk of Lyme disease in this new endemic region.



[33] THE EPIDEMIOLOGY OF *SALMONELLA* IN NEW ZEALAND ISLAND FAUNA

Danielle M. Middleton,¹ Anne C. La Flamme,¹ Brett D. Gartrell,² and Nicola J. Nelson¹

¹Allan Wilson Centre for Molecular Ecology and Evolution, Victoria University of Wellington, New Zealand; ²New Zealand Wildlife Health Centre, Massey University, Palmerston North, New Zealand.

Presenting author: Middleton, Danielle (danielle.middleton@vuw.ac.nz)

A wide variety of *Salmonella* serotypes occur within reptilian hosts but the ecology and relationship of this organism with its hosts is poorly understood. We investigated the spatial and temporal distribution of *Salmonella* within wildlife in New Zealand. Cloacal swabs were collected from a variety of native species on Stephens Island (Takapourewa), New Zealand between October 2009 and March 2011. Soil samples were also collected from across the island. These samples were tested for *Salmonella* using standard isolation techniques. Over 1000 cloacal swabs were collected from tuatara during this study and no intestinal carriage of *Salmonella* was detected. In contrast, *Salmonella* was isolated from soil samples and 19% of skinks caught in tuatara habitat. Absence of *Salmonella* in tuatara may indicate a lack of exposure or an innate resistance of tuatara to this bacterium. Hence, tuatara were targeted for in depth immunological analyses and blood samples were collected from tuatara at the time of cloacal sampling. We tested the hypothesis that tuatara are resistant to *Salmonella* colonisation by determining if tuatara have developed anti-*Salmonella* antibodies. Using western blot and flow cytometry we have demonstrated that tuatara possess antibodies which recognise *Salmonella* antigens and have ruled out cross-reactivity with two closely related bacteria, *E. coli* and *Citrobacter* as a possible source of these antibodies. This is the first investigation into the immune response of tuatara to this pathogenic bacterium and will help to establish greater knowledge of the threat of salmonellosis to tuatara and within the natural environment.



[34] A RETROSPECTIVE ANALYSIS OF KILLER WHALE STRANDINGS IN THE NORTH PACIFIC OCEAN AND THE BENEFITS OF A COORDINATED STRANDING RESPONSE PROTOCOL

Michelle M. Barbieri,¹ Stephen Raverty,² M. Bradley Hanson,³ Stephanie Wong,⁴ John K. B. Ford,⁵ and Joseph K. Gaydos¹

¹UC Davis Wildlife Health Center - Orcas Island Office, Eastsound, Washington, USA; ²British Columbia Ministry of Agriculture and Food, Animal Health Center, Abbotsford British Columbia, Canada; ³NOAA/NMFS/Northwest Fisheries Science Center, Seattle, Washington, USA; ⁴U.S. Navy Marine Mammal Program, Biosciences Division, Code 2351, Space and Naval Warfare Systems Center - San Diego, San Diego, California, USA; ⁵Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo, British Columbia, Canada.

Presenting author: Barbieri, Michelle (mmbarbieri@ucdavis.edu)

Killer whales (*Orcinus orca*) are widely distributed throughout the world's oceans, and some populations in the eastern North Pacific are particularly well studied. However, little is known about their diseases or stranding patterns. We used published reports and electronically solicited information about killer whale strandings and postmortem examinations in the North Pacific Ocean to evaluate stranding patterns and to study opportunities for learning about their diseases. Between 1944 and 2011, 230 stranded animals were reported in the North Pacific with the majority occurring in Alaska (34.3%), British Columbia (30.4%) and Japan (19.1%). Fewer strandings were reported from Russia (5.7%), Washington (5.2%), California (3.5%), Oregon (0.9%), Hawaii (0.4%) and Mexico (0.4%). Stranding data consistently collected over the last two decades suggest that an average of seven dead killer whales per year are found in the North Pacific, making each stranding event a rare opportunity to collect information on the natural history and diseases of killer whales. Prior to the 2004 publication of a standardized killer whale necropsy protocol 1.7% of stranded killer whales received complete postmortem necropsies per year, while 33.9% per year were examined at necropsy after the protocol was written and distributed to marine mammalogists and veterinarians. This significant increase in animals examined at necropsy ($p < 0.0001$) suggests that standardized necropsy protocols and communication associated with publication of such protocols can improve our ability to collect disease information on understudied marine mammals. Continued use of this protocol is encouraged in order to expand our knowledge about where, when, and why killer whale strandings occur.



[35] *GIARDIA* IN SYMPATRIC WILDLIFE IN VOLCANOES NATIONAL PARK, RWANDA

Jennifer Hogan,¹ James Hassell,² Jean Bosco Noheri,³ Jan Ramer,³ Michael Cranfield,⁴ Woutrina Miller,¹ and Kirsten Gilardi⁴

¹Veterinary Medicine: Pathology, Microbiology, Immunology, UC Davis, California, USA; ²Royal Veterinary College, University of London, London, UK; ³Mountain Gorilla Veterinary Project; ⁴Mountain Gorilla One Health Program, UC Davis Wildlife Health Center, California, USA.

Presenting author: Hogan, Jennifer (jnhogan@ucdavis.edu)

The mountain gorilla (*Gorilla beringei beringei*) is a critically endangered species, with 480 living within the Virunga Massif in Rwanda, Democratic Republic of Congo, and Uganda, and approximately 300 living in Bwindi Impenetrable National Park in Uganda. Limited habitat coupled with increased contact with humans and livestock is a concern for pathogen introduction into this species. Protozoa such as *Giardia* spp. have been found in gorillas, humans, and domestic cattle in the region. Parasite infection has been linked to increased mortality and reduced fitness in gorillas. In 2010, we conducted a survey of feces from mountain gorilla, domestic cattle, and forest buffalo (*Syncerus caffer*) residing in and near Volcanoes National Park, Rwanda. Using direct fluorescent antibody tests, we determined that 8.5% of gorilla (n=130) feces sampled were positive for *Giardia*, and present within 33% of the gorilla groups (5/15 groups surveyed). By comparison, 5.9% of cattle (n=137) and 1.8% of forest buffalo (n=56) feces were positive for *Giardia*. While cattle have been identified as a potential source of pathogens for mountain gorilla, forest buffalo in this park had not been studied previously. Our findings suggest that forest buffalo may be a potential source or route of pathogen transmission between cattle and gorilla. Protocols are implemented to reduce human-gorilla contact, and a park boundary fence helps reduce domestic animal entry into the forest. Disease introduction to the critically endangered mountain gorilla remains a constant concern, and preventive measures must continue to be implemented to effectively protect this species.



[36] PREDICT: SURVEILLANCE FOR EMERGING INFECTIOUS ZONOTIC DISEASES OF WILDLIFE ORIGIN

Jonna Mazet,¹ William Karesh,² Peter Daszak,² Damien Joly,³ Nathan Wolfe,⁴ Suzan Murray,⁵ Stephen Morse⁶

¹University of California at Davis, Davis, California, USA; ²EcoHealth Alliance, New York, New York, USA; ³Wildlife Conservation Society, Nanaimo, British Columbia, Canada; ⁴Global Viral Forecasting Initiative, San Francisco, California, USA; ⁵Washington DC, USA; ⁶Columbia University, New York, New York, USA.

Presenting author: Joly, Damien (djoly@wcs.org)

Based on the premise that the majority of emerging infectious zoonotic diseases originate in wildlife species, the United States Agency for International Development has created Emerging Pandemic Threats Program to develop capacity in the developing world to detect and respond to emerging threats. A coalition of organizations led by the University of California at Davis, and including EcoHealth Alliance, Wildlife Conservation Society, Global Viral Forecasting Initiative, and the Smithsonian Institution, are implementing PREDICT, the component of the program tasked with developing the capacity for early detection of these emerging threats. Based on an iterative process of field and digital data collection and statistical computer modeling, PREDICT identifies geographic, taxonomic, and behavioural interfaces likely to lead to disease emergence. Sampling of free-ranging wildlife as well as those in the wildlife trade is occurring in 18 countries in Latin America, Central and East Africa, South and Southeast Asia. At the time of abstract submission, a total of 20,962 samples from 5,441 animals were added to the GAINS database. Samples were collected from free-ranging wildlife and hunted wildlife (74.7%), traded and market wildlife (10.7%), and other sampling sources (14.6%). A total of 24 novel viruses across 5 viral families have been discovered, based on 1) molecular characterisation only, and 2) on the percentage sequence identity between established species. Implementation of the PREDICT surveillance strategy and prioritization process will improve the capacity in hotspot countries to detect and respond to emerging disease threats.



[37] *BARTONELLA* IN KENYAN CARNIVORES: AN EMERGING PATHOGEN OF CONSERVATION AND PUBLIC HEALTH CONCERN

Krista L. Jones,¹ Katie C. Prager,¹ Rosie Woodroffe,² Rick W. Kasten,¹ David Y. Namekata,¹ and Bruno B. Chomel¹

¹University of California - Davis, Davis, California, USA; ²Zoological Society of London, London, UK.

Presenting author: Jones, Krista (kljones@ucdavis.edu)

Bartonella species are emerging bacterial pathogens of concern in wildlife, domestic animals, and people, perhaps particularly in sub-Saharan Africa. 1) Wildlife: exposure has been noted in several rare carnivore species, where infection may reduce population health; common carnivores could serve as a bridge for transmission between domestic dogs and wildlife of conservation concern. 2) Domestic animals: domestic dogs may serve as a pathogen reservoir and/or a bridge for transmission between humans and wildlife; yet, infection is likely to go unrecognized due to lack of veterinary care. 3) People: high incidence of HIV in Africa increases the risk that infection will lead to acute symptoms. Determining current prevalence is the first step in understanding the role carnivores play in the ecology of *Bartonella* and in exploring the potential for such infections to negatively affect these carnivore populations. Therefore, we used IFA on serum samples to investigate the hypotheses that: 1) carnivores of the Ewaso ecosystem of Kenya serve as hosts of *Bartonella*; and 2) seroprevalence in common carnivores (jackals and hyenas) is high on community lands, where the domestic dog population is dense and receives low veterinary care. Members of all species tested were seropositive for *Bartonella*, with seroprevalence varying from 1.9% (spotted hyenas) to 66.7% (African lions). Logistic regression indicated that site and year of capture had significant effects on seroprevalence, while land type did not. Further research is needed to determine whether these patterns were transient or remain constant over time and to elucidate factors contributing to these trends.



[38] PREDICTING TICK INVASION: SPREAD OF THE LYME DISEASE VECTOR *IXODES SCAPULARIS* IN CANADA

Patrick Leighton,¹ and Nicholas Ogden^{1,2}

¹*Faculty of Veterinary Medicine, University of Montréal, Saint-Hyacinthe, Québec, Canada;* ²*Centre for Food-borne, Environmental & Zoonotic Infectious Diseases, Public Health Agency of Canada – Agence de la santé publique du Canada, Ottawa, Ontario, Canada.*

Presenting author: Leighton, Patrick (patrick.a.leighton@umontreal.ca)

Over the past two decades *Ixodes scapularis*, the primary tick vector of Lyme disease in eastern North America, has expanded its range northward from the USA to colonize new regions in southern Canada. Since 1990, ticks have been collected across Canada and submitted to national authorities by veterinarians, medical practitioners, and the general public, providing a unique picture of the northward spread of *I. scapularis* populations. We used this 19-year time series to model the spread of *I. scapularis* in Canada in order to identify factors influencing the speed and direction of spread. Our results point to both long-distance dispersal of ticks by migratory birds and local dispersal by resident hosts as important mechanisms underlying patterns of range expansion for *I. scapularis*. Annual temperature (degree-days) was the most important determinant of environmental suitability for tick establishment, suggesting that tick range expansion may be facilitated by climate warming. Model projections suggest that *I. scapularis* range will expand substantially in the coming decade, resulting in a substantial increase in the risk to humans of Lyme disease, with the proportion of the human population of eastern Canada inhabiting areas with established tick populations increasing from approximately 20% in 2010 to over 80% by 2020. This first empirical model of *I. scapularis* range expansion provides an important estimate of the relative influence of host dispersal mechanisms and habitat suitability on the process of tick invasion at the continental scale, and a new tool to guide surveillance and focus interventions on the most critical areas.



[39] GASTROINTESTINAL PARASITES IN NON-HUMAN PRIMATES (NHPS) WITH CLOSE CONTACT TO HUMANS IN THE PERUVIAN AMAZON

Marieke H. Rosenbaum,¹ Jorge Núñez,² Carmen Lucas,² Bruno Gherzi,³ Patricia Mendoza,⁴ Silvia M. Montano,⁵ Kimberly A. Edgel,² Andres G. Lescano,², and Joseph R. Zunt⁶

¹Cummings School of Veterinary Medicine at Tufts University, Grafton Massachusetts, USA; ²Department of Parasitology, NAMRU-6, Lima Peru; ³Emerging Infections Department, NAMRU-6, Lima Peru; ⁴Wildlife Conservation Society, Lima Peru; ⁵Department of Bacteriology, NAMRU-6, Lima Peru; ⁶Department of Global Health, University of Washington, Seattle Washington, USA.

Presenting author: Rosenbaum, Marieke H. (marieke.rosenbaum@tufts.edu)

Similar and identical species of gastrointestinal parasites are known to infect humans and non-human primates (NHPs), however Peru has little published research on parasites in NHP populations, and a rich human-NHP interface exists that has not been systematically studied. Because of their physiological similarity and sympatry with humans, understanding the degree to which NHPs harbor zoonotic parasites will further our understanding of the role human-NHP interactions play in bidirectional parasite transmission. We examined the prevalence of gastrointestinal parasites in captive NHPs that had close contact with humans. Thirty-six fecal samples from spider monkeys (*Ateles chamek*, n=8; *Ateles belzebuth*, n=1) and woolly monkeys (*Lagothrix lagothricha*, n=27) have been analyzed from 2 sanctuaries housing NHPs rescued from homes, zoos, markets, and circuses. Fresh and sodium acetate formalin (SAF) fecal concentration smears were evaluated by microscopy to detect gastrointestinal helminths and protozoa. Kinyoun acid-fast staining was performed using both fresh and SAF-concentrated samples to identify coccidial species via microscopy. Gastrointestinal helminths or protozoal parasites were found in 91.7% (n=33/36) of NHPs, the most common being *Trichomonas* sp. (75%, n=18/24), *Blastocystis* sp. (63.8%, n=23/36), *Entamoeba* sp. (63%, n=23/36), *Cryptosporidium* sp. (59.3%, 16/27), hookworm (47%, n=17/36). *Trichuris trichiura* (11%, n=4/36), *Ascaris* sp. (11%, n=4/36), and *Giardia* sp. (2.7%, n=1/36). PCR and genetic sequencing will be used to confirm and identify species. These preliminary results provide an initial cross-sectional view of parasitic infections in NHPs and will serve as base-line data for future descriptive studies of zoonotic parasitism in NHPs.



[40] B-VIRUS SHEDDING RATES DETERMINED BY PCR IN CULLED FREE-RANGING LONG-TAILED MACAQUES (*MACACA FASCICULARIS*) IN MALAYSIA

Melinda K. Rostal,¹ Mei-Ho Lee,¹ Tom Hughes,¹ Anthony Griffiths,² Mallory Harden,² Jeffrine Japning Rovie-Ryan,³ Frankie Thomas Sitam,³ Mislih M. Basir,^(3,4) Joseph Fair,⁵ Jonathan H. Epstein,¹ and Peter Daszak¹

¹EcoHealth Alliance, New York, New York, USA; ²Texas Biomedical Research Institute, San Antonio, Texas, USA; ³Wildlife Genetic Resource Banking Laboratory (WGRB), Department of Wildlife and National Parks Peninsular Malaysia (PERHILITAN), Kuala Lumpur, Malaysia; ⁴Office of The Deputy Director General, Department of Wildlife and National Parks Peninsular Malaysia (PERHILITAN), Kuala Lumpur, Malaysia; ⁵Global Viral Forecasting Initiative, San Francisco, California, USA.

Presenting author: Rostal, Melinda (mrostal@gmail.com)

B-virus (Macacine herpesvirus 1) is an emerging infectious disease that is endemic to Southeast Asia and has a human case fatality rate approaching 70% in untreated patients. Despite being endemic in Asia, the virus has only been diagnosed in humans having close contact with macaque monkeys in the US and Canada. Studies in free-ranging macaques suggest an 81% seroprevalence of B-virus antibodies; however, this does not necessarily correlate with the threat of human transmission as they only shed sporadically. The Malaysian Department of Wildlife and National Parks is culling free-ranging, long-tailed macaques (*Macaca fascicularis*) to control the urban population. PCR to detect B-virus was performed on 82 samples from 41 culled macaques. Of these, 73% of animals (30/41) tested positive, 64% (27/42) and 55% (22/40) of oropharyngeal and urogenital samples (respectively) were positive. Fourteen of the 30 positive animals tested were positive on both oropharyngeal and urogenital swabs. Fourteen samples were partially sequenced and were 97-100% identical at the nucleotide level to the B-virus genome from GenBank. While it is well documented that nearly all adult macaques are seropositive, the rate of viral shedding has not been previously documented. Viral isolation was not attempted, as this requires a biosafety level 4 laboratory, but the presence of viral DNA in saliva and urine is suggestive of current or recent shedding. These results have implications for the risk of transmission to humans in many public recreational or religious (e.g. temples) areas where human-macaque contact frequently occurs.



[41] PREVALENCE OF ZONOTIC ENTERIC PATHOGENS IN WILDLIFE, LIVESTOCK, AND SOIL ON BEEF, DAIRY, AND SWINE FARMS IN ONTARIO

Sarah Totton,¹ Logan Flockhart,¹ Nicol Janecko,^{2,3} Jane Parmley,² Angela Cook,⁴ Richard Reid-Smith,² and Claire Jardine¹

¹Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ²Laboratory for Foodborne Zoonoses, Public Health Agency of Canada, Guelph, Ontario, Canada; ³Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ⁴Integrated Enteric Pathogen Surveillance Division, Public Health Agency of Canada, Guelph, Ontario, Canada.

Presenting author: Jardine, Claire (cjardi01@uoguelph.ca)

Zoonotic enteric pathogen control begins on the farm; however, little is known about the farm environment's role in pathogen maintenance. To estimate prevalence of enteric pathogens we collected fecal samples from livestock and wildlife (skunks and raccoons) and soil from outside barns on eight swine, eight beef and nine dairy farms in Ontario in 2010. *Campylobacter* was isolated from livestock and wildlife on all farm types. Prevalence of *Campylobacter* did not differ ($p>0.05$) between wildlife samples collected from beef (28%; 5/18), dairy (60%; 3/5) or swine (56%; 19/34) farms. Prevalence of *Campylobacter* was higher ($p=0.01$) in pigs (88%; 19/32) than dairy cattle (58%; 21/36); prevalence in pigs was not different ($p=0.7$) from that in beef (71%; 17/24). Prevalence was higher in livestock than wildlife on beef and swine farms ($p=0.01$ and 0.006, respectively). Soil was not tested for *Campylobacter*. *Salmonella* was found in wildlife, livestock and soil samples from all farm types. There were no significant differences in prevalence of *Salmonella* in livestock, wildlife or soil between farm types. However, on dairy farms, prevalence in wildlife (40%; 2/5) was higher ($p=0.01$) than that from soil (1%; 1/89). On beef and dairy farms, wildlife and livestock shared no *Salmonella* serotypes. On swine farms *S. Agona*, *Braenderup*, *Livingstone*, and *Typhimurium* were identified in both pigs and wildlife. The high prevalence of *Salmonella* and *Campylobacter* in feces from wildlife near farms suggests that wildlife may play a role in the epidemiology of these enteric pathogens. This may have important implications for pathogen control on the farm.



[42] HOW MANY PARASITES ARE THERE IN A HEALTHY ECOSYSTEM?

Andy Dobson,¹ Ryan Hesinger,² Armand Kuris,² and Kevin Lafferty³

¹*EEB, ENo Hall, Princeton University, Princeton, New Jersey, USA;* ²*Ecology Department, UC Santa Barbara, Santa Barbara, California, USA;* ³*USGS, Santa Barbara, California, USA.*

Presenting author: Dobson, Andy (dobson@princeton.edu)

We present results that describe large scale sampling dissections of three relatively healthy salt-marshes in coastal California and Baja, Mexico. The analysis allows us to estimate the abundance and biomass of all free-living and parasitic species (visible by light-microscopy) in the ecosystem. Apparently healthy ecosystems are dominated by many species of parasites and pathogens! We initially use these data to illustrate how intimately embedded parasites and pathogens are in the food web of each ecosystem. We then estimate the total biomass of the parasite species – this exceeds that of the major vertebrate group in the ecosystem. Finally we describe the underlying allometric and energetic scaling laws that provide a good quantitative description for the abundance of parasites and free-living species at each trophic level. The results provide important insights that need to be tested in other ecosystems.



[43] RETROSPECTIVE SEROSURVEY FOR *NEOSPORA CANINUM* IN A HERD OF PERE DAVID'S DEER (*ELAPHURUS DAVIDIANUS*)

Priya Bapodra,¹ Michael T. Barrie,² Michelle Verant,³ Summet Gupta,⁴ and Barbara A. Wolfe¹

¹The Wilds, Cumberland, Ohio, USA; ²Columbus Zoo and Aquarium, Powell, Ohio, USA; ³University of Minnesota, College of Veterinary Medicine, Saint Paul, Minnesota, USA; ⁴Ohio State University, Veterinary Medical Center, Columbus, Ohio, USA.

Presenting author: Bapodra, Priya (pbapodra@thewilds.org)

Neospora caninum is a coccidian parasite shown to cause abortion and serious production losses in cattle. Canids are definitive hosts and ungulate species function as intermediate hosts. To date, neosporosis in nondomestic ungulates has not been well characterized. The Wilds, a 10,000 acre conservation facility in southeastern Ohio, manages a large herd of Pere David's deer (*Elaphurus davidianus*) in a semi-free ranging setting on 250-plus acres. In 2008, a suspected increase in abortions led to a study of potential causes of abortion in this herd. The only consistent finding in the study was seropositivity to *N. caninum*. Unmanaged species on Wilds land that are likely involved in the *N. caninum* cycle include white-tailed deer (*Odocoileus virginianus*) and coyotes (*Canis latrans*). A current study has identified 68.2% of coyote feces collected at the Wilds to contain *Neospora*-like oocysts. A retrospective serosurvey for *N. caninum* exposure was conducted on serum samples banked from the Pere David's deer herd between 2002 and 2009. Samples were analyzed by competitive ELISA using 30% inhibition as a minimal positive result. Of 30 animals tested, 22 (73.3%) were persistently positive with high titers. Of these, 18 were seropositive within the first year of life. Four females, all original founders, have remained seronegative or borderline. While calving rates have declined over the past four years, no correlation has been found between seropositivity and poor fertility on an individual basis. Further studies will investigate the association of seropositivity with transmission potential in this cervid model.



[44] WIND FARMS, BIRDS, AND BATS: HOW MUCH MORTALITY IS ACCEPTABLE?

Renee Carleton

Berry College, Mount Berry, Georgia, USA

Presenting author: Carleton, Renee (rcarleton@berry.edu)

Towerkills, caused when migrating birds collide with tall man-made structures (radio, television, and cell-phone towers, sky scrapers, bridges, etc.), account for a significant proportion of mortality each year. As reported at our WDA annual conference in 2000, 2 to 4 million songbirds died as a result of towerkills in the late 1990's. An additional hazard, in the form of wind farms, is becoming more prevalent because of the increasing world-wide demand for energy. Wind turbines present a danger to not only birds, but bats as well. An estimated 4,700 birds, including endangered golden eagles, are killed annually at California's Altamont Pass Wind Farm and as many as 4,000 bats per year are killed at a single facility in West Virginia. These mortality estimates are likely to increase with more and more wind farms coming online around the world. The U.S. is dedicated to increasing the amount of electric power generated by wind farms from the current level of 3% to 20% by 2030. A review of wind farm-associated bird and bat mortality, planned wind power expansion, and ongoing research aimed at reducing bird and bat deaths will be presented.



[45] AN INCREASE IN ROE DEER TRAFFIC VICTIMS IN UTRECHT: IS DISEASE A CONTRIBUTING FACTOR?

J.M. Rijks,¹ J. IJzer,¹ M.J.L. Kik,¹ J.C.M..Vernooij,² R. Schoon,³ J. Nuijsl,⁴ and A. Gröne¹

¹Dutch Wildlife Health Centre (DWHC), Utrecht, The Netherlands; ²Department of Farm Animal Health, Veterinary Faculty, Utrecht University, The Netherlands; ³Terra Salica, de Zilk, The Netherlands; ⁴Fauna Management Unit Utrecht, Veenendaal de Klomp, The Netherlands.

Presenting author: Rijks, Jolianne (j.m.rijks@uu.nl)

Traffic accidents involving roe deer (*Capreolus capreolus*) are on the rise in the Province of Utrecht, The Netherlands. An investigation into the reasons for this increase included post-mortem examination of roe deer to explore the possibility of an underlying health problem in the roe deer population (N=± 2000). All roe deer with closed thoracic and abdominal cavities that died in traffic accidents during week days in 2010 were examined (n=64, out of a total of 363 killed on the road in 2010). Based on the lesions found, the roe deer were classified into three categories: healthy (only traumatic lesions), incidental findings (lesions present but unlikely to have contributed to an accident occurring), debilitating lesions (lesions likely to have contributed to the accident). In total, 47% of the roe deer was healthy, 44% had incidental findings and 9% had debilitating lesions. The debilitating lesions were all of a different nature, suggesting there was no single specific health problem in the roe deer population of Utrecht that contributed to the occurrence of the accidents. The results suggest that the increase in the number of traffic accidents was unlikely to be due to disease.



[46] PARANASAL SINUS TUMORS OF ROCKY MOUNTAIN BIGHORN SHEEP

Karen Fox,¹ Terry Spraker,² Sarah Wootton,³ Michael Miller,⁴ Ivy LeVan,⁴ Natalie Rouse,⁴ Lisa Wolfe,⁴ and Sandra Quackenbush¹

¹Colorado State University, Department of Microbiology, Immunology, and Pathology, Fort Collins, Colorado, USA;

²Colorado State University, Diagnostic Laboratory, Fort Collins, Colorado, USA; ³Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ⁴Colorado Division of Wildlife, Wildlife Research Center, Fort Collins, Colorado, USA.

Presenting author: Fox, Karen (karen.fox@colostate.edu)

The purpose of this study was to describe the gross features, histological features, and preliminary diagnostic findings for a previously undescribed lesion in bighorn sheep: paranasal sinus masses. From February, 2009 through January, 2011, we examined 75 bighorn sheep carcasses from a total of 24 herds in Colorado, and we identified 26 cases of paranasal sinus masses. Defining gross features of these masses included unilateral or bilateral diffuse thickening of the respiratory linings of the maxillary and/or frontal sinuses, with abundant seromucinous exudate in the affected sinus cavities. Defining histological features of these masses included chronic inflammation, and proliferation of both epithelial and mesenchymal cells of the mucosa and submucosa. Epithelial changes included hyperplasia of the mucosal surface epithelium, hyperplasia of submucosal glands and ducts, and neoplasia (adenocarcinoma). Mesenchymal changes included submucosal myxedema, submucosal fibroplasia/fibrosis, bone destruction, and neoplasia (myxomatous fibroma). We examined tissue samples using polymerase chain reaction (PCR) and immunohistochemistry (IHC) for Jaagsiekte sheep retrovirus (JSRV) and enzootic nasal tumor virus (ENTV) with negative results. We also performed PCR using degenerate primers for herpesviruses and identified a novel herpesvirus associated with the masses, and also present in tissues acquired from bighorn sheep lacking these masses. Ongoing efforts to identify an infectious cause for these masses include: quantitative PCR for the novel herpesvirus; PCR using degenerate primers to detect retroviruses; an experimental inoculation study; and the use of primary tissue cultures of cells derived from these masses.



[47] SURVEY OF *LEISHMANIA* SP. IN FREE RANGING NEOTROPICAL PRIMATES OF ATLANTIC AND AMAZON RAIN FOREST, BRAZIL

Marina Galvão Bueno,¹ Marcia Dalastra Laurenti,² Vania Lucia Ribeiro da Matta,² Thaíse Yumie Tomokane,² Fernando Tobias Silveiram,³ Rodrigo Del Rio do Valle,⁴ Fabio Höre,⁵ and José Luiz Catão-Dias¹

¹Universidade de São Paulo, Faculdade de Medicina Veterinária/Departamento de Patologia, São Paulo, Brasil;

²Universidade de São Paulo /Faculdade de Medicina/LIM50/HCFMUSP, São Paulo, Brasil; ³Instituto Evandro Chagas (IEC), Ananindeua/Pennsylvania, Brasil; ⁴WildLife Management /WLM, São Paulo, Brasil; ⁵ Wildlife Conservation Society/WCS, Manaus, Brasil.

Presenting author: Bueno, Marina Galvão (buenomg@gmail.com)

Leishmaniasis is a global zoonosis, with great effects on public health due to high rates of incidence, morbidity and mortality. Several studies on the role of wild mammals as reservoirs of *Leishmania* sp. have been conducted. However, little is known about the importance of neotropical primates (NTP) in the epidemiological chain of this disease. Therefore, the goal of this study was to investigate the occurrence of *Leishmania* sp. infection in free ranging NTP from the Brazilian Amazon (Rondônia and Amazonas states; n = 18) and Atlantic Forest (São Paulo state; n = 81), using an ELISA test for the presence of anti-*Leishmania* sp. antibodies. The results showed that nine *Callithrix penicillata* (11.0%), from the Atlantic forest, and one *Cebus macrocephalus* (5.5%), from the Amazon region were positive, suggesting a difference in the prevalence of *Leishmania* sp. infection between the animals from the different regions. Despite the low prevalence observed, the present results suggest the occurrence of transmission of *Leishmania* sp. among the NTP. Complementary studies, including immunohistochemistry for *Leishmania* in intact skin from ELISA- positive animals, serological TEZA-blot to investigate possible cross-reaction with *Trypanosoma cruzi* and molecular analyzes (PCR and real time PCR) searching for *Leishmania* sp. DNA, are in progress and will be correlated to serologic results in order to clarify the role played by NTP in this important zoonotic process.



[48] COMPARING POST-RELEASE MOVEMENT OF REHABILITATED HARBOR SEAL PUPS TO AGE-MATCHED WILD SEALS

Joseph K. Gaydos,¹ Ignacio Vilchis,¹ Monique Lance,² Steven Jeffries,² Austen Thomas,³ Penny Harner,⁴ Vanessa Greenwood,⁴ and Michael Ziccardi⁵

¹UC Davis Wildlife Health Center - Orcas Island Office, Eastsound, Washington, USA; ²Washington Department of Fish and Wildlife, Lakewood, Washington, USA; ³University of British Columbia, Vancouver, British Columbia, USA; ⁴Wolf Hollow Wildlife Rehabilitation Center, Friday Harbor, Washington, USA; ⁵UC Davis Wildlife Health Center, Davis, California, USA.

Presenting author: Gaydos, Joseph K. (jkgaydos@ucdavis.edu)

In the inland waters of Washington and British Columbia, the harbor seal (*Phoca vitulina*) population is considered robust and believed to be nearing carrying capacity. Females give birth in June and July and nurse for three to four weeks until weaning ends the maternal-pup bond. In areas of high human density, stranded pups often are collected and admitted to rehabilitation centers. We do not know, however, how released rehabilitated pup movement compares to that of wild weaned pups in Washington State. To help answer this question we outfitted ten rehabilitated pups and ten wild weaned pups with satellite transmitters to track and compare post-release movements between the two groups. Because of a timing disparity in the weaning of wild pups and pup release post-rehabilitation, wild seals were outfitted an average of 49 Julian days earlier than rehabilitated seals. At release, rehabilitated seals were longer and heavier than wild pups at capture, while wild pups had a larger axillary girth (all tests $P < 0.05$). After release, rehabilitated seals transmitted for shorter periods of time ($P = 0.006$), an average of 76 days compared to 135 days for wild weaned pups. Rehabilitated seals also moved a greater average daily distance ($P = .02$) and showed a greater overall movement away from the release site than wild seals ($P = .04$). Learned behavior during the brief 3-4 week nursing period when a pup is with its mother likely enables wild harbor seal pups to move less daily and remain closer to their weaning site than rehabilitated pups.



[49] CAUSES OF DEATH OF STRANDED HARBOUR SEALS (*PHOCA VITULINA*) AND GREY SEALS (*HALICHOERUS GRYPUS*) IN THE NETHERLANDS DURING A THIRTY-YEAR PERIOD, 1975-2008

Nynke Osinga,^{1,2} M. Mostafa Shahi Ferdous,¹ Danny Morick,¹ Helias A. Udo de Haes,² Paul M. Brakefield,^{2,3} Ab D.M.E. Osterhaus,⁴ and Thijs Kuiken⁴

¹Seal Rehabilitation and Research Centre, Pieterburen, The Netherlands; ²Science Faculty, Leiden University, Leiden, The Netherlands; ³Department of Zoology, University of Cambridge, Cambridge, UK; ⁴Department of Virology, Erasmus Medical Centre, Rotterdam, The Netherlands.

Presenting author: Kuiken, Thijs (t.kuiken@erasmusmc.nl)

Most postmortem studies of marine mammals last no longer than a few years, and therefore do not necessarily represent the long-term situation. We analysed strandings (n = 1286) and necropsies (n = 379) of harbour seals (*Phoca vitulina*) and grey seals (*Halichoerus grypus*) in the Netherlands from 1975 to 2008. Harbour seal strandings increased gradually during this period in correspondence with population growth, except for peaks in 1988 and 2002, when phocine distemper outbreaks reduced the population by half. Besides phocine distemper, the most common causes of death in harbour seals (n = 286) examined at necropsy were possible or known by-catch (19%), pup starvation (7%), intestinal volvulus (7%), and parasitic pneumonia (6%). Grey seal strandings were sporadic until the 1990's and increased thereafter with the species' recolonisation of Dutch waters. The most common causes of death in grey seals (n = 93) examined at necropsy were possible or known by-catch (16%), pup starvation (11%), and trauma (5%). Phocine distemper did not affect grey seals. Diagnosis of by-catch in grey seals did, but in harbour seals did not, decrease significantly between the first and second halves of the study period. These results show that harbour seals are affected more by infectious causes of death than grey seals, both sporadically from phocine distemper and annually from parasitic pneumonia. Also, by-catch remains a substantial cause of mortality, despite measures in recent years to reduce this problem. In conclusion, knowledge of long-term trends in causes of death is important to guide management of these populations of harbour and grey seals.



[50] IDENTIFICATION OF MYCOPLASMAS IN AUSTRALIAN FUR SEALS AND POSSIBLE ASSOCIATION WITH GESTATIONAL FAILURE

Michael Lynch,¹ Trevor Taylor,² Pádraig J. Duignan,³ Jane Swingler,² Marc Marenda,³ John P. Y. Arnould,⁴ and Roger Kirkwood⁵

¹Veterinary Department, Melbourne Zoo, Parkville, Victoria, Australia & School of Life and Environmental Sciences, Deakin University, Burwood, Victoria 3125, Australia; ²CSIRO Animal Health, Australian Animal Health Laboratory, Geelong, Victoria 3220, Australia; ³Faculty of Veterinary Science, University of Melbourne, Werribee, Victoria 3030, Australia; ⁴School of Life and Environmental Sciences, Deakin University, Burwood, Victoria 3125, Australia; ⁵Phillip Island Nature Parks, Cowes, Victoria 3922, Australia.

Presenting author: Lynch, Michael (mlynch@zoo.org.au)

Bacteria from the genus *Mycoplasma* are common inhabitants of the respiratory, gastrointestinal and genital tracts of mammalian species. The understanding of the pathological significance of mycoplasmas in seals is poor as few studies have utilized the specific culture techniques required to isolate these bacteria. This study surveyed for the species present in Australian fur seals (*Arctocephalus pusillus doriferus*) and investigated the association between infection and pathology. Mycoplasmas were found in the nasal cavities of 55/80 (69%) apparently healthy individuals. Eighteen isolates were identified by 16S rRNA sequencing and 3 species were identified, *M. zalophi*, *M. phocae* and *Mycoplasma* sp.-GenBank Ref. EU714238.1, all of which had previously been isolated from Northern Hemisphere pinnipeds. In addition, mycoplasmas were isolated from 5/22 (23%) of lung swabs collected at post mortem from pups, juveniles and adults. Five isolates were sequenced and *M. zalophi*, *Mycoplasma* sp.-GenBank Ref. EU714238.1 and *M. phocicerebrale* were identified. Infection was not associated with lung pathology in these age classes. Inflammatory lesions were seen in 14/36 (39%) aborted fetuses. Interstitial pneumonia characterized by a predominantly mononuclear infiltrate was observed in 6/32 individuals and 8/32 individuals had cardiac inflammatory infiltrates. *Mycoplasma. phocicerebrale* was isolated from the thymus of an aborted fetus and, 3/11 (27%) fetuses with inflammatory heart or lung lesions were PCR-positive for *Mycoplasma*. This study concludes that several species of *Mycoplasma* are part of the normal flora of the nasal cavity of Australian fur seals, and that mycoplasmas may be associated with abortion in this species.



[51] POSITIVE RESULTS IN BRUCELLOSIS SEROLOGICAL TESTS: WHAT IS YOUR DIAGNOSIS?

Jacques Godfroid,^{1,2} Ingebjørg Nymo,¹ Anett Larsen,¹ Kjetil Åsbakk,¹ Carlos G. das Neves,¹ and Morten Tryland¹

¹Section of Arctic Veterinary Medicine, Norwegian School of Veterinary Science, Tromsø, Norway; ²Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa.

Presenting author: Godfroid, Jacques (jacques.godfroid@nvh.no)

Besides *Brucella ceti* and *Brucella pinnipedialis* infections in marine mammals, *Brucella suis* biovar 4 infection in reindeer and caribou, and *B. suis* biovar 2 infection in wild boar and hare, *Brucella* spp. infection spills over from infected livestock to wildlife. This has been documented in South Carolina (USA) where feral pigs are infected with *B. suis* biovar 1 and *Brucella abortus*. Conversely, wildlife acts as a reservoir of *Brucella* spp. for livestock as shown in the Yellowstone ecosystem (USA) for bison and elk transmitting *B. abortus* to nearby cattle. Not all *Brucella* spp. are zoonotic agents (*B. suis* biovar 2) neither do all *Brucella* spp. induce gross pathology (*B. pinnipedialis* in seals). Positive serology does not allow ascertaining which *Brucella* species sensitize animals (or humans). Another limitation of serology is that exposure to bacteria such as *Yersinia enterocolitica* O:9 will induce serological cross-reactions virtually impossible to differentiate from *Brucella*. When performing serology for *Brucella* the following 2 questions must always be answered: 1) Are positive serological results indicative of a sensitization to *Brucella* spp.? 2) Which *Brucella* species is/are likely to have induced positive serology? In Alaska, it has been speculated that polar bears were exposed to *B. suis* biovar 4. In Africa, wild suidae are believed to be infected with *B. suis* although its isolation has never been reported. *Brucella* spp. could not be isolated from aborted material in seropositive Antarctic seals. These examples challenge our understanding of *Brucella* spp. at the wildlife/livestock/human interface.



[52] EXPERIMENTAL INFECTION OF BAR-HEADED GEESE (*ANSER INDICUS*) AND RUDDY SHELDUCKS (*TADORNA FERRUGINEA*) WITH A CLADE 2.3.2 H5N1 HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS

Nicole M. Nemeth,¹ Justin D. Brown,¹ David E. Stallknecht,¹ Scott H. Newman,² and David E. Swayne³

¹*Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, Georgia, USA;* ²*EMPRES Wildlife Unit, Animal Production and Health Division, Food and Agriculture Organization of the United Nations (FAO), Rome, Italy;* ³*Southeast Poultry Research Laboratory, United States Department of Agriculture/ Agricultural Research Service, Athens, Georgia, USA.*

Presenting author: Nemeth, Nicole (nmnemeth@uga.edu)

The emergence of H5N1 highly pathogenic avian influenza (HPAI) viruses has caused numerous epizootics among wild and captive waterfowl in Eurasia and Africa, with recent circulation of clade 2.3.2 viruses. Consequently, research has focused on the potential role of migratory waterfowl in virus spread and maintenance. Both Bar-headed geese (*Anser indicus*) and Ruddy shelducks (*Tadorna ferruginea*) have been implicated in the spread of H5N1 HPAI virus based on migratory patterns and involvement in multiple wild bird outbreaks in Eurasia. To examine their potential to contribute to the geographic spread of H5N1 HPAI, individuals of both species were inoculated with a clade 2.3.2 H5N1 HPAI virus. Viral shedding via the oropharyngeal cavity occurred between 1-7 days post-inoculation (DPI) in individuals of both species. Cloacal shedding was detected between 2-4 DPI in shelducks, and 3-7 DPI in geese. Four of five shelducks died or were euthanised due to severe neurologic signs between 4-7 DPI. Two of the three inoculated geese exhibited mild, transient lethargy between 6-7 DPI. Geese had relatively mild histologic lesions, with mild gliosis and perivascular cuffing in cerebrum and corresponding immunohistochemical staining of a small number of neurons. Ducks had more severe and widespread histologic lesions and corresponding immunohistochemical staining. Lesions in ducks included lymphoplasmacytic encephalitis with perivascular cuffing, vasculitis, hemorrhage, and vacuolization, pancreatic necrosis, hepatic necrosis and inflammation, and renal and myocardial degeneration. The varied susceptibility to H5N1 HPAI virus and subsequent pathogenesis between these species has important implications for viral transmission dynamics and possibly future conservation strategies.



[53] PREDICTING TRANSMISSION RATE OF AVIAN INFLUENZA VIRUS IN WILD WATERFOWL

Viviane Hénau¹, Michael D. Samuel² and Jane Parmley³

¹Department of Forest and Wildlife Ecology, University of Wisconsin, Madison, Wisconsin, USA; ²U. S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Madison, Wisconsin, USA; ³Canadian Cooperative Wildlife Health Centre, Department of Pathobiology, University of Guelph, Ontario, Canada.

Presenting author: Hénau, Viviane (henau@wisc.edu)

Wild aquatic birds play an important role in the maintenance and spread of all low pathogenic avian influenza (LPAI) viruses, which provide the precursor for the development of highly pathogenic avian influenza (HPAI) affecting domestic animals and humans. However, there is currently little scientific information about the epizootiology of avian influenza (AI) in wild birds. Based on published laboratory studies, we previously developed an AI epidemic model ("Susceptible-Exposed-Infectious-Recovered") which described the course of LPAI and HPAI infection in individual hosts. However, predicting AI dynamics in wild bird populations remains challenging because LPAI data from field studies are usually incomplete and HPAI outbreaks are rare, typically discovered after epizootiological dynamics have occurred and/or affected birds have migrated. We used a maximum likelihood approach to estimate the rate of AI infection in wild waterfowl populations by fitting the AI epidemic models to disease surveillance data. Using weekly prevalence data in hatch-year birds at post breeding and migration stopover sites in North America, we predicted probabilities of LPAI infection ranging from 0.07 to 0.27 day⁻¹. We found lower daily probabilities of infection at sites in the Pacific flyway (0.05-0.07), high probabilities in prairie Canada (0.21-0.27), and variable probabilities in eastern Canada (0.02-0.18). In addition, we used this method to estimate an infection probability of 0.03-0.06 day⁻¹ during the HPAI outbreak in mute swans (*Cygnus olor*) in France during 2006. Such information is critical for the prediction of AI dynamics in wild bird populations and the risk of spread to domestic birds.



[54] EFFECTS OF A NATURAL INFECTION WITH AN AVIAN INFLUENZA VIRUS (H13N2) ON MIGRATING LESSER BLACK-BACKED GULLS

Inge Müller,¹ Timm Harder,³ Christian Grund,³ Kamran Safi,¹ and Martin Wikelski^{1,2}

¹Max-Planck Institute for Ornithology, Department of Migration and Immuno-ecology, Schlossallee 2, 78315 Radolfzell, Germany; ²Konstanz University, Chair of Ornithology, 78457 Konstanz, Germany; ³Friedrich-Loeffler-Institute, Institute of Diagnostic Virology, Suedufer 10, 17493 Greifswald-Insel Riems, Germany.

Presenting author: Müller, Inge (imueller@orn.mpg.de)

We observed an ongoing natural infection with avian influenza virus in a population of lesser black-backed gulls (*Larus fuscus fuscus*; LBBG). Gulls are, besides ducks and shorebirds, a major reservoir for low-pathogenic avian influenza viruses. The LBBG population originated from Finland and was studied in the context of a research project on navigation and orientation during the migratory period. The birds were caught and kept in captivity for several days before they were translocated to Heligoland. Oropharyngeal and cloacal swabs for virological examination were taken immediately after catch and a second time at the day of translocation. The samples were tested for influenza A viruses by PCR and subsequently propagated on embryonated chicken eggs. An influenza A virus of the subtype H13N2 was isolated (A/lesser black-backed gull/Finland/R2265/09 [H13N2]). Through the repeated sampling we were able to observe the infection dynamics within the population. Local movements and mortality of the birds were monitored by satellite telemetry and compared to the infection status of the bird. We could show that the infection with a H13N2 low-pathogenic avian influenza virus had no effect on mortality and local movements of the birds. This suggests that the strong selection of low-pathogenic avian influenza viruses cause minimal impairment to their hosts, which facilitates the spread of the virus within a local population as well as over large distances during migration.



[55] ESTIMATION OF A DYNAMIC INDICATOR OF INDIRECT CONTACT BETWEEN WILD BIRDS AND POULTRY BASED ON REMOTE SENSING AND SATELLITE TELEMETRY

Julien Cappelle,¹ Nicolas Gaidet,¹ Sam Iverson,² John Takekawa,² Scott Newman,³ Bouba Fofana,⁴ and Marius Gilbert^{5,6}

¹CIRAD-ES, UR AGIRs, F34398 Montpellier, France; ²US Geological Survey, Western Ecological Research Center, Vallejo California, USA; ³FAO, EMPRES Wildlife Unit, Infectious Disease Group Animal Health Service, Animal Production and Health Division, Rome, Italy; ⁴Ministère des Eaux et Forêts du Mali, Bamako, Mali; ⁵LUBIES, Université Libre de Bruxelles, Bruxelles, Belgique; ⁶Fond National de la Recherche Scientifique, 1000 Bruxelles, Belgique.

Presenting author: Cappelle, Julien (julien.cappelle@cirad.fr)

Understanding and modeling the wildlife-livestock interface is essential for controlling emerging infectious diseases (EIDs). The contact rate between hosts is a key parameter for mathematical modeling of EIDs dynamics. Because modifications of the contact rate can modify greatly the epidemiologic dynamics, it is important to take into account its seasonal variability. We developed a distribution model based on satellite telemetry and remote sensing data to estimate an indicator of contacts between wild birds and domestic poultry in African villages. In the Inner Niger Delta of Mali, five Comb ducks (*Sarkidiornis melanotos*), were tracked with satellite transmitters providing GPS data for seven months. We used 250-meter spatial resolution and 8-day temporal resolution remotely sensed environmental indicators to model the distribution of these wild birds with the MaxEnt method. For each 8-day period, we estimated the potential contacts between wild and domestic birds by calculating the number of villages harbouring predicted suitable habitats for Comb ducks. A period of increased potential contacts occurred at the end of the dry season when wild birds were looking for the last suitable habitats. Comb ducks subsequently performed regional movements to reach their breeding grounds during the rainy season. We could estimate the seasonal variation of potential contacts between Comb ducks and domestic poultry. It allowed us to identify periods of potential transmission and spread of pathogens by wild birds. The estimation of the dynamics of contacts between wild and domestic animals with our method could feed epidemiological models of the wildlife-livestock interface.



[56] LAST HOPE FOR THE GREATER SAGE GROUSE (*CENTROCERUS UROPHASIANUS*) IN CANADA? LAUNCH OF A TRANSBOUNDARY, INTERDISCIPLINARY RECOVERY PROGRAM

Judit Smits,¹ Alessandro Massolo,¹ Cormack Gates,² Greg McDermid,³ and Dale Eslinger⁴

¹*Department of Ecosystem & Public Health, Veterinary Medicine, University of Calgary, Calgary, Canada;*

²*Environmental Design, University of Calgary, Calgary, Canada;* ³*Geography, University of Calgary, Calgary, Canada;*

⁴*Alberta Sustainable Resource Development, Medicine Hat, Canada.*

Presenting author: Smits, Judit (judit.smits@ucalgary.ca)

Headlines in a local newspaper “Industry blamed for bird’s demise; Sage grouse on path to extinction in Alberta” succinctly describe the problem that our interdisciplinary group of university researchers with state and provincial governments are addressing. We are applying conservation tools and actions at a regional scale, to increase the abundance and distribution of a critically endangered Greater Sage Grouse (*Centrocercus urophasianus*) subpopulation in southern Alberta. In keeping with one of WDAs priority areas, safe and effective wildlife translocation, we aim to prevent the introduction of disease, and to monitor the health of animals following translocation. This is year I of a 5-year program to augment this population on silver sagebrush ecosystems of southern Alberta. Ten adult females were captured from large, active leks in southcentral Montana. After health examinations, plus blood, choanal, cloacal and fecal samples for disease and parasite testing, the birds were identified, radio-collared and released onto two of the remaining, active leks in southern Alberta. Serology was carried out for common and important pathogens. Spatial tracking of the birds continues as their distribution and survival are being followed and all mortalities investigated. Recognizing the causal role of energy and agricultural developments in fragmenting sage-grouse habitat, industry is now working with the recovery team to restore habitat and connectivity between adjacent sage-grouse populations. The success of this program is dependent upon its cohesive, interdisciplinary and collaborative nature, involving government agencies, academia and the energy industry.



[57] FIRST REPORT OF *ECHINOCOCCUS MULTILOCULARIS* IN URBAN AND RURAL COYOTES (*CANIS LATRANS*) FROM ALBERTA, CANADA

Stefano Catalano,¹ Guilherme G. Verocai,¹ Manigandan Lejeune,² Stefano Liccioli,¹ Carmen Fuentealba,¹ Padraig J. Duignan,¹ Susan Kutz,¹ and Alessandro Massolo¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada; ²Canadian Cooperative Wildlife Health Centre Alberta, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada.

Presenting author: Catalano, Stefano (ste.cata85@gmail.com)

Hunted and road-killed coyotes (n = 90) were collected in 2009/2010 from sites within, or adjacent to, Calgary (n = 83) and Edmonton (n = 7). Full necropsy to determine cause of death and prevalence of infectious or parasitic diseases was conducted. All gastrointestinal parasites were collected in 70% ethanol and sorted using a dissecting microscope. *Echinococcus* sp. was found in 22 (24.4%) animals. Of these, 18 (21.7%) were from Calgary and 4 (57%) from Edmonton. Following initial examination using light microscopy, species identification was confirmed by multiplex PCR on adult parasites (Trachsel et al. 2007). Other parasites isolated and identified based on morphology included: *Toxascaris leonina*, *Uncinaria stenocephala*, *Ancylostoma caninum*, *Pterygodermatites* sp., *Taenia* sp., and *Alaria* sp. *Echinococcus multilocularis* is a zoonotic agent, responsible of alveolar echinococcosis in humans. Few parasitological surveys have been conducted on coyotes in Canada. A comparable survey carried out in southwestern Manitoba in the 1970's found that the prevalence of *E. multilocularis* was 23% in 43 coyotes (Samuel et al. 1978). However, the only previously reported survey for helminths in Alberta reported no *Echinococcus* species in 75 animals (Holmes and Podesta 1968). This suggests that *E. multilocularis* may be expanding its geographical range in wild canids in western Canada. The presence of this parasite within urban areas poses a potential transmission risk among coyotes, dogs and humans that warrants further investigation and development of a predictive approach to disease emergence, as well the implementation of preventive strategies.



[59] *ECHINOCOCCUS GRANULOSUS* (CYSTIC HYDATID DISEASE) IN CERVIDS IN CANADA

Janna Schurer,¹ Karen Gesy,¹ Todd Shury,² and Emily Jenkins¹

¹*Veterinary Microbiology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada;* ²*Parks Canada and Department of Veterinary Pathology, Saskatoon, Saskatchewan, Canada.*

Presenting author: Jenkins, Emily (emily.jenkins@usask.ca)

In the past, surveillance for the zoonotic parasite *Echinococcus granulosus*, the causative agent for hydatid disease, has been limited to opportunistic reports across Canada. The life cycle of sylvatic *E. granulosus* requires a canid definitive host as well as a cervid intermediate host. People become infected through the accidental ingestion of eggs passed in the feces of the definitive host. We report findings based on a literature review, search of the Canadian national wildlife database, and ongoing research in order to better characterize the current distribution and genetics of this parasite in Canada. As part of a broader geographic survey, we determined the genotype and viability of hydatid cysts recovered from 104 elk (*Cervus elaphus*) removed in the 2010 and 2011 disease control programs in Riding Mountain National Park, Manitoba. The prevalence of hydatid cysts was 8.7%, few cysts were fertile (i.e. contained protoscolices), and all cysts examined to date were the G10 cervid genotype of *E. granulosus*. All cysts found in a sympatric moose were viable, and contained large numbers of protoscolices. Cervid species may naturally vary in host suitability for *E. granulosus*; alternatively, immune response may also limit the viability of hydatid cysts in these elk. Since local indigenous people hunt both moose and elk in Riding Mountain National Park and surrounding area, further research should address whether carcass butchering and disposal practices facilitate transmission to domestic or wild carnivores, and if this parasite represents a significant public health risk in this region.



[58] SERIAL OVARIAN ULTRASONOGRAPHY IN WILD-CAUGHT WOOD BISON (*BISON BISON ATHABASCAE*)

Robert B. McCorkell,¹ Murray R. Woodbury,² and Gregg P. Adams²

¹*Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada;* ²*Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

Presenting author: Woodbury, Murray (murray.woodbury@usask.ca)

The wood bison (*Bison bison athabasca*) has been declared a threatened species. One method to ensure bison conservation is the cryopreservation of genetically significant gametes and embryos. As a first step, a detailed understanding of female bison reproductive physiology is required. Our objectives were to determine if wood bison are amenable to daily ultrasound examination and to characterize ovarian function during the non-breeding season. Ten two-year-old wood bison heifers obtained from Elk Island National Park were placed in a corral next to a handling system designed for bison and systematically trained to our routine over a period of 2 months. Once animals were conditioned to be restrained, daily transrectal examination of the ovaries was completed in 100% of attempts for 30 days (January-February). Follicle size and numbers were recorded, and individual follicles were identified serially. Blood samples were collected daily and the serum analyzed for FSH concentrations. Non-random changes were detected in the number of follicles ≥ 4 mm in diameter per day ($P < 0.05$). Each peak in follicle numbers was associated with the development of a single dominant follicle. The interval between the emergence of successive dominant follicles was 6.8 ± 0.6 days (mean $\pm$ se). The maximum diameter of the dominant follicle was 9.9 ± 0.4 mm. In conclusion, wild-caught wood bison were amenable to daily examination and blood sampling, and ovarian dynamics were characterized by wave-like development of anovulatory antral follicles. This information is useful in the development of bison-specific protocols for controlling ovarian function and subsequent assisted reproductive techniques.



[60] FAILURE TO DETECT RANAVIRUS IN TOE CLIPS AND BLOOD OF WILD GREEN FROGS, *LITHOBATES (RANA) CLAMITANS*, THROUGH PCR TESTING

María Forzán,¹ Raphaël Vanderstichel,² and John Wood³

¹Canadian Cooperative Wildlife Health Centre, Dept. of Pathology and Microbiology, Atlantic Veterinary College, Univ. of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; ²Dept. of Health Management, Atlantic Veterinary College, Univ. of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; ³Pisces Molecular LLC, Boulder, Colorado, USA.

Presenting author: Forzán, María (mforzan@ccwhc.ca)

Ranavirus (Iridoviridae) infection is a significant cause of mortality in amphibians. Detection of infected individuals, particularly reservoirs/carriers, is necessary to prevent and control outbreaks. Recently, the use of toe clips to detect ranavirus infection through PCR was proposed as a viable alternative to lethal liver sampling in green frogs (*Lithobates (Rana) clamitans*). The present study attempted to evaluate the use of blood on filter paper (FTATM cards) as a less invasive alternative to toe-clipping. A toe clip and blood sample were obtained from 118 green frogs from five separate ponds on Prince Edward Island, Canada, and tested for ranavirus DNA through PCR. Fifty-three of the frogs sampled came from ponds with confirmed ranavirus outbreaks in the past year, the remaining 65 inhabited ponds of unknown infection status. Unexpectedly, all samples (118 toe-clips and 116 blood samples, as bleeding was unsuccessful in two frogs) were negative for ranavirus DNA. The quality of the DNA in the samples and the success of the DNA extraction method were confirmed through amplification of an amphibian gene (CO1) in 14 randomly chosen samples. Results suggest that either green frogs are poor reservoirs of ranavirus and the prevalence in the wild populations of PEI is very low (<2.5%), or that toe clips and blood may be unreliable samples in detection of sub-clinical infections in frogs.



[61] SUSCEPTIBILITY OF COLOSTRUM-DEPRIVED LAMBS AND LAMBS RECEIVING COLOSTRUM TO THE CERVID ADENOVIRUS THAT CAUSES HEMORRHAGIC DISEASE IN DEER

Jennifer K. Arnall,¹ Leslie W. Woods,^{1,2} and Howard Lemkuhl³

¹*Wyoming State Veterinary Laboratory, University of Wyoming, Laramie, Wyoming, USA;* ²*California Animal Health and Food Safety Laboratory System, School of Veterinary Medicine, University of California, Davis, California, USA;* ³*National Animal Disease Center, USDA-ARS, Ames, Iowa, USA.*

Presenting author: Woods, Leslie W. (lwwoods@ucdavis.edu)

Fourteen 3-week-old Rambouillet/Hampshire lambs were inoculated via the mucous membranes of the eyes, nose and mouth and transtracheally with cervid adenovirus and monitored for clinical signs until necropsy three weeks post-inoculation. Seven lambs were colostrum-deprived and seven had received colostrum. Pre-inoculation and post-inoculation serum samples were tested for antibody to the cervid adenovirus, ovine adenovirus type 7, bovine adenovirus type 7 and goat adenovirus type 1. Virus isolation was performed using fetal deer lung cells, on pre-inoculation and 4-day post-inoculation nasal swabs, and on homogenates of tissues collected at necropsy. A complete selection of tissues was evaluated for microscopic changes, and immunohistochemistry was performed on a select group of tissues using a polyclonal antibody to cervid adenovirus. Polymerase chain reaction tests were performed on pre-inoculation and 4- and 8-day post-inoculation nasal, tonsil, urine and rectal swabs and all tissues collected at necropsy using primers that identify the fiber portion of the cervid adenovirus genome. No clinical signs, gross or microscopic lesions consistent with cervid adenovirus infection of deer were seen. Results of PCR tests were all negative for cervid adenovirus. Virus was not isolated from the nasal swabs or lung/tonsil/nasal swab homogenates. Immunohistochemistry results did not demonstrate cervid adenovirus in any of the tissues examined. Results of this study demonstrate that lambs (receiving colostrum and colostrum-deprived) do not develop clinical disease when exposed to the cervid adenovirus that causes hemorrhagic disease in deer. This study also suggests lambs do not become infected with, replicate and shed the cervid adenovirus.



[62] *CRYPTOSPORIDIUM PARVUM* AND *GIARDIA LAMBLIA* IN SMALL AND MEDIUM SIZE MAMMALS IN FRAGMENTED LANDSCAPES ALONG THE CUITZMALA RIVER IN THE STATE OF JALISCO, MEXICO

Omar García-Suárez,¹ Antonio Tapia-Palacios,² Ana Cecilia Espinosa,² Mariza Mazari-Hiriart,² and Gerardo Suzán¹

¹Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Circuito Exterior, Ciudad Universitaria, Coyoacán, México, México; ²Instituto de Ecología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Circuito Exterior, Ciudad Universitaria, Coyoacán, México, México.

Presenting author: García-Suárez, Omar (ogs_concolor@hotmail.com)

Cryptosporidium parvum (CP) and *Giardia lamblia* (GL) are distributed worldwide affecting several domestic animal hosts with little known in wildlife. We identified: 1) the prevalence of these parasites among small and medium-size mammals in western Mexico, 2) the relationship of prevalence with richness and diversity, and 3) the relationship of prevalence with habitat fragmentation. We selected 12 sites along the Cuitzmala River, state of Jalisco, Mexico. We classified 6 sites as forested and 6 sites as disturbed using GIS. Animals were captured with Sherman and tomahawk traps and we collected feces for all individuals in September 2010. We used immunofluorescent microscopy to identify both parasites. Species richness and diversity was compared with the Shannon index (SI). A total of 89 individuals were captured and the prevalence of CP was 23% and no individuals were positive to GL; forested sites showed lower richness (7 species), higher diversity (1.304 SI) and lower CP prevalence (14.2%), while disturbed sites showed higher richness (8 species) and lower diversity (1.244 SI) with a higher prevalence (20%). The dominant species *Liomys pictus* had the highest prevalence (27%) followed by *Oryzomys cuesi* (20%). To our knowledge, this is the first report of CP in these species, and further studies are needed to understand the dynamics of this parasite and the presence of GL in other species. Larger spatial-scale studies should be implemented to understand the relationship of habitat fragmentation with pathogen dynamics.



[63] BODY CONDITION, IMMUNOCOMPETENCE AND PARASITES IN CONTRASTED POPULATION OF ROE DEER: A FIRST SIGHT INTO THE VICIOUS CIRCLE

Gilot-Fromont Emmanuelle,¹ Ferté Hubert,² Benoit Etienne,³ Gaillard Jean-Michel,¹ Gibert Philippe,⁴ Bonenfant Christophe,¹ Mastain Olivier,⁴ and Klein François⁴

¹Université de Lyon, Villeurbanne cedex, France; ²JE 2533 -USC ANSES « VECPAR » UFR de Pharmacie, Université de Reims Champagne -Ardenne, Reims, France; ³UMR INRA ENVL ISARA 1233, VetAgro-Sup, Marcy l'Etoile, France; ⁴Office National de la Chasse et de la Faune Sauvage, Studies and Research Department, Paris, France.

Presenting author: Gilot-Fromont, Emmanuelle (e.gilot@vetagro-sup.fr)

Parasites are generally expected to stimulate immunity and host protection. However, the recent hypothesis of “vicious circle” proposes that, by altering host body condition, parasites decrease the level of resources available for immunity, thus favouring new infections in the same hosts. According to this hypothesis, the most heavily parasitized individuals should have the lowest body condition and immunocompetence. We report results of a cross-sectional survey comparing two populations of roe deer (*Capreolus capreolus*) living in habitats with different climate and resources in France. Blood and feces were sampled from 186 individuals captured between December 2009 and March 2010. Hematological, biochemical and immunological parameters were determined and parasites were detected by coproscopy. We analyzed variations in parasite abundance estimated as fecal egg/larval counts for gastrointestinal strongyles, *Nematodirus*, *Trichuris*, *Capillaria*, *Dictyocaulus*, *Protostrongylids* and *Eimeria*. After taking into account age, sex, date and population, we tested if parasite abundance was correlated to 1) host body condition (body mass, red blood cell parameters, proteins and carbohydrates levels) and 2) humoral and cellular measures of immunocompetence (globulins, haptoglobin, natural antibodies, complement, neutrophils, eosinophils, lymphocytes, monocytes). Parasite abundance was generally negatively correlated to host body condition as measured by body mass, hemoglobin, albumin and creatinine levels. However it was always positively related to immunocompetence: significant relationships were obtained with alpha1- and alpha2-globulins, natural antibodies, complement, neutrophils and lymphocytes, suggesting that parasitism was not accompanied by immune impairment, at least in a cross-sectional scheme. Longitudinal analyses are now required to further analyze these relationships.



[64] SEASONAL FLUCTUATIONS IN RUMINANT BODY CONDITION: EFFECTS OF RAINFALL, PARASITES AND SEX

Wendy C. Turner,¹ Wilferd D. Versfeld,² J. Werner Kilian,² and Wayne M. Getz^{3,4}

¹Department of Environmental Science, Policy & Management, University of California, Berkeley, Berkeley, California, USA; ²Etosha Ecological Institute, Ministry of Environment and Tourism, Etosha National Park, Namibia; ³Department of Environmental Science, Policy & Management, University of California, Berkeley, Berkeley, California, USA and

⁴Mammal Research Institute, Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa.

Presenting author: Turner, Wendy C. (wturmer@berkeley.edu)

Ruminant body condition fluctuates seasonally in response to changes in energy requirements, foraging patterns and resource availability. Gastrointestinal (GI) parasite infections also fluctuate seasonally and can reduce host body condition and enhance predation risk in heavily parasitized individuals. Our goals were to a) examine the effects of rainfall and parasitism on body condition of a ruminant species and b) assess how the expected relationship between GI parasite infection and reduced host body condition varied for a species with known sex differences in predation risk. Using data from four years and three study areas, we investigated the influence of rainfall on GI parasite prevalence and intensity and how these factors influenced springbok (*Antidorcas marsupialis*) body condition in Etosha National Park, Namibia. Rainfall affected body condition through multiple pathways: increased rainfall improved body condition as a result of nutrient gains from improved vegetation, though increased rainfall also led to an increase in parasite infections, which limited the ability of parasitized individuals to improve body condition. Strongyle nematodes were associated with reduced host condition in adult females but not in males, perhaps due to sexual segregation and differential predation risk between social groups. Adults were more likely to be parasitized by strongyle nematodes and to be in poorer body condition than other age classes. Parasitism fluctuated strongly between wet and dry seasons but was minimally affected by variation in rainfall abundance between wet seasons, indicating that the detrimental effects of parasites may be amplified in drier years when animals have reduced forage abundance and quality.



[65] THE CURRENT STATUS AND THE PREVENTION OF RABIES IN KOREAN RACCOON DOGS (*NYCTEREUTES PROCYONOIDES KOREENSIS*)

Sun-A Kim and Nam-Shik Shin

Lab of Zoo & Wildlife Medicine, College of Veterinary Medicine, Seoul National University, Seoul, Korea.

Presenting author: Kim, Sun-A (sunakim@snu.ac.kr)

Raccoon dogs (*Nyctereutes procyonoides*) are mainly distributed in eastern Siberia, eastern China, northern Vietnam, Japan, and Korea. It has become increasingly one of the important rabies hosts. This fatal zoonosis has become an important public health concern in South Korea because of a recent epidemic of rabies virus that spread through the raccoon dog population. First reported in a canine in 1906, after the intensive introduction of the vaccine program, cases of rabies dramatically decreased and no outbreaks were seen from 1985 to 1992. However, in 1993, there was an outbreak of rabies in several species of animals. Since then, cases of rabies were observed among dogs, cattle and raccoon dogs until 2010. The national animal rabies eradication program has been formed to reduce rabies outbreaks by annual vaccination of dogs and cattle since 1995, and oral vaccination of raccoon dogs has been used with annual vaccinia-rabies glycoprotein (V-RG) bait vaccine in Gyeonggi and Gangwon provinces since 2001. To evaluate the efficacy of the oral rabies vaccination in applied areas, antibodies against rabies were measured by the fluorescent antibody virus neutralization (FAVN) test in 50 captured raccoon dogs resulting in 20 raccoon dogs testing sero-positive against rabies. This study showed the importance of rabies prevention among wild animals in order to determine the suitability of various management techniques associated with veterinary and ecological programs.



[66] THE *CHRYSO Sporium* ANAMORPH OF *NANNIZZIOPSIS VRIESII* IN FREE RANGING REPTILES

Jean A. Paré

Global Health Program, Wildlife Conservation Society, Bronx, New York, USA.

Presenting author: Paré, Jean A (jpare@wcs.org)

The *Chrysosporium* anamorph of *Nannizziopsis vriesii* (CANV), an ascomycetous onygelanean fungus, has emerged as the most important fungal pathogen of captive reptiles over the last few decades. This white, powdery, keratinophilic fungus has limited thermotolerance and is characterized microscopically by a combination of aleurioconidia and arthroconidia. It has been, and still is repeatedly misidentified as *Trichophyton*, *Geotrichum*, *Malbranchea*, among others. The ecology of the CANV is poorly understood, but it is not part of the cutaneous mycobiota of healthy reptiles. All but one of the 30 + deposited CANV reptile isolates were recovered from reptiles with lesions. Molecular data shows that CANV isolates, although morphologically indistinguishable, are a cluster of closely-related organisms, of which two have now been renamed. The CANV causes progressive, often disfiguring, deep granulomatous fatal dermatomycosis in squamates and sometimes crocodilians, and is the agent of “Yellow Fungus Disease” in bearded dragons (*Pogona vitticeps*). This fungus can act as a primary pathogen and is contagious with the potential for epidemics to occur. CANV affects captive terrestrial and aquatic reptiles, but evidence now strongly suggests it also can cause disease in free-ranging reptiles. The CANV has been diagnosed in wild, or very recently caught, file snakes (*Acrochordus* spp.) in Australia, and water snakes (*Nerodia* spp.) and massasauga rattlesnakes (*Sistrurus catenatus*) in North America. Only through a heightened awareness among wildlife professionals will this condition be recognized and recorded so that we gain a better understanding of its significance and potential impact in wild reptile populations.



[67] OCCURRENCE OF THE PATHOGENIC FUNGUS, *BATRACHOCHYTRIUM DENDROBATIDIS*, AMONG AMPHIBIANS OF THE SIERRA GORDA BIOSPHERE RESERVE, QUERÉTARO, MEXICO

Richard G. Botzler,¹ Sean Rovito,² Cinthya Mendoza Almeralla,² and Gabriela Parra Olea²

¹Peace Corps México, Querétaro, México; ²Instituto de Biología, Universidad Nacional Autónoma de México, Mexico, D.F.

Presenting author: Botzler, Richard (botzlerr@sbcglobal.net)

The chytrid fungus, *Batrachochytrium dendrobatidis*, has been linked with the extinction of over 100 species of amphibians in the world, and the decline of numerous others. To date, it has been found in 8 of the 32 states of Mexico. The Sierra Gorda Biosphere Reserve, Querétaro, Mexico, has many unique amphibian species in an area rich with biodiversity; many are known to be vulnerable or are closely related to vulnerable species. Skin swabs were made of 90 metamorphosed amphibians, and buccal swabs were made from 17 tadpole samples in five regions of the Reserve ranging from pine oak forests to semi-desert, with elevations ranging from 491 to 2102 meters. Of 52 samples tested to-date using a real-time polymerase chain reaction test, 10 (19%) were positive for *B. dendrobatidis*: among metamorphosed animals this included 4/28 *Incilius (Bufo) nebulifer*, 4/9 *Rhinella (Bufo) marinus*, 0/4 *Bufo* spp. (Bufonidae), 1/4 *Lithobates (Rana) berlandieri* (Ranidae), and 1/2 *Smilisca baudini* (Hylidae); chytrid levels generally were low. Among buccal swabs, prevalence was 0/5 for *Lithobates* spp. tadpoles. These are the first known reports for *B. dendrobatidis* among all four infected amphibians and this is a range extension for chytrids to the State of Querétaro, México.



[68] ASSESSMENT OF REPTILE AND MAMMAL DISEASE PREVALENCE ON CHRISTMAS ISLAND

Jane Hall,¹ Karrie Rose,¹ Shannon Donahoe,¹ David M. Spratt,² Craig Smith,³ Carol De Jong,³ and Hume E. Field³

¹Australian Registry of Wildlife Health, Taronga Zoo, Mosman NSW Australia; ²CSIRO Ecosystem Sciences, Canberra ACT, Australia; ³Queensland Centre for Emerging Infectious Diseases, Biosecurity Queensland, Department of Employment, Economic Development and Innovation, Coopers Plains Qld, Australia.

Presenting author: Rose, Karrie (krose@zoo.nsw.gov.au)

Christmas Island, an Australian territory located in the Indian Ocean, has undergone significant ecological alterations over the past century including; human settlement and infrastructure development, vegetation shifts, phosphate mining, and multiple introductions of invasive plants, vertebrate and invertebrate animals. Christmas Island has had a well documented history of endemic species extinctions and recently, a marked decline in the remaining endemic species has been documented. Current fieldwork indicates that the reptilian fauna of Christmas Island is most at risk, with four or five of the six native reptile species nearing extinction. At the request of the Director of National Parks (DNP), we assembled a diverse, multi-disciplinary team to undertake an assessment of the health of the reptile and mammal fauna of the island that dovetails with other ecosystems-based research. Although the investigation did not identify a single organism or toxin of high pathogenicity, we did identify: multiple parasites with a new host or geographic record; multiple parasites with the ability to be transmitted from feral and native host species; undescribed parasite species; the absence of widespread, naturally occurring or anthropogenic heavy metal toxins; no evidence of viral pathogens within reptiles; seven potentially zoonotic agents, identified within both native and feral wildlife. The results of this study have been used to develop a disease risk assessment for species conservation activities including recommendations for captive breeding, animal translocation and re-introduction. A program for additional investigations and ongoing health monitoring has also been developed.



[69] HEALTH ASSESSMENTS OF RADIATED TORTOISES (*ASTROCHELYS RADIATA*) IN MADAGASCAR

Bonnie L. Raphael,¹ Berni Leahy,¹ Brian D. Horne,¹ Herilala Randriamahazo,² and Richard D. Hudson²

¹Wildlife Conservation Society global Health Program, Central Park Zoo and Global Conservation Program, Bronx, New York, USA; ²Turtle Survival Alliance, Fort Worth, Texas, USA.

Presenting author: Raphael, Bonnie L. (braphael@wcs.org)

Radiated tortoises (*Astrochelys radiata*), endemic to southern Madagascar, are undergoing a rapid and drastic decline of numbers in the wild due to anthropogenic habitat alterations and overharvesting for food and the pet trade. Health assessments, consisting of physical exams, sample collection (blood, choanal and cloacal swabs, feces, ectoparasites, and nasal flushes), weights and measurements, were performed in Madagascar during 1999 and 2010. Two free-ranging populations of animals at Cap Sainte Marie and Lac Tsimanampetsotsa, and two captive groups, at the Parc Ivoloïna in Tamatave and the Tortoise Village in Ifaty, were evaluated. White blood cell counts, total solids, hematocrit determinations and fecal analysis were performed in the field. Swabs and nasal flushes screening for mycoplasmas, herpesvirus, and ranavirus using PCR or culture, and plasma biochemistries and mycoplasma serology were performed in the USA. All samples were negative for presence of infectious disease. In one captive group there was evidence of possible plant toxicosis. The data obtained will be used to refine protocols for introductions, repatriations and translocations of animals in order to protect the health of wild populations.



[70] VARIATION OF WEST NILE VIRUS EXPOSURE IN AVIAN SPECIES WITH LAND USE

Natalie Randall,¹ Bradley Blitvich,² and Julie Blanchong¹

¹*Department of Natural Resource Ecology and Management, Iowa State University, Ames, Iowa, USA;* ²*Department of Veterinary Microbiology and Preventive Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa, USA.*

Presenting author: Randall, Natalie (nrandall@iastate.edu)

Wildlife management agencies' ability to predict where risk of disease exposure may be greatest, and to which populations, is important in devising surveillance strategies. In the Midwest U.S., existing research suggests the prevalence of West Nile Virus (WNV) in humans and mosquitoes is linked to land use, but no data are currently available for birds. Our study evaluated whether the risk of exposure to WNV in Midwestern peridomestic birds varied with land use in order to identify locations where birds were at greatest risk of encountering the virus. In addition, we explored whether a bird's likelihood of having WNV antibodies was associated with its family, age, and sampling season/year. Over two summers, we collected blood samples from birds captured in sites comprising gradients of different land uses, and tested them for exposure to WNV. Our results suggest a bird's risk of WNV exposure increased in urban areas, possibly because urban landscapes often harbor standing water favorable for mosquito vector reproduction. We also found that exposure risk was significantly greater in 2009 than in 2010. This disparity appears to be related to differences in weather, suggesting annual variation in environmental conditions may strongly influence WNV activity. Lastly, our results indicated seroprevalence was higher within the Cardinalidae, Columbidae, and Turdidae families relative to other families sampled. Heterogeneity among taxa may be due to variation in exposure, physiological response to infection, or survival. Overall, we identified several factors associated with WNV exposure in Midwestern peridomestic birds that might be useful for tailoring disease surveillance activities.



[71] VIRULENCE EVOLUTION AND HOST SUSCEPTIBILITY OF *MYCOPLASMA GALLISEPTICUM* CONJUNCTIVITIS IN HOUSE FINCHES

David H. Ley,¹ Dana M. Hawley,² Erik E. Osnas,³ Andy P. Dobson,³ Keila V. Dhondt,⁴ JL Grodio,⁴ Karel A. Schat,⁴ Wesley M. Hochachka,⁵ and André A. Dhondt⁵

¹Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina, USA; ²Department of Biology, Virginia Tech, Blacksburg, Virginia, USA; ³Department of Ecology and Evolutionary Biology, Princeton University, Princeton, New Jersey, USA; ⁴Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, New York, USA; ⁵Laboratory of Ornithology, Cornell University, Ithaca, New York, USA.

Presenting author: Ley, David H. (david_ley@ncsu.edu)

We are working to understand the evolution of *Mycoplasma gallisepticum* virulence in the ongoing epidemic of House Finch (*Carpodacus mexicanus*) conjunctivitis. These investigations were motivated by the observation that prevalence rates were far lower in western than eastern North America, and that disease prevalence had also declined in eastern North America over time. Our goal was to understand whether these spatial and temporal differences in disease prevalence were the result of host and/or pathogen evolution. We compared the responses of two populations of House Finches (east and west of the Great Plains) to experimental infections with one of two isolates of *M. gallisepticum*: the original 1994 isolate from Virginia, and a 2006 isolate from northern California. We found that differences in virulence were entirely caused by differences between the two isolates of *M. gallisepticum*, indicating that pathogen evolution was the predominant reason for virulence variation in House Finches. This raised the question as to whether the pathogen has evolved through space (from emergence in the mid-Atlantic to the Pacific coast), or time (decline in virulence in both eastern and western North America). To answer this question we compared the virulence of two eastern North American isolates of *M. gallisepticum*: the original 1994 isolate from Virginia and a 2006 isolate from North Carolina. We found increased virulence with the 2006 isolate compared to the 1994 isolate. In eastern North America, *M. gallisepticum* has apparently evolved towards increased virulence since its emergence as a pathogen of House Finches.



[72] THE ROLE OF RACCOONS IN THE EVOLUTION OF CANINE AND FELINE PARVOVIRUSES

Andrew Allison,¹ Justin Brown,¹ Mark Ruder,¹ Kevin Keel,¹ Carole Harbison,² Karla Stucker,² Jason Kaelber,² Edward Holmes,³ Israel Pagan,³ Edward Dubovi,⁴ and Colin Parrish²

¹Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA; ²Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Ithaca, New York, USA; ³Center for Infectious Disease Dynamics, Department of Biology, The Pennsylvania State University, University Park, PA 16802, USA; ⁴Department of Population Medicine, College of Veterinary Medicine, Cornell University, Ithaca, New York, USA.

Presenting author: Brown, Justin (jubrown1@uga.edu)

Canine parvovirus (CPV) is a host range variant of feline panleukopenia virus (FPV) which emerged as a pathogen in 1978 (CPV-2) and subsequently spread worldwide, infecting >80% of the world's dog population. In 1979, a variant of CPV-2 (CPV-2a) also spread globally and by 1980 had supplanted CPV-2. Although the molecular changes between CPV-2 and CPV-2a are known, the evolutionary pathways by which they arose remain obscure. Our knowledge on parvoviruses in wild carnivores is incomplete. Gastroenteritis in raccoons has historically been associated with FPV, and existing field and experimental data suggest raccoons are poor hosts for CPV. Since 2006, this paradigm has changed, as outbreaks of gastroenteritis associated with novel CPV variants have been diagnosed at rehabilitation centers throughout the Southeast. Herein we genetically and functionally characterize FPV- and CPV-derived viruses from raccoons and show that raccoons served as the intermediate host in the evolution of CPV-2a from CPV-2, and possibly in the emergence of CPV-2 from FPV. All raccoon viruses derived from FPV or CPV had substitutions in the VP2 capsid protein that altered their interactions with the cellular transferrin receptors (TfR) of different host species. The mutations also altered the antigenic structure of the capsids, as determined by virus-specific monoclonal antibody binding. Cloning and expression of the raccoon TfR showed it was genetically intermediate between the feline and canine TfRs and that it was bound by both FPV and CPV-2, supporting the role of raccoons in the host adaptation of these parvoviruses in dogs and cats.



[73] PARASITE COMMUNITY STRUCTURE, SOCIAL ORGANIZATION AND HETEROZYGOSITY IN ALPINE MARMOTS

Marie-Pierre Callait-Cardinal,^{1,2} Florence Wolff,¹ Bastien Teton,² and Dominique Allainé²

¹Université de Lyon, F-69000 Lyon; Vetagro-Sup, veterinary campus, F-69280, Marcy l'Etoile, France; ²Université de Lyon, F-69000, Lyon; Université Lyon 1; CNRS, Department of Biometry and Evolutionary Biology, LBBE UMR 5558, F-69622 Villeurbanne, France.

Presenting author: Callait-Cardinal, Marie-Pierre (mp.callait@vetagro-sup.fr)

For Alpine marmots as for a lot of other species, parasite community structure is highly unequal between individuals in the same environment, highlighted by the aggregated distribution of intestinal parasites. For this territorial, socially monogamous and cooperative breeding mammal, parasite infection is expected to be a general cost of sociality. Using capture-mark-recapture models, the effect of age, sex, dominance, family group organization and individual heterozygosity (measured at 16 microsatellites markers) on intestinal parasite community structure – prevalence, abundance, aggregation, diversity – (measured by coproscopic examination), was estimated using a Generalized Linear Model (GLM). The Alpine marmot population is dominated by 4 gut parasites: the anoplocephaloid cestode *Ctenotaenia marmotae*, the ascarid nematode *Ascaris laevis* (both in the small intestine), the oxyurid nematode *Citellina alpina* (in the large intestine) and the coccidian *Eimeria* sp. (in the small intestine). Taking into account seasonal variations of infection synchronized with hibernation, overall we found that prevalence and abundance were low in dominant adults, in juveniles (2 years-old), in females, when heterozygosity increased, for home ranges facing north and on lower altitudes. Analyses also revealed that individual parasite richness increased in dense groups one year before, and for yearlings or subordinate adults. We discuss these results in relation to promiscuity in burrows, social interactions, well developed in socially monogamous species, host immunity and different transmission strategies of parasites. Finally, the epidemiological consequences of host sociality on infection risk are relevant to understand well the role of parasites in wild populations.



[74] USE OF OTHER INFECTIOUS AGENTS IN DEER TO UNDERSTAND CWD EPIDEMIOLOGY

Champika Fernando,¹ Trent Bollinger,^{2,3} Asha Perera,² and Janet Hill¹

¹Department of Veterinary Microbiology and Immunology, Saskatoon, Saskatchewan, Canada; ²Canadian Cooperative Wildlife Health Centre, Saskatoon, Saskatchewan, Canada; ³Department of Veterinary Pathology, Saskatoon, Saskatchewan, Canada.

Presenting author: Bollinger, Trent (trent.bollinger@usask.ca)

Since being introduced into Saskatchewan with infected farmed elk in the late 1980's, chronic wasting disease (CWD) has spread into wild deer throughout western Saskatchewan and eastern Alberta. Estimates of CWD prevalence within infected Wildlife Management Zones are less than 5% but appear to be slowly increasing. Wildlife agencies are typically attempting to manage CWD by reducing deer densities through depopulation and increased hunting but measuring response to these programs is difficult due to the large sample sizes required to detect changes and by the long incubation period and environmental persistence of CWD which delays the response. Monitoring other infectious agents which have a higher initial prevalence and which have transmission characteristics similar to that of CWD but lack a prolonged incubation period may be useful in predicting changes in CWD prevalence in the longer term. Beginning in 2006 deer populations in southern Saskatchewan were surveyed using serology, fecal parasite assessment and PCR in order to identify infectious agents which may be suitable for this purpose. Based on relative host specificity, moderate prevalence and horizontal routes of transmission, herpesvirus, parainfluenza 3, *Eimeria* and *Skrjabinema* were identified as good candidates for evaluating effectiveness of disease management strategies. Mule deer lymphotropic herpesvirus is particularly promising because of its moderate prevalence, ease of sample collection and the availability of a rapid and low-cost method for its detection. The potential use of these markers to monitor disease management responses and to understand host population structure will be discussed.



[75] MODELING TRANSMISSION DYNAMICS OF CHRONIC WASTING DISEASE IN WISCONSIN WHITE-TAILED DEER

Christopher Jennelle,¹ Bala Thiagarajan,¹ Gideon Wasserberg,² and Michael D. Samuel³

¹Department of Forest and Wildlife Ecology, University of Wisconsin, Madison, Wisconsin, USA; ²Department of Biology, University of North Carolina, Greensboro, North Carolina, USA; ³U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, University of Wisconsin, Madison, Wisconsin, USA.

Presenting author: Jennelle, Christopher (jennelle@wisc.edu)

Chronic wasting disease (CWD) is a fatal neurodegenerative prion disease, occurring in free-ranging cervids. At the population level, CWD epizootic dynamics accelerate slowly and operate on the scale of decades. Management efforts (culling) have failed to eradicate or prevent the geographic spread of CWD in free-ranging white-tailed deer (*Odocoileus virginianus*) in South-Central Wisconsin. Mathematical models of wildlife diseases are useful for understanding transmission dynamics, making predictions about population trajectories, and evaluating alternative management strategies. We develop previous work by fitting harvest data from southern Wisconsin for 2002 to 2009 using a multi-state non-spatial deterministic matrix model and a maximum likelihood approach. We evaluated the effect of sex within the context of density and frequency dependent transmission, a non-linear transmission function intermediate between density- and frequency-dependence, time since disease introduction, geographic rate of spread, and the basic disease reproductive rate (R_0). Using parameter estimates from our best model (evaluated by AIC), we explored the implications of several harvest strategies with respect to projected white-tailed deer population dynamics. The model best supported by the data was a frequency-dependent sex-specific transmission model with transmission coefficients (β) of 0.60 (95% CI: 0.56-0.63) and 1.07 (95% CI: 1.00-1.14) for females and males, respectively. Using these transmission coefficients we estimated the rate of CWD spread to be between 0.43 and 1.2 miles per year. These results underscore the potential heterogeneity in mechanisms driving dynamics between sexes in this system and have direct bearing on Wisconsin's adaptive CWD management strategy.



[76] EFFECTS OF CHRONIC WASTING DISEASE ON REPRODUCTION AND RECRUITMENT IN WISCONSIN WHITE-TAILED DEER

Julie Blanchong,¹ Daniel Grear,² Byron Weckworth,³ Delwyn Keane,⁴ Kim Scribner,³ and Michael Samuel⁵

¹*Department of Natural Resource Ecology and Management, Iowa State University, Ames, Iowa, USA;* ²*Department of Forest and Wildlife Ecology, University of Wisconsin, Madison, Wisconsin, USA;* ³*Department of Fisheries and Wildlife, Michigan State University, East Lansing, Michigan, USA;* ⁴*Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin, Madison, Wisconsin, USA;* ⁵*U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, University of Wisconsin, Madison, Wisconsin, USA.*

Presenting author: Blanchong, Julie (julieb@iastate.edu)

Chronic wasting disease (CWD) is a fatal, transmissible spongiform encephalopathy affecting cervids. Although impacts of CWD on cervid survival have been documented, little is known about the disease effects on reproduction and recruitment. We used genetic methods and harvest data to reconstruct parentage for a cohort of white-tailed deer fawns born in spring 2002 and evaluated the effects of CWD infection on reproduction and recruitment. There was no difference between CWD-positive and CWD-negative male deer in the probability of being assigned as parents. However, CWD-positive females were more likely to be assigned as parents than CWD-negative females. Because our results are based on harvested animals, we evaluated the hypothesis that higher parentage assignment occurred because fawns with CWD-positive mothers were more vulnerable to harvest. Male fawns with CWD-positive mothers were harvested much earlier (>1 month) and farther away from their mothers than male fawns with CWD-negative mothers. We conclude that pre-clinical stages of CWD infection do not prohibit white-tailed deer from successfully reproducing. However, higher harvest vulnerability of male fawns with CWD-positive mothers suggests that CWD infection makes females less capable of providing adequate parental care to ensure the survival and recruitment of their fawns. Given that dispersing male deer are suspected to be primarily responsible for CWD spread, higher harvest vulnerability or lower survival rates for male fawns with CWD-positive mothers may be a mechanism for containing disease spread. Alternatively, earlier dispersal or more wide ranging movements of potentially infected fawns with CWD-positive mothers could promote disease spread.



[77] SPREAD OF CHRONIC WASTING DISEASE: DID MULE DEER DRAW THE SHORT STRAW?

Margo Pybus,¹ Mark Ball,¹ James Allen,¹ Evelyn Merrill,² Tom Habib,² Barry Nobert,² Alex Potapov,² and Eric Brownrigg²

¹*Alberta Fish and Wildlife Division, Edmonton, Alberta, Canada;* ²*Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada.*

Presenting author: Pybus, Margo (margo.pybus@gov.ab.ca)

Chronic wasting disease (CWD) is an infectious and fatal prion disease of cervids now found in over 20 states or provinces across the United States and Canada. In Canada, CWD was detected in wild deer in the prairie regions of Saskatchewan (SK) in November 2000 and in Alberta (AB) in September 2005, and has increased steadily in both provinces. Active surveillance in AB since 1998 detected 94 deer with CWD (85 mule deer, 9 white-tailed deer). The two deer species are sympatric in affected areas, and reasons for the high prevalence in mule deer in both AB (and SK) are not known. We assess information on behavioral and demographic differences between the species to try to understand why the CWD occurrence is predominantly in mule deer in the prairie-parkland system, and what this tells us about CWD transmission and spread. In terms of behavior, the home range sizes, daily movements, and migration rates were similar, but mule deer exhibited more concentrated spatial distribution, and had larger group sizes, which modelling shows increased contact rates. We also show how higher rates of reproduction in white-tailed deer may contribute to lower CWD prevalence in white-tailed deer compared to mule deer in sympatry. We discuss the implications of these findings for comparing prevalence rates among cervid species and for CWD management in this region.



[78] SUMMARY OF NATIONAL CHRONIC WASTING DISEASE (CWD) SURVEILLANCE IN WILD CERVID POPULATIONS IN THE USA BETWEEN 2003 - 2010 AND ITS APPLICATION TO FEDERAL/STATE REGULATORY POLICIES FOR PREVENTION AND CONTROL OF CWD

Patrice Klein,¹ Dallas Meek,² Dianne Norden,³ Lynn Creekmore,³ Sandra Wallace,¹ and Jennifer Dartez¹

¹USDA APHIS Veterinary Services, CWD Program, Riverdale, Maryland, USA; ²USDA APHIS Veterinary Services, Eastern Regional Office, Raleigh, North Carolina, USA; ³USDA APHIS Veterinary Services, Western Regional Office, Ft. Collins, Colorado, USA.

Presenting author: Klein, Patrice (Patrice.N.Klein@aphis.usda.gov)

National Chronic Wasting Disease (CWD) surveillance in wild cervid populations in the USA has been supported by USDA APHIS Veterinary Services (VS) since 2003. Annual surveillance data is reported to VS by each participating state and confirmatory testing of initial positive findings in wild cervid populations is conducted by USDA's National Veterinary Services Laboratory (NVSL). Since 2003, 47 - 50 states have participated annually in national CWD surveillance efforts in wild cervids. To date, an approximate total of 773,000 samples have been collected and tested for CWD from wild cervids (averaging 96,600 per year), of which, approximately 3200 have been reported to VS as CWD positive. States with CWD reported in wild cervid populations have been classified as Tier 1 states. States adjacent to Tier 1 states and/or have reported CWD in farmed cervid herds are classified as Tier 2 states. States without CWD in any cervid population are classified as Tier 3 states. Analysis of this national CWD surveillance data over the 7 year time period, which is currently underway, will guide future surveillance strategies and inform federal/state regulatory partners on future policies for prevention and control of CWD in both wild and farmed cervid populations.



[79] EXPERIMENTAL PARAPOXVIRUS INFECTION IN SEMI-DOMESTICATED REINDEER (*RANGIFER TARANDUS TARANDUS*)

Morten Tryland,¹ Jörn Klein,² Therese Berger,¹ Terje D. Josefsen,³ Carlos G. das Neves,¹ and Kjetil Åsbakk¹

¹Section of Arctic Veterinary Medicine, Department of Food Safety and Infection Biology, The Norwegian School of Veterinary Science, Tromsø, Norway; ²Department of Microbiology and Virology, University of Tromsø, Tromsø, Norway; ³National Veterinary Institute Tromsø, Tromsø, Norway.

Presenting author: Tryland, Morten (morten.tryland@nvh.no)

Contagious ecthyma occurs world-wide in sheep and goats and is caused by Orf-virus (genus Parapoxvirus, Poxviridae family). Contagious ecthyma has been described in semi-domesticated reindeer (*Rangifer tarandus tarandus*) in Sweden, Finland and Norway, sometimes with high mortality. Fourteen one-year-old semi-domesticated reindeer were corralled in mid-April, ear-tagged and adapted to feeding (lichen, hay, reindeer pellets) during five weeks. Two animals were vaccinated (Scabivax®) one week after arrival. Purified Parapoxvirus from reindeer with contagious ecthyma was inoculated in scarified oral mucosa of the two vaccinated and six additional animals, the remaining six reindeer being sentinels, all sharing feed and water. A small whitish lesion appeared on the inoculation site and the labial skin-mucosa junction of three animals five days post inoculation (p.i.). Twelve days p.i., typical ecthyma lesions were visible on the inoculation site in six of eight animals (including both vaccinees). Four inoculated animals (including both vaccinees) and one sentinel seroconverted 12 days p.i., and five animals (including two sentinels) seroconverted 20 days p.i. No contagious ecthyma-like lesions were detected in the sentinels, but four of them had small ulcers in the oral mucosa. All animals were slaughtered at 26-28 days p.i. Histological examination of lesions showed proliferative dermatitis with epidermal hyperplasia, hyperkeratosis, intra-epithelial pustules and ulcers. Orf-virus DNA was detected in lesions, mandibular lymph nodes and tonsils of four animals, including one sentinel. The incubation period for Parapoxvirus infection in reindeer is short. Virus was transmitted to sentinel animals. The commercial Orf-vaccine did not protect reindeer.



[80] VIRUS INFECTIONS IN REINDEER: A REVIEWED ASSESSMENT

Carlos G. das Neves, Alina Evans, Hanne Ihlaebek, Ingebjørg H. Nymo, Kjetil Aasbakk, Jacques Godfroid, and Morten Tryland

Section of Arctic Veterinary Medicine, Department of Food Safety and Infection Biology, The Norwegian School of Veterinary Science, Tromsø, Norway.

Presenting author: Das Neves, Carlos G. (carlos.dasneves@nvh.no)

Reindeer/caribou (*Rangifer tarandus*) is a circumpolar species and previous studies have demonstrated the presence of viruses known to cause disease in other wild and domestic ruminants. Serosurveys, PCR and cell culture have been carried out on samples from Norway, Svalbard, Greenland, Finland, Sweden, Alaska and Canada. Alpha herpesvirus have been detected in all locations except Svalbard. A specific Cervid herpesvirus 2 has been detected in Alaska and isolated in Norway where it has been reported as the primary agent of Infectious Keratoconjunctivitis. The presence of a new gamma herpesvirus in Norwegian reindeer has been shown by serology and viral DNA amplification. Parapoxvirus infections causing contagious ecthyma in the mouth of reindeer have been reported in Norway and Finland, whereas in Alaska it has been reported only in sheep. Pestivirus has been identified by serosurveys in Norway and Alaska. Parainfluenza virus type 3 has been identified in Norway by serology but is absent in Svalbard reindeer which have been negative to all tested viral agents. Results show a variety of viruses in reindeer across the Arctic, with some active episodes of disease, for which it is necessary to evaluate transmissions to other ruminants. While many of these viruses have been documented in Scandinavia, there is a lack of information about them in the rest of the Arctic. Likewise, other viruses such as bluetongue, known to infect reindeer, should be investigated. Viruses present in the Arctic can pose a risk to reindeer health and should be part of an integrated health management approach.



[81] *ECHINOCOCCUS CANADENSIS* IN FINNISH WOLVES – HOST POPULATION CHANGES, PARASITE DISTRIBUTION NOT

Marja Isomursu,¹ and Samuli Heikkinen²

¹The Finnish Food Safety Authority Evira, Production Animal and Wildlife Research Unit, Oulu, Finland; ²The Finnish Game and Fisheries Research Institute, Oulu, Finland.

Presenting author: Isomursu, Marja (marja.isomursu@evira.fi)

Echinococcus canadensis is a zoonotic tapeworm using wolves as definitive hosts and cervids, *Alces alces* or *Rangifer tarandus*, as intermediate hosts. In Finland, the parasite started re-emerging in the 1990's, shown by hydatid cysts found at reindeer meat inspection. Subsequently, surveillance in wolves was started. The Finnish wolf population is concentrated in the eastern, least human populated part of the country but during 2004-2010, the range has expanded markedly to the west with more human settlement. Contacts between wolves and people have increased and raised concerns also about zoonoses carried by wolves. The Finnish Food Safety Authority Evira carries out surveillance of wildlife diseases, including echinococcosis. All available wolf carcasses are screened for echinococcosis. Several methods have been used: sedimentation, coproantigen-ELISA and worm egg isolation with egg PCR. During 2000-2010, a total of 252 wolves were examined, 25 of which (9.9%) *Echinococcus* positive. The prevalence was highest (23%) in 2000-2002 and has since decreased to 7-9%. In the core area with high density of wolves and moose, prevalence was 46% in 2000-2010. Most positives (17) originated from known wolf pack territories whereas only two individuals were outside of any known territory. One positive wolf was juvenile (< 1 yr), 56% of the positives were aged 1-2 years and 36% 3-8 years. The prevalence of *E. canadensis* in wolves has nationally remained constant since 2003. The parasite has failed to expand its range along that of the definitive host, but the distribution remains stable in persistent core areas with wolf pack territories.



[82] SURVEILLANCE, FIRST DETECTION AND EARLY MANAGEMENT OF *ECHINOCOCCUS MULTILOCULARIS* IN SWEDEN

Erik O. Ågren,¹ Ulla Carlsson,¹ Maria Cedersmyg,² Dan Christensson,¹ Marianne Elvander,¹ Sören Höjgård,⁵ Birger Hörnfeldt,³ Mikael Juremalm,¹ Ann Lindberg,¹ Gert Olsson,³ Eva Osterman Lind,¹ Henrik Uhlhorn,¹ Helene Wahlström,¹ and Stefan Widgren¹

¹National Veterinary Institute (SVA), Uppsala, Sweden; ²Swedish Board of Agriculture, Jönköping, Sweden; ³Swedish university of agricultural sciences, Umeå, Sweden, ⁴Swedish university of agricultural sciences, Uppsala, Sweden.

Presenting author: Ågren, Erik (erik.agren@sva.se)

Surveillance of the fox tapeworm *Echinococcus multilocularis* (EM) has been carried out in Sweden by analyzing 300 hunter shot red foxes (*Vulpes vulpes*) annually since year 2000, when three positive red foxes were found in neighboring Denmark. The first EM positive fox finding in Sweden was in February 2011. This led to an intensified nation-wide surveillance, with almost 3,300 hunter shot foxes collected during the hunting season. Intestines were examined with the segmental sedimentation and counting technique followed by PCR confirmation of positive findings. In one infected area 119 fecal samples from hunting dogs were negative for EM. Vole trapping designed to identify the intermediate host has been initiated. As a more cost effective surveillance is needed, a baseline study based on systematic sampling of fox feces has been initiated in an infected area. Several authorities, including veterinary and human health institutes held weekly teleconferences to coordinate further actions as well as recommendations and information to the public. The general protective measure to prevent human infection is to have good hand hygiene routines. In the intensified surveillance, 2,996 foxes have been analyzed and another three EM positive foxes (0.11%) have been identified. As positive foxes originate from three different counties it was concluded that EM is endemic at a very low prevalence in Sweden. The extent of the infection as well as the time and route of introduction of the parasite in Sweden is still unknown.



[83] MANAGEMENT OF *TRICHODECTES CANIS* INFESTATION OF WOLVES IN INTERIOR ALASKA

Craig Gardner and Kimberlee Beckmen

Alaska Department of Fish & Game, Division of Wildlife Conservation, Fairbanks, Alaska, USA.

Presenting author: Beckmen, Kimberlee (kimberlee.beckmen@alaska.gov)

The dog louse, *Trichodectes canis*, was first detected on Interior Alaska wolves in 2004. We suspected infested wolves dispersing from Southcentral Alaska were the source. We hypothesized that louse infestation would continue to spread to other areas via wolf dispersal. Our objectives were to determine the extent of louse infestation on wolves within the Tanana Flats and to develop and test a management technique to reduce louse infestation and transmission rates. Previous attempts to eliminate lice from wolves by single treatment failed in Southcentral. We employed multiple treatments of ivermectin containing baits distributed by airplane at den and rendezvous sites during May-August. From 2005-2010 we evaluated 19 of the 22-25 packs in the study area. Estimated infestation rates were < 15% in 2005, 50% in 2006, 25% in 2007, 6% in 2008 and 0% in 2009-2010. We treated 50%, 71% and 75% of the known infested packs during 2005-2007, respectively. During 2007-2010, as a control, we monitored but did not treat 2 infested packs adjacent to and 1 within the study area. All treated packs were louse free the following winter after treatment whereas all 3 control packs remained infested. The chance of being infested following treatment was significantly lower and transmission rates within and out of the area was low. We documented the dispersal records for 14 wolves from within the treatment area; 9 were local dispersers and 5 left the area. We treated 7 of the local dispersers and 2 of the long distance dispersers prior to dispersal.



[84] MONITORING WILDLIFE DISEASES: SYNDROMIC SURVEILLANCE FOR THE DETECTION OF UNUSUAL EVENTS

Eva Warns-Petit,¹ Eric Morignat,² and Didier Calavas,² and Marc Artois³

¹UMR 5525, Laboratory TIMC, Team « Environnement et Prédiction de la Santé des Populations », VetAgro Sup – Veterinary campus of Lyon, Marcy l'Étoile, France; ²French Food Safety Agency (AFSSA)LYOntario, Lyon, France;

³VetAgro Sup – Veterinary campus of Lyon, Marcy l'Étoile, France.

Presenting author: Artois, Marc (m.artois@vetagro-sup.fr)

Our aim was to develop tools capable of detecting unusual disease events in free ranging wildlife, by adopting a syndromic approach, as used for human health surveillance. We propose to use the information registered by a national network monitoring causes of death in wildlife in France since 1986, called SAGIR. More than 50.000 cases of mortality in wildlife were recorded up to 2007, representing 244 species of terrestrial mammals and birds, and were attributed to 220 different causes of death. Facing the multiplicity of species and causes of death, syndromic classes were defined by a statistical typology of the lesions observed on the carcasses. We then carried out time series analyses on overall mortality and syndromes, using two complimentary methods of detection, one robust detection algorithm developed by Farrington and another generalized linear model with periodic terms. We established the historical trends of occurrence of these syndromes and identified greaterthanexpected counts. The revealed signals were then characterized by species and diagnosed causes of death. Reporting of unusual mortality events in the network bulletin was used to interpret the identified signals. The study analysed the relevance of the use of syndromic surveillance on this type of data and gives arguments in favour of its ability to detect some unusual disease events. It is part of a European project on the development of novel technologies for the surveillance of emerging and re-emerging infections in wildlife (WildTech).



[85] DO COYOTES (*CANIS LATRANS*) REALLY MAKE GOOD SENTINELS FOR THE DETECTION OF PLAGUE (*YERSINIA PESTIS*)?

Laurie A. Baeten,¹ Martin E. Schriefer,² Thomas W. Gidlewski,³ and Richard A. Bowen⁴

¹Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, Colorado, USA;

²Division of Vector-Borne Infectious Diseases, National Center for Infectious Diseases, Centers for Disease Control and Prevention, Fort Collins, Colorado, USA; ³National Wildlife Disease Program, USDA-APHIS-Wildlife Services, Fort Collins, Colorado, USA; ⁴Department of Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA.

Presenting author: Baeten, Laurie A (labaeten@lamar.colostate.edu)

Over the years, multiple publications have reported the use of coyotes (*Canis latrans*) in animal-based surveillance efforts for the detection of *Yersinia pestis*. Coyotes are likely exposed via both flea bite or oral routes and appear to be resistant to the development of clinical disease. This historical data has only been useful for the evaluation of the geographic distribution of *Y. pestis* in the landscape. As the canid immunological response to *Y. pestis* has not been thoroughly characterized, we experimentally inoculated captive reared juvenile coyotes with *Yersinia pestis* CO92 wild type via oral or intradermal routes. The serological response to F1 capsule was measured by passive hemagglutination over a 20 week period. Differences were noted between inoculation groups in the magnitude and duration of anti-F1 capsule antibody production. The intradermal group anti-F1 titers peaked at day 10 post-inoculation (range of 1:32 to 1:128) with titers remaining stable at 1:32 through week 12. In contrast, orally inoculated animals had higher anti-F1 titers (range of 1:256 to 1:1024) that remained stable at 1:256 to 1:512 through week 6. Re-challenge at 14 weeks post-inoculation using similar dosage and routes resulted in marked differences in antibody titers between groups. The oral group produced a striking increase in anti-F1 titer to 1:4068 within three days while there was minimal to no increase in antibody response noted in the intradermal group. Information gathered from this experimental trial may provide additional information allowing for the spatial and temporal evaluation of coyote plague serology.



[86] MANAGEMENT OF BOVINE TUBERCULOSIS IN FREE-RANGING MICHIGAN WHITE-TAILED DEER: PREDICTIONS FROM A NEW SPATIALLY-EXPLICIT MODEL

David S.L. Ramsey,¹ Daniel J. O'Brien,² Melinda K. Cosgrove,² Stephen M. Schmitt,² and Brent A. Rudolph³

¹Arthur Rylah Institute for Environmental Research, Heidelberg, Victoria, Australia; ²Wildlife Disease Laboratory, Michigan Department of Natural Resources, Lansing, Michigan, USA; ³Rose Lake Wildlife Research Center, Michigan Department of Natural Resources, East Lansing, Michigan, USA.

Presenting author: O'Brien, Dan (obriend@michigan.gov)

Bovine tuberculosis (Tb) is enzootic in free-ranging white-tailed deer (*Odocoileus virginianus*) in Michigan's northeast lower peninsula, most prevalent within Deer Management Unit (DMU) 452. While current broad management strategies (increased hunting pressure and restricted feeding and baiting) have been partially effective, refinement is needed. The extent to which hunter harvest must be increased to eradicate Tb, and the timeframe to achieve eradication, are currently unknown. To address these issues, we developed a computer simulation model of Tb in deer. Adapted from a model of Tb in New Zealand brushtail possums (*Trichosurus vulpecula*), the model is spatially explicit (to account for variation in Tb occurrence and management) and stochastic (to account for uncertainty). The model simulates behavior of individual deer with sex- and age-specific home ranges and dispersal, and sex specific Tb transmission rates. Potential management scenarios include sex- and age-specific hunter harvest, culling and vaccination, as well as local congregation of deer around bait and supplemental feed. Spatial variation in carrying capacity and the application of management are incorporated as GIS layers. Simulations in DMU 452 over thirty years suggest at least a doubling of current harvest rates is required to eradicate Tb in the presence of baiting. However, relatively small increases in harvest coupled with elimination of baiting rapidly decrease prevalence. Vaccination alone will only eradicate Tb if 90% of susceptible deer are covered annually. Tb establishment in a previously Tb-free region is substantially more likely if baiting occurs. Work to incorporate deer to cattle transmission is underway.



[87] NOVEL APPLICATION OF WIRELESS SENSOR NETWORKS TO MONITOR WILDLIFE INTERACTIONS WITH THEIR ENVIRONMENT

Lauren Charles-Smith,¹ Douglas McClusky,² Robert Fornaro,² and Suzanne Kennedy-Stoskopf¹

¹North Carolina State University, College of Veterinary Medicine, Raleigh, North Carolina, USA; ²North Carolina State University, Computer Science-Engineering, Raleigh, North Carolina, USA.

Presenting author: Charles-Smith, Lauren (lecharle@ncsu.edu)

Understanding the spatiotemporal patterns of wildlife interactions with resources in response to environmental changes is often lacking or difficult to obtain. Through advanced hardware and software programming, we have adapted micro-scale integrated processor/radio boards for placement on animals that wirelessly transmit selected information, such as temperature, humidity, atmospheric pressure and light, through an ad hoc network directly to the user's computer. This system is called a wireless sensor network (WSN). The inexpensive WSN is a unique and versatile monitoring device that is programmed so that real-time data can be wirelessly accessed from any offsite location and uploaded to a user-friendly designed GIS interface. The data can then be analyzed and incorporated into simulation models that investigate questions concerning disease transmission, resource utilization, animal interactions and movement patterns as they relate to climatic factors. The goal of this project is to show that the WSN can provide a cost effective, easy, and reliable method for monitoring the spatial and temporal relationships of wildlife, resources, and environmental factors within a given landscape. The WSN units used in stationary field trials are outfitted with GPS, thermometers, barometers, anemometers, and lumen microsensors. In addition to the sensor data, they are programmed at user-defined intervals to record date, time, and battery power. All information is sent via VHF beacons at radial distances of 0, 12, 25, and 50 meters to other nearby units, all equipped with receivers. Ultimately, data from instrumented animals will be used to develop models of disease transmission relating to climate.



[88] ASSESSMENT OF IMMUNOLOGICAL HEALTH AND MERCURY EXPOSURE IN ADIRONDACK COMMON LOONS

Keith A. Grasman,¹ and Nina Schoch²

¹*Calvin College, Dept. Biology, Devries Hall 103, 3201 Burton SE, Grand Rapids, Michigan, USA;* ²*Biodiversity Research Institute, 19 Flaggy Meadow Rd., Gorham, Maine, USA.*

Presenting author: Schoch, Nina (nina.schoch@briloon.org)

This study investigated the adaptation of lymphocyte cryopreservation and culture methods to wild loons to evaluate the effect of mercury contamination on immune function in these birds. Blood samples for mercury and immune function analyses were collected in 2008 and 2009 from 25 adult and 4 juvenile loons on 19 Adirondack lakes in New York. Lymphocytes were isolated using a slow spin technique at 150xg, and samples were frozen in culture medium containing 10% DMSO, then stored in liquid nitrogen up to 22 months, which did not significantly reduce post-thaw viability. Samples were thawed, and proliferation of specific classes of lymphocytes was induced via mitogens (phytohemagglutinin (PHA), Concanavalin-A (Con-A), lipopolysaccharide (LPS), and phorbol myristate acetate (PMA)). Proliferation was assessed by an ELISA measuring the incorporation of bromodeoxyuridine (BrdU) into newly synthesized DNA. The lymphocyte isolation, cryopreservation, thawing, and cell proliferation methods worked well for common loons. The proliferation results demonstrated low variability amongst replicates, high reproducibility upon re-running samples, and good agreement amongst mitogen treatments. Blood mercury concentrations were not directly associated with any lymphocyte proliferation indices in adult loons. In chicks, mercury showed nearly linear relationships with several lymphocyte proliferation indices, but evaluation of these potential relationships was hampered by low sample sizes. These potential relationships between altered immune function and mercury exposure in young loons are consistent with the general sensitivity of the developing immune system to contaminants, and with a previous laboratory study that demonstrated immunotoxicity of environmentally relevant exposures of mercury in young loons.



[89] NEW TOOLS FOR ELECTRONIC REPORTING AND ANALYSIS OF WILDLIFE DISEASE EVENTS

Joshua Dein,^{1,2} Megan Hines,^{1,3} Cris Marsh,^{1,3} and Xiaojin Zhu⁴

¹*Wildlife Disease Information Node;* ²*National Wildlife Health Center, US Geological Survey, Madison, Wisconsin, USA;* ³*Nelson Institute for Environmental Studies, University of Wisconsin-Madison, Madison, Wisconsin, USA;*

⁴*Department of Computer Sciences, University of Wisconsin-Madison, Madison, Wisconsin, USA.*

Presenting author: Dein, Joshua (fjdein@usgs.gov)

Early detection of health events that affect wildlife is often difficult to achieve. Once enough animals are affected, and not removed by scavengers, there must be observers in the area to take note of the event, and then have knowledge of what to do with that information. These observations are commonly made by the public and usually reported by telephone to natural resources agency personnel. However, all too often people might see such events but not know how or where to deliver this information. We will present two sets of tools. To encourage an increase of reported events, the web-based Wildlife Health Event Reporter (WHER) was developed and deployed for public use. In addition, reporting tools using mobile phones are also available through applications such as Outbreaks Near Me and Epicollect, which also can be monitored. This presentation will discuss the operation of WHER and mobile phone apps, and the findings of approximately nine months of reports. While these mechanisms are most likely used by persons such as those active in “Citizen Science” projects, others may simply be passive incidental observers who communicate through social media networks such as Twitter. Twitter “tweets” represent a very large amount of machine readable data that can be mined for potential indicators of health events. The collection, processing, and analysis of Twitter feeds to extract wildlife disease event information will also be discussed. Lastly, we will explore how the combination of these two channels of observational information can potentially improve early detection.



[90] STALKING A KILLER: WHITE-NOSE SYNDROME IN NORTH AMERICAN CAVE BATS

Anne Ballmann, David Blehert, Carol Meteyer, David Green, Valerie Shearn-Bochsler, Nancy Thomas, Brenda Berlowski-Zier, Jeff Lorch, and Laura Muller

US Geological Survey-National Wildlife Health Center, Madison, Wisconsin, USA.

Presenting author: Ballmann, Anne (aballmann@usgs.gov)

White-nose syndrome (WNS) is an emerging disease believed responsible for causing mortality of over one million insectivorous bats in the eastern United States since it was first recognized in winter 2006. WNS has been observed among bats at more than 100 sites in 17 states and 4 Canadian provinces. Thus far, six species of North American bats that rely on winter hibernation as a survival strategy are known to be susceptible, including the federally-listed endangered Indiana bat (*Myotis sodalis*). Cutaneous infection by the cold-obligate fungus, *Geomyces destructans*, causes wing damage in bats that is thought to ultimately cause death by physiological, behavioral, and/or mechanical alterations. While there is still much to be learned about disease pathogenesis, several important epidemiological factors have been identified from evaluating over 600 bat submissions to the USGS-National Wildlife Health Center. Submissions were analyzed based on date of collection, on-site location, euthanised versus dead, body condition, and WNS status. Subclinical infections were identified as early as late September and were not detected in bats submitted after the end of May. The earliest visible manifestation of infection by *G. destructans* occurred in early November. Both adult and juvenile bats are susceptible. Emaciation is not a prerequisite for WNS as live, affected bats in fair to good body condition collected inside hibernacula have been diagnosed with the disease. Conversely, the majority of bats found dead outside of affected hibernacula were emaciated. The presence of wing damage alone was a poor predictor of WNS, particularly during the summer months.



[91] LONG-WAVE ULTRAVIOLET LIGHT AS A SCREENING TECHNIQUE FOR WHITE-NOSE SYNDROME IN HIBERNATING BATS

Gregory G. Turner,¹ Carol U. Meteyer,² Hazel Barton,³ John F. Gumbs,⁴ David S. Blehert,² Laura K. Muller,² Mitzi Kaiura,⁴ and Mick Valent⁵

¹Pennsylvania Game Commission, Harrisburg, Pennsylvania, USA; ²USGS National Wildlife Health Center, Madison, Wisconsin, USA; ³Northern Kentucky University, Highland Heights, Kentucky, USA; ⁴BATS Research Center, Shohola PA USA; ⁵New Jersey Division of Fish and Wildlife, Clinton, New Jersey, USA.

Presenting author: Meteyer, Carol (cmeteyer@usgs.gov)

Geomyces destructans causes the flocculent white growth on the muzzles of hibernating bats for which white-nose syndrome (WNS) is named. Although the white muzzle is the most obvious field sign of WNS, the wing membrane is the primary site of infection, and damage to this physiologically dynamic membrane is the proposed cause of mortality associated with WNS. Identification of the characteristic histologic pattern of fungal colonization and erosion of skin is the current 'gold standard' for diagnosing WNS. Surface illumination and transillumination of wings with long-wave ultraviolet light (UV) causes a characteristic fluorescence of wings in bats with WNS. This fluorescence correlates with defined histologic sites of infection by *G. destructans*. The fluorescence of bat wings is a non-invasive field technique to screen bats for WNS and to optimize selection of wing tissue samples for confirming infection by *G. destructans*.



[92] FEATURES OF *GEOMYCES DESTRUCTANS* INFECTIONS REVEALED BY ELECTRON MICROSCOPY THAT MAY BE ASSOCIATED WITH VIRULENCE OF THE FUNGUS FOR BATS AND THE DEVELOPMENT OF WHITE-NOSE SYNDROME

Kevin Keel,¹ Katie Haman,¹ Craig Stihler,² and Mary Ard³

¹*Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, Georgia, USA;* ²*West Virginia Division of Natural Resources, Elkins, West Virginia, USA;* ³*Department of Pathology, College of Veterinary Medicine, The University of Georgia, Athens, Georgia, USA.*

Presenting author: Keel, Kevin (mkkeel@uga.edu)

Skin samples from two little brown bats (*Myotis lucifugus*) and four tricolored bats (*Perimyotis subflavus*) infected with *G. destructans*, the fungus associated with white-nose syndrome, were examined by scanning-electron microscopy (SEM) and transmission-electron microscopy (TEM). Muzzle samples examined by SEM had diffuse growth of hyphae, in contrast to multifocal proliferation on the patagia. Hyphae were few to nonexistent on the skin of the abdomen and thorax. On the muzzle and patagial skin, hyphae adhered tightly to the epidermal surface and occasionally extended under the edges of cornified epithelial cells. They frequently invaded hair follicles by diving between the hair shaft and follicle wall. Damage to hair shafts was never observed and hyphae generally did not adhere to hair shafts. Erosion or inflammation of the epidermis was not evident. Sporogenesis was observed on all bats and adherent conidia were very numerous on some. Varied bacteria were abundant in areas with fungal hyphae but were absent on regions of the skin lacking fungal proliferation. Sections examined by TEM demonstrated early invasion of the stratum corneum with minimal or no alteration of the epithelium. However, fungal hyphae invaded epithelial cells of the patagium at other foci and were associated with dissolution of the basement membrane prior to dermal invasion. Potentially important features of *G. destructans* infection, identified in this study, were specific adhesion to the epidermis but not hair shafts, an apparent tropism for hair follicles, correlation with increased bacterial growth and direct invasion of intact epithelium with disruption of the basement membrane.



[93] TERBINAFINE DOSAGE AND SAFETY IN WNS INFECTED *MYOTIS LUCIFUGUS*: CORRELATION OF SURVIVAL, DRUG TISSUE LEVELS, AND TOXIC EFFECTS

Alison Robbins,¹ Flo Tseng,¹ Richard Reynolds,² Erika Beck,¹ DeeAnn Reeder,³ George Lathrop,¹ Lara Helwig,¹ Elizabeth Buckles,⁴ and Michael Court⁵

¹Cummings School of Veterinary Medicine at Tufts University, North Grafton, Massachusetts, USA; ²Virginia Department of Game and Inland Fisheries, Verona, Virginia, USA; ³Bucknell University, Lewisburg, Pennsylvania, USA; ⁴Cornell University, College of Veterinary Medicine, Ithaca, New York, USA; ⁵Tufts University School of Medicine, Boston, Massachusetts, USA.

Presenting author: Robbins, Alison (alison.robbs@tufts.edu)

This study was conducted to determine whether the antifungal drug terbinafine administered to captive, naturally WNS infected *Myotis lucifugus* increases survival over the hibernation period. One hundred nineteen *Myotis lucifugus* were captured from a known WNS infected site in Northern Virginia in December 2010, and transported live to Tufts Cummings School of Veterinary Medicine. Bats were divided into 6 groups; a cold control group placed directly into an environmental chamber, a treatment control group given the drug vehicle, and 4 treatment groups receiving 6, 20, 60 and 200 mg/kg/day terbinafine given subcutaneously for 10 days. The five treatment groups were kept at room temperature in cages with heat lamps, hand fed meal worms, weighed, examined, and given an injection daily. After the treatment period, bats were transferred to an environmental chamber held at 8°C and 99% humidity for hibernation, and checked daily for survival. Toxic effects of the drug were apparent in the 200 mg/kg/day group by day 5: Nine of 19 bats died in the group by day 10 of the treatment period. Bat survival for all 5 treatment groups held at room temperature was longer than the cold control group placed directly into the environmental chamber. Bat survival by treatment groups will be presented. Terbinafine dosage will be correlated with drug tissue concentrations in hair, pelt, wing, and liver. Histological exam of each bat will be conducted to determine WNS infection status, extent, and intensity, and to identify potential toxic drug effects on the treated bats.



[94] PARASITES AND PATHOGENS OF BATS (MICROCHIROPTERA) ON ST. KITTS, WEST INDIES

Amanda Loftis,¹ Jason Beck,² Will Reeves,³ Floyd Revan,¹ Chelsea Faircloth,¹ and Kristi Pippin¹

¹Ross University School of Veterinary Medicine, Basseterre, St. Kitts, St. Kitts and Nevis; ²Idaho Department of Fish and Game, Pocatello, Idaho, USA; ³USAF School of Aerospace Medicine, Wright-Patterson AFB, Ohio, USA.

Presenting author: Loftis, Amanda (adloftis@gmail.com)

Bats are susceptible to a variety of infectious diseases and can serve as a reservoir for diseases of veterinary and public health concern. Previous studies on St. Kitts identified seven species of bats, including Antillean endemics and more widely distributed species. We undertook a survey to determine the presence and prevalence of ectoparasites and blood-borne pathogens in these bats. Between November 2010 and April 2011, 200 bats were mist-netted, examined for ectoparasites, and blood was sampled via the brachial vein. Bats included: 45 *Ardops nicholsii*, 85 *Artibeus jamaicensis*, 31 *Brachyphylla cavernarum*, 1 *Chiroderma* sp., and 38 *Molossus molossus*. Ectoparasites were found on 141 bats and included four streblid bat fly species and two species of parasitic mites. Streblid bat flies infested 56% of *A. jamaicensis* and 97% of *B. cavernarum*, but were not found on the other species. Mites were found on *A. nicholsii* (80%), *A. jamaicensis* (72%), *B. cavernarum* (13%), and *M. molossus* (3%). The majority of the mites collected were wing mites, *Perigilischrus iheringi*. Blood smears were prepared from 168 bats; microfilariae were seen in 15% of *A. jamaicensis*, but no other blood-borne parasites were seen. A novel *Bartonella* was detected by PCR in one pool of streblid bat flies. Cultures for fastidious bacteria were performed on 85 whole bloods; preliminary results suggest the presence of *Bartonella* and *Mycoplasma* spp. These data reveal the presence of several pathogens that could affect bat populations and will help establish a baseline for future research.



[95] RABIES IN FOUR VAMPIRE BAT POPULATIONS (*DESMODUS ROTUNDUS*) IN CENTRAL MEXICO

Fernández-González Adriana,¹ Suzán Gerardo,² Rojas Edith,³ Loza-Rubio Elizabeth,³ Ávila-Flores Rafael,⁴ and Medellín Rodrigo⁴

¹Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma del Estado de México. El Cerrillo Piedras Blancas, Toluca, Estado de México; ²Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Cto. Interior s/n Copilco, Coyoacan, Ciudad de México; ³Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Km 15.5 Carretera México-Toluca Col. Palo Alto Delegación Cuajimalpa, Ciudad de México; ⁴Instituto de Ecología, Universidad Nacional Autónoma de México, anexo al Jardín Botánico Exterior, s/n Copilco, Coyoacan, Ciudad de México.

Presenting author: Fernández-González Adriana (frogaf@gmail.com)

The vampire bat (*Desmodus rotundus*) has a broad geographical distribution ranging from northern Mexico to Argentina including Trinidad Island. It is one of the three haematophagus bats and it's considered the competent reservoir for rabies. The infection dynamics in haematophagus bats populations is poorly known. We sampled four vampire bat populations in the state of Mexico (central Mexico) to determine seroprevalence and detect rabies virus. We examined the relationship between age, sex and reproductive condition and infection in two seasons in 2010 and 2011. We mist-netted bats and collected blood samples for the Eli-rab immunoenzymatic test and brain tissues for direct immunofluorescence (IFD). A total of 70 blood samples were obtained and the seroprevalence was 18.6% (13/70). Of these, we collected 15 brains and none was seropositive to IFD. Only adults showed antibody prevalence (22.4%, 13/58) and higher prevalence was detected in males (21.9%, 9/41) than females (13.8%, 4/29). No reproductively inactive females and juveniles were seropositive. The seroprevalence in the wet season was lower (17.8%, 8/37) than in the dry season (20%, 5/20). Additional data on species richness was taken, and interesting, caves with high species richness showed higher prevalence than caves with low species richness. We conclude that vampire bat populations have been exposed to the virus, however, we could not find the virus. High interspecific interaction rates in reproductively active adults may explain high prevalence. Further studies with larger spatial and temporal scales should be implemented to understand the relationship between population dynamics, season, and species diversity and infection dynamics.



[96] THE MOUNTAIN GORILLA VETERINARY PROJECT: 25 YEARS OF MEDICINE, RESEARCH, AND CONSERVATION

Michael Cranfield,^{1,2} Kirsten Gilardi,¹ Kristin Benjamin,³ and Robert Hilsenroth^{2,4}

¹Mountain Gorilla One Health Program, UC Davis Wildlife Health Center, Davis, California, USA; ²Mountain Gorilla Veterinary Project (MGVP), Davis, California, USA; ³Denver, Colorado, USA; ⁴American Association of Zoo Veterinarians, Yulee, Florida, USA.

Presenting author: Cranfield, Michael (cranfield.mike@gmail.com)

The Mountain Gorilla Veterinary Project (MGVP), launched in 1986 by Morris Animal Foundation at the request of the late Dian Fossey, provides veterinary care in situ to wild mountain gorillas (*Gorilla beringei beringei*) in Rwanda, Uganda and Democratic Republic of Congo that are affected by human-induced illness or injury. In the 25 years since its inception, the MGVP has evolved from serving as a first-aid responder treating gorillas caught in poachers' snares, to implementing a comprehensive One Health program that is integral to the conservation of this endangered species. The MGVP became a stand-alone non-profit organization in 2006, and subsequently partnered with the UC Davis Wildlife Health Center in 2009. In addition to daily health monitoring of all habituated gorillas and veterinary intervention on individual gorilla cases (10-20 clinical cases or necropsies annually), the focus is now also on minimizing the risk of disease transmission from people to gorillas through an employee health program, conducting research on diseases affecting wild gorillas, and building capacity for wildlife veterinary medicine and disease surveillance in countries with gorillas. There are now 786 mountain gorillas in the world; some would argue this is the result of "extreme conservation" – an unprecedented and seemingly unsustainable level of engagement. Alternatively, one could argue that "extreme conservation" is the success story: that it is an outstanding example of how veterinary medicine can ensure the survival of a wildlife species through direct intervention and investment – in the animals, their habitats, and in the human communities that surround them.



[97] SEROLOGIC SURVEYS FOR VIRUS EXPOSURE IN WILD AND CONFISCATED MOUNTAIN AND GRAUER'S GORILLAS IN EAST CENTRAL AFRICA

Kirsten Gilardi,¹ Christopher Whittier,² and Michael Cranfield^{1,3}

¹Mountain Gorilla One Health Program, UC Davis Wildlife Health Center, Davis, California, USA; ²Smithsonian Institution, Washington DC, USA; ³Mountain Gorilla Veterinary Project, Davis, California, USA.

Presenting author: Gilardi, Kirsten (kvgilardi@ucdavis.edu)

To characterize risk factors for emergence of pathogens of human pandemic potential from wildlife (USAID Emerging Pandemic Threats PREDICT project), we tested 77 sera collected from 41 wild and captive (confiscated) mountain (*Gorilla beringei beringei*) and 10 wild and captive Grauer's (*G. beringei graueri*) gorillas between 2001 and 2009 for evidence of exposure to known viruses. We tested sera for antibodies to retroviruses (simian immunodeficiency virus (SIV), simian retrovirus (SRV), human T-lymphotropic virus (HTLV) and simian foamy virus (SFV) by immunoassay), paramyxoviruses (measles by immunoassay, parainfluenza 1-3 and respiratory syncytial virus (RSV) by complement fixation), herpesviruses (rhesus rhadinovirus, lymphocryptovirus, and simian varicella by immunoassay), influenza viruses (A and B by complement fixation), flaviviruses (West Nile virus and Dengue fever by ELISA), and hantavirus (by ELISA). Diagnostics were conducted by the California National Primate Research Center (Davis, CA) and Focus Diagnostics, Inc. (Cypress, CA). All samples were antibody-positive for lymphocryptovirus. One Grauer's gorilla was antibody-positive for varicella, two Grauer's gorillas were antibody-positive for hantavirus, and six gorillas were antibody-positive at least once for both Dengue fever and West Nile virus. Three serial samples from a Grauer's gorilla tested antibody-positive for HTLV. Two Grauer's gorillas were antibody-positive for SRV-1. SRV has not yet been detected in a wild African ape. No samples tested antibody-positive for SIV, influenza A and B, parainfluenzas 1-3 or RSV. Our results were comparable to previous surveys that detected herpesvirus exposure, but were inconsistent with earlier detection of influenza and morbillivirus, but not retrovirus, exposure.



[98] GASTRO-INTESTINAL HELMINTHS IN THREE SYMPATRIC SPECIES SHARING THE BOUNDARY OF THE VOLCANOES NATIONAL PARK, RWANDA

James Hassell,¹ Jennifer Hogan,² Jean Bosco Noheri,³ Jan Ramer,³ Michael Cranfield,⁴ Michael Waters,¹ and Carlos Hermosilla⁵

¹Pathology and Infectious Disease, Royal Veterinary College, London, UK; ²Veterinary Medicine: Pathology, Microbiology, Immunology, UC Davis, California, USA; ³Mountain Gorilla Veterinary Project, Musanze, Rwanda; ⁴Mountain Gorilla One Health Program, UC Davis Wildlife Health Centre, California, USA; ⁵Institute of Parasitology, University of Giessen, Giessen, Germany.

Presenting author: Hassell, James (jhassell@rvc.ac.uk)

Helminth infection is widely documented in the critically endangered mountain gorilla (*Gorilla gorilla beringei*) and parasites are routinely described on both ante-mortem and post-mortem examination. Indications of a transmission cycle for *Cryptosporidium parvum* infections involving cattle have been identified in the Ugandan population of these animals. The Rwandan population are exposed to more extreme agricultural pressures and a relatively large wildlife reservoir, concentrated at the park boundary. In 2010 a study was conducted to investigate the potential for gastrointestinal parasite transmission between domestic cattle, forest buffalo (*Syncerus caffer nanus*) and mountain gorilla at the boundary of the Volcanoes National Park, Rwanda. Helminth eggs recovered by fecal flotation (gorilla[n=130]; cattle[n=127]; buffalo[n=55]) included Strongylida, Rhabditoidea and *Nematodirus* (gorilla, cattle and buffalo), Ascaridoidea (gorilla and cattle), *Trichuris* and *Capillaria* (cattle and buffalo), *Anoplocephala gorillae* (gorilla) and *Skrjabinema* (buffalo). Additionally, protozoal oocysts including *Coccidia* (*Eimeria* spp. from gorilla and cattle), *Buxtonella sulcata* from buffalo and a cyst morphologically resembling *Balantidium coli* (gorilla) were identified. Trematode eggs were also recovered from all three species by sedimentation. There was evidence to support transmission of helminths. The ruminant strongylid *Nematodirus* was described for the first time as an accidental infection of gorilla, and overlapping geographical ranges of buffalo and cattle shedding *Fasciola* spp. may indicate the contamination of shared water supplies. *Balantidium coli*, as yet undescribed in wild populations of mountain gorilla, may represent a protozoal cause of typhlitis in these animals. Further surveillance is required to interpret and address parasitic transmission cycles in mountain gorilla conservation.



[99] REMOTE MONITORING AS A TOOL FOR TRANSMISSION STUDIES OF EBOLAVIRUS AND OTHER EMERGING INFECTIOUS DISEASES

Patricia Reed,¹ Kenneth Cameron,¹ Alain U. Ondzie,² David Morgan,^{1,3} and Crickette Sanz⁴

¹Wildlife Conservation Society, Bronx, New York, USA; ²Wildlife Conservation Society, Brazzaville, Republic of Congo; ³Lincoln Park Zoo, Chicago, Illinois, USA; ⁴Washington University, St. Louis, Missouri, USA.

Presenting author: Reed, Patricia (PReed@wcs.org)

Ebolavirus (EBOV) has caused human epidemics and resulted in massive declines of African great apes. The wildlife trade (hunting) is a major driver for EBOV emergence in humans, but transmission in great apes and other wildlife is poorly understood, as is the full range of susceptible hosts. We used remote monitoring techniques to further elucidate transmission dynamics of EBOV and other infectious diseases among wildlife. We achieved this by placing motion activated video cameras on wildlife carcasses located and sampled as part of our large scale surveillance and hunter-based reporting network in high-risk EBOV regions in the Republic of Congo. Carcasses were scavenged by a variety of species, with those of apes being of particular interest to other taxa. Scavenging species and visitation rates changed as carcasses decayed, which may be relevant to disease transmission risk. Knowing which animals contact potentially EBOV-infected carcasses may contribute to public health protection by identifying high-risk species in the trade. Furthermore, rates of visitation or contact are essential to the most basic susceptible-infected-recovered (SIR) models of disease transmission. This information helps determine spatial spread dynamics after “founder” events and aides prediction of future epidemics. In terms of wildlife conservation, information on vulnerable species, combined with health education, has the potential to reduce hunting pressure on wildlife and lead to new epizootic control strategies. In conclusion, remote monitoring techniques have potential in epidemiological studies in which traditional investigative methods prove difficult.



[100] INVESTIGATING THE ROLE OF WILD PIGS IN EBOLAVIRUS ECOLOGY IN CENTRAL AFRICA

Kenneth Cameron,¹ Alain Ondzie,² Sarah H. Olson,³ David Morgan,^{4,5} Crickette Sanz,⁴ and Patricia Reed¹

¹Wildlife Conservation Society, Bronx, New York, USA; ²Wildlife Conservation Society, Brazzaville, Republic of Congo; ³Wildlife Conservation Society, Nanaimo, British Columbia, Canada; ⁴Washington University, St. Louis, Missouri, USA; ⁵Lincoln Park Zoo, Chicago, Illinois, USA.

Presenting author: Cameron, Kenneth (kcameron@wcs.org)

Ebola hemorrhagic fever (EHF), caused by the Ebola virus (EBOV), has produced high mortality among people and great apes in the Congo Basin of Central Africa, with Zaïre ebolavirus (ZEBOV) of greatest concern. Despite years of research, relatively little is known of ZEBOV's ecology, including reservoirs and modes of transmission to great apes. The role of fruit bat species as putative reservoirs of EBOV remains unconfirmed and theories of bat-to-ape transmission remain unproven. Mitigation strategies to protect great apes from EHF are being pursued, but without a more complete understanding of EBOV ecology and transmission, may not be fully effective. Interest has begun to focus on pigs as potential players in EBOV ecology. Reston ebolavirus was detected in pigs in the Philippines. A recent study shows that domestic pigs are susceptible to ZEBOV infection, develop severe respiratory disease, shed the virus in large quantities and can infect co-housed pigs. Field studies suggest red river hogs (*Potamochoerus porcus*) are voracious scavengers of great ape carcasses, with peak scavenging activity at days 2-3 and 5-6 post-mortem, placing them at high risk of infection from an EBOV-infected carcass. Given the extensive overlap in range and foraging between red river hogs and great apes, this raises the question of wild pigs as potential amplifying hosts for EBOV and sources of infection of great apes. We are currently testing tissues from 17 hunter-killed *P. porcus* for EBOV by PCR and are conducting EBOV serologic studies of free-ranging *P. porcus*. Results of both studies are pending.



[101] GORILLA DENSITY AND EBOLA FECAL ANTIBODY PREVALENCE - STEP 1. OPTIMIZING EMERGING INFECTIOUS DISEASE SPATIAL SURVEILLANCE

Sarah H. Olson,¹ Patricia Reed,² Alain Ondzie, 3) Kenneth Cameron,² and Damien Joly¹

¹*Wildlife Conservation Society, Nanaimo, British Columbia, Canada;* ²*Wildlife Conservation Society, Bronx, New York, USA;* ³*Wildlife Conservation Society, Brazzaville, Republic of Congo.*

Presenting author: Olson, Sarah H. (solson@wcs.org)

Ebola hemorrhagic fever is considered a minacious driver of gorilla extinction in the wild, yet the relationship of present day great ape density and prior Ebola exposure is unclear. A new assay to detect Ebola virus antibodies in gorilla and chimpanzee fecal samples can provide data on population exposure history (Reed, pers. commun.). We simulate and compare reconnaissance walks (recces) and distance-based fecal sampling methods to estimate relative ape densities on a virtual landscape, across different densities and distributions of ape populations, for accuracy as well as cost and time efficiencies. Since 2005, scientists have performed recces at 13 different locations and collected more than 250 fecal samples in the Republic of Congo. Each recce resembles a cross pattée, with eight 10 km segments radiating from a central point every 45° and four 7.6 km segments connecting alternate ends. Recce collection paths are not straight lines, but rather the path of least resistance through thick jungle and swamps, so sine curves are used in the simulation to approximate the wandering path of a collector. Distance 6.0 software, past ape density surveys, and dung deposition/decay rates will be used to parameterize the simulated field studies. Fecal sample collection along a straight transect and random walk are simulated with R Statistical Software. This research is the first part of a larger study relating great ape densities to antibody prevalence. We will discuss results and the next steps towards understanding the relationship of gorilla density and Ebola fecal antibody prevalence.



[102] IDENTIFICATION OF RISK FACTORS ASSOCIATED WITH BOVINE TUBERCULOSIS IN FERAL SWINE POPULATIONS: IMPLICATIONS FOR MITIGATION OF RISK IN NORTH AMERICA

Ryan S. Miller,¹ Steven J. Sweeney,¹ Jennifer L. Malmberg¹

¹*Animal Plant Health Inspection Service, Centers for Epidemiology and Animal Health, Fort Collins, Colorado, USA;*

²*Animal Plant Health Inspection Service, Veterinary Services, Salem, Oregon, USA.*

Presenting author: Miller, Ryan S. (ryan.s.miller@aphis.usda.gov)

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, occurring in free ranging swine has been reported in fourteen countries and is considered endemic in five. Recent evidence supports the role of wild boar as competent maintenance hosts for bTB, posing a serious risk for livestock, human health and the recreational hunting industry in North America. The goal of this study was to identify potential risk factors associated with the maintenance of bTB in free ranging swine and determine if risk factors are present in North America. A systematic structured literature review was conducted to identify scientific peer reviewed publications related to bTB in feral or free ranging swine. The review procedure involved three processes: 1) identification of keywords, 2) systematic review of PubMed, Scopus, and Web of Science 3) review and identification of risk factors associated with bTB. Searches identified 236 scientific publications with 107 relevant to the topic, explicitly addressing *M. bovis* in free ranging swine. The majority of publications (53%) addressed issues related to surveillance and epidemiology. The remaining publications addressed pathology (31%) and disease control tools (16%). Risk factors identified included concentration of swine for hunting, supplemental feeding, congregation at watering or feeding sites, and interactions with cattle or other wildlife. While bTB has not been identified in North American feral swine, risks for disease emergence are present – high densities, robust hunting industry, and significant baiting and feeding. Development of a robust program of feral swine control together with surveillance for bTB may help mitigate risks.



[103] ANTIBIOTIC RESISTANT BACTERIAL STRAINS IN TRADED WILDLIFE IN PERU

A. Patricia Mendoza,¹ Maria Bernal,² Nancy Caverio,¹ Yocelinda Meza,² Bruno Gherzi,² Donald J. Brightsmith,³ Joel M. Montgomery,⁴ Alberto Perez,⁴ and Marcela Uhart⁴

¹Wildlife Conservation Society, Lima, Perú; ²US Naval Medical Research Unit 6, Callao, Perú; ³Schubot Exotic Bird Health Center at Texas A&M University, College Station, Texas, USA; ⁴Wildlife Conservation Society, Global Health Program, Puerto Madryn, Argentina; ⁵Centers for Disease Control and Prevention, Atlanta, Georgia, USA.

Presenting author: Mendoza, A. Patricia (pmendoza@wcs.org)

Wetmarkets are common in all regions of Peru. In these markets, wildlife and domestic species are offered as pets, food and traditional medicine in the vicinity of produce and meat, raising the possibility of cross-contamination of human foodstuffs. The purpose of this study was to detect bacteriological risks associated with the wildlife trade. We surveyed confiscated and for sale wildlife from 4 wetmarkets between May 2010 and April 2011. Cloacal and rectal swabs were collected from apparently healthy animals. Swabs were also obtained from fresh droppings in single-species cages. Secretions and altered tissues were collected from sick and dead animals. Specimens were cultured by routine methods and Kirby-Bauer disk diffusion antimicrobial susceptibility tests were performed. A total of 177 samples from 24 bird, 8 mammal and 8 reptile species were collected and analyzed. Bacterial pathogens were detected in 41/164 samples from live animals and 4/13 necropsy samples. All isolates were resistant to at least one antibiotic. *Aeromonas* spp. were the most commonly isolated (35/45) and found resistant to Ampicillin, Cefalotin, Amoxicillin/Clavulanic Acid, Azithromycin and Erythromycin. *Salmonella enterica* was isolated from 3/45 samples and found resistant to Eritromicine. *Klebsiella* spp. was isolated from a parakeet and found resistant to Ampicillin, Sulfamethoxazole/trimethoprim and Tetracycline. Our study shows that opportunistic, zoonotic enteropathogens are frequently isolated from wild-caught animals in Peruvian wetmarkets. Under current conditions, wildlife trade may be facilitating the selection and spread of antimicrobial resistant pathogens of public health concern.



[104] A MULTIVARIATE ASSESSMENT OF ORAL VACCINATION CAMPAIGNS WITH ONRAB® BAITS FOR THE CONTROL OF RABIES IN RACCOONS AND STRIPED SKUNKS IN SOUTHERN QUÉBEC, CANADA

Julien Mainguy,¹ Erin Rees,² Pierre Canac-Marquis,¹ Denise Bélanger,² Christine Fehlner-Gardiner,³ Guylaine Séguin,^{1,2} Sylvain Larrat,² François Landry,¹ Daniel Guérin,¹ Hélène Jolicoeur,¹ Nathalie Côté,⁴ and Stéphane Lair²

¹Ministère des Ressources naturelles et de la Faune, Direction de l'expertise sur la faune et ses habitats, Québec, Québec, Canada; ²Faculté de médecine vétérinaire de Saint-Hyacinthe, Université de Montréal, Saint-Hyacinthe, Québec, Canada; ³Canadian Food Inspection Agency, Ottawa Laboratory Fallowfield, Ottawa, Ontario, Canada; ⁴Ministère de l'Agriculture, des Pêcheries et de l'Alimentation, Direction de la santé animale et de l'inspection des viandes, Québec, Québec, Canada.

Presenting author: Mainguy, Julien (julien.mainguy@mrnf.gouv.qc.ca)

Oral vaccination with ONRAB® baits has been advocated as a tool to eradicate raccoon variant rabies (RVR) in wildlife. The objective of this study was to determine rabies antibody seroprevalence in raccoons (*Procyon lotor*) and striped skunks (*Mephitis mephitis*) following oral rabies vaccination (ORV) campaigns in which ONRAB® was distributed aerially and by hand in southern Québec, Canada, in 2007–2009. The annual mean percentage of raccoons and skunks considered seropositive for rabies antibodies after the distribution of 150 ONRAB®/km² varied from 48.5–56.2% and 11.0–16.7%, respectively. At the individual level in raccoons, seropositivity was positively associated with the density of ONRAB® distributed, the number of previous ORV campaigns experienced, and age. Conversely, seropositivity was negatively associated with the estimated density of raccoons and the proportion of residential areas near the raccoon capture location. None of the variables examined explained variation in the seropositivity of skunks. Our results indicate that the ONRAB® density employed during ORV campaigns should be adjusted to account for variations in raccoon density and presence of residential areas to establish an adequate immunological barrier. The high percentage of juvenile raccoons (annual mean = 45%) and skunks (66%) captured during post-ORV studies also suggests that ORV campaigns must be conducted at least annually. In southern Québec, the use of ONRAB® has apparently contributed to the elimination of RVR. Nonetheless, our results indicate that improvements to this bait or the distribution techniques used are required to increase its efficacy in skunks.



[105] CLIMATE CHANGE, CATASTROPHES AND DOGS IN DEVELOPING COUNTRIES: A RECIPE FOR WILDLIFE DISASTERS?

Elena Garde, and Guillermo Pérez

Veterinarians Without Borders - Canada, Valdivia, Chile.

Presenting author: Garde, Elena (elena.garde@vwb-vsfc.ca)

In developing countries around the world, the inability to control free-roaming dogs is a common yet complex problem. In these regions national infrastructure, veterinary services and expendable income of residents are all limited and effective dog management may not be feasible nor a priority for governments or individual owners. Large-scale disaster events are increasing world-wide in part due to climate change, and millions of people are affected annually. Developing countries are disproportionately affected, and the human public health and welfare risks typically following natural disasters are well-described. Although there is a growing body of literature describing disease and predation risks that free-roaming dogs present to wildlife, information on the impacts and potential for increased risk in the post-disaster setting is scarce. We report here on a canine distemper virus outbreak in central Chile following the 2010 earthquake and tsunami, and review the changed human and canine dynamics that potentially increase risks to wildlife.



[105] CLIMATE CHANGE, CATASTROPHES AND DOGS IN DEVELOPING COUNTRIES: A RECIPE FOR WILDLIFE DISASTERS?

Philippe Berny,¹ Julie Vein,¹ Danièle Vey,¹ and Olivier Mastain²

¹Université de Lyon, VetAgro Sup, Marcy l'étoile, France; ²Office National de la Chasse et de la Faune Sauvage, Auffargis, France.

Presenting author: Berny, Philippe (p.berny@vetagro-sup.fr)

The EU has re-evaluated all the existing pesticides and, as a result, only 300-400 active substances are now available instead of over 900 in the late 90's. Among the reasons for banning pesticides, ecological effects including non-target poisoning, have been considered. The SAGIR network has been established in 1986 in order to monitor wildlife diseases in France. All toxicological analyses are conducted at the same laboratory. Cases were retrieved from the SAGIR database. Several pesticides were selected for investigation: strychnine, some cholinesterase inhibitors (aldicarb, carbofuran, furathiocarb, mevinphos), and anticoagulant rodenticides. Information regarding species and circumstances of exposure were taken into consideration. Time-series analyses from 1995 until 2010 clearly indicate that banning may be effective if the products are actively eliminated and not available from other sources or countries. Strychnine, for instance, is still detected, although it was partially restricted in 1984 and completely banned in 2000. A surprising result of our analyses is the detection of shifts in pesticide poisoning cases with obvious "re-emerging" toxicants in recent years, such as lindane and alpha-chloralose. These results will be compared with toxicological accidents observed in domestic animals with the same products. Trends are very similar, and even more pronounced in domestic species. A review of the circumstances of exposure clearly points out that pesticide poisoning is commonly associated with deliberate abuse and that the persisting chemicals, as well as the "re-emerging" ones are all mostly detected in illicit use against wildlife. Most species of concern are protected and/or endangered species.