

66th WDA Annual International Conference

5th Kalaan Kab
International Congress
on Disease Ecology

3rd Conference of the WDA
Latin American Section



Book of Abstracts

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San Cristóbal de Las Casas, Chiapas, México 2017



**GRUPO DE ECOLOGÍA DE ENFERMEDADES
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Jean-François Guégan

French Institute for Research on Sustainable Development (IRD), France

Jean-François Guégan is a 56 years old theoretical ecologist interested in the ecology, evolution and policy-decisions on human infectious diseases and their host vectors or reservoirs. He obtained his Ph.D. in parasite ecology in 1990 from the University of Montpellier (France), and did a post-doc in 1990-1991 at Exeter University in Great Britain where he worked on patterns and processes in parasite communities. In 1991, he was hired as a junior researcher at IRD, the French Institute for Research on Sustainable Development. He is currently Senior Research Director, with the highest rank (“de classe exceptionnelle”), in the same Institute where he led a research group on Dynamics of Systems and Infectious Diseases in the joint national team called UMR MIVEGEC.

He is involved in research on the neglected emerging tropical disease, Buruli ulcer in Africa and French Guiana, southern America and more generally on the theoretical relationships between biodiversity and emerging infectious diseases. As part of his duties at IRD, JFG is also an adjunct professor at Montpellier University where he is teaching a course on global environmental changes and emerging infectious diseases, and a professor at EHESP, the French School of Public Health, where he is a track leader for courses on Environmental and Occupational Health Sciences, an Erasmus Mundus Excellence in European Education training from both the EHESP’s Master of Public Health and EuroPubHealth. He is responsible for the writing of up to 140 international scientific papers (Nature, PLoS Biology, PLoS Medicine, PLoS Pathogens, PLoS Neglected Tropical Diseases, American Journal of Epidemiology, Annual Review Ecology, Evolution and Systematics, Global Ecology and Biogeography...), 11 hard-books and up to 85 international conferences. As a former fellow of the French High Council for Public Health, he (co)-led different French national reports on Climate Change and Health, Adaptation to Climate Change and Emerging Infectious Diseases: research actions and planning. He is responsible for organizing an annual research action Seminar, called School of Val-de-Grâce Seminar, on emerging infections to improve sensitization of political leaders and civil society actors on societal risks associated with these new emerging threats. He has been the PI or co-Pi of 12 national and international grants, 8 of which on the ecology and evolution of infectious diseases.

Carol Meteyer, DVM

Diplomate, American College of Veterinary Pathologists

Senior Science Advisor

Health and Environment, U.S. Geological Survey National Center, Reston VA

Carol Meteyer specializes in the ecology and comparative pathophysiology of disease in wild populations of birds, terrestrial and marine mammals, reptiles and amphibians. Prior to her work in wild populations, she determined causes of morbidity and mortality in industrial and backyard poultry, zoological collections, laboratory animals, and companion animals. This comparative perspective across taxa and life histories has led to multidimensional applications of data, shifting investigation of disease into new paradigms of study and understanding. Meteyer moved to Washington DC in 2012 to serve as the USGS Deputy Program Coordinator for Contaminant Biology bringing into focus the roles of both biotic and abiotic forces and their relationship to disease ecology. She is currently the Senior Science Advisor for Health and Environment at the USGS. In her roles at USGS headquarters, she has worked with others providing science and science guidance on Presidential Committees and Working Groups in support of wildlife and ecosystem conservation, and human health.

Meteyer received her doctorate of veterinary medicine from Iowa State University, completed an Internship in Small Animal Medicine and Surgery in Los Angeles, California, worked in private practice, and earned board certification from the American College of Veterinary Pathologists after completing a Residency in Comparative Pathology at the University of Southern California and the County of Los Angeles. She was Assistant Professor with the University of California, Davis teaching and serving as diagnostic pathologist, and Branch Chief for the UC Davis Diagnostic Laboratory in Fresno, California before joining the USGS National Wildlife Health Center (NWHC), the singular U.S. national laboratory focused solely on wildlife health.

During her 21 years at the NWHC, Meteyer was the forensic pathologist for US Fish and Wildlife Service and wildlife pathologist. Dr. Meteyer's investigations contributed to the discovery of novel diseases including white-nose syndrome in bats; the NSAID, diclofenac as the cause of the population crash of Gyps vultures in Pakistan; virulent Newcastle disease virus as a cause of mortality in young cormorants; *Mycoplasma gallisepticum* conjunctivitis in finches; avian vacuolar myelinopathy in American eagles and American coots; protozoal encephalitis in southern sea otters; investigations into mortality due to legacy organochlorines, toxic metals associated with mining, pesticides, lead, and deliberate poisonings. Additional studies defined the pathology of amphibian malformations and amphibian infectious diseases, monkeypox in rodents native to the US, plague in prairie dogs, Asian HPAI H5N1 in North American raptors and shore birds, and effects of anticoagulant rodenticides in raptors. Invertebrate studies have included the ecology of *Atta cephalotes* (leaf-cutter ant) in the 1970s as a research assistant in the Guanacaste National Forest Costa Rica, and workshops to define pathology associated with diseases in coral. Carol has been a member of WDA since 1980.

Rodolfo Dirzo
Stanford University

Rodolfo Dirzo studied Biology at the University of Morelos, Mexico. He completed his Masters (M.Sc.) and Doctorate (Ph.D.) in Ecology at the University of Wales, Great Britain. He has been a Professor at the National University of Mexico (UNAM), where he was researcher and chair of the Evolutionary Ecology Department, and Director of the Los Tuxtlas Tropical Research Station. Currently he is a Professor at Stanford University in the Biology Department, where he teaches Ecology and Natural History, Field Ecology, Conservation Science, and Bio-Cultural Diversity.

His research centers on the study of the ecological and evolutionary relationships between plants and animals and on the impact of human activities on natural ecosystems. His recent work includes studies on the evolution of plant defenses; ecology and evolution of tropical plants; and a documentation of the global magnitude of animal extinction (Defaunation), and how this affects ecosystems and ecosystem services, such as regulation of disease risks in humans. Most of his work is carried out in tropical ecosystems of Latin America (Mexico, Costa Rica, Brazil), the Central Pacific, and East Africa.

He also runs science education programs for high school students from under-represented communities in Northern California. These programs focus on students from underserved communities in the Bay Area. He participated in and co-authored the Framework for K-12 Science Education.

He is member of the Mexican Academy of Sciences, the US National Academy of Sciences, the American Academy of Arts and Sciences, and the California Academy of Sciences.

Frances M. D. Gulland, Vet MB, PhD, MRCVS

Marine Mammal Center

Sausalito, California, USA

Frances Gulland is a veterinarian at The Marine Mammal Center in Sausalito, California. She has been actively involved in the veterinary care and rehabilitation of stranded marine mammals and research into marine mammal diseases there since 1994. Her interests include determining the impacts of human activities on marine mammal health, and how marine mammals can in turn serve as indicators of ocean health. She received a veterinary degree from the University of Cambridge, U.K., in 1984, and a PhD in Zoology there in 1991. Before moving to California in 1994, she worked as a veterinarian and research fellow at the Zoological Society of London. She currently serves as Commissioner on the U. S. Marine Mammal Commission

Emerging Disease and Wildlife Conservation - When does intervention work?

09:00 - Monday, 24th July, Solar Square

*Dr. Carol Meteyer*¹

1. U.S. Geological Survey-Environmental Health

Wildlife disease was once viewed as part of the natural ecological cycle; 'Nature's' tool for rebalancing populations - intervention was controversial. We have moved beyond this philosophical controversy to one that questions when to intervene, and what intervention should look like. Disease is now accepted as one of many threats to wildlife populations and it would be hard to find a wildlife resource manager that would consistently argue a hands-off approach. Wildlife diseases with the potential to cause species extirpations are emerging more frequently, leading natural resource managers and policy makers to search for effective intervention strategies. Optimizing management approaches to these high-consequence diseases under the constraints of time, incomplete data, and limited resources, can be critical for the survival of some wildlife species. But defining and clearly communicating the limits of what can be reasonably accomplished is a science in itself. This disciplined assessment of what research and management actions can realistically achieve, balanced with the potential ecological ramifications, is critical to keeping the trust and good faith of managers who are using the science; of the taxpayers and constituents who pay for the science and management; and of the policy makers who determine priorities and allocate funds.

Multidisciplinary groups are attempting to establish risk/benefit models to assist in management decisions for emerging wildlife disease and research prioritization while acknowledging the difficulty and risks of embarking on management actions in the context of limited information.

This presentation will review recent publications and case study data to discuss:

- Criteria that constitute an 'emerging wildlife disease event'
- How minimum data can be optimized to enhance early predictive modeling
- Conditions that are present when emerging wildlife diseases are successfully eliminated
- Potential usefulness of approaching wildlife disease agents within the context of environmental toxicology as 'environmental contaminants' of concern.

First Cases Of Peste Des Petits Ruminants Virus In Saiga Antelope

10:30 - Monday, 24th July, Solar Square

Prof. Richard Kock¹, Dr. Enkhtuvshin Shiilegdamband Shiilegdamband², Dr. Bayarbaatar Buuveibaatar², Dr. Amanda Fine²

1. Royal Veterinary College 2. *Wildlife Conservation Society*

Saiga *Saiga tatarica*, a critically endangered antelope lives in Central Asia. It survives in fragmented populations, totalling under 100,000 individuals across Russia, Kazakhstan and Mongolia. The main threats are poaching and episodic mass mortality, the latter a problem in the Western sub-species (*S.t. tatarica*). With conservation support over the last decade or more, the population of the subspecies *S.t. mongolica* had increased from as few as 750 individuals, to an estimated 10,000 individuals by 2016. This unique population occupies semiarid deserts of the Gobi Altai in Western Mongolia. In December 2016, they became infected with peste des petits ruminants virus which infected Mongolian livestock for the first time in August 2016. This disease has been spreading through Africa and Asia over the last decade or so and was reported for the first time in China in 2013, Kazakhstan in 2014 and now Mongolia with over 60 million livestock and at least million small wild ruminants threatened. The epidemic was first reported in saiga by local herders on 22nd December 2016, mid-winter when the animals were at their most vulnerable. It has now killed over 54% of the population and this has occurred within the first 3 months, and the epidemic is still ongoing. Deaths from PPR have now also been confirmed, in goitered gazelle (*Gazella subgutturosa*), Sibirian Ibex (*Capra sibirica*) and Argali sheep (*Ovis ammon*) in the infected area. Since January 2017, a team of veterinarians and biologists comprised of Mongolian and international colleagues coordinated by the Wildlife Conservation Society have been investigating this die off, and some preliminary findings will be presented. Including evidence of high susceptibility to the disease (unlike its African antelope cousins), a description of rapid diagnostic approaches in the field, preliminary findings on virology and pathology and discussion of predisposing factors.

Conservation Implications of Herpesviruses in Free-ranging Mountain Gorillas (*Gorilla beringei beringei*) in the Bwindi Impenetrable Forest and Virunga Massif Conservation Area

10:30 - Monday, 24th July, Solar Square

Dr. Tierra Evans¹, Dr. Kirsten Gilardi¹, Prof. Linda Lowenstine¹, Dr. Mike Cranfield¹, Prof. Peter Barry², Dr. Tracey Goldstein¹, Dr. Benard Ssebide¹, Dr. Jean Felix Kinani¹, Dr. Fred Nizeyimana¹, Dr. Jean Bosco Noheli¹, Dr. Antoine Mudakikwa³, Prof. Jonna Mazet¹, Dr. Christine Johnson¹

1. Gorilla Doctors, Karen C. Drayer Wildlife Health Center, University of California Davis School of Veterinary Medicine) 2. Center for Comparative Medicine, University of California Davis 3. Rwanda Development Board

Free-ranging mountain gorillas (*Gorilla beringei beringei*) are frequently in contact with humans through research activities, ecotourism and habitat encroachment. Herpesviruses, which are ubiquitous in primates, have the potential to be shared in these settings. Based on serology and lesions seen in infant gorillas, a gamma-herpesvirus similar to Epstein-Barr virus (EBV) is suspected to infect the majority of mountain gorillas. Similarly, serology and observations of orofacial lesions suggest that an alpha-herpesvirus is present in human-habituated mountain gorillas. While the etiology of orofacial lesions has not been confirmed, it is known that human herpes simplex virus type 1 (HSV-1) has been transmitted to juvenile eastern gorillas in rehabilitation. In order to better characterize herpes viruses infecting mountain gorillas, and to determine whether human herpesviruses have been introduced into the free-ranging population, we conducted a population-wide survey to test for the presence of orally-shed viruses in mountain gorillas. DNA was extracted from discarded chewed plants collected from 294 individuals from 26 groups, and samples were screened by PCR using pan-herpesvirus assays. We found new mountain gorilla-specific homologs to human herpesviruses, including a lymphocryptovirus (GbbLCV-1), cytomegaloviruses (GbbCMV-1 and 2) and a rhadinovirus (GbbRHV-1) with similar characteristics (i.e. timing of primary infection, shedding in multiple age groups and likely modes of transmission) to human EBV, human cytomegalovirus and Kaposi's sarcoma-associated herpesvirus, respectively. We also identified GbbLCV-1 in lungs from infants with histopathological lesions consistent with pulmonary reactive lymphoid hyperplasia (PRLH) a condition associated with EBV in immune deficiency children, suggesting that primary infection with GbbLCV-1 in infant gorillas may be associated with PRLH. We found no evidence that human herpesviruses have infected free-ranging mountain gorillas. Because the health effects of HSV-1 in mountain gorillas is unknown, reintroduction of formerly captive individuals with human herpesvirus infections may pose an unacceptable risk to this critically endangered species.

Clinical babesiosis and suspected coinfection with *Borrelia* in a North American River Otter: A Consideration for Reintroduction Programs?

10:30 - Monday, 24th July, Solar Square

*Dr. Nancy Boedeker*¹, *Mrs. Brittany Thomas*², *Dr. Adam Birkenheuer*², *Dr. Catherine Brown*³

1. Zoo New England, 2. North Carolina State University Vector Borne Disease Diagnostics Laboratory, 3. Massachusetts Department of Public Health

Background: North American river otters, historically overharvested, have been translocated for reintroduction in many regions of the US over decades. Tick-borne diseases affecting human and animal health are increasingly being reported and expanding geographically.

Objective: An orphaned North American river otter brought to a Massachusetts wildlife rehabilitation center developed severe splenomegaly and anemia (hematocrit 14%). Tick-borne diseases were considered as differentials and diagnostic testing was conducted.

Methods: Samples were submitted for a biochemistry panel and infectious disease testing (serology and/or PCR) for *Borrelia*, *Babesia*, *Bartonella*, *Anaplasma*, *Ehrlichia*, *Rickettsia*, and *Mycoplasma*.

Results: Abnormal results included elevations in ALT, AST, and total bilirubin, anti-*Borrelia* antibodies at 1:1600, and PCR positivity for *Babesia* sp. Sequencing identified a *Babesia* microti-like organism identical to that previously documented in 80% of otters from North Carolina without apparent clinical signs. After treatment for borreliosis and babesiosis with doxycycline, atovaquone, and azithromycin, the splenomegaly resolved and the hematocrit, ALT, AST, and total bilirubin normalized. Post-treatment *Borrelia* titer was negative at 1:100. The *B* microti-like organism was still detectable as has been reported in some dogs post-treatment.

Conclusions: Results strongly suggest the anemia, splenomegaly, and hepatopathy in this otter were due to *Babesia* microti-like organism infection. This represents the first antemortem diagnosis of clinical babesiosis in otters. Immunocompromise associated with orphan status and/or *Borrelia* co-infection may have contributed to disease severity. The incidence of borreliosis and babesiosis in species including dogs and humans has significant geographic variation and this is likely also true for otters. As the pathogenicity of these organisms in wildlife species and the prevalence and geographic distribution of these organisms in otters are not well documented, screening for these and other tick-borne diseases as well as ectoparasite treatment of otters involved in reintroductions should be considered to minimize anthropogenic spread of disease to potentially naïve populations.

Suspected Feline Immunodeficiency Virus Infection In Eurasian Lynx During A Translocation Program - A Veterinary Challenge At The Interface Among Health Risks, Species Conservation, Animal Welfare And Politics

10:30 - Monday, 24th July, Solar Square

Dr. Marie-Pierre Ryser-Degiorgis¹, Ms. Iris Marti¹, Mr. Simone Pisano¹, Dr. Martin Wehrle², Prof. Regina Hofmann-Lehmann³, Dr. Urs Breitenmoser⁴, Dr. Francesco Origgi¹, Dr. Anna Küber-heiss⁵, Dr. Felix Knauer⁵, Dr. Marina Meli³

1. Centre for Fish and Wildlife Health, Vetsuisse Faculty, University of Bern, 2. Natur- und Tierpark Goldau, 3. Clinical Laboratory and Centre for Clinical Studies, Vetsuisse Faculty, University of Zurich, 4. KORA (carnivore ecology and wildlife management), 5. Research Institute of Wildlife Ecology, University of Vienna

The Eurasian lynx (*Lynx lynx*) population in Switzerland serves as a source for reintroductions in neighbouring countries. In 2016/2017, three lynx from the same geographical region were found seropositive for feline immunodeficiency virus (FIV) in the framework of an international translocation program. This unexpected finding raised questions about the origin of the virus and its pathogenicity to lynx, the emerging character of the infection, and the interpretation of serological results regarding the management of lynx caught for translocation. A decision scheme was required to minimize health risks both in the recipient and source populations, considering animal welfare (no prolonged stay in quarantine), the political situation (no repatriation to the source population), and conservation goals (use of the source population for translocations). The seropositive lynx were examined, sampled and observed in quarantine enclosures for several weeks, prior to euthanasia and necropsy. Archived samples from 83 live lynx captured in 2001-2016 were tested for FIV antibodies by Western blot (gold standard), including older samples of the three positive individuals. Clinical signs and organ lesions described in FIV-infected cats were observed in the seropositive lynx but their association with the FIV infection is questionable and attempts to characterize the virus have failed so far. None of the archived samples were positive for FIV antibodies. The proposed decision scheme considered the main route of infection (bites) and expected antibody dynamics, and distinguished between three scenarios: left in the field, translocated, or euthanized. In conclusion, data suggest a recent emergence of FIV in the Swiss lynx population, possibly resulting from a spillover from domestic cats. Nevertheless, the infection remains to be confirmed by virus isolation and sequencing. The FIV pathogenic potential in lynx is still unclear. In this context, the implementation of a cautious decision scheme for the management of seropositive lynx is particularly challenging.

Potential origin of hemoplasma infection in the endangered Darwin's fox (*Lycalopex fulvipes*)

10:30 - Monday, 24th July, Solar Square

Dr. Javier Millán¹, Mr. Aitor Cevidanes¹, Mr. Javier Cabello², Mrs. Sophia Di Cataldo¹, Ms. Irene Sacristan¹, Mrs. Carla Barría¹, Ms. Katy Chirgwin³, Dr. Dario Moreira⁴, Dr. Constanza Napolitano⁴, Mr. Ezequiel Hidalgo⁵

1. Universidad Andres Bello, 2. Universidad San Sebastián 3. Fundación de la Palma Chilena y el Bosque Nativo, 4. Universidad de Chile, 5. Parque Zoológico Buin Zoo

Background: In a previous study, we found that hemotropic mycoplasma infection (chiefly by *Mycoplasma hemocanis*, Mhc) was highly prevalent (57%) in the endangered Darwin's fox (*Lycalopex fulvipes*) in its main stronghold, the island of Chiloé (Southern Chile). Whether Mhc is enzootic in fox populations or the infection is the result of periodic spill-overs from dogs is unknown.

Objectives: To increase our knowledge about the epidemiology of hemoplasma infection in foxes and to determine the prevalence of hemoplasma in sympatric dogs.

Methods: Between 2013-2016, we captured 37 additional free-living foxes from Chiloé (n=32) and the mainland (n=5). We also sampled 198 rural dogs from three areas of Chiloé (Inio, far south, n=33; Yungai, south, n=103; Ancud, north, n=62). Blood was analyzed by conventional and real-time PCR targeting a ≈350 bp sequence of the 16S RNA gene.

Results: Prevalence in fox was 63% (65% in Chiloé, 40% in the mainland), without differences between sex and age groups, seasons, years, or areas into Chiloé. Prevalence in dogs was 24% (Inio 45%; Yungai 24%; Ancud 13%). In Chiloé, prevalence was significantly higher in foxes than in dogs. Sequencing revealed that all the positive cases in foxes showed the highest identity with Mhc, whereas in dogs, only 60% were similar to Mhc, and 40% to *Candidatus M. haematoparvum* or *C. M. hemominutum*. Ten Mhc haplotypes were identified, 3 of which were shared by foxes and dogs.

Conclusions: Hemoplasma infection is still prevalent in Darwin's fox, confirming that is enzootic in this species. Determining the reasons for the differences in prevalence in dogs from different areas of the island will be helpful to determine the way of transmission in the "tick-free" Chiloé. Mhc was probably introduced with dogs, but might be currently being transmitted between foxes. Ongoing molecular characterization will help in confirming this hypothesis.

Impact of disease on recovery of an endangered large carnivore: Canine parvovirus and canine distemper virus in the Mexican wolf (*Canis lupus baileyi*) population in Arizona

10:30 - Monday, 24th July, Solar Square

Dr. Anne Justice-Allen¹, Dr. Matthew Clement¹, Dr. Ole Alcumbrac², Dr. Susan Dicks³

1. Arizona Game and Fish Department, 2. Wildlife Health Services, 3. United States Fish and Wildlife Service

Mexican wolves (*Canis lupus baileyi*) are classified as endangered in Mexico and the United States. Recovery efforts began in 1977; in 1998 wolves were reintroduced into Arizona. Annually, wolves are captured, and tested for exposure to diseases including canine distemper virus (CDV) and canine parvovirus (CPV), viruses implicated in declines of several endangered species. We used annual serologic results and survival data from 99 wolves born in the recovery area from 2003 to 2014 to evaluate whether exposure to CDV or CPV was associated with a greater risk of mortality before 2 years. We used mixed-effects logistic regression to estimate the effect of CDV and CPV on the probability of mortality, while controlling for pack effects and nuisance variables. Seroprevalence rates for CDV and CPV ranged from 0 to 62% and 33% to 100%, respectively (median 14.24% and 90.28%, respectively). The nuisance variable “age at testing” had a negative effect on mortality, while “pack” had little effect. Overall, neither CDV nor CPV seroprevalence had a biologically or statistically significant effect on mortality. For cohorts born in 2002, 2007, and 2010, the mortality rate for wolves <2 exceeded the 95% confidence level of the mean rate (mean 27.21, 2002 = 50.0, 2007 = 67, 2010 = 62.5). In 2006, 5 of 8 wolves were seropositive for CDV indicating an increased circulation of CDV and a possible cause for increased mortality. Necropsy results are pending for 6 of 14 wolves for that period. While statistical analysis demonstrates that the effect of these viruses is small, in 2017 CDV was identified as the cause of mortality in 2 individuals with clinical signs. Necropsy results are pending for 11 of 22 wolves dying in 2015-2016. Additional information regarding the true impact of these diseases could be revealed through comprehensive post-mortem examinations.

Environmental Persistence of *Streptococcus infantarius ss coli* and *Streptococcus phocae*: Bacteria Responsible for Significant Mortality of Northern Sea Otters in Resurrection and Kachemak Bays, Alaska

10:30 - Monday, 24th July, Solar Square

Mrs. Natalie Rouse¹, Mrs. Katrina Counihan¹, Mrs. Deborah Boege-Tobin², Mrs. Khrystyne Duddleston²

1. Alaska SeaLife Center, University of Alaska, 2. University of Alaska

The USFWS declared an unusual mortality event (UME) in 2002 when a high number of sea otters in Alaska were found dead due to severe vegetative valvular endocarditis and septicemia. Culturing of heart valves and biochemical testing of isolates revealed that *Streptococcus infantarius ss coli* and *Streptococcus phocae* were the primary bacteria present in affected cases. We are investigating the persistence of *S. infantarius ss coli* and *S. phocae* in the marine environment by 1) developing a molecular method to detect *S. infantarius ss coli* 2) examining potential microbe-habitat associations and 3) determining the competency of otter prey species to act as reservoirs for these pathogens. A PCR assay was developed to detect the *sodA* gene of *S. infantarius ss coli* in both environmental and clinical samples. Water and blue mussels were collected from 162 sites around the perimeters of Kachemak and Resurrection Bays in the summer of 2016 and pathogen presence was determined using PCR to detect the *sodA* gene. Habitat attributes were recorded onsite and determined using ShoreZone. Prey competency was tested via a dosing experiment in the lab. Our primer set for *S. infantarius ss coli* *sodA* and a previously published primer set for the *S. phocae* *sodA* gene successfully identified our targets in clinical and environmental samples using conventional PCR and quantified the *sodA* gene in dosed prey samples using qPCR. *S. infantarius ss coli* and/or *S. phocae* were present in water and mussels at 61 sites. Statistical analyses to determine bacterial correlations with habitat attributes are currently underway. Prey competency experiments showed that bivalves were the most competent pathogen reservoirs. Results will inform wildlife managers of the environmental risk factors for *S. infantarius ss coli* and *S. phocae* infection and add to knowledge about bacterial ecology in the marine environment.

Infectious disease and toxins as causes of unusual mortality events in penguins

10:30 - Monday, 24th July, Solar Square

*Dr. Marcela Uhart*², *Dr. Ralph E. T. Vanstreels*¹, *Dr. Jessica Kemper*³, *Dr. Nola J. Parsons*⁴, *Dr. Ursula Ellemberg*⁵, *Dr. Patricia Serafini*⁶, *Dr. Renata Hurtado*⁷, *Prof. José Luiz Catão-Dias*⁸, *Dr. Pierre A. Pistorius*¹

1. Marine Apex Predator Research Unit (MAPRU), Nelson Mandela Metropolitan University, Port Elizabeth, South Africa 2. Wildlife Health Center, School of Veterinary Medicine, University of California, Davis, United States, 3. African Penguin Conservation Project, Lüderitz, Namibia, 4. Southern African Foundation for the Conservation of Coastal Birds (SANCCOB), Cape Town, South Africa, 5. Department of Ecology, Environment and Evolution, La Trobe University, Melbourne, Australia 6. National Center for Research and Conservation of Wild Birds (CEMAVE), Chico Mendes Institute for Biodiversity Conservation (ICMBio), Florianópolis, Brazil, 7. Institute of Research and Rehabilitation of Marine Animals (IPRAM), Cariacica, Brazil, 8. Laboratory of Wildlife Comparative Pathology (LAPCOM), School of Veterinary Medicine, University of São Paulo, São Paulo, Brazil

Penguins (Spheniscidae) are one of the world's most endangered seabird groups, with 83% (15/18) of species threatened with extinction at some level. Most penguin species breed colonially in aggregations that range from hundreds to millions of individuals. This makes them particularly vulnerable to spatially-clustered impacts such as disease outbreaks, harmful algal blooms, anthropogenic disturbance and natural disasters. As a result, even geographically limited events have the potential to produce significant penguin morbidity/mortality. We compiled information on 227 penguin unusual mortality events from 1888 to 2016, 26 of which were attributed to infectious disease or toxins. The most common infectious disease leading to mass mortality was pasteurellosis (7 incidents), followed by pox-like and puffinosis-like disease (3), hyper-infestation by ticks (2) and leucocytozoonosis (1). Mortality events attributed to toxins were related to harmful algal blooms, particularly paralytic or neurotoxic shellfish poisoning (5 and 1 incidents, respectively). There were seven incidents where clinical signs and/or necropsy findings were strongly suggestive of a pathogen and/or poison, yet the aetiology could not be conclusively established. Ten penguin species were affected by disease or toxic events, particularly gentoos (*Pygoscelis papua*; 5 events), Magellanics (*Spheniscus magellanicus*; 4) and yellow-eyed (*Megadyptes antipodes*; 4). Geographical distribution was broad, with more events in subtropical and temperate zones. Areas most affected were New Zealand and Southeast Atlantic. Age categories more commonly impacted were pre and post-fledging chicks. Death tolls ranged from <100 to 10,000, but most events did not exceed 1,000 individuals. Higher numbers of events were recorded in the 2000s followed by 2010s. This assessment illustrates that disease and toxins can impact penguin populations, that their trend seems to be increasing, and that careful monitoring and investigation are needed for reducing under-reporting and under-diagnosis biases.

Intermediate Host Of The Necrotic Oropharyngeal Disease (Nod) In Scops Owl (*Otus Scops*): Implications In Public Park Management

10:30 - Monday, 24th July, Solar Square

Dr. Fernando Esperon¹, Dr. Francisca Lopes², Dr. Raúl Alonso², Ms. Verónica Delicado³, Dr. Carlos Sacristán⁴, Dr. Matilde Carballo⁵, Dr. Francisco José Cabrero⁶, Dr. Patricia Orejas²

1. Centro de Investigación en Sanidad Animal (INIA-CISA), 2. Brinjal Owl Rescue Centre, Madrid, Madrid, Spain, 3. Animal Health Research Center (INIA-CISA), Valdeolmos, Madrid, Spain, 4. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, 5. Group of Epidemiology and Environmental Health, Animal Health Research Centre (INIA-CISA). Valdeolmos, Madrid, 28130, Spain., 6. Department of Zoology and Physical Anthropology, School of Biology. University Complutense of Madrid, Spain.

The scops owl (*Otus scops*), an inhabitant of urban parks, has experienced declines in the range of 20%–50% in several European countries, including Spain. The necrotic oropharyngeal disease (NOD) is caused by the third-stage larva of *Gongylonema* sp. (Nematoda: Spiruroidea) and characterized by proliferative necrotic lesions in the oral cavity, and even bone lesions in severe cases, leading to starvation and death. This condition has only been described in scops owl fledglings (an accidental host) in Madrid (Spain) during every breeding season since 1997, with an estimated prevalence of 90%. Spiruroidea parasites have an indirect life cycle, being transmitted to the definitive hosts (mammals or birds) through the ingestion of intermediary hosts, mainly coprophagic insects. In order to identify the *Gongylonema* sp. intermediate host, we analyzed the diet of scops owls: (1) map georeferenciation of over 650 NOD cases (1997-2014) (through placement of camera traps in four nests located in the most prevalent areas); (2) sampling and identification of invertebrates in radio telemetry established owl hunting areas, and (3) employment of a novel highly sensitive real-time TaqMan PCR method to detect *Gongylonema* sp. in the captured arthropods. We captured a low diversity of invertebrates, mainly cicadas (20%) and oriental cockroaches (*Blatta orientalis*) (49%), the latter positive to *Gongylonema* sp. (66.7%). Oriental cockroaches were not registered (photographed) at the nests; however, a previous study reported their predation by scops owls in the studied area. Thus, oriental cockroaches may be considered intermediate hosts of *Gongylonema* sp. and responsible for the transmission of the parasite to scops owl chicks. In the analyzed parks, scops owls are forced to predate on cockroaches due to the absence of their naturally preferred preys, possibly due to management practices that dramatically decrease arthropod diversity. Further studies are currently under development to clarify this hypothesis.

Morbidity And Mortality In Key Deer Caused By An Epizootic Of New World Screwworm Infestation

10:30 - Monday, 24th July, Solar Square

*Dr. Mark Cunningham*¹, *Dr. Samantha Gibbs*², *Dr. Lara Cusack*², *Dr. Heather Fenton*², *Ms. Rebecca Shuman*¹, *Ms. Katherine Watts*², *Mr. Michael Milleson*⁴, *Mr. Daniel Clark*²

1. Florida Fish and Wildlife Conservation Commission, 2. US Fish and Wildlife Service, 3. Florida Fish and Wildlife Conservation Commission, 4. USDA/APHIS/WS

An epizootic of New World screwworm (NWS, *Cochliomyia hominivorax*) in the Florida Keys (USA) in 2016 had a significant impact on the endangered Key deer (*Odocoileus virginianus clavium*). The epizootic, which lasted from 5 July 2016 to 7 January 2017, resulted in the deaths of at least 135 Key deer. The total extent of affected cases and mortality are estimated to be higher, but are unknown. Survival of many deer is attributed to treatment. Of the documented cases, infestations were most frequently seen in male deer (139 of 149 [92%] total documented cases), and males were 73 times (CI 37.4 – 142.5) more likely to be infested than female deer. Lesions in males were most frequently seen on the head, neck, and forelimbs, likely associated with injuries sustained during fighting. Only 10 (8%) females were infested and the distal extremities and vulva were most often affected– the latter likely associated with fawning out of season. Lesions were usually extensive, had multiple larval stages indicative of multiple ovipositions, and extended deep into the surrounding tissues. Histologically, lesions were characterized by necrosis, eosinophilic and pyogranulomatous inflammation, edema, hemorrhage, neovascularization, and secondary bacterial infections. Anemia, neutrophilia, eosinophilia, and hyperglobulinemia were documented in immobilized deer with NWS. The high density of Key deer, optimum environmental conditions for NWS flies, and the occurrence of the outbreak during the rut likely contributed to the severity of the outbreak. Management strategies included the release of sterile male flies, euthanasia of severely affected deer, topical and oral administration of anti-parasitics to free-ranging deer, and immobilization and treatment of deer with mild to moderate infestations. Together these multi-agency management practices contributed to the eradication of NWS in the Keys with the last documented case in a Key deer occurring 7 January 2017.

Co-Infection And Its Consequences For Wildlife Disease Emergence And Control

15:15 - Monday, 24th July, Solar Square

*Prof. Andy Dobson*¹

1.Princeton University

Most wildlife populations are infected with a diversity of infectious agents; some of these interact directly with each other, others interact indirectly through their influence on host immunity, fecundity and survival. I will present some simple mathematical models based on studies of *Mycoplasma* and *Plasmodium* infections in house finches that examine how the presence of a second pathogen modifies the establishment and emergence of a second pathogen: *Mycoplasma gallisepticum*. In the second part of the talk, I will use a closely related mathematical framework to examine how control and eradication of viral infections by vaccinations is impacted by the presence of a second viral pathogen. Here I will specifically consider interactions between CDV (canine distemper virus) and CPV (canine parvovirus). In both halves of the talk new results emerge that suggest our understanding of the dynamics of wildlife diseases may be misleading if we fail to consider the modifications to host-parasite dynamics that occur in host populations that harbor multiple pathogen species.

Surveillance for *Erysipelothrix rhusiopathiae* in Arctic ruminants using data-driven calibration of an ELISA test in the absence of “gold standard”

15:15 - Monday, 24th July, Solar Square

*Mr. Fabien Mavrot*¹, *Mrs. Karin Orsel*¹, *Mrs. Wendy Hutchins*¹, *Mr. Layne Adams*², *Mrs. Michele Anholt*¹, *Dr. Kimberlee Beckmen*³, *Mrs. Kristin Bondo*¹, *Mrs. Marsha Branigan*⁴, *Mr. Mitch Campbell*⁵, *Mrs. Sylvia Checkley*¹, *Mr. Steeve D. Côté*⁶, *Mrs. Christine Cuyler*⁷, *Mrs. Tracy Davison*⁴, *Mr. Brett Elkin*⁴, *Mrs. Lisa-Marie Leclerc*⁵, *Mr. Bryan Macbeth*¹, *Mrs. Angie Schneider*¹, *Mrs. Helen Schwantje*⁸, *Ms. Matilde Tomaselli*¹, *Mrs. Susan Kutz*¹

1. Faculty of Veterinary Medicine, University of Calgary, 2. USGS Alaska Science Center, 3. ADFG Fairbanks Alaska), 4. Government of the Northwest Territories, 5. Government of Nunavut, 6. Département de Biologie et Centre d'Études Nordiques, Université Laval, 7. Greenland Institute of Natural Resources, 8. British Columbia Ministry of Forests, Lands and Natural Resource Operations,

Erysipelothrix rhusiopathiae, a common bacterium of pigs and poultry, was recently isolated from muskoxen (*Ovibos moschatus*) for the first time in the Canadian Arctic. Although serology is an invaluable tool for monitoring diseases in wildlife, serological tests such as enzyme-linked immunoassays (ELISA) are almost exclusively developed for domestic animals. This can lead to misclassification when those tests are directly applied to wild species without adaptation. Typically, adapting a test for a species involves a “gold standard” (i.e. known positive and negative animals) against which the evaluated test is calibrated. This is not always feasible with wildlife species due to financial, ethical and logistical constraints. Here we explore the applicability of a data-driven approach, the so-called mixture distribution modelling to calibrate an ELISA in the absence of “gold-standard”. We then use the calibrated ELISA to monitor exposure to *E. rhusiopathiae* in arctic ruminants.

We used a set of ELISA results (expressed as Optical Density Ratios [ODR]) from 500 free-ranging caribou (*Rangifer t. caribou* and *Rangifer t. groenlandicus*) and 650 muskoxen tested against *E. rhusiopathiae*. We assumed a bi-modal Gaussian distribution of the ODR-values, corresponding to a mixture of two distributions (negative and positive populations) and used maximum likelihood estimation to fit the most likely distributions to our set of ODR-values and determine an optimal cut-off for each species. In a second step, we used bootstrapping to compute a confidence interval around our new cut-off values.

Using those cut-offs on our dataset, we confirmed a widespread exposure to *E. rhusiopathiae* in both species, with large variability in prevalence between populations and years. Additionally, in muskoxen, high seroprevalence seems associated with local population declines or die-offs. Those results highlight the need for reliable diagnostic tests in wildlife monitoring and raise new questions regarding the impact of *E. rhusiopathiae* on arctic wildlife.

Erythroparvovirus, Bocaparvovirus and Tetraparvovirus (PARV4) in Non-Human Primates of Costa Rica

15:15 - Monday, 24th July, Solar Square

Mrs. Andrea Chaves¹, Mr. Roberto Avendaño², Dr. Carlos Ibarra-Cerdeña³, Mrs. Hilary Ureña-saborío⁴, Mr. Francisco A. Venegas⁵, Dr. Max Chavarría⁵, Dr. Edgar Ortiz-Malavasi⁶, Dr. Mauricio Jimenez⁷, Dr. Gustavo Gutiérrez-Espeleta¹

1. Escuela de Biología, Universidad de Costa Rica, 2. Centro Nacional de Innovaciones Biotecnológicas (CENIBiot), CeNAT- CONARE, 3. Departamento de Ecología Humana, Centro de Investigaciones y de Estudios de Avanzados (Cinvestav) del IPN Unidad Mérida, Mérida), 4. Centro Nacional de Innovaciones Biotecnológicas, CeNAT- CONARE, 5. Centro Nacional de Innovaciones Biotecnológicas (CENIBiot), CeNAT- CONARE. Escuela de Química & Centro de Investigaciones en Productos Naturales (CIPRONA), Universidad de Costa Rica. 6. Escuela de Ingeniería Forestal, Instituto Tecnológico de Costa Rica, 7. Escuela de Medicina Veterinaria, Universidad Nacional, 8. Escuela de Biología, Universidad de Costa Rica

The *Parvoviridae* family is composed of rapidly evolving viruses that infect a wide range of hosts. Within the subfamily *Parvovirinae*, which infects vertebrates, we recognize the following genus: *Erythroparvovirus* including the human parvovirus B19 and other related virus, *Bocaparvovirus* including human parvovirus (HBoV1-4) and other parvovirus and the newly classified *Tetraparvovirus*, which includes the human PARV4. There are still many questions about the transmission, classification and dissemination of these three genera, which have been detected in addition to humans in old world primates (*e. g.* gorilla, chimpanzee, rhesus and macaques). In the Americas these viruses have been reported in humans in both North and South America, however, to date there has been not known evidence of its presence in new world primates. We set out to determine the presence of *Erythroparvovirus*, *Bocaparvovirus* and *Tetraparvovirus* in the four species of monkeys of Costa Rica (*Alouatta palliata*, *Cebus imitator*, *Saimiri oerstedii* and *Ateles geoffroyi*). We analyzed 387 samples of blood or plasma from monkeys captured from 2001 to 2016 from free-living populations and captivity. The presence of parvovirus was determined through PCR and the results were confirmed through sequencing and phylogenetic analyzes. We detected 2 (0.5%) individuals that were positive to *Erythroparvovirus*, 10 (2.6%) that were positive to *Boca parvovirus*, and 44 (11.4%) positive to *Tetraparvovirus* (PARV4). *Erythroparvovirus* and *Bocaparvovirus* were detected in *A.palliata* and *C.imitator* in the wild. However, PARV4 was detected in *A.palliata*, *C.imitator* and *A.geoffroyi*, in both, captivity and free-living individuals. Through this research in monkeys of Costa Rica, the presence of these *Parvovirinaes* in new world primates was established. Moreover, PARV4 is widespread in three out of the four monkey species of Costa Rica. Taking into account that this parvovirus has the capacity of hosts shift, it is important to analyze the zoonotic potential that may exist.

The feasibility of controlling rabies in vampire bats (*Desmodus rotundus*) through topical application of vaccine

16:30 - Monday, 24th July, Solar Square

Tonie Rocke, Ben Stading, Daniel Streicker, Kevin Bakker, Jorge Osorio

1.USGS National Wildlife Health Center, 2. University of Wisconsin - Madison, 3.University of Glasgow,
4.University of Michigan

Rabies transmitted by vampire bats (*Desmodus rotundus*) in Central and South America is a significant threat to humans and domestic animals, and also a tremendous economic burden, due to widespread cattle mortality. Current efforts to minimize this threat focus on vaccination of livestock and culling of vampire bats through topical application of anticoagulants that are transferred between bats via mutual grooming. However, studies have shown that despite these efforts for more than 40 years, rabies in vampire bats has increased over time and vampire bats continue to expand their distribution in Central and South America, with corresponding increases in rabies. We recently developed a new recombinant rabies vaccine specifically for bats using an *in silico* antigen designer tool to create a mosaic glycoprotein (MoG) gene with available sequences from the rabies Phylogroup I glycoprotein. This sequence was cloned into raccoonpox virus (RCN) and the efficacy of this novel RCN-MoG vaccine was tested in big brown bats (*Eptesicus fuscus*). Bats immunized with RCN-MoG by the oronasal route (100%) or treated topically with the vaccine in glycerin jelly (83%) survived rabies challenge at a much higher rate than control bats (11%). Field studies are currently being conducted in Peru and Mexico to test the feasibility of oral and topical delivery of vaccine and transfer rates between vampire bats using biomarker-labelled jelly (without vaccine). Initial results are quite promising, indicating that topical application of vaccine, with subsequent spread via mutual grooming, could be an effective method of vaccinating large numbers of vampire bats, providing another tool for managing rabies.

Going Batty: Disease Surveillance of Bats in British Columbia, Canada

16:30 - Monday, 24th July, Solar Square

Glenna McGregor

1. British Columbia Ministry of Agriculture, Canadian Wildlife Health Cooperative

In the fight to protect North America's bats, surveillance of mortalities is important; both to detect movement of White Nose Syndrome (WNS), a devastating fungal disease of bats caused by the fungus *Pseudogymnoascus destructans*, and to determine other common causes of mortality. Understanding health threats may illuminate new ways to minimize mortality and increase resilience of bat populations. In 2016, 190 bat mortalities, comprising 10 species, were collected throughout British Columbia, Canada. A full necropsy by a veterinary pathologist and rabies testing by immunohistochemistry was performed for all bats in an adequate state of post-mortem preservation. WNS testing was done on bats found between November 1 and May 31 by histologic examination of patagium, ears and nose in combination with PCR of cutaneous swabs for *P. destructans*. The cause of death was trauma in 42%, emaciation with no apparent significant concurrent disease in 28%, infectious/inflammatory disease in 22% and undetermined in 8%. Cat predation was the most common source of trauma, accounting for 30% of traumatic deaths. Rabies was the most common infectious disease, affecting 19% of all tested bats. All bats were negative for WNS; however, non-WNS fungal skin disease was surprisingly common in the spring. In bats found between March 1 and May 31, 58% (11/19) bats had histologically appreciable fungal hyphae on their patagium, nose or ears. These fungi were histologically distinct from *P. destructans* and included at least 5 morphologically-distinct fungal species. Fungal hyphae were often associated with an inflammatory response. Fungal infection was rare in bats during the summer. This suggests an increased susceptibility to fungal skin infection by a variety of fungi in bats during hibernation. The presence of inflammation associated with some fungi indicates bats are capable of inciting or maintaining an inflammatory response to a cutaneous fungal pathogen during hibernation.

The Mule Deer Genome: Insights On Past And Future Retrovirus Epizootics

16:30 - Monday, 24th July, Solar Square

Mary Poss, Lei Yang, Theodora Maravegias, Raunaq Malhotra

1. Pennsylvania State University

Raunaq Malhotra (PSU) Genomic analysis can show how historic virus infections shape the allele frequency of host defense genes. However, only retroviruses leave evidence of the actual virus involved in a prior virus outbreak. During a retrovirus epizootic, a germ cell can by chance be infected resulting in acquisition of a new host gene called an endogenous retrovirus [ERV]. We recently identified a new cervid ERV [CrERV] that has been actively colonizing the mule deer genome. We ask how these ERVs have impacted the mule deer genome and whether the dynamics of colonizing ERVs can inform future retroviral epizootics in mule deer or other cervids. The mule deer genome was *de novo* assembled and novel algorithms were used to obtain CrERV sequence at each location in the genome. Bayesian coalescent methods and recombination analysis were used to estimate virus evolutionary dynamics. Impact on host gene expression was assessed by RNA-seq.

Mule deer have experienced five distinct retrovirus epizootics. Because few CrERV are fixed in the mule deer population, there are extensive differences in number and location of CrERV in mule deer genomes. The contemporary epizootic contributed full length CrERV that have extensively recombined with CrERV in the same and older lineages and that retain infectious capability. These data support a process by which an infectious retrovirus recombines with an existing ERV and generates a new recombinant retrovirus, which can reinfect a germ cell and, by analogy to the dynamics of a related feline retrovirus, FeLV, can have new host tropism. We further demonstrate that CrERV now regulates key genes involved in DNA repair and gene expression in some mule deer. Our research provides important genome resources for cervid biologists, provides a history of recent retrovirus infections in mule deer, and suggests a novel mechanism of retrovirus emergence that could impact other cervids.

Demographic Perturbation And Recovery Dynamics Following The Emergence Of Avian Cholera Outbreaks At An Arctic Common Eider Breeding Colony

16:30 - Monday, 24th July, Solar Square

Samuel Iverson Mark Forbes Catherine Soos, Grant Gilchrist

1. Canadian Wildlife Service, Environment and Climate Change Canada,
2. Carleton University,
3. Science and Technology Branch, Environment and Climate Change,
4. Science and Technology Branch, Environment and Climate Change

Emerging infectious diseases are on the rise globally; however, determining the acute and long-term conservation impacts of disease epidemics on wildlife population dynamics remains a significant challenge. In this study, we take advantage of a unique opportunity to examine the transmission dynamics and the demographic impact of a new series of avian cholera outbreaks on a marked population of northern common eiders (*Somateria mollissima borealis*) at a breeding colony in the Canadian Arctic subject to long-term monitoring (1997-2016). Consistent with expectations for a novel pathogen invasion, case incidence increased exponentially during the initial wave of exposure ($R_0 = 2.5$). Disease conditions gradually abated, but only after several years of smouldering infection. In total, >6000 eider deaths were recorded during outbreaks spanning eight consecutive breeding seasons. Breeding pair abundance declined by 56% from the pre-outbreak peak; however, a robust population of breeding pairs remained upon apparent epidemic fade-out. While the arrival of avian cholera coincided with a precipitous decline in the survival rates of both male and female eiders, the disease did not have an appreciable influence on eider nest success. Rather, nest success was most strongly influenced by clutch initiation date, weather conditions, and the frequency of polar bear (*Ursus maritimus*) incursions onto the colony. The latter has exhibited a directional increase in association with anthropogenic climate change and as such constitutes a shift beyond the normal scope of annual variability that could potentially constrain population recovery. The results of our research constitute a step forward in determining disease impacts in a free-ranging wildlife population subject to a variety of limiting factors and for which basic epidemiological information has been lacking.

Viral families in the rectum of migratory wild ducks in a Mexican wetland using high-throughput sequencing

16:30 - Monday, 24th July, Solar Square

Luis Ramírez-Martínez, Elizabeth Loza-rubio, Juan Mosqueda-gualito, Gary García-Espinosa

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. Departamento de Biotecnología en Salud Animal, Centro Nacional de Investigación Disciplinaria en Microbiología Animal, Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, 3. Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro

Waterfowl are considered reservoirs of the *Influenza A virus*, besides, in wild ducks the *Avian avulavirus 1* and the *Avian coronavirus* are also identified commonly. Other viral genera have been described in wild ducks, but they have only been reported during an outbreak or an epidemiological surveillance. Moreover, several viruses have been identified that were not known in wildlife species before. Since it is not well researched the viral diversity that may be found in wild ducks in wetlands, it is not completely understood their role in these species and the ecosystems. The aim of this study was to describe the avian and non-avian viruses in migratory wild ducks during the winter season in a marsh in the central high plateau of Mexico, to assess an initial description of the virome in free-living wild ducks. During January to February 2016, sixty five hunted migratory wild ducks of eight species were collected in the Chignahuapan marsh, and the feces were obtained directly from the rectum of the specimens. The nucleic acids from the virus-like particles were purified and the nucleotide sequences were obtained by next-generation sequencing (Illumina). A taxonomic classification detected eighteen viral families in all samples and up to 54 viral families. The *Alloherpesviridae* and *Herpesviridae* were the most abundant families, nevertheless several viral genera from insects, plants and bacteria were also detected. All of them represent known viral families and they concurred with the expected species from marches so far. No viral families involved with humans or farm animals were detected so far. Since the virome of the wild ducks shows a great diversity of viruses from different hosts, others than ducks, it is important to continue investigating their role in these species to assess their potential transmission to others animals that inhabit the marshes (Project PAPIIT IN218716).

A small leap. Spillover of Morbillivirus into novel hosts exerts divergence on its H protein

16:30 - Monday, 24th July, Solar Square

Maricarmen Villalobos, Gabriel E García Peña, Rosa Elena Sarmiento-Silva, Oscar Rico-Chavez

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México

Morbilliviruses are RNA virus that infects a variety of mammals, including cetaceans, primates, carnivores and ruminants. This genus of viruses is deteriorating human and wildlife health, and the wide diversity of its hosts suggests that some have jumped and specialized into new hosts. Nonetheless, the mechanisms by which Morbillivirus adapts to a wide spectrum of hosts are poorly understood. To advance on this issue we reviewed the associations between host diversity and the primary structure of the Hemagglutinin protein (H), which binds Morbillivirus with the host cellular receptor, SLAM (Signaling Lymphocyte Activation Molecule); this event represents an essential step in the Morbillivirus infection. In our bioinformatic review we analysed 645 sequences, and identified 52 non-synonymous changes in the primary structure of the H protein of the most generalist Morbillivirus, Canine Distemper Virus (CDV). Measles virus (MeV), which is more specific than CDV and only infects primates, had 62 non-synonymous changes in the H protein. Five of the amino acids in CDV and none in MeV, are known to interact with the SLAM; and only three of these are common between CDV and MeV. Hence, this evidence suggests that host jumps in CDV, and specialization in MeV may exert divergent selection on the H protein, in sites not known to interact with the SLAM molecule. Moreover, because currently there is no evidence that these positions modulate SLAM, we argue that changes in the tertiary structure of the H protein may facilitate or prevent infection of diverse hosts with Morbillivirus. Together, this review provides some insight on the properties of Morbillivirus that may help controlling epidemic outbreaks that jeopardize wildlife and human health.

Chagas Disease Ecology Near Its Northern Edge Of Endemicity

16:30 - Monday, 24th July, Solar Square

Sarah Hamer

Texas A&M University

Despite over 100 years of research on *Trypanosoma cruzi*, this parasite continues to cause significant morbidity and mortality in human, dog, and nonhuman primate populations across the Americas, with unmeasured impacts on other domestic mammals and wildlife reservoirs. Parasite transmission networks are vastly different across geographic regions, ranging from domestic infestations of triatomine vectors with high human contact to predominantly sylvatic transmission among wildlife with only occasional spillover to humans. In a one health approach, our objective was to develop a multidisciplinary program to address Chagas disease ecology in the southern US, where there is now increasing recognition of locally-acquired disease despite endemic triatomines and infected wildlife for many decades. We use citizen science to empower the public with disease prevention information while accepting citizen-collected triatomines for analysis. Molecular analysis of over 3500 insects from this program revealed >60% *T. cruzi* infection prevalence and bloodmeals acquired from diverse wildlife, domestic animals, and humans. In our comparative wildlife evaluations in Texas, raccoons (*Procyon lotor*) have emerged as a key, infectious reservoir with over 70% of raccoons (n=99) from central Texas having *T. cruzi*-infected heart tissue. In contrast, 0-14% of feral hogs, bats, bobcats, coyotes, fox, and rodents were infected (n=844). We have studied *T. cruzi*-infected shelter dogs, government working dogs, and pet dogs to link epidemiology with pathology, and found that infection with parasite discrete typing unit TcIV is more likely to result in asymptomatic infections relative to TcI which is more commonly associated with myocarditis. Finally, we have detected *T. cruzi* exposure in 1.8% of humans (n=233) and 19.6% of their pet dogs (n=209) in impoverished communities along the Texas-Mexico border. Together, these studies emphasize wildlife and animal research in the Chagas system will benefit not only animal health, but also human health.

Hantavirus Infection From Humans To Rodents

15:15 - Monday, 24th July, Real Room

Dr. Gabriel E García Peña¹, Dr. Benjamin Roche², Dr. Ivan Castro-Arellano³, Dr. Marion Vittecoq⁴, Dr. Constantino González-Salazar⁴, Dr. Christopher Stephens⁵, Prof. Jean Francois Guegan², Dr. Gerardo Suzán

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. IRD, 3. Texas State University, 4. Tour du Valat, 5. C3 – Centro de Ciencias de la Complejidad, Universidad Nacional Autónoma de México

Wildlife's diseases are emerging in humans, impairing health and global economy. On this matter, quantitative analyses on massive large scale datasets of public domain can aid in surveilling zoonosis. We illustrate this, by analysing the evolution of Hantavirus (Bunyaviridae) across the Americas. Particularly, the Andes Virus genotype is of concern because it is a virus transmitted from rodents *Oligoryzomys longicaudatus* to humans, which develop Hantavirus Pulmonary Syndrome. Unlike other hantavirus forms, it has been suggested that Andes Virus can be transmitted from person-to-person and generate small epidemics in human populations; thus (reverse zoonosis) transmission from humans to rodents is plausible. To investigate this controversial hypothesis, we first performed geographic analysis on 264,543 reports of rodent specimens preserved in museum collections, to identify co-occurrence of rodent species susceptible of infection with hantaviruses. Second, we performed phylogenetic inference on the transmission network, by analyzing 339 nucleotide sequences of the hantavirus's nucleocapside. Together, these results revealed three stages of hantavirus transmission: i) sylvatic enzootic cycles of hantavirus, ii) transmission of epizooties to humans, and iii) humans may transmit Andes Virus to the rodent reservoir. Overall, these findings militate for integrative comparative analyses at smaller scales to investigate transmission pathways at the interface between human and the wild.

Andes hantavirus infection in rodents from a landscape dominated by exotic plantations in Chile: Identifying risky habitats

15:15 - Monday, 24th July, Real Room

Dr. André V. Rubio¹, Dr. Fernando Fredes², Dr. Javier A. Simonetti¹

1. Facultad de Ciencias, Universidad de Chile, 2. Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile

The expansion of human activities at expenses of natural environments may result in changes in hantavirus infection dynamics, sometimes creating conditions for the emergence of Hantavirus Pulmonary Syndrome in humans. Therefore, the study of the effects of land use change on host and hantavirus dynamics is relevant for a better understanding of risk for hantavirus exposure. Andes virus (ANDV) is a hantavirus strain that cause 40% case fatality rate in humans in Chile. In this country, forest industry is based mostly on Monterrey pine (*Pinus radiata*) plantations. To date, there is no information regarding the effects of this land use change on ANDV prevalence in rodents. Our aim was to study ANDV seroprevalence in a landscape that contains extensive stands of Monterrey pine and interspersed remnants of Maulino forest, a native temperate forest located in central Chile. Rodents were sampled in four types of habitats (3 replicates for each): Native forest, adult pine plantation, young pine plantations with high understory cover and young pine plantation with low understory cover. In each habitat type, trapping was undertaken for four consecutive nights, during each four season, using a 7 × 10 grid of Sherman traps. Blood was tested for antibodies against ANDV using a strip immunoblot assay. To date, we have conducted four trapping periods capturing 698 individuals from 6 species. Habitat types differed in the structure of small mammal assemblages. The native forest harbors more abundance of *Oligoryzomys longicaudatus*, the main ANDV reservoir, and preliminary results indicates that ANDV seroprevalence in *O. longicaudatus* is higher in native forest with overall seroprevalence of 7.7% compared to the other habitats in which the overall seroprevalence range from 0% to 2%. Our preliminary data showed that land conversion to pine plantations, including adult and young plantations would not increase ANDV risk exposure to humans.

Modeling filovirus maintenance in nature by experimental transmission of Marburg virus between Egyptian rousette bats

15:15 - Monday, 24th July, Real Room

Amy Schuh, Brian Amman, Megan Jones, Tara Sealy, Luke Uebelhoer, Jessica Spengler, Brock Martin, Jo Ann Coleman-McCray, Stuart Nichol, Jonathan Towner

1. Centers for Disease Control and Prevention, 2. San Diego Zoo Global 3. Oregon Health and Science University

The Egyptian rousette bat (*Rousettus aegyptiacus*) is a natural reservoir host for Marburg virus; however, the mechanisms by which the virus is transmitted bat-to bat and to other animals are unclear. In this study, we co-housed Marburg virus inoculated donor Egyptian rousette bats with naive contact Egyptian rousette bats. Marburg virus shedding was detected in oral, rectal and urine specimens from inoculated bats from 5–19 days post infection. Simultaneously, Marburg virus was detected in oral specimens from contact bats, indicating oral exposure to the virus. In the late study phase, we provided evidence that Marburg virus can be horizontally transmitted from inoculated to contact Egyptian rousette bats by finding Marburg virus RNA in blood and oral specimens from contact bats, followed by Marburg virus IgG antibodies in these same bats. This study demonstrates that Marburg virus can be horizontally transmitted from inoculated to contact Egyptian rousette bats, thereby providing a model for filovirus maintenance in its natural reservoir host and a potential mechanism for virus spillover to other animals.

From dead duck to national announcement – HPAIV H5N8 in the UK 2017

16:30 - Monday, 24th July, Real Room

J. Paul Duff , Paul Holmes, Richard M Irvine

1. Animal and Plant Health Agency, Diseases of Wildlife Scheme, England and Wales

It is one thing diagnosing a wild waterbird infected with Highly Pathogenic Avian Influenza virus (HPAIV) H5N8 and another to ensure that the laboratory result from the wild bird is assessed, prioritised and escalated, by correct routes, to the highest veterinary authority of the country, usually the Chief Veterinary Officer (CVO). This presentation takes the audience through the process from dead duck to HPAIV announcement in England, by looking at the steps in the process. In most countries the pathways for notifiable disease reporting in domesticated animals are well rehearsed but they may not be so clearly marked out for notifiable disease in wild animals. The authors, between them, have many years' experience in these steps along the pathway, from their own pathological examinations of submitted water birds, to the co-ordination of national surveillance and diagnostic examinations, and finally to the reporting of threats in wildlife to the veterinary and medical authorities. The process starts with the diagnosis of H5N8 infected wild birds in January 2017. Although isolation of pathogens may be reported directly to Policy divisions, following the England Wildlife Health Strategy, threats from all vertebrate wild species are reported monthly to a Veterinary Risk Group and this will be described. This talk also covers the pathways that have been devised in England and Wales for wildlife threats, from the original pathology and surveillance results, to the assessment of the findings, their dissemination and their risk assessments (when appropriate) reported to the Policy customers from the medical, veterinary and biodiversity authorities. Ways to improve this movement of data from the post-mortem room table to the Policy desks will be discussed.

West Nile virus infection in elk and moose in Michigan

16:30 - Monday, 24th July, Real Room

Julie Melotti, Thomas Cooley, Daniel O'Brien, Scott Fitzgerald, Steven Bolin, Kimberly Signs, Kelly Straka

1. Michigan Department of Natural Resources, Wildlife Disease Lab, 2. Michigan State University, Diagnostic Center for Population and Animal Health, 3. Michigan Department of Health and Human Services

Following the detection of West Nile virus (WNV) in North America in 1999, the Michigan Department of Natural Resources Wildlife Disease Lab (WDL), in collaboration with other agencies, has monitored for infection of avian and mammalian species with WNV. West Nile virus has been detected in a large number of mammalian species worldwide. From 2002 through 2016, twenty free-ranging mammals were diagnosed with WNV infection as the primary cause of death in Michigan, including eight eastern fox squirrels (*Sciurus niger*), eight white-tailed deer (*Odocoileus virginianus*), two elk (*Cervus canadensis nelsoni*), one big brown bat (*Eptesicus fuscus*) and one moose (*Alces alces*). While exposure and fatal infection has been documented in big brown bats and eastern fox squirrels, clinical disease in white-tailed deer is infrequently documented and this represents the first reports of clinical disease caused by WNV in elk and moose. Both elk were yearling animals displaying signs consistent with a neurological disorder and were subsequently euthanized and submitted to the WDL as suspects for infection with *Parelaphostrongylus tenuis*. The moose was a 4 year old bull involved in a vehicle strike. All three animals had histopathological lesions in the brain consistent with a viral infection and a real-time PCR assay that included an hydrolysis probe confirmed WNV was present in the brain.

Invasive Macaques In Florida Carry And Shed A Herpes Virus Of Public Health Concern

16:30 - Monday, 24th July, Real Room

Samantha Wisely, Jane Anderson, Carisa Boyce, Katherine Sayler, Amy Klegarth, Steve Johnson

1. University of Florida, 2. University of Washington

Rhesus macaques (*Macaca mulatta*) are an invasive species in Florida and Puerto Rico and host to *Macacine herpesvirus 1* (MaHV1), a pathogen that is typically asymptomatic in macaques, but is fatal if untreated in 70% of cases in humans. In Silver Springs State Park, Florida, a breeding population of macaques has been established for >80 years. The goal of our study was to estimate the proportion of animals that were actively shedding virus in their saliva and feces and estimate the risk of transmission to humans. We collected samples non-invasively at two times of year when animals may be stressed and therefore shedding virus: during gestation in Spring 2016 (n=22 saliva samples representing 5 to 22 individuals, and 1 fecal sample) and during the breeding season in October 2016 (n=48 saliva samples representing 28 to 45 individuals and 22 fecal samples). We used real time polymerase chain reaction (qPCR) to detect viral DNA from samples. Zero animals were detected shedding virus in March, but 3 saliva samples were positive for viral DNA in October for a minimum prevalence of 4 to 11%. For years in which data were available, the park averaged 3 macaque bites to visitors per year. Although the risk of a human coming into contact with an actively shedding animal is low, the consequences are great. This public health issue needs to be addressed in Florida.

Orf Virus In Alaskan Mountain Goats, Dall's Sheep, Muskoxen, Caribou And Sitka Black-Tailed Deer – A Zoonotic Risk For Hunters And Game Managers

16:30 - Monday, 24th July, Real Room

Morten Tryland, Kimberlee Beckmen, Kathleen Burek-huntington, Eva Breines, Jörn Klein

1. UiT - Arctic University of Norway, 2. ADFG Fairbanks Alaska, 3. Alaska Veterinary Pathology Services, 4. UiT - Arctic University of Norway, 5. University College of Southeast Norway

Study background: The zoonotic Orf virus (ORFV; genus *Parapoxvirus*, *Poxviridae* family) occurs worldwide and is transmitted between sheep and goats, wildlife and man.

Objectives: The aim of this study was to address the presence of parapoxvirus in Alaskan game species having clinical signs suspicious of ORFV infection.

Methods: Fifteen animals reported dead or euthanized for animal welfare reasons had lesions on the mucocutaneous margins and/or on coronary bands consistent with or suspicious of contagious ecthyma, representing mountain goat (*Oreamnos americanus*, $n=8$), Dall's sheep (*Ovis dalli dalli*, $n=3$), muskox (*Ovibos moschatus*, $n=3$), and caribou (*Rangifer tarandus granti*, $n=1$). In addition, one Sitka black-tailed deer (*Odocoileus hemionus sitkensis*) had lesions consistent with a fibroma. Archived tissue samples from these cases were analyzed with PCRs targeting four different genes (putative viral envelope antigen; *B2L*, GM-CFS IL 2; *GIF*, putative Viral interleukin 10; *vIL-10*, and putative homolog to orthopox A type inclusion protein and viral fusion peptide).

Results: All four PCRs demonstrated ORFV specific DNA in all cases. Phylogeny revealed that sequences from Dall's sheep formed a separate cluster, with sequences comparable to ORFV from domestic sheep. In contrast, sequences from all the other species were different from the Dall's sheep sequences but almost identical to each other, despite of originating from animals separated by geography and ten years of sampling.

Discussion and conclusions: This is the first report of parapoxvirus infection in caribou and Sitka black-tailed deer. This study revealed that ORFV is present in many of the large ruminant game species in Alaska. These findings call for attention to potential transmission of ORFV from wildlife to domestic sheep and goats, as well as to people handling game, such as hunters, subsistence harvesters, and wildlife biologists.

Plasmid-Mediated Antimicrobial Resistance Genes In House Sparrows (*Passer Domesticus*): A Comparative Study Between Livestock And Urban Environments

16:30 - Monday, 24th July, Real Room

Verónica Delicado, Carlos Sacristán, Matilde Carballo, José Ignacio Aguirre, Ana De La Torre, Fernando Esperon

1. Animal Health Research Center (INIA-CISA), Valdeolmos, Madrid, Spain, 2. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, 3. Group of Epidemiology and Environmental Health, Animal Health Research Centre (INIA-CISA). Valdeolmos, Madrid, 28130, Spain, 4. Department of Zoology and Physical Anthropology, School of Biology. University Complutense of Madrid, Madrid, Spain, 5. Centro de Investigación en Sanidad Animal (INIA-CISA)

Antimicrobial resistance (AMR), particularly of plasmid-mediated AMR genes (PM-ARGs), is an emerging threat to public health whose presence and impact in wildlife is widely unknown. We assessed the impact of livestock on the acquisition of PM-ARGs by a synanthropic species; the house sparrow *Passer domesticus*. We evaluated house sparrows (n=38) from two populations; an intensive sheep farm (n=17; 8 in 2013, 9 in 2015) and an urban environment (n=21; 8 in 2013, 13 in 2015). A common garden experiment was performed in all the individuals captured in 2013, which were maintained in captivity for 21 days under the same standardized conditions, and had fecal samples collected at three different moments: trapping (t_0), 11th (t_1) and 21st day in captivity (t_2). Real-time PCRs were employed to detect and quantify six PM-ARGs (*sull*, *sullI*, *qnrS*, *tet(A)*, *tet(Q)*, *mecA*) on the intestinal bacterial metagenome of the studied birds. PM-ARGs levels found in both scenarios were low, most frequently *sull*. Two urban-samples were positive to *mecA*, a gene present in methicillin-resistant *Staphylococcus aureus* strains. At t_0 , captive house sparrows from farm areas presented a larger percentage of individuals positive to *sullI* (75% vs. 0%, $p=0.000$) and an increased mean number of PM-ARGs per sample (2.5 vs. 0.75, $p=0.000$) in comparison with the urban sparrows. Furthermore, the percentage of *sull* gene copies (8.5×10^{-2} vs. 1.4×10^{-3} *sull* copies /100 16S rRNA gene copies, $p=0.013$) and a mean number of PM-ARGs per sample (2.5 vs 1.4 genes/sample, $p=0.008$) decreased in farm sparrows between t_0 and t_2 . This is the first report of *mecA* in house sparrows worldwide. Our findings show the impact of livestock on the presence of ARGs in wildlife, how ARGs levels decrease following farm exposure withdrawal, and the use of PM-ARGs as indicators of the degree of wildlife exposure to farming environments.

Integrated Social-Behavioral And Ecological Risk Maps To Prioritize Local Public Health Responses To Lyme Disease

16:30 - Monday, 24th July, Real Room

Catherine Bouchard, Cécile Aenishaenslin, Erin Rees, Jules Konan Koffi, Yann Pelcat, Marion Ripoche, François Milord, Robbin Lindsay, Nicholas Ogden, Patrick Leighton

1. Public Health Agency of Canada, 2. University McGill, 3. Université de Montréal, 4. DSP Montérégie

Lyme disease (LD) risk exhibits spatial variability that challenges public health authorities to prioritize prevention and control interventions that are adapted to the local context. The objective of this study was to link social-behavioral and ecological risk measures to create enhanced risk maps for public health decision-making: a social/behavioral-ecological vulnerability index map and a prioritization index map.

The study was conducted in the Montérégie region of Southern Quebec, Canada, where LD is an emerging disease. Spatial variation in LD knowledge, risk perceptions and behaviors in the population were measured using websurvey data collected in 2012, and used as a proxy for the social-behavioral risk. Tick vector population densities were measured in the environment during field surveillance from 2007 to 2012 to provide an index of the ecological risk. Social-behavioral and ecological risk measures were combined to create integrated risk maps and, with addition of human population densities, prioritization index maps. Map predictions were validated by testing the association between high risk areas identified by the risk maps and the current spatial distribution of human LD cases.

Social-behavioral and ecological risks had incongruent distributions suggesting that both factors should be considered when making decision about locally adapted interventions. The occurrence of human LD cases in a municipality was positively associated with high tick density ($P < 0.01$) but was not significantly associated with social-behavioral risk. This result suggest that ecological risk is still the main driver of human cases in the study region, an observation that fits with its emerging epidemiological status, but that could be reversed in different epidemiological contexts.

To our knowledge, this study is the first to develop integrated social/behavioral-ecological risk maps for LD to assist decision-making. Such maps provide a novel and valuable tool for prioritizing and adapting interventions to the local characteristics of targeted populations.

Health screening of Chiricahua leopard frogs (*Lithobates chiricahuensis*) at the Fort Worth Zoo as a tool for conservation programs In situ: The Sorta Situ link

09:00 - Monday, 24th July, Solar Square

Dr. Hugo Alejandro Gonzalez Jassi¹, Dr. Carlos Sánchez¹, Dr. Emily E. Brenner¹

1. Fort Worth Zoo

The Chiricahua leopard frog (*Lithobates chiricahuensis*) has been listed by the IUCN as a vulnerable species since 2004 and designated as threatened by the U.S Fish and Wildlife Services in 2000. As a part of a multi-institutional conservation effort, the Fort Worth Zoo (FWZ) began housing a captive group to establish a headstart program. A retrospective mortality assessment showed that some of the most common pathologies in this species at the FWZ included skin ulcerations, joint degeneration, and granulomatous disease. As a part of the headstart program, the Fort Worth Zoo has established a strict biosecurity program and routine health screening surveillance. The routine health surveillance includes a complete physical exam and diagnostic tests, such as whole body radiographs, blood samples, bacterial cultures, intra-articular and bone fine needle aspirates (FNA for acid fast stains ([AFS]), and PCR to rule out mycobacteriosis.

In 2016, results of 19 health screenings revealed that 70% of the population presented bone lesions related to chronic osteomyelitis. The carpal regions were most commonly affected. From the 13 animals suspected for chronic osteomyelitis, 4 animals were positive to AFS in FNA. Histologically, 2 cases showed lesions suggestive of *Mycobacterium* and 2 cases were positive for (*Mycobacterium chelonae*) by PCR. The incidence of *M. chelonae* in frogs with bone lesions was 10.5%.

The low prevalence of *M. chelonae* in this study, supported by literature findings, suggests that this organism is an opportunistic pathogen commonly found in the soil or water of amphibian environments. This is the first report of osteomyelitis bone lesions caused by *Mycobacterium chelonae* in this specie of anuran. Health screenings of the captive colony remains a paramount component of the *Sorta Situ* approach and must be performed in all captive colonies of amphibians that will be reintroduced into the wild to avoid introducing emerging pathogens.

From science to policy: management of health when wildlife is involved, an inquiry in France

09:00 - Monday, 24th July, Solar Square

Mr. Sebastien Gardon¹, Dr. Sylvie Mialet¹, Prof. Marc Artois¹

1. VetAgro-Sup

The management of health crisis situations pose peculiar problems when wild plants or animals are deemed source of a disease of the humans or their livestock. A group of students at the National school for veterinary services, in France, was in charge of an inquiry on the social or political dimensions of these crisis situations. After reviewing the recent history of health events linked with wildlife in this country, a focus was made on four case studies: allergies due to ambrosia, Lyme disease management, HPAI avian influenza during the years 2005/2007 and finally a recent outbreak of two cases of human brucellosis linked to infection of a free living ibex population. The students have led 25 semi-structured interviews of various involved people: stakeholders, heads of associations, government workers, professionals... to collect their views on the management of health in this context. The purpose of the report was to draw recommendations for an appropriate and proportionate management of the health in epidemiological situations leading to the emergence of diseases resulting from direct or indirect exposure to wild plants or animals in a natural environment.

As a result of the interviews and literature review, three areas should be explored to reduce the risk of crisis outbreak:

- A better communication scheme when things go well (media coverage on emergency plan exercises, explanations of sanitary measures).
- A better preparation for communication through training of government workers, scientists and experts.
- A better use of the the social networks that allow to communicate quickly and directly to the targeted public in a way avoiding the spread of rumours.

The final version of the report will be publicly published after an external review.

co-authors: Hervé Sevestre, H el ene Renault, C ecile Balon, Nathalie Riverola, (all veterinary officers) and Alice Delarue, Marie-claude Lemaistre (*Master 2 PAGERS IEP Lyon*). xx

Infestation of *Hopilas malabaricus* (Teleostei, Characiformes, Erythrinidae) with nematode parasite *Eustrongyloides* spp. in the Arena Dam of Trinidad, West Indies

09:00 - Monday, 24th July, Solar Square

Dr. Rod Suepaul¹, Prof. Asoke Basu¹, Mr. Ryan Mohammed¹

1. The University of the West Indies

Background: “*Hopilas malabaricus*”, is found in Trinidad, locally called ‘guabine,’ but referred to as ‘wolf fish’ in the ornamental trade. After discovering “worms” in the flesh, a local fisherman brought seven *H. malabaricus* for necropsy.

Methodology: Necropsy was performed and the helminths were preserved in 70% alcohol for identification. Tissue samples were fixed in 10% buffered formalin for 48 hours, embedded in paraffin and stained with haematoxylin and eosin for histological examination. Sections of the gastrointestinal tract were also examined for parasite.

Results: In 4 out of 5 fish, 14 to 18 worms approximately 30.0 mm long with a 2.0 mm diameter were isolated. Amongst the muscle fibres, there were multiple sections of large helminth parasites within a dense fibrous capsule which was infiltrated by granulocytes and macrophages. The nematodes were identified as “*Contracaecum* sp.” and “*Eustrongyloides* sp.”

Conclusions: This is the first report of *Eustrongyloides* sp. in Trinidad. The parasites were found in a similar anatomical location as other fish and, typical histological lesion were present. The guabine were caught during a metrological drought. *Eustrongyloides* sp. are capable zoonotic agents.

Responses of Juvenile Black-Tailed Prairie Dogs to a Commercially-Produced Oral Plague Vaccine Delivered at Two Doses

09:00 - Monday, 24th July, Solar Square

*Ms. Elsa Cárdenas-Canales¹, Dr. Lisa Wolfe¹, Mr. Daniel Tripp¹, Dr. Tonie Rocke²,
Dr. Rachel Abbott², Dr. Michael Miller¹*

1. Colorado Parks and Wildlife, 2. USGS National Wildlife Health Center

The damaging effects of plague- an exotic disease to North America- have depressed prairie dog (*Cynomys* spp.) abundance. Recently, oral vaccination of prairie dogs has emerged as a potential tool for combating plague. To support landscape-level vaccination efforts, we used off-the-shelf technology to mass-produce vaccine-laden baits carrying an experimental, commercial-source plague vaccine (RCN-F1/V307). We then conducted laboratory trials to confirm its safety and immunogenicity and also measured black-tailed prairie dog (*C. ludovicianus*) responses to a lower vaccine dose in order to begin exploring the potential for cost savings. Forty-five juvenile black-tailed prairie dogs were divided into three treatment groups ($n=15$ animals/group). The first group received one standard dose vaccine bait (5×10^7 plaque forming units [pfu]; STD) and the second group received a lower dose bait (1×10^7 pfu; LOW). In the third group, five animals received two standard-dose baits (DD) and 10 were left untreated but in-contact (C). We tested for seroconversion using a lateral flow assay that detects antibodies against *Yersinia pestis* V antigen. During the study, two vaccinated prairie dogs died, but laboratory analyses ruled out vaccine involvement. Overall, 17 of 33 (52%; 95% confidence interval for binomial proportion [bCI] 34-69%) prairie dogs receiving vaccine-laden bait showed a positive antibody response on at least one sampling occasion after bait consumption, and eight (24%; bCI 11-42%) showed sustained antibody responses. STD and LOW groups did not differ ($P \geq 0.78$) in their proportions of overall or sustained antibody responses to vaccine bait consumption. We did not observe any adverse effects related to oral vaccination. Lowering the annual cost of plague management seems necessary in order to facilitate its sustained, large-scale use as a conservation tool. Our data suggest that lowering vaccine dose could be explored as a means of further reducing the overall cost of oral vaccination for landscape-level plague control.

Molecular evidence of *Toxoplasma gondii* in synanthropic rodents (*Mus musculus* and *Rattus rattus*) captured in Yucatán, México

09:00 - Monday, 24th July, Solar Square

Mr. Torres Marco¹, Mr. Rodrigo Medina-Pinto¹, Mr. Alonso Panti-May¹, Prof. Silvia Hernández-betancourt¹, Mr. Henry Noh-Pech¹, Mr. Aarón Yeh-Gorocica¹, Prof. Edwin Gutiérrez-Ruiz¹, Prof. Jorge Zavala-Castro¹, Prof. Fernando I. Puerto¹

1. Universidad Autónoma de Yucatán

Introduction. *Toxoplasma gondii* is an obligate intracellular parasite recognized as the etiological agent of Toxoplasmosis, a zoonotic disease endemic in different countries worldwide. The definitive host of this parasite are individuals of the *Felidae* family, including domestic cats (*Felis catus*). In Mexico, the disease is recognized as a human and animal health problem. *Toxoplasma gondii* sporozoites have the capacity of been released from the gut lumen and infect several tissues, including kidneys. Rodents have been identified as intermediate hosts of *Toxoplasma gondii*; nevertheless, no previous reports exist in Yucatán, México, about their role in the infectious cycle.

Objective. Report the circulation of *Toxoplasma gondii* in biological samples of synanthropic rodents (*Mus musculus* and *Rattus rattus*) captured in a rural community from Yucatán, México.

Methods. A total of 187 rodents were studied: 130 (69.5 %) *Mus musculus* and 57 (30.5 %) *Rattus rattus*. Total DNA was extracted from renal tissue and was utilized in the identification of *Toxoplasma gondii* with the end-point PCR method. Positive products were purified and sequenced to confirm and validate the results through the BLAST Sequence Analysis Tool.

Results. The PCR provided a global positivity of 5.34% (10/187). The BLAST analysis found a direct homology for *Toxoplasma gondii* with identities and coverage of 96-98% and 98-100%, respectively.

Discussion. Rodents have an important role as intermediate hosts of *Toxoplasma gondii*, and are involved in the domestic, peridomestic and wild infection cycles. Predation of these animals is a fundamental element for the dissemination of *Toxoplasma gondii*, because they are important sources of infection for domestic and wild cats. Our results confirm the role of *Mus musculus* and *Rattus rattus* in the biological cycle of Toxoplasmosis. This converts to both studied species in potential transmission pathways, which represents an epidemiological risk to domestic animals and inhabitants of community studied.

Ebola virus surveillance and capacity building in Sierra Leone

09:00 - Monday, 24th July, Solar Square

Dr. Brian Amman¹, Dr. Amy Schuh¹, Ms. Tara Sealy¹, Mr. James Graziano, Mr. Ibrahim Abu-bakarr, Jonathan Johnny², Celine Taboy, John Klena, Stuart Nichol, Aiah Lebbie², Jonathan Towner¹

1. Centers for Disease Control and Prevention, 2. Njala University

The December 2013 emergence of Ebola virus in multiple West African countries resulted in over 28,600 cases with over 11,300 deaths from Ebola virus disease. Sierra Leone reported over 14,100 cases with 8,706 laboratory confirmed cases and 3,956 deaths. Beginning in June 2015, the Centers for Disease Control and Prevention's Viral Special Pathogens Branch (CDC VSPB) initiated a multi-year collaboration with Njala University in Sierra Leone to establish an in-country disease ecology surveillance program aimed at detecting filoviruses and other zoonotic pathogens in wildlife, primarily bats. Through a cooperative agreement between the VSPB and Njala University, a team of local investigators is being trained to perform ecological surveillance on potential and confirmed zoonotic disease reservoirs. This effort includes the establishment of a high-throughput molecular diagnostic laboratory on the Njala University campus for testing collected field samples. Ecological surveillance methods and laboratory training began in October 2015, and the first trapping efforts were conducted in January 2016 in eastern Sierra Leone, near the Guinea border and roughly 50 km from the epicenter of the 2014 Ebola outbreak. To date over 2400 tissues from 300 bats and representing 20 species have been collected for initial qRT-PCR testing. Serological testing, as well as additional training in serologic testing methods for local investigators, will be carried out at the CDC in Atlanta, GA.

Molecular identification of *Toxoplasma gondii* in road-killed wild animals from Yucatán, México

09:00 - Monday, 24th July, Solar Square

*Mr. Torres Marco*¹, *Mr. Rodrigo Medina-Pinto*¹, *Mr. Alonso Panti-May*¹, *Prof. Silvia Hernández-betancourt*¹,
*Mr. Henry Noh-Pech*¹, *Mr. Aarón Yeh-Gorocica*¹, *Prof. Edwin Gutiérrez-Ruiz*¹, *Prof. Jorge Zavala-Castro*¹,
*Prof. Fernando I. Puerto*¹

1. Universidad Autónoma de Yucatán

Introduction. *Toxoplasma gondii* is an obligate intracellular protozoan parasite, recognized as the causal agent of toxoplasmosis, zoonotic endemic disease in many countries, including México. In Yucatán, México, this disease is important in public and animal health. Wild animals are host of zoonotic pathogens as *Toxoplasma gondii*. Utilizing road-killed wild animals for molecular detection of *Toxoplasma gondii* and other zoonotic pathogens, represents a feasible and efficient alternative to the use of live animals in research.

Objective. Report the circulation of *Toxoplasma gondii* DNA in different tissue samples from road-killed wild animals from Yucatán, México.

Methods. Four road-killed wild animals were studied: 1 coatimundi (*Nasua narica*), 1 greater grison (*Galictis vittata*), 1 Yucatan squirrel (*Sciurus yucatanensis*), and 1 tayra (*Eira barbara*). A necropsy was performed and were taken different tissues samples for DNA extraction. The molecular identification of a fragment of the B1 *Toxoplasma gondii* gene was pretended through final point PCR. Positive products were sequenced and analyzed by BLAST tool; additionally, a phylogenetic tree was constructed.

Results. *Toxoplasma gondii* DNA was detected in brain, lung, liver, kidney, and spleen from a Yucatecan squirrel (*Sciurus yucatanensis*), in a lung, and femoral muscle of a greater grison (*Galictis vittata*), and in a kidney from a coatimundi (*Nasua narica*)

Discussion. Our results confirm that *Toxoplasma gondii* is present in wild mammals, which act as sources of infection for humans and animals. This is the first molecular report of the *Toxoplasma gondii* circulation in a squirrel and coatimundi from Yucatan, and maybe is the first in a greater grison around the world. Squirrels are important in the *Toxoplasma gondii* infectious cycle. In this study, we did not find evidence of *Toxoplasma gondii* DNA circulating in tayra, but this fact can be a consequence to the small sample size.

Molecular detection of pathogenic leptospiras in synanthropic and wild rodents, captured in Yucatán, México

09:00 - Monday, 24th July, Solar Square

Torres Marco , Bayron Cruz-Camargo, Rodrigo Medina-Pinto, Carlos Moguel-Lehmer, Rolando Medina ,José Ortiz-Esquivel, William Arcila-Fuentes, Henry Noh-Pech, Alonso Panti-May, Aarón Yeh-Gorocica, Iván Rodríguez-Vivas, Fernando I. Puerto

1. Universidad Autónoma de Yucatán

Introduction. *Leptospira* spp. is the causal agent of leptospirosis; zoonotic disease endemic in Mexico, recognized as a public health and veterinary problem. Rodents are the most relevant reservoirs of *Leptospira* spp., because the bacteria establish and reproduces in their renal tissue. In Yucatán, there are reports of leptospirosis in humans, domestic and wild animals.

Objective. To report the presence of pathogenic *Leptospira* in renal tissue from synanthropic and wild rodents captured in Yucatán, México.

Methods. Synanthropic and wild rodents were captured in the rural municipality of Cenotillo, Yucatán, México. A kidney was recollected and total DNA was extracted. The identification of *Leptospira* spp. was made by the amplification of two fragments of 16S rRNA gene, trough polymerase chain reaction (PCR) final point. The positive products were sequenced and analyzed by alignment tools; also, was constructed a phylogenetic tree for the determination of the isolated species.

Results. Were captured a total of 92 rodents belonging to seven different species: *Rattus rattus* (27.2 %), *Mus musculus* (27.2 %), *Heteromys gaumeri* (23.9 %), *Ototylomys phyllotis* (10.9 %), *Peromyscus yucatanicus* (8.8 %), *Peromyscus leucopus* (1.0 %), and *Sigmodon hispidus* (1.0 %). The PCR yielded a global positivity of 5.4 % (5/92). The alignment analysis of the sequenced products demonstrated an 100 % of coverage and 93-100 % of identity whit *Leptospira interrogans* species; which was also identified in the phylogenetic tree.

Discussion. Rodents of Yucatán are reservoirs of *Leptospira* spp. and may participate in the infection cycle of leptospirosis. We present the first molecular evidence of the circulation of *Leptospira* spp. in a *Heteromys gaumeri* captured in Yucatán, México. Also, we confirm previously reports in *Mus musculus* and *Rattus rattus*. Presence of infected rodents is considered a risk factors for the presentation of leptospirosis in humans and domestic animals.

Presencia de genes de resistencia a antimicrobianos en felinos silvestres

09:00 - Monday, 24th July, Solar Square

Dr. Kinndle Blanco-Peña³, Ms. Ana Sofía Angulo¹, Dr. Fernando Esperon¹, Mr. Roberto Salom-Pérez²

1. Posgrado Regional en Ciencias Veterinarias, Universidad Nacional Centro de Investigación en Sanidad Animal (INIA-CISA), 2. Programa Jaguar Panthera, 3. Instituto Regional de Estudios en Sustancias Tóxicas (IRET), Universidad Nacional de Costa Rica)

La resistencia a antimicrobianos es un riesgo emergente con efectos poco conocidos sobre los ecosistemas. Los mecanismos por los que una bacteria es resistente son múltiples, sobresaliendo los genes de resistencia (ARGs) mediados por plásmidos.

En esta investigación se buscaron 16 ARGs (*tet*, *sul*, *cat*, *qnrS*, *vanA* y *mecA*) en heces de 14 jaguares (*Panthera onca*) y 13 pumas (*Puma concolor*) de Costa Rica mediante qPCR. La cuantificación fue relativa (% de bacterias con un gen) y la resistencia se categorizó en: baja ($\geq 10^{-6}$ - 10^{-4} %), intermedia ($> 10^{-4}$ - 10^{-1} %) y alta ($> 10^{-1}$ -100%). Las muestras negativas se asignaron un valor de un punto logarítmico por debajo del límite de cuantificación (10^{-7} %). Se hallaron 14 de los 16 ARGs en al menos una muestra. Los jaguares presentaron mayor promedio de genes por muestra (7,4) que los pumas (5,0; $p=0,026$), y mayor concentración de *tet*(W) (jaguares=0,15%; pumas=0,033%; $p=0,016$). Los ARGs más hallados fueron: *tet*(Q) (85%) y *tet*(Y), *sulI* y *sulII* (70%). El *qnrS*, que codifica a quinolonas, fue hallado solo en jaguares (21,4%).

Cuantitativamente, 6,2% de los resultados fueron de alta resistencia, 23,6% intermedia y 8,8% baja; 61,3% estaban debajo del límite de detección. No se observaron diferencias entre especies.

En conclusión, los grandes felinos podrían ser reservorios de bacterias con ARGs, algunos de los cuales, como *qnrS*, son de especial importancia en ganadería y salud pública. Las diferencias halladas en concentraciones, número de genes y perfiles, pueden estar relacionadas con las vías de exposición, principalmente de naturaleza antropogénica, muy especialmente la agropecuaria. Esto puede relacionarse con la interacción entre felinos y ganado, factor a tener en cuenta fuera de áreas protegidas (ej. en gestión de corredores biológicos). Para dilucidar si existe una relación entre ganadería y perfiles de ARGs, se ampliará el número de muestras analizadas y se representarán geográficamente en futuros estudios.

“Making the most of precious data – building a wildlife health database for Nepal”

09:00 - Monday, 24th July, Solar Square

Dr. Deborah McCauley¹, Dr. Amir Sadaula², Dr. Gretchen Kaufman¹

1. Veterinary Initiative for Endangered Wildlife 2. National Trust for Nature Conservation

Nepal has recently begun to invest in wildlife health infrastructure to better understand and protect species that are important to them. We previously reported on the development of a strategy to prioritize disease investigation in endangered and threatened species. Wildlife health data is now being collected and must be handled in the most efficient and responsible manner to lead to evidence based research and policy development.

VIEW has spearheaded the creation of a wildlife health database system that is responsive to local needs. All data is considered property of the Government of Nepal and access will be bound by strict confidentiality agreements. Data is generated in several ways: 1) when an animal is brought into a wildlife facility for treatment, 2) when an animal is captured for conflict or management reasons, 3) when an animal is found dead and a necropsy is performed, and when health data is generated as part of a research study. All data is collected by authorized wildlife professionals, processed and entered into the database by designated individuals.

The database is structured to collect data on individual animals identified through a unique identifier/microchip, and basic information such as species, gender, age, and location. This information is tagged to all subsequent data points associated with that animal. Biological samples are linked to the animals unique identity through a bar coding system. Health data is entered on a Medical History form (repeatable), and/or a Necropsy form. Standard report modules are available to generate paper or electronic reports, such as laboratory and necropsy reports. In addition, specific queries can be made to generate customized reports based on any of the database parameters.

This simple database provides access to wildlife health information for the first time and forms the basis for better understanding the health threats faced by Nepal's wildlife.

Frecuencia de *Toxoplasma Gondii* en Félidos Silvestres en Cautiverio de México

09:00 - Monday, 24th July, Solar Square

Mr. Antonio Gomez¹, Dr. Matilde Jiménez Coello¹, Dr. Karla Acosta Viana¹, Dr. Eugenia Guzmán Marín¹, Dr. Ivonne Hernández Cortazar¹, Dr. Antonio Ortega Pacheco¹, Dr. Darío Guiris Andrade², Mr. Rubén López Alonso³

1. Universidad Autónoma de Yucatán, 2. Universidad Autónoma de Chiapas, 3. Zoológico Zoofari

Toxoplasma gondii es un parásito zoonótico mundial del cual se desconoce su carga de ooquistes, período de eliminación y biotipos en félidos silvestres. En estas especies, se han reportado altas seroprevalencias del parásito (54-81%), pudiendo afectar negativamente la conservación, reintroducción y/o translocación de estas y otras especies, dependiendo de la susceptibilidad, virulencia del biotipo involucrado y estatus inmune del hospedero. Asimismo se han asociado estas especies con casos de toxoplasmosis en humanos. El objetivo de esta investigación fue determinar la frecuencia de *T. gondii* en félidos de cuatro zoológicos mexicanos. De noviembre de 2015 a septiembre de 2016, se colectaron muestras de sangre de 42 félidos de diez especies en cuatro zoológicos mexicanos, así como 35 muestras de heces de estos mismos ejemplares. El suero fue analizado mediante una ELISA IgG indirecta. Las heces se analizaron por microscopia directa posterior a una flotación (con solución de Seather, densidad 1.27) para determinar ooquistes del parásito. Asimismo, se obtuvo el ADN genómico de sangre completa y heces, y se evaluó la ausencia de inhibidores por amplificación de los genes constitutivos GAPDH (sangre) y 18s (heces); las muestras positivas se utilizaron para la amplificación del gen SAG1 de *T. gondii*, mediante una PCR anidada (PCRa). Se detectaron anticuerpos anti-*T. gondii* en el 100% de los sueros analizados, en contraste, no se detectaron al microscopio ooquistes en las muestras de heces. Por otra parte, en el 9.5% (4/42) y en el 14.3% (5/35) de las muestras de ADN obtenidas de sangre y heces respectivamente, se amplificó un fragmento de 390 pares de bases, correspondiente a SAG1. Existe una alta seroprevalencia de *T. gondii* en las poblaciones estudiadas, asimismo el detectar parasitemia y eliminación de ooquistes pueden indicar una reactivación o reinfección con un biotipo diferente. Posteriormente se identificarán los biotipos circulantes en estas especies

Transmission of influenza A virus from mallards to European starlings via shared water

09:00 - Monday, 24th July, Solar Square

Dr. Susan Shriner¹, Mr. Jeremy Ellis¹, Dr. Jeff Root¹, Mr. Kevin Bentler¹, Ms. Nicole Mooers¹, Ms. Kaci VanDalen¹,
Ms. Katherine Dirsmith¹

1. National Wildlife Research Center

Influenza A viruses (IAV) have the potential to cause serious economic harm to poultry and when highly pathogenic strains emerge they may be problematic. While mallards (*Anas platyrhynchos*) are a very common reservoir host for IAVs, these birds are infrequently found on farms. Thus, we are studying IAV bridge hosts which are species that come into contact with both maintenance hosts (aquatic birds) and/or their habitats and poultry and/or their environment. In this study, we first assessed the susceptibility of European starlings (*Sturnus vulgaris*) to a low pathogenic IAV by experimentally inoculating starlings with an H4N6 virus. We then evaluated the transmission of IAV from experimentally infected mallards by inoculating three mallards in a pen that shared water with three other pens, each of which housed three starlings. We replicated this experiment three times. For both the experimental inoculation and the transmission experiments, we collected oral, cloacal, and fecal swabs daily and then tested the swabs for viral RNA by qPCR. All ten experimentally inoculated starlings became infected with a mean peak in oral shedding of $10^{4.09}$ EID₅₀/mL on the first day post inoculation. In the transmission experiments, all starlings (N = 9 per replicate) became infected in each of the three replicates. Peak oral shedding varied from $10^{3.38}$ EID₅₀/mL to $10^{3.51}$ EID₅₀/mL and transmission was evident in different individuals between days three and seven post inoculation of the mallards. In all three replicates, the viral RNA load in the water peaked at around 10^4 EID₅₀/mL. This study demonstrates that starlings can be infected with low pathogenic IAV from water contaminated by infected mallards. Accordingly, starlings should be considered in the development of farm biosecurity plans in order to minimize the potential risk of IAV transmission to poultry.

Notoedric Mange In Fox Squirrels From Kansas, USA

09:00 - Monday, 24th July, Solar Square

*Dr. Heather Fenton*¹, *Dr. Devinn Sinnott*², *Dr. Elizabeth Elsmo*³, *Ms. Sarah Peltier*⁴, *Dr. Michael Yabsley*¹

1. Southeastern Cooperative Wildlife Disease Study 2. The Ohio State University College of Veterinary Medicine 3. Marshfield Labs 4. Florida Fish and Wildlife Conservation Commission

Notoedres is a genus of sarcoptiform mites that have been documented in numerous mammalian hosts worldwide, most commonly rodents and bats. Most of what is known about this genus is related to *Notoedres cati*, the causative agent of mange in domestic cats. However, other mammalian hosts, including humans, have been diagnosed with *Notoedres* sp. infections. This case report describes the lesions in two, adult, male fox squirrels (*Sciurus niger*) from Kansas that were observed with bilateral alopecia along the dorsal midline. Deep skin scrapings of the alopecic skin revealed numerous adult mites with two pairs of anterior and posterior legs, long unbranched pedicels, and a dorsal anus, consistent with the genus *Notoedres*. Amplification and sequencing of the ITS-2 region of mite DNA revealed 99.4% similarity to a *N. centrifera* sequence (KF278482). *Notoedres centrifera* seems to be endemic in some wild squirrel populations in the United States, but periodic outbreaks of notoedric mange, sometimes associated with significant mortality events, have been reported in Western gray squirrels in California and Washington, Eastern gray squirrels in Massachusetts, and fox squirrels in Indiana and Illinois. Most recently, *N. centrifera* has been associated with a large die-off in Western gray squirrels in the San Bernardino mountains in California. Risk factors that have been proposed to predispose free-ranging squirrels to outbreaks include: poor nutritional condition (e.g. due to crop failure), habitat loss, mild winter conditions, and stress. The objectives of sharing these cases are to describe the lesions of notoedric mange in fox squirrels to promote recognition of the gross appearance of this condition, describe diagnostic methods used to confirm infection with this mite, and to raise awareness that equipment used to trap, handle, and ear tag free-ranging mammals could potentially act as fomites and potentially transmit mites to other hosts.

Assessing the impact of monk parakeets in Santiago: Ecological and public health implications of a neglected invasive species in Chile

09:00 - Monday, 24th July, Solar Square

*Prof. Cristóbal Briceño¹, Dr. Cintia Munita¹, Dr. Paola Sanhueza¹, Mrs. Gabriela Contreras¹, Prof. Héctor Hidalgo¹, Dr. Sofía Egaña-Labrín¹, Prof. Jaime Hernández², Dr. Dominique Surot¹, Prof. Daniel González-Acuña¹,
Dr. Fernando Fredes*

1. Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, 2. Facultad de Ciencias Forestales y de la Conservación de la Naturaleza, Chile

Invasive species are one of the major threats to biodiversity and the first in insular ecosystems. Chile is geographically isolated and consequently, it has high levels of endemism. This natural heritage is important in central Chile, where the highest anthropic pressure is found.

The monk parakeet (*Myiopsitta monachus*) is one of the most problematic introduced birds in Chile, successfully established in Metropolitan Region. Its biology, such as monogamy, non-migration behaviour and the unique ability among psittacids to build their nests, has proven useful for invasion. Despite decades since first observed in Chile, almost no literature is available. Furthermore, globally there is little information on their impact and no records or their potential zoonotic pathogens.

Our objective is to assess the origin, extent and dispersion of the parakeets' invasion in Metropolitan Region of Chile, and to evaluate their ecological impact and risks to human and animal populations.

Mapping nest distribution we are establishing variables that determine the presence of nests in certain trees. Through capture, we are assessing parakeets' health status using clinical pathology, pathogen culture and molecular detection of viruses, bacteria, protozoa and parasites. Using molecular genetics at genomic scale we aim to elucidate the origin and extent of the invasion.

Nineteen percent of sampled adult parakeets were positive to *Cryptosporidium* spp. We have also detected positive chicks to *Giardia* spp., being most of these chicks positive to *Streptococcus* alpha haemolyticus in palatine swabs. Forty six percent of the adults had the louse *Paragoniocolotes fulvofasciatum*, never found in Chile before.

Combining ecological, genetic and diagnostic tools we aim to determine risk factors to the health of humans and animals from this synanthropic parakeet. Through colony management, we are building capacity to reduce the impact of monk parakeets and their associated risks.

Financed by VID, Universidad de Chile and Fondecyt 11160852

The Microbiome Of Ticks At The Interface Of Domestic Animals And Wildlife In Nicaragua

09:00 - Monday, 24th July, Solar Square

*Dr. Aubrey Tauer*¹, *Dr. Christiane Düttman*², *Dr. Christine Fiorello*³

1. Cura Earth, 2. Universidad Nacional Autunoma de Nicaragua, 3. University of California Davis School of
Veterinary Medicine

The microbiome of important disease vectors can affect vector competence, and thus the transmission of pathogens of importance to wildlife, domestic animal, and public health. Little is known about how global climate change and anthropogenic disturbance affect the microbiome of ticks, an important vector of diseases worldwide in wildlife, and especially little work has been done in identifying both the microbiomes and pathogens of importance in neotropical ticks. Ticks removed directly from horses, cattle, dogs, and cats in close proximity to nature reserves or rural areas were donated from Düttman's collection at the Universidad Nacional Autónoma de Nicaragua, Fiorello's collection from Bowawas Biosphere Reserve, and Tauer's collection from area's adjacent to the Reserva Padre Ramos. Ticks were preserved in ethanol and shipped to the United States. Tick species were identified to the species level using morphology and sexed. The ticks' GI tracts was dissected and DNA extracted, 16s rRNA PCR was completed with Illumina MiSeq and operational taxonomic units were identified. Analysis was done in Geneious and R. Of the species of ticks identified, 43 ticks were *Amblyomma maculatum*, 1 was *A. mixtum*, 3 *Dermacenter dissimilis*, 2 *D. imitans*, 9 *D. nitens*, and 36 *Rhipicephalus sanguineus*. Tick species varied by region and host species. Operational taxonomic unit composition and diversity varied by tick species and region. The microbiome of ticks in this study lay the ground work for further research into vector competence in ticks in the neotropics and the ecology of disease transmission, but also emphasize the importance for surveillance for pathogens of importance using other molecular methods.

Evaluation Of High-Risk Human-Wildlife Interfaces In Myanmar For Emerging Viral Threats

09:00 - Monday, 24th July, Solar Square

*Dr. Marc Valitutto¹, Dr. Ohnmar Aung¹, Dr. Kyaw Yan Naing Tun¹, Ms. Megan Vodzak¹, Dr. Dawn Zimmerman¹,
Dr. Suzan Murray¹*

1. Global Health Program, Smithsonian Conservation Biology Institute

Over 70% of emerging infectious diseases (EIDs) in humans originate from animals, prompting a global focus on the human-wildlife interface for the prediction and prevention of future pandemics. Opportunities for ‘spill-over’ of these viruses from wildlife to human populations are facilitated with increased interactions at the human-wildlife interface. The Republic of the Union of Myanmar, located entirely within the Indo-Burma “biodiversity” hotspot, is classified as a region where EIDs are more likely to occur based on environmental, socio-economic, geographical, and ecological factors. Recent changes in the Myanmar government have expanded economic development, and opened borders to globalization offering access to foreign tourists and investors with increased incidence of exposure to these high-risk human-wildlife interfaces. Traditional high-risk interactions persist including wildlife consumption and guano collection, with intensification of other practices such as wildlife trade, poaching, ecotourism, and unregulated deforestation. Despite this increase, there is not only a paucity of data, but also limited surveillance on EIDs in Myanmar, due in part to almost five decades of political isolation. Thus, understanding the intersection between wildlife and humans is a critical step for recognizing patterns of disease emergence in Myanmar. In this investigation, two geographic regions in Myanmar, including Hpa-an of Kayin State, and Hlawga National Park of Northern Yangon, were thoroughly evaluated for the presence of high-risk human-wildlife interfaces and for the potential impact on human health. Both regions boast a thriving ecotourism industry, religious shrines, wildlife trade markets, and nearby livestock farms offering visitors and local communities direct interaction with wildlife including non-human primates, bats, and rodents. The increased exposure of humans to wildlife in Myanmar poses a risk to human health and highlights the need for a multi-sector approach to effectively protect public health.

Surveillance of select arboviruses in farmed and wild white-tailed deer (*Odocoileus virginianus*) in Florida, USA

09:00 - Monday, 24th July, Solar Square

Ms. Carisa Boyce¹, Dr. Samantha Wisely¹, Dr. Katherine Saylor¹

1. Department of Wildlife Ecology and Conservation, University of Florida

As part of the objectives of the University of Florida Cervidae Health Research Initiative (CHeRI), we perform surveillance for epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) in farmed and wild white-tailed deer (*Odocoileus virginianus*). These two pathogens are vectored by biting midges (*Culicoides* spp.). In addition, we test a subset of deer specimens for the presence of two reportable mosquito-borne viruses: eastern equine encephalitis virus (EEEV) and West Nile virus (WNV). From April 2015 to April 2017, whole blood and tissue specimens were collected throughout Florida, from both live (n=610) and dead (n=64) white-tailed deer. Specimens were tested for EHDV and BTV RNA using reverse-transcriptase quantitative polymerase chain reaction (RT-qPCR). Over half of post-mortem specimens tested positive for either EHDV or BTV (39/64); 6.3% were co-infected with both viruses. In live deer, nearly 21% (127/610) of specimens tested positive; 1.8% had co-infections of both EHDV and BTV. Temporal variability in seasonal effect was observed with the majority of deer testing positive during the month of September in both 2015 and 2016. All white-tailed deer specimens have tested negative for both EEEV and WNV. In Florida, EHDV and BTV are significant causes of morbidity and mortality in white-tailed deer. Cases of EEEV and WNV are rare in white-tailed deer, but necessitate surveillance due to the zoonotic nature of these viruses. Florida is an epicenter for many vector-borne diseases; thus it is important to screen for select arboviruses. We plan to continue our surveillance efforts as part of the ongoing CHeRI project.

Orthopoxvirus and Rabies Seroprevalence in Wild Carnivores of Northwestern Chihuahua, Mexico

09:00 - Monday, 24th July, Solar Square

Mr. Clint Morgan¹, Mr. Andres Lopez-Perez², Mrs. Paola Martínez Duque², Mr. Felix R. Jackson¹, Dr. Gerardo Suzán², Dr. Nadia F. Gallardo-Romero³

1. Poxvirus & Rabies Branch, Centers for Disease Control and Prevention Atlanta GA, USA, 2. Departamento de Etología, Fauna Silvestre y Animales de Laboratorio, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México 3. Poxvirus & Rabies Branch, Centers for Disease Control and Prevention A

The distribution of Orthopoxviruses (OPXV) across the North American continent is suggested by previous serosurveillance studies to be widespread, and OPXV seroprevalence reported in these studies indicates a wide range of mammalian hosts. To further investigate the OPXV distribution within Mexico, wild carnivores were collected via live-trapping from fall of 2013, and spring of 2014 within the Janos Biosphere Reserve (JBR) in northwestern Chihuahua, Mexico at five sampling sites categorized by vegetation type. After species and sex identification the animals were ear-tagged and blood samples were collected from cephalic or femoral veins for diagnostic testing. Anti-Orthopoxvirus IGG Enzyme-Linked Immunosorbent Assay (ELISA) and Rapid Fluorescent Focus Inhibition Test (RFFIT) assay for the detection of rabies virus neutralizing antibodies (RVNA) were conducted. Preliminary ELISA results show that around 30% of the carnivores tested were seropositive for anti-Orthopoxvirus neutralizing antibodies, and all carnivores tested were negative for RVNA by RFFIT. Orthopoxvirus antibodies have been identified in previous studies within three genera of Procyonidae from Central and Southeast Mexico. These results may indicate a widespread distribution of OPXV within carnivores throughout Mexico.

Valores hematológicos y de química sanguínea de *Cebus imitator* (*Cebidae*) sanos en condiciones de vida libre en Costa Rica

09:00 - Monday, 24th July, Solar Square

*Mrs. Sofia Bernal*¹, *Dr. Mauricio Jimenez*¹, *Mrs. Ana Meneses-guevara*¹

1. Escuela de Medicina Veterinaria, Universidad Nacional

Cebus imitator habita en ambas vertientes de Costa Rica, considerado bajo amenaza de extinción. La determinación de valores hematológicos y de química sanguínea, proporciona una herramienta útil y confiable para complementar la evaluación del estado de la salud, contribuyendo a realizar diagnósticos, pronósticos y medir la evolución de la afección o un tratamiento. Este estudio en monos de vida libre, es pionero en su área en Costa Rica. El objetivo del mismo fue establecer valores de referencia preliminares hematológicos y de química sanguínea para *Cebus imitator* en condiciones de vida libre en Costa Rica. Se evaluaron muestras de sangre y suero de 26 monos aparentemente sanos *in situ*, habitantes de nueve áreas protegidas y fincas privadas. Los animales se capturaron mediante la inyección intramuscular de Ketamina 10% (10-20mg/kg) y Xilacina 2% (0.5-2mg/kg). Para determinar los parámetros hematológicos se utilizaron métodos manuales convencionales, mientras la química sérica se analizó bajo métodos colorimétricos y cinéticos automáticos y debidamente estandarizados. Al obtener las medidas estadísticas descriptivas: media, desviación estándar, valores mínimos y máximos, se observó que algunas variables hematológicas como la concentración de leucocitos, neutrófilos segmentados y linfocitos, presentaron una gran dispersión de los datos (alta desviación estándar), mientras que los datos de la química sérica, mostraron menor dispersión, por ende, ámbitos más estrechos. A pesar de lo anterior, común hallazgo en animales de vida libre, los resultados son razonables en el contexto de literatura de primates no humanos y se ubican dentro del ámbito reportado para el género *Cebus* y la especie en estudio. Estos valores sanguíneos pueden considerarse un acercamiento a los ámbitos fisiológicamente normales, válidos para animales *in situ*, bajo circunstancias de muestreo, semejantes. Para realizar una correcta interpretación de los resultados del hemograma y química sanguínea, estos deben integrarse a la clínica del animal y a otros exámenes colaterales.

Analysis of Morbidity and Mortality of Wild Koalas in South-East Queensland using Passive Surveillance Data

09:10 - Tuesday, 25th July, Solar Square

Viviana Gonzalez-Astudillo, BVSc, MNR

PhD Supervisors: A/Prof. Rachel Allavena, Dr. Joerg Henning

The koala is a tree-dwelling marsupial and iconic representative of Australia's native fauna, with a current population estimate of >300,000. Despite these estimations, it is listed as 'vulnerable to extinction' due to the high variation in population densities across regions and time and relative persistence of population threats across its range. Habitat loss is the most important conservation threat for koalas, and relates to many factors driving local declines, of up to 80% in certain regions within South-East Queensland since the 1990s. Several hospitals have provided specialised care to injured and diseased koalas for decades, collecting data on major causes of admission. Nevertheless, the lack of standardised pathological analysis and data management procedures to compile and analyse data are primary constraints for understanding koala threats. To determine local threats and examine risk factors driving admissions, a government-managed database of N=20,250 koalas (1997-2013) was utilised for an epidemiological retrospective analysis via multinomial logistic regression models in addition to exploratory spatial analysis. In addition, a large-scale prospective post-mortem survey (N=519; 2013-2016) was conducted. Trauma, chlamydiosis, and wasting, were the leading causes of admission, each of these revealed to be regionally clustered in potential hotspots by space-time permutation scans. Although similar numbers of males and females were admitted to hospitals in both datasets, demographic factors as well as temporal variables, were found to strongly drive the dynamics of koala disease and injury. Koalas were also frequently diagnosed with more than one aetiology, with chlamydiosis frequently co-occurring (39% vs. 48% retrospective and prospective study, respectively). Alarming, 50% of injured koalas that underwent a post-mortem examination had evidence of underlying disease or were wasted. Results suggest that locally, the koala decline involves a complex interplay of aetiologies, primarily due to anthropogenically-driven factors, that require immediate attention and application of mitigation and management strategies.

Novel and Highly Sensitive SYBR Green Real-Time PCR for Poxvirus Detection in Odontocetes

09:10 - Tuesday, 25th July, Solar Square

Carlos Sacristán, José Luiz Catão-Dias, Carol Ewbank, Elena Neves, Elitieri B. Santos-neto, Alexandre Azevedo, José Jr. Lailson-brito, Pedro V. De Castilho, Fábio Gonçalves Daura-jorge, Paulo César Simões-Lopes, Matilde Carballo, Fernando Esperon

1. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, 2. Laboratory of Wildlife Comparative Pathology (LAPCOM) – Pathology Department – School of Veterinary Medicine and Animal Science – FMVZ. University of São Paulo, São Paulo state, 05508-270, Brazil, 3. Group of Epidemiology and Environmental Health, Animal Health Research Centre (INIA-CISA). Valdeolmos, Madrid, Spain, 4. Laboratório de Mamíferos Aquáticos e Bioindicadores “Profa Izabel M. G. do N. Gurgel” (MAQUA), Faculdade De Oceanografia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil, 5. Universidade do Estado de Santa Catarina, Departamento de Engenharia de Pesca, Laguna, SC, Brazil, 6. Centro de Investigación en Sanidad Animal (INIA-CISA

Poxviruses are considered emerging pathogens in cetaceans, currently temporarily named “cetacean poxviruses” (CePV, family *Poxviridae*). These viruses are further classified into two main lineages: CePV-1 in odontocetes and CePV-2 in mysticetes. These viruses have been associated to benign cutaneous lesions known as “tattoos” or “pinholes”. Only a few studies performed the molecular detection of CePVs, via DNA polymerase gene (DNA-pol) and/or DNA topoisomerase I gene (DNA-topo) amplification. Herein we reported a new real-time PCR (rt-PCR) assay based on SYBR® Green and a new primer set to detect a 150 bp fragment of CePV DNA-pol gene also effective for conventional PCR diagnosis. To assess the efficacy of the method, we tested tattoo-skin lesions from twelve dolphin specimens: 10 from the Mediterranean coast of Spain {Atlantic bottlenose dolphin (*Tursiops truncatus*) (n=1), Risso’s dolphin (*Grampus griseus*) (n=1), and striped dolphins (*Stenella coeruleoalba*) (n=8)} and 02 from Brazil {*T. truncatus* (n=1) and Guiana dolphin (*Sotalia guianensis*) (n=1)}. Five individuals were positive to both novel rt- and conventional PCR methods (*G. griseus*, 02 *S. coeruleoalba*, and the *S. guianensis* and *T. truncatus* from Brazil), even two specimens previously negative to current conventional DNA-pol and DNA-topo PCR methods (*G. griseus* and 01 *S. coeruleoalba*). Relative sensitivity of the novel and current methods was based on the comparison of the results obtained from 10-fold dilution series of one strain (*T. truncatus*, Brazil), showing that our novel PCR methods are 1000- to 10000-fold more sensitive. To the authors’ knowledge, this is the first report of a *Cetaceanpoxvirus* rtPCR detection method, demonstrably a much more sensitive tool in the diagnosis of CePV-1 infections and able to potentially contribute to the diagnosis of subclinical poxvirus infections, especially in cases of compromised DNA integrity (e.g., autolysis, formaldehyde-fixed samples, etc) and low number of viral copies.

Are fungi present in octocoral lesions in the Costa Rica Caribbean during El Niño 2015-2016?

09:10 - Tuesday, 25th July, Solar Square

Alejandra Calderón Hernández, Andrea Urbina Villalobos, Juan Alberto Morales, Jorge Cortés

1. Universidad Nacional de Costa Rica

Octocorals (Cnidaria: Octocorallia) are important components of marine ecosystems. Octocorals create environmental complexity, leading to higher biodiversity, are important producers of secondary metabolites and are attractive animals for tourism. Four infectious diseases described in octocorals have been associated with fungi and one of them has caused high rates of mortalities in the sea fans (*Gorgonia* spp.) in different countries of the Caribbean during the last El Niño events. The aim of this study was to describe macroscopic and microscopic lesions, isolate and identify fungi in octocorals, and to investigate fungal involvement. During El Niño 2015 - 2016 dives were conducted at 11 sites of La Amistad Caribe Conservation Area, Limón, Costa Rica. Tissue samples were collected, and temperature, pH, depth, salinity variables as well as geographical coordinates and dimensions of octocorals were recorded. Description of lesions and identification of fungi were based on reference guides. PCR using B-tubulin primers followed by sequencing for *Aspergillus* identification were used. Fifty five colonies from five genera (*Gorgonia*, *Eunicea*, *Plexaurella*, *Pseudopterogorgia* and *Muricea*) were studied, 30.9 % had lesions and the rest had no evident lesions. Eight genera of fungi were isolated from healthy tissues whereas three genera were identified in affected tissues; *Aspergillus*, *Penicillium*, *Fusarium* and *Scopulariopsis* were the most frequent genera in healthy colonies, while *Aspergillus*, *Penicillium* and *Zygosporium* in affected colonies. No relationship between octocoral dimensions and abiotic parameters and the presence of lesions and / or isolation of fungi was found. Fungal hyphae associated with tissue reaction were demonstrated by histopathology in 17.6 % of the affected colonies and the parasitic adaptation matched with the isolated fungi. Multidisciplinary and longitudinal studies are necessary to elucidate the pathogenic or opportunistic role of these fungi and the factors involved in tissue damage in order to provide knowledge leading to the octocorals conservation.

The Effect Of Diet On The Gastrointestinal Microbiome Of Rehabilitating Green Sea Turtles (*Chelonia Mydas*) And Its Implications For Released Individuals

09:10 - Tuesday, 25th July, Solar Square

Jennifer Bloodgood, Terry Norton, Lisa Hoopes, Patrick Thompson, Thomas Waltzek, Sonia Hernandez

1. Daniel B. Warnell School of Forestry and Natural Resources, University of Georgia; Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, 2. Georgia Sea Turtle Center, 3. Georgia Aquarium, 4. Department of Infectious Diseases and Pathology, College of Veterinary Medicine, University of Florida; Small Animal Clinical Sciences, College of Veterinary Medicine, University of Florida

The gastrointestinal microbiota (GIM) is an emerging area of research because of its complex association with health. Microbiota composition is associated with diet, and in humans, disruption is associated with problems such as obesity and diabetes. This is the first report of the GIM of green sea turtles (*Chelonia mydas*), whose unique physiology presents a valuable opportunity to further understanding of the chelonian microbiome. Hatchlings and pelagic juveniles are primarily carnivorous, while coastal juveniles and adults are primarily herbivorous. Dietary requirements at each life stage are poorly understood, making diet selection during rehabilitation of injured and sick animals challenging. Although turtles are transitioned to an herbivorous diet before release, items high in animal protein (e.g. fish, squid) are often offered early in rehabilitation to combat poor appetite and emaciation. To understand the impact of diet on the GIM, we analyzed fecal samples from green sea turtles in rehabilitation (N=19) at the Georgia Sea Turtle Center on Jekyll Island, GA. Samples were collected at admission (fed primarily animal protein diets), mid-rehabilitation (consumed at least 25% vegetables), and recovery (consumed at least 75% vegetables).

Fecal samples were extracted and sequenced using the Illumina MiSeq next generation sequencing platform. The dominant phyla across the three timepoints were Firmicutes and Bacteroidetes. Admission samples were primarily Firmicutes (55.0%) with less Bacteroidetes (11.1%), while recovery samples were primarily Bacteroidetes (45.3%) with less Firmicutes (32.5%). Firmicutes play an important role in metabolizing dietary plant polysaccharides, and fewer of these organisms may result in underutilization of wild diet items (i.e. seagrass and algae) in coastal juveniles. The role of the GIM in health is only recently being investigated, but it is important to consider potential impacts that rehabilitation diets and various medications can have to ensure individuals are released back to the wild with optimum probability of survival.

Toxoplasma gondii in Hunter-Harvested Wildlife of the Eastern Canadian Arctic

09:10 - Tuesday, 25th July, Solar Square

Nicholas Bachand, Gregor Gilbert, Stas Olpinski, Patrick Leighton, André Ravel, Craig Stephen, Emily Jenkins, Asma Iqbal, Momar Ndao

1. University of Saskatchewan, 2. Makivik Corporation, 3. Université de Montréal, 4. Canadian Wildlife Health Cooperative, 5. University McGill

Toxoplasma gondii, a zoonotic apicomplexan protozoal parasite, infects mammals and birds worldwide. Infection is asymptomatic, though illnesses occur in immunocompromised people and fetuses of susceptible women. In Nunavik, Canada, 60% of Inuit are seropositive to *T. gondii* compared to 33% of the global population. Despite studies highlighting wildlife consumption as a risk factor for Inuit, no information exists on the *T. gondii* infection status of wildlife tissues. Until recently, knowledge of this disease in wildlife has been based mostly on serology as a proxy for exposure, but infection status of animal tissues has been scarce since very small quantities of tissue (100 milligrams) are used to extract parasite DNA. Being able to detect and quantify *T. gondii* in animal tissues harvested for food is important to ensure food safety, but also to better understand implications for wildlife health. A recently developed magnetic capture DNA extraction and Taqman real-time PCR protocol was optimised to detect *T. gondii* from large amounts of tissues (up to 100 grams) of 453 hunter-harvested animals: 166 ptarmigan, 156 geese, 61 ringed seals, 39 foxes and 31 caribou. DNA from the type II *T. gondii* strain was detected in 44% (CI: 28-60%) of foxes and 9% (CI: 3-15%) of geese, but was not detected in other wildlife including seropositive ringed seals and caribou. In tissue-positive geese, parasite DNA was present in brain, heart, muscle, liver and gizzard with concentrations ranging between 150-2500 tachyzoites per 100 grams of tissue. This is the first account of *T. gondii* detection and quantification in tissues of hunter-harvested wildlife in the Arctic. A risk assessment of Inuit exposure to *T. gondii* from the consumption of geese will now be developed.

Potential bioindicator species to monitor heavy metals in different taxa in three hydrological regions in Northwestern Mexico

10:40 - Tuesday, 25th July, Solar Square

Julio José Barron-Rodríguez¹, Andres Lopez-Perez¹, Jesús Sotomayor-Bonilla¹, Omar García-Suárez¹, Shiara Kirana González-Padrón¹, Jonathan López-Islas¹, Ana Cecilia Espinosa¹, Marisa Mazari-Hiriart², Gerardo Suzán¹

1. Universidad Nacional Autónoma de México

Heavy metals are released into the biosphere from natural and anthropogenic sources. Because of their toxicity, bio-accumulative and non-biodegradable nature metals are considered a global and One Health problem. Biota can be used as a bio-indicator for monitoring environmental conditions, including the presence of contaminants. The objective of this study was to compare heavy metals concentrations in terrestrial vertebrates of regions with different degrees of mining activities and to evaluate vertebrate species as potential bio-indicators. We captured birds, rodents and carnivores during summer in 2015 in 11 locations within three regions in Northwestern Mexico. Different tissues were collected to determine concentrations of Al, As, Cd, Cu, Fe, Mn, Ni, Pb, Zn by ICP-MS. ANOVA tests were used to evaluate the differences in metal concentrations between regions for each vertebrate group, tissue and metal. A total of 2,857 samples of tissues were collected from 1,443 animals belonging to different groups: 64 bird species, 20 rodent species and four carnivore species. We found statistically significant differences between metal concentrations: Zn in bird's liver; As and Fe, Cu, and Pb in rodent's liver, brain and muscle, respectively; As and Pb, and As and Cu in carnivore's hair and blood, respectively. Our findings suggest that 11 vertebrate species (four birds, five rodents and two carnivores) might be used as potential bio-indicators for heavy metal contamination. Concentrations of Cu in rodent's brain and carnivores' blood from the highest mining region suggest a bio-magnification process explained by predator-prey interaction. To our knowledge this is the first-time that heavy metals have been monitored at different trophic levels in Mexico. Results can be used as a reference in an area with abundant metal presence that is being impacted by important extraction activities.

Trypanosoma cruzi infection prevalence and pathology among coyotes (*Canis latrans*) and raccoons (*Procyon lotor*) of Texas, USA

10:40 - Tuesday, 25th July, Solar Square

Carolyn Hodo, Edward Wozniak, Erin Edwards, Rosa Bañuelos, Elise Birkner, Sarah Hamer

1. Texas A&M University, 2. Texas Department of State Health Services

Trypanosoma cruzi, agent of Chagas disease, is a zoonotic vector-borne protozoan that infects a range of mammalian hosts throughout the Americas. Spillover from sylvatic cycles can occur when triatomine vectors bridge the parasite from wildlife to humans or dogs. Although knowledge of reservoir capacity of diverse wildlife could provide an ecological basis for disease management, most wildlife studies only document exposure with little attention to infectiousness to vectors. Additionally, pathology investigations are rarely conducted in these populations, but can provide key information on pathogenesis and population impacts. Our objectives were to characterize the *T. cruzi* reservoir status and associated pathology in coyotes (*Canis latrans*) and raccoons (*Procyon lotor*) in Texas, an area with increasingly documented locally-acquired infections in humans and dogs. We hypothesized that infection prevalence and parasitemia would be higher in raccoons, while coyotes would develop more severe pathology similar to domestic dogs. We collected hearts and/or blood from hunter-harvested animals in Central and South Texas, including 120 coyotes and 24 raccoons. Infection prevalence determined via qPCR of blood or heart was significantly greater in raccoons (62.5%) than coyotes (8.3%; p-value <0.0002). Most raccoons with *T. cruzi*-infected hearts also had positive blood (83%), in contrast to coyotes (17%). Because parasite DNA in the blood may correspond to infectiousness to vectors, these data implicate raccoons as important sylvatic reservoirs. Histologic lesions were more severe in coyotes, with 4/6 PCR-positive coyotes exhibiting mild to moderate lymphoplasmacytic inflammation and occasional myodegeneration and fibrosis. In contrast, raccoons had only very mild inflammation. Pathology variation among host taxa may result from host associations of *T. cruzi* genetic strains. We will build upon these findings to quantify the impact of *T. cruzi* on wildlife reservoir populations, as well as how infection in wildlife relates to disease risk in domestic dogs and humans.

Risk Factors for Snare-related Injuries in Mountain Gorillas (*Gorilla beringei beringei*) and Implications of Veterinary Intervention on Survival

10:40 - Tuesday, 25th July, Solar Square

Marlene Haggblade, Woutrina Smith, Jean Bosco Noheri, Mike Cranfield, Kirsten Gilardi

1. University of California Davis School of Veterinary Medicine
2. University of California Davis School of Veterinary Medicine)
3. Gorilla Doctors,
4. University of California Davis School of Veterinary Medicine

Mountain gorillas (*Gorilla beringei beringei*) are one of the most critically endangered great apes. Gorilla Doctors (a partnership between the non-profit Mountain Gorilla Veterinary Project and the Karen C. Drayer Wildlife Health Center at UC Davis), have been providing *in situ* health care to human-habituated gorillas since 1986, thereby contributing to population growth from a low of 200 individuals to almost 900 gorillas currently. The most common cause of gorilla morbidity and mortality requiring clinical intervention is trauma (e.g., injury from conspecifics or snare entrapment). In 2016, we conducted a retrospective case-control study of free-ranging mountain gorillas (*Gorilla beringei beringei*) to: (1) evaluate risk factors associated with snare entrapment of mountain gorillas, and (2) evaluate whether clinical intervention affected gorilla survival to one month post-intervention. Data were collected from clinical records on all intervention cases in Volcanoes National Park, Rwanda conducted between 1995 – 2015 (n=132). Within that time period, Gorilla Doctors treated 37 gorillas entrapped in snares, and 95 gorillas for other clinical conditions (including trauma and respiratory illness). Risk factor analysis revealed that young gorillas (age<8 years old) were more likely than older gorillas to become snared. Co-morbidities (presence of a simultaneous disease process), delayed intervention (≥ 3 days), and severity of wounds (e.g. necrotic and ischemic) at the time of intervention were associated with increased risk of death within one-month post-intervention. The results of this study may inform decisions for future priorities for gorilla health monitoring and treatment decisions, in order to most effectively conserve this critically endangered species.

Prevalence and pathological significance of leptospirosis in California mountain lions (*Puma concolor*)

10:40 - Tuesday, 25th July, Solar Square

Mary H. Straub, Jaime L. Rudd, Leslie W. Woods Deana L. Clifford, Janet E. Foley

1. (University of California Davis School of Veterinary Medicine, 2. California Department of Fish and Wildlife, Wildlife Investigations Lab, 3. California Animal Health and Food Safety Laboratory System, University of California Davis School of Veterinary Medicine, 4. California Department of Fish and Wildlife, Wildlife Investigations Lab, University of California, Davis School of Veterinary Medicine

Background: Mountain lions (*Puma concolor*) are the largest free-ranging felid species in California. A newly initiated state-wide mountain lion population and health assessment program, managed by the California Department of Fish and Wildlife, is seeking to estimate the size of the lion population, characterize population genetics and identify diseases affecting the population. One disease suspected to be of importance in mountain lions is leptospirosis.

Objectives: To determine the sero- and PCR-prevalence of leptospirosis in California mountain lions as well as to investigate the pathological significance of leptospirosis in this species. We hypothesize that leptospirosis (defined as being sero- and/or PCR-positive) is associated with interstitial nephritis in mountain lions.

Methods: Blood and kidney samples were collected from 122 lions necropsied by California Department of Fish and Wildlife during 2016. Seroprevalence was determined using the microscopic agglutination test (MAT) and active infection was determined by real-time PCR of kidney tissue. Pathological significance was investigated by histological examination of formalin-fixed kidney tissue.

Results: Overall seroprevalence was 49.1% (56 positive/114 tested; 95% CI=39.9-58.3) with *Leptospira interrogans* serovar Pomona being the most commonly detected serovar. *Leptospira* spp. DNA was detected in 22.6% (26 positive/115 tested; 95% CI=14.9-30.2) of kidney samples tested. Lions with interstitial nephritis, ranging from mild to severe, and primarily lymphocytic, were 34.5 times more likely to test positive for leptospirosis by real-time PCR and/or serology ($p < 0.0001$).

Conclusions: California mountain lions face a variety of challenges to survival including habitat loss and fragmentation as well as mortalities resulting from conflicts with domestic animals and humans. Diseases, such as leptospirosis, may represent additional ecological pressures impacting the population. Our results demonstrate that exposure to and infection by leptospires are very common in California mountain lions and that leptospirosis should be considered as a potentially important cause of disease in these wild felids.

Evidence Of Small Rodent Involvement In Plague Outbreaks On Prairie Dog Colonies

10:40 - Tuesday, 25th July, Solar Square

Bieneke Bron, Katie Richgels, Carly Malave, Jorge Osorio, Tonie Rocke

1. University of Wisconsin - Madison, 2. USGS National Wildlife Health Center, 3. USGS National Wildlife Health Center

Across the world rodent-borne diseases are public health challenges. Rodents are highly abundant and often co-habit with humans. In the U.S., *Sin nombre virus (SNV)*, *Borrelia burgdorferi* (causative agent of Lyme) and *Yersinia pestis* (causative agent of plague) are the most well known pathogens maintained by wild rodents. SNV and Lyme disease dynamics are fairly well understood, but how plague is maintained in prairie ecosystems remains uncertain. In the early 1900's the causative bacterium was introduced to the western U.S., spread eastwards with rodents and their fleas, and became established in 'wild rodent' reservoirs with recurring outbreaks in highly susceptible species like squirrels (*Spermophilus* spp.) and prairie dogs (*Cynomys* spp.). Some investigators have hypothesized that other small rodents, like deer mice (*Peromyscus maniculatus*), voles (*Microtus* spp.) and northern grasshopper mice (*Onychomys leucogaster*) act as maintenance or amplifying hosts, and drivers of plague outbreaks by transporting infectious fleas, but others argue they are not important. Thus we assessed small rodent - flea dynamics in six different study areas to further evaluate the role of short-lived rodents and their fleas in plague disease ecology. We trapped small rodents (n=3,585), other than prairie dogs, and collected their fleas (n=~6,100) on 15 prairie dog colonies for three years. Our rodent and flea communities were related by study area, but geographically distinct. During plague outbreaks we did not detect prairie dog fleas on small rodents, but we did find potentially infectious (*Y. pestis* DNA positive) fleas on two small rodents preceding plague outbreaks and prior to detection of plague positive prairie dog fleas. This unique finding implies that small rodents could be involved in the initiation of plague outbreaks in prairie dogs. We will discuss this finding and its implications for plague disease ecology in prairie ecosystems.

Effect of land use change on bat communities of Mexico: Implications for their viral richness

12:10 - Tuesday, 25th July, Solar Square

Citlali C Mendoza Guevara, Gabriel E García Peña, Heliot Zarza Villanueva, Oscar Rico

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In the last 50 years, land use change has increased globally at an alarming rate, causing changes in the composition and structure of host communities. This has led to increased contact rates between humans, domestic animals and wildlife, favoring outbreaks of infectious diseases. We studied the effect of land use change on the bat communities composition from Mexico through alpha and beta diversity measurement, in order to present a tool for conservation planning and epidemiological surveillance. Bat species were classified according to their tolerance to the type of land use (dependent, vulnerable and adaptable), so we could model the loss of species through three time periods (1993, 2002 and 2011). To know the viral communities associated to bats, we used the Database of Bat-associated Viruses. Bats and viral richness was determined by the total number of species in each cell, conformed by a grid of 500 km² across Mexico. The loss of bat species and viruses over time was quantified by the nestedness component of taxonomic and phylogenetic beta diversity. A general linear model was performed to explore the correlation between the beta diversity of bats and the change of their viral communities. The results showed that land use change altered the composition of bat communities, decreasing the number of species, particularly in the southeast of Mexico. However, no significant changes were observed in viral communities. The beta diversity of the viral communities was not explained by the taxonomic (LR = 0.095, p = 0.758), nor phylogenetic beta diversity (LR = 0.086, p = 0.770) of the bats. This could be associated with low sampling efforts on the detection of viruses from rare bat species. The present study is the first to determine the effect of land use change on bat communities and their associated viruses at a regional scale.

Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus

12:10 - Tuesday, 25th July, Solar Square

Amanda Vicente-Santos, Andrés Moreira-soto, Claudio Soto-garita, Luis Guillermo Cgaverri, Andrea Chaves, Jan Felix Drexler, Juan Alberto Morales, Alejandro Alfaro, Bernal Rodríguez Herrera, Eugenia Corrales-agui-lar

Emory University, 2. University of Bonn, 3. University of Costa Rica, 4. Universidad Estatal a Distancia

Studies have shown Dengue Virus (DENV) presence in neotropical wildlife including bats, suggesting that bats may be susceptible to DENV infection. We aim to elucidate the role of house-roosting bats in DENV transmission cycle. Households were sampled from high and low dengue incidence regions during rainy and dry seasons in Costa Rica. We captured 318 bats from 12 species in 29 households. Necropsies were performed in 205 bats to analyze virus presence in heart, lung, spleen, liver, intestine, kidney, and brain tissue. Histopathology studies from all organs showed no manifestation of disease or infection. Sera were analyzed by PRNT₉₀ for a seroprevalence of 22% (53/241), and by PCR for 8.8% (28/318) positive bats for DENV RNA. From these 28 bats, 2 intestines were DENV RNA positive for the same dengue serotype detected in blood. Viral isolation from all positive organs or blood was unsuccessful. Viral load analysis in positive blood samples by qRT-PCR showed virus concentrations under the minimal dose required for mosquito infection. Simultaneously, 651 mosquitoes were collected and analyzed for DENV and feeding preferences (bat cytochrome b). Three mosquitoes were found DENV positive and none was positive for bat cytochrome b. Our results suggest an accidental presence of DENV in bats probably caused from oral ingestion of infected mosquitoes. Phylogenetic analyses suggest also a spillover event from humans to bats. We conclude that bats in these urban environments do not sustain DENV amplification; not having a role as reservoirs, but function as an epidemiological dead-end host for DENV.

Beyond abundance: microenvironmental and weather characteristics associated with zoonotic pathogens in urban Norway rats (*Rattus norvegicus*)

12:10 - Tuesday, 25th July, Solar Square

Jamie Rothenburger Chelsea Himsworth, Nicole Nemeth, David Pearl, Claire Jardine

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Norway rats (*Rattus norvegicus*) inhabit cities worldwide and carry a number of zoonotic pathogens. Although many studies investigate rat-level risk factors, there is limited research on the effects of weather and environment on zoonotic pathogen carriage in rats. The objective of this study was to examine associations between abundance, microenvironmental and weather features with *Bartonella tribocorum*, *Clostridium difficile*, methicillin-resistant *Staphylococcus aureus* (MRSA) and antimicrobial resistant (AMR) *Escherichia coli* in urban rats. During a systematic trap-removal study, city blocks were evaluated for 48 environmental variables related to waste, land/alley use and property condition, as well as rat abundance. We constructed 32 temperature/precipitation variables with time lags prior to rat capture date. We fitted multivariable logistic regression models with rat pathogen status as the outcome. *Bartonella tribocorum* was positively associated with city blocks with < 25% low-rise apartments. *Clostridium difficile* was negatively associated with mean maximum temperatures between 12.89-20.29°C on days 84-90 prior to capture. AMR *E. coli* was positively associated with alleys bordered by non-paved surfaces and negatively associated with any of the alley surfaces in fair condition. MRSA was positively associated with city blocks with >25% institutional parcels, food gardens and when the total precipitation in the 15 days prior to capture was <49.40mm. The identified features may relate to pathogen survival/exposure in the environment for all pathogens and also vector ecology for *B. tribocorum*. None of the pathogens were associated with rat abundance, suggesting a lack of density-dependent transmission. There are no consistent environmental/weather variables that are associated with all pathogens, meaning that a single focus of control/surveillance is not possible. However, this study is an important first step to understanding how environment/weather impacts rat infections in urban ecosystems.

Effect of the landscape over rodent diversity and Hantavirus antibody prevalence in Yucatan, Mexico

12:10 - Tuesday, 25th July, Solar Square

Deyra Ortiz Chabolla, Oscar Rico, Rafael Avila-Flores, Francisco Galindo Maldonado, Gerardo Suzán

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Biodiversity loss and habitat fragmentation due to anthropogenic factors, such as land-use change for livestock production have enhanced the risk and the incidence of zoonotic diseases. In the present study, we measured the effect of taxonomic and phylogenetic diversity of rodents over antibody seroprevalence in agricultural landscapes in the east of Yucatan, Mexico. We evaluated a landscape composed of 8 sites, each with different spatial configuration and habitat composition. Antibody (IgG) detection for Hantavirus (Sin Nombre virus genotype) was performed via an indirect enzyme immunoassay (ELISA). A comparison of the rank-abundance curves for the 8 sampled landscapes was made through an ANOVA. Taxonomic diversity of each site was calculated with the Effective Number of Species (True diversity), whereas phylogenetic diversity was determined using the Faith Index. Preliminary results do not suggest a negative correlation between seroprevalence and taxonomic and phylogenetic diversity (adjusted $R^2=0.42$, $P>0.05$). Statistically significant differences were found in rodent rank-abundance curves as a result of landscape type ($F=2.133$, $df=7$, $P<0.05$). Higher abundance of competent hosts was observed in landscapes with higher spatial homogeneity. We noticed that landscape configuration determines the species composition and competent host abundance, regardless of failing to detect a significant correlation between rodent diversity and prevalence of antibodies for hantavirus. The present study proves the relevance of spatial configuration as persistence factor of a zoonosis in an anthropogenic-dominated landscape.

Modelling rabies dynamics in red foxes (*Vulpes vulpes*) and domestic animals in Ukraine

14:30 - Tuesday, 25th July, Solar Square

Sreejith Radhakrishnan Pierre Nouvellet, Mykola Ivanov, Emmanuelle Robardet, Florence Cliquet, Christl Donnelly

1. Imperial College London, UK, 2. Rabies Detection Laboratory, State Veterinary and Phytosanitary Service 3. Anses - Laboratoire de la Rage et de la Faune Sauvage de Nancy

Widespread implementation of oral rabies vaccination (ORV) campaigns has resulted in eradication of terrestrial animal rabies in Western and Central Europe. Most rabies cases are reported from the Russian Federation, Ukraine and Belarus. Since 2006, Ukraine has implemented ORV campaigns with financial support from the European Union. Utilizing open-access data, this study analyzed rabies incidence trends between 2001 and 2016 in Ukraine and used a three-host Susceptible-Exposed-Infectious (SEI) compartmental mathematical model fitted to this data to elucidate rabies dynamics in red foxes (*Vulpes vulpes*), cats (*Felis catus*) and dogs (*Canis familiaris*) in Ukraine. The relative roles of species in driving peaks in rabies cases was analyzed using Relative Risk (RR) estimates. Most rabies cases in Ukraine occurred in foxes, but domestic animal cases outnumbered wildlife cases. Cats (*Felis catus*) were the most commonly affected domestic species, followed by dogs and cattle. Rabies incidence declined in East Ukraine after 2009, possibly because of ORV campaigns. The SEI model captured the varying rabies surveillance in Ukraine and provided estimates of rates of transmission in foxes and dogs. The model also highlighted the strong links between rabies dynamics in these species, with fox rabies significantly influencing disease dynamics in cat populations, and these in turn affecting dog rabies dynamics. Seasonal hunting also influenced the number of cases detected and corresponding estimates of rabies prevalence. The RR estimates indicated that cats were driving peaks in rabies cases at the national and regional levels, particularly among domestic animals. Dogs were rarely found to drive a rise in rabies incidence, pointing to the need for ensuring adequate rabies vaccination coverage in cats to reduce the risk of exposure to humans. Implications of these findings in informing rabies surveillance strategies and the role of cats as an important rabies host in Ukraine are discussed.

Drivers underlying the retreat of fox rabies from Western Europe

14:30 - Tuesday, 25th July, Solar Square

Micaela De la Puente, Conrad Freuling, Thomas Mueller, Patrick Wysocki, Laurie Baker, Jason Matthiopoulos, Katie Hampson

1. Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, 2. Friedrich-Loeffler-Institute), 3. Institute of Epidemiology, Friedrich-Loeffler-Institute, 4. Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow

Oral Rabies Vaccinations (ORV) have successfully eliminated fox rabies from 10 previously endemic countries in Western Europe. Yet, fox rabies circulates in Eastern Europe where it threatens humans and wildlife and is economically costly. Understanding the spatiotemporal drivers of fox rabies retreat from Western Europe should inform future ORV programmes and help to secure and maintain rabies-free areas. Using a generalized linear hurdle model, we assessed the effects of epidemiological, geographical and control-related variables on the retreat of fox rabies from Western Europe, exploring predictors of rabies presence using a logistic regression model, and using a gamma model to examine the conditional distribution of intensity of rabies infection. Considerable variability was observed in the retreat of the infected area, which initially receded rapidly by around 100,000 km²/year from 1990 until 1997 and thereafter retreated more slowly and stochastically until elimination in 2006. Presence of fox rabies in the previous year was the most important influence on fox rabies retreat, followed by ORV. Campaigns the previous year only had a short-term effect on reducing rabies intensity, but were associated with an increased likelihood of rabies presence. In contrast, sustained ad-hoc ORV over a 5-10-year period reduced rabies intensity and created rabies-free areas, with significant differences in the effect on intensity depending on the bait distribution mode (aerial or manual). Land use and elevation also influenced fox rabies presence and intensity, but mechanisms underlying these effects need further exploration. Our findings suggest considerable potential to improve our understanding of mechanisms driving rabies persistence using long-term fox rabies surveillance data, and to improve the efficiency of rabies elimination programmes. Our findings demonstrate that sustained ORV (5-10 years) should drive rapid and predictable retreats of infected areas, but elimination of remaining foci becomes increasingly unpredictable.

Mapping spatial and temporal patterns of hemorrhagic disease infection in deer and biting midges (Diptera: *Culicoides*) for vector incrimination in Florida, USA

14:30 - Tuesday, 25th July, Solar Square

Kristin Sloyer, Gregory Ross, Stacey Vigil, Joseph Corn, Jason Blackburn, Erik Blosser, Katherine Sayler, Carisa Boyce, Samantha Wisely, Nathan Burkett-Cadena

1. University of Florida, 2. Southeastern Cooperative Wildlife Disease Study

Epizootic Hemorrhagic Disease virus (EHDV) and Blue Tongue virus (BTV) cause hemorrhagic disease in wild and domestic ungulates including sheep, cattle, and white-tailed deer, resulting in large economic losses to deer and cattle farmers. These diseases are transmitted between animal hosts by *Culicoides* biting midges. *Culicoides sonorensis* is a confirmed vector of EHDV and BTV throughout the western United States, while *Culicoides insignis* is a vector of BTV throughout the American Tropics. In Florida, where *C. sonorensis* is exceedingly rare, recent epizootics of EHDV highlight the need for delineating vectors of the virus. An association in time and space between the a suspected vector species and cases of disease is a major criteria for incrimination of a vector species, which in turn is necessary information for vector control interventions aimed at protecting animals from outbreaks of disease. The current study used seasonal mapping to implicate suspected vectors of EHDV and BTV in Florida. From 2015 to 2017, virus was detected in both wild and farmed white-tailed deer in 21 different locations throughout Florida. *Culicoides* trapping data from 194 sampling locations (2007-2016) compiled by Southeastern Cooperative Wildlife Disease Study and Florida Medical Entomology Laboratory (n=171,033 *Culicoides*) was used to generate virus and *Culicoides* distribution maps by season, in ArcGIS. Comparing the overlapping distributions of 39 potential *Culicoides* Orbivirus vectors with incidence of the disease in domestic and wild white-tailed deer supports the incrimination of *C. insignis* as a vector of BTV in Florida. For EHDV, incidence of the disease coincided spatially and temporally with that of *C. insignis*, *C. venustus*, and *C. stellifer*, suggesting that these species warrant further study as potential vectors of EHDV.

Ecology and differential rates of range expansion of protostrongylid nematodes in muskoxen and caribou in the changing Arctic

14:30 - Tuesday, 25th July, Solar Square

Pratap Kafle, Lisa-Marie Leclerc, Peter Peller, Tracy Davison, Marsha Branigan, Morgan Anderson, Shane Blackm, Donald McLennan, Matilde Tomaselli, Susan Kutz

1. University of Calgary, 2. Government of Nunavut, 3. Government of the Northwest Territories, 4. Canada North Outfitting, 4. Polar Knowledge Canada

Protostrongylids are common, and often pathogenic nematode parasites of northern ungulates. This family of parasites are of interest in the Arctic because of their recent invasion and rapid range expansion. Our objectives were: to determine the diversity of protostrongylids in muskoxen and caribou in the Canadian Arctic, and, examine the impacts of climate change on the ongoing range expansion of two protostrongylids *Umingmakstrongylus pallikuukensis*(UP) and *Varestrongylus eleguneniensis*(VE). We used: widespread fecal surveys (n>1500 muskox and caribou fecal samples) across Canadian Arctic from 2013-2017; lab experiments on the temperature sensitivities of UP and VE, and predictive habitat modelling using field and laboratory data, together with state-of-art global climate model outputs, to understand the climate-mediated historical to future range expansion of these lungworms. We found that protostrongylid diversity in muskoxen varies geographically, with UP limited to the west-central Canadian Arctic, VE distributed broadly across muskox range except for the high Arctic, and *Protostrongylus stilesi* present only in northern Yukon, in areas of sympatry with Dall's sheep. Caribou of the west-central Canadian Arctic were infected with VE and the muscle worm, *Parelaphostrongylus andersoni*, in single and co-infections, the latter being the first report in the Dolphin-Union caribou herd. No protostrongylids were detected in Peary caribou. On Victoria Island, UP and VE are expanding rapidly northwards, but at differential rates with UP expanding faster over a broader geographical range. In lab experiments, VE has a higher temperature threshold ($T_0=9.6^\circ\text{C}$) and requires more heating ($DD=173$) for development than UP ($T_0=8.5$, $DD=167$), and this may be one reason for differential range expansion. Both UP and VE are extremely freeze tolerant with a survival rate of >80% after six months at -10 to -80°C. Predictive habitat modelling suggests the comparatively faster range expansion of UP, and future invasion of other Arctic islands currently free of lungworms.

Potential spread of flaviviruses in dynamic community structures of migratory and resident birds, Bahía Kino, Sonora-México

14:30 - Tuesday, 25th July, Solar Square

Paulina Alvarez, Gabriel E García Peña, Tracey Goldstein, Jesús Sotomayor-Bonilla, Hugo Mendoza-Gutiérrez, María José Tolsá-García

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. One Health Institute, University of California-Davis

Bird migration is an important mechanism for the spread of avian pathogens into new regions. Wild bird species can carry zoonotic pathogens (i.e. *flaviviruses*) and if migrating they can transmit them into resident species at stopover or wintering sites. However, pathogen persistence in bird communities is not as simple or immediate. To understand these infection dynamics it is important to consider ecological attributes of bird communities, as the distribution of certain hosts can influence the transmission and persistence of a pathogen in a region. The two main topics this study seeks to investigate are: (1) the ecological effects of migration in the distribution of resident birds at Bahía Kino, Sonora-México, and (2) the implications that distribution and co-occurrence patterns of species may have in the spread of flaviviruses. We hypothesized that the arrival of migratory birds may modify competent host distributions across a metacommunity generating structures that may facilitate or impede their interactions and the spread of their pathogens. Metacommunity structure was assessed by analyzing three parameters of species distribution (coherence, turnover and boundary clumping) in a site-by-species incidence matrix during a three-month survey. In order to infer potential interactions between hosts we also quantified co-occurrence between birds by using the Chao's dissimilarity index. All communities exhibited Gleasonian structures in which competent migratory species arriving from latitudes where flaviviruses have been reported are co-occurring significantly with highly competent and abundant resident species of birds. This implies a widespread distribution of competent vertebrate hosts, which are available for feeding mosquitos and which are prone to sustain infection across both the community and metacommunity levels. These results suggest an ecological scenario in which flaviviruses may spread. Our approach represents a multidisciplinary methodology to identify communities where zoonotic pathogens can be maintained and may help identify epidemiological hazards for wildlife and public health.

Public Motivations for Feeding Birds and the Relationship of Supplemental Feeding to Urban Avian Health

14:30 - Tuesday, 25th July, Solar Square

Shannon Curry , Sonia Hernandez, Gary Green , Lincoln Larson, Catharine Welch, Whitney Kistler, Michael Yabsley

1. Daniel B. Warnell School of Forestry and Natural Resources, University of Georgia; Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, 2. Department of Parks, Recreation, and Tourism Management, College of Natural Resources, North Carolina State University

Supplemental wildlife feeding can facilitate the public's connection to nature and may provide important resources to wildlife; however, it alters pathogen dynamics between wildlife and to the public by affecting wildlife nutrition and increasing densities and inter- and intra-specific contact. We assessed the public's role in supplemental feeding and pathogen prevalence at Palm Beach County, Florida (PBC) urban parks where people commonly feed birds including ducks, gulls, and White Ibis (*Eudocimus albus*). We quantified ibis diet, site fidelity, and pathogen prevalence, and assessed the public's motivations for feeding. Ibis regularly consumed anthropogenic foods, exhibited high fidelity to PBC parks, and had high prevalence of *Salmonella* spp. infection (13%) and antibodies against avian influenza viruses (71%) and paramyxoviruses (45%). Most people that fed birds brought children (65%), and 12% were >65 years old—both groups are most at risk for serious disease from *Salmonella* spp. infection. Most people that fed birds were unaware that birds carry pathogens of wildlife and public health concern, and would stop feeding birds if they understood this. However, those who most strongly enjoyed feeding birds were least likely to stop feeding based on information about pathogen transmission risk ($X^2(12)=22.04$, $p=0.04$). People fed birds to connect to nature (65%), and those who more strongly enjoyed feeding birds felt stronger connections to birds and wildlife ($X^2(18)=34.71$, $p<0.01$). Ibis visit PBC parks to capitalize on supplemental feeding, which allows the public to interact with birds and connect to nature. However, ibis are exposed to aforementioned pathogens of concern via contaminated soil/water and aggregation with reservoir species (e.g., ducks, gulls). Management of supplemental feeding to reduce pathogen transmission must address public motivations for and benefits from feeding, and public education to encourage compliance with management actions should preserve support for, and provide alternatives for people to maintain beneficial interactions with, wildlife.

Endemism of *Salmonella* Typhimurium does not compromise reproductive success in Great (*Parus major*) and Blue (*Cyanistes caeruleus*) Tits

16:00 - Tuesday, 25th July, Solar Square

Roschong Boonyarittichaij, Elin Verbrugghe, Daan Dekeukeleire, Lieze Rouffaer, Roel Haesendonck, Diederik Strubbe, Robbe Debeelde, Wesley Mattheus, Sophie Bertrand, Frank Pasmans, Dries Bonte, Kris Verheyen, Luc Lens, An Martel

1. Ghent University, 2. University of Copenhagen, 3. Scientific Institute of Public Health,

Endemic infections with the common avian pathogen *Salmonella enterica* subspecies *enterica* serova Typhimurium (*Salmonella* Typhimurium) may impose a significant cost on host fitness and reproduction. In this study, we determined the potential of endemic *Salmonella* infections to reduce reproductive success of blue (*Cyanistes caeruleus*) and great (*Parus major*) tits by correlating eggshell infections and reproductive parameters (egg volume, clutch size, number of nestlings and number of fledglings). The fifth egg of each clutch was collected from the nest boxes in 53 ancient deciduous forest plots in Flanders that differ in forest fragmentation and tree species composition. Out of 101 sampled eggs (65 great tit eggs, 36 blue tit eggs), seven *Salmonella* Typhimurium were recovered from 7 different forest plots by isolation methods (ISO 6579-2000). The low bacterial prevalence was reflected by a similarly low serological prevalence in fledglings, determined by indirect-ELISA procedures. Presence of *Salmonella* did not affect reproductive parameters, not body condition of the fledglings. Phage typing showed that the isolates belonged to the definitive phage types (DT) 193 and 99. Multi-locus variable number tandem repeat analysis (MLVA) demonstrated a high similarity among the tit isolates. These findings suggest endemism of passerine-adapted *Salmonella* strains in wild blue and great tit populations with host-pathogen co-existence.

Developing tools to monitor the health of wild muskoxen: the effect of sex, season, and year of collection on qiviut cortisol levels

16:00 - Tuesday, 25th July, Solar Square

Juliette Di Francesco, Nora Navarro-gonzalez, Katherine Wynne-edwards, Stephanie Peacock, Lisa-Marie Leclerc, Matilde Tomaselli, Tracy Davison, Anja Carlsson, Susan Kutz

1. University of Calgary, 2. Government of Nunavut, 3. Government of the Northwest Territories

Muskoxen (*Ovibos moschatus*) in some areas of the Canadian Arctic are undergoing population declines that may be linked to multiple stressors, including disease emergence and ecosystem changes associated with climate warming. Cortisol is produced in response to stress and has been measured in the hair of several wild mammals. We validated the use of liquid-chromatography coupled to tandem mass spectrometry (LC-MS/MS) for quantifying cortisol in the qiviut (undercoat) of muskoxen and then evaluated qiviut cortisol levels in 150 muskoxen from seven different locations. Qiviut, collected from the rump of adult muskoxen harvested by subsistence and sport hunters in Nunavut and the Northwest Territories between 2012 and 2016, was washed and cortisol was then cold-extracted in methanol, and quantified using LC-MS/MS. The effects of sex, season, and year of collection on qiviut cortisol levels were assessed using linear mixed-effects models that included location as a random effect, and were compared using the corrected Akaike information criterion. There was a high inter-individual variability in qiviut cortisol concentrations, ranging from 3.51 to 48.92 pg/mg (median of 11.73 pg/mg). The final model included sex, season, year of collection, and no interactions and there was a trend towards higher cortisol levels in the locations where muskoxen are declining. The high inter-individual variability is in accordance with results from other species and shows the potential utility of qiviut cortisol levels as markers of individual health in muskoxen. Significant differences in qiviut cortisol levels between sexes, seasons, and years are linked to the diverse stressors experienced.

Investigating toxoplasmosis risk at Eastern barred bandicoot reintroduction sites

16:00 - Tuesday, 25th July, Solar Square

Katherine Adriaanse Michael Lynch, Jasmin Hufschmid, Duncan Sutherland, Rebecca Traub

1. University of Melbourne, Melbourne Zoo, 2. Melbourne Zoo, 3. Phillip Island Nature Parks

The Eastern barred bandicoot (*Perameles gunnii*) is considered extinct in the wild, and is extant only as intensively managed captive or reintroduced populations. Phillip Island in Westernport Bay, Victoria, Australia, has been proposed as a potential site for the introduction of *P. gunnii*. Feral cats, the definitive host of the coccidian parasite *Toxoplasma gondii*, are present on the island. *P. gunnii* is known to be fatally susceptible to toxoplasmosis, however, the risk of exposure to *T. gondii* on Phillip Island is not known. The overall aim of this study is to ascertain whether *T. gondii* infection in feral cats and rabbits on Phillip Island, as well as levels of soil contamination with oocysts, can be used as indirect measures of toxoplasmosis risk in relocated *P. gunnii*. The prevalence of *T. gondii* in the feral cat and rabbit populations will be determined by detecting tissue cysts using real-time PCR targeting the highly repetitive REP-529 gene. *T. gondii* oocyst levels in soil at the release site will also be measured directly using real-time PCR. *P. gunnii* released onto Phillip Island in spring 2017 will be followed longitudinally, and seroconversion to *T. gondii* will be determined using the Modified Agglutination Test. Where possible, any deceased *P. gunnii* will be recovered, and a full necropsy and *T. gondii* testing conducted to determine cause of death. These data will be combined to estimate the risk toxoplasmosis poses to the successful establishment of *P. gunnii* at Phillip Island. Furthermore, this project will provide a risk-analysis framework for toxoplasmosis that will be applicable to future sites proposed as habitat for *P. gunnii*.

Rabies Transmission Within Wild Dog Populations In Northern Australia

16:00 - Tuesday, 25th July, Solar Square

Vanessa Gabriele-Rivet, Julie Arsenault, Victoria Brookes, Michael Ward

1.The University of Sydney, 2.Université de Montréal

Australia's canine-rabies free environment is threatened by the current spread of the disease across the Indonesian archipelago, which has brought rabies 300 km from northern Australia. Remote Indigenous communities in northern Australia are situated within complex ecosystems containing large populations of free-roaming domestic dogs. Such communities are surrounded by widely dispersed wild dog populations. Therefore, the incursion of rabies into northern Australia, via or with spillover to wild dogs, is a genuine threat. The goal of this project is to evaluate strategies for controlling the spread of rabies in wild dog populations in northern Australia, should an incursion occur. The distribution and density of wild dogs across the study area, as well as the extent of interactions between wild and domestic dogs, is currently being evaluated using a range of field approaches, including camera traps placed at strategic locations and interviews with local residents who use community dogs for feral-pig hunting activities. Based on this data, a stochastic model of rabies spread in wild dogs will be developed and tested using different control scenarios. For the first nine months of the one-year camera trap study, 986 502 photographs were captured from 28 cameras deployed for 5940 camera trap nights along trails and at focal points. Dogs were active at all sites and visualized in 2.9% of the photographs; of these, 56.2% showed dingo phenotypic characteristics. Dingo-like dogs were predominantly recorded during nocturnal hours. Results from interviews with hunters suggest that wild dogs tend not to approach domestic dogs during hunting trips. Areas reported by hunters as having a high dingo density are consistent with dingo-like dog sightings from the camera traps. The decision-support system developed in this project will help prepare for a rabies incursion impacting Indigenous communities, wildlife populations and the ecosystem in Australia.

First detection of *Brucella* spp. in a *Clymene* dolphin (*Stenella clymene*) stranded in Brazil

16:00 - Tuesday, 25th July, Solar Square

Angélica Sánchez-Sarmiento, Vitor L. Carvalho, Carlos Sacristán, Kátia R. Groch, Rodrigo A. Réssio, Natalia A. C. Fernandes, Juliana M. Guerra, Samira Costa-Silva, Josué Díaz Delgado, Cintia M. Favero, Nairléia Dos Santos Silva, Jose Soares Ferreira Neto, Ana C.O. Meirelles, José Luiz Catão-Dias

1. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, 2. (Associação de Pesquisa e Preservação de Ecossistemas Aquáticos-AQUASIS, Caucaia, CE), 3. Instituto Adolfo Lutz, São Paulo, SP, 4. Laboratory of Wildlife Comparative Pathology, College of Veterinary Medicine and Animal Science of the University of São Paulo (LAPCOM/FMVZ/USP), 5. Laboratório de Zoonoses Bacterianas, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, 6. Associação de Pesquisa e Preservação de Ecossistemas Aquáticos-AQUASIS, Caucaia, CE

Brucella ceti is one of the most important emerging pathogens affecting cetaceans. The ST27 genotype has been associated with zoonotic disease, raising concern about the occurrence and distribution of *B. ceti* strains, particularly in regions not extensively studied to date, such as the Southwest Atlantic Ocean. On March 2012, a debilitated Clymene dolphin (*Stenella clymene*) stranded alive in Ceará state, Brazil, and died shortly after. A necropsy was followed and tissues were collected for diagnostics. Major histopathological findings included: moderate chronic pyogranulomatous bronchopneumonia associated with adult and nematode larvae (*Halocercus* sp.); moderate pulmonary edema, congestion and hemorrhage; moderate mesenteric and splenic lymphoid depletion; moderate mesenteric pyogranulomatous lymphadenitis; mild eosinophilic splenitis; mild lymphoplasmacytic glandular gastritis; chronic ulcerative and hyperplastic pyloric gastritis associated with adult nematodes (*Anisakis typica*); mild to moderate multifocal eosinophilic enterocolitis; moderate centrilobular congestion with minimal portal lymphoplasmacytic infiltrates; mild to moderate multifocal lymphoplasmacytic interstitial nephritis; focal necroulcerative glossitis. Sera agglutinated via Rose Bengal Test using a cell suspension of inactivated *B. abortus* (1119-3 strain, Instituto Biológico-Brazil). Immunolabeling for *Brucella* sp. was detected in alveolar macrophages by immunohistochemistry (polyclonal antibody anti-*B. abortus* (1:500, Biorbyt®). A 223 bp fragment of the gene encoding the 31 kDa protein, specific for the genus *Brucella* was amplified from lung by conventional PCR presenting a 100% BLAST identity to *Brucella* species (Genbank®). These results provide evidence of a localized *Brucella* sp. pulmonary infection, and to the best knowledge of the authors, constitutes the first record of brucellosis in odontocetes in the Southwest Atlantic Ocean, widening the spectrum of susceptible species and geographic location and rising significant public health concerns on the zoonotic potential of this strain and possible aerogenous route of transmission. Ongoing research on marine *Brucella* in Brazil is focused on occurrence, host range, molecular characterization of circulating strains and associated pathology.

From the darkness: cryptic diversity of *Strongyloides* in a community of Bornean primates

16:00 - Tuesday, 25th July, Solar Square

Liesbeth Frias, Danica J. Stark, Milena Salgado Lynn Senthilvel K. S. S. Nathan, Benoit Goossens, Munehiro Okamoto, Andrew J. J. MacIntosh

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Strongyloides is a gastrointestinal nematode infecting a wide range of vertebrates, and reported from several primate species in Africa and Asia. Parasites circulating within communities of closely-related host species are often assumed to belong to the same species, based on morphological similarities between parasites, but information about the diversity within parasite genus and host range remains scarce. Here we aimed to assess *Strongyloides* diversity and host range in a community of Bornean primates living sympatrically in the Lower Kinabatangan Wildlife Sanctuary, Malaysian Borneo. We tested whether variation within the parasite species followed the taxonomy of its primate host, i. e. whether there are different *Strongyloides* strains for each primate host. We collected fecal samples from six primate species, and cultured nematode larvae for DNA extraction and phylogenetic analyses. Parasite sequences for most sampled primates were identified as *S. fuelleborni*, showing considerable within/between host species variation, and clustering into two major clades with no correspondence to any particular primate host. In contrast, sequences obtained from a Bornean slow loris clustered closely to *S. stercoralis* into a different group, being genetically distinct to sequences reported for other primate species, humans included. Our study identified *S. fuelleborni* in five out of six sympatric primates examined, with the exception of the slow loris, suggesting that while *S. fuelleborni* infects all the haplorrhines in the primate community, a different species infects the slow loris, only strepsirrhine in Borneo. We propose that *Strongyloides* in primates is more diverse than previously thought, and show that although generalist *Strongyloides* isolates exist in the primate community, such generalism does not necessarily extend to the entire host community. The extent to which parasites are distributed in the wild and transmission ecology of multi-host parasites is fundamental to understand ecological and evolutionary host-parasite associations, and the epidemiological consequences of these dynamics.

Flow cytometric characterization of oxidative burst and phagocytosis activities of snakes' peripheral blood leukocytes

16:00 - Tuesday, 25th July, Solar Square

Marcelo Pires Nogueira de Carvalho, Nicolle Gilda Teixeira Queiroz-Hazarbassanov, Cristina De Oliveira Massoco, Sávio Stefanini Sant'Anna, Mariana Mathias Lourenço, Gabriel Levin, Mari Cleide Sogayar, Kathleen Fernandes Grego, José Luiz Catão-Dias

1. Laboratory of Wildlife Comparative Pathology (LAPCOM), College of Veterinary Medicine and Animal Science of the University of São Paulo (FMVZ/USP), 2. (School of Veterinary Medicine and Animal Science, University of São Paulo), 3. (School of Veterinary Medicine and Animal Science, University of São Paulo), 4. (Laboratory of Herpetology, Butantan Institute), 5. (NUCEL/NETCEM (Cell and Molecular Therapy Center), Internal Medicine Department, Medical School, University of São Paulo, São Paulo, Brazil)

Reptiles are the unique ectothermic amniotes becoming an important group to study with the aim of providing important knowledge into the evolutionary history of vertebrate immunity. Besides its importance, classification systems for reptiles' leukocytes have been described by their appearance rather than function, being still inconsistent. With the establishment of analytical protocols for snakes' blood, we bring a qualitative and quantitative flow cytometric analysis of oxidative burst and phagocytosis activities presented by snakes' peripheral blood leukocytes. For this purpose, we used 72 snakes from *Bothrops jararaca* (n=30), *Crotalus durissus* (n=30) and *Boa constrictor* (n=12) species. Blood samples were collected from the ventral coccygeal vein in vipers or from the paravertebral sinus in boas, and immediately transferred to tubes containing sodium heparin. Blood leukocytes were isolated using one-step Percoll gradient. As bacterial and fungi challenges for phagocytosis, respectively *Staphylococcus aureus* stained with propidium iodide (SAPI) and Zymosan A were used. Oxidative burst activity was evaluated with SAPI and phorbol 12-myristate 13-acetate (PMA) stimuli. Cell suspensions were incubated with antigens for 60min at 25°C-28°C, in agitation, in the dark. After incubation, samples were washed with EDTA 3mM solution, suspended in PBS and analyzed by flow cytometry. Considering the percentage of cells that undergo phagocytosis activities upon SAPI treatment, heterophils presented the highest phagocytic percentage, when compared to azurophils and lymphocytes. With Zymosan A particles, heterophils and azurophils presented a major phagocytic percentage, when compared to lymphocytes. Results patterns were similar in all snake species. Analysis of snakes' leukocytes oxidative burst activity demonstrated that azurophils reflected strong oxidative burst and were the only cells to show statistically significant difference between baseline and activated oxidative burst. With these results we provide novel and additional information which may contribute to snake leukocytes classification and to better understand the development of the immune system of vertebrates.

Spontaneous pathology of wild urban rats

16:00 - Tuesday, 25th July, Solar Square

Jamie Rothenburger, Chelsea Himsworth, Nicole Nemeth, Piper Treuting, Claire Jardine

1. Ontario Veterinary College, University of Guelph, 2. School of Population and Public Health, University of British Columbia, BC Ministry of Agriculture, Canadian Wildlife Health Cooperative, 3. University of Washington

Norway and black rats (*Rattus norvegicus* and *R. rattus*, respectively) are considered among the most successful of invasive species, inhabiting cities worldwide. Despite their significant role in zoonotic pathogen transmission, agricultural damage and as urban pests, remarkably little is known about naturally occurring diseases in rats. The objective of this study is to describe the gross and microscopic pathology in a population of 725 live-caught urban rats from Vancouver, Canada. The most frequent histological lesions included cardiomyopathy, respiratory tract inflammation, esophageal and stomach *Eucoleus sp.* (nematode) infection associated with proliferative and hyperkeratotic gastritis, hepatitis associated with *Capillaria hepatic* infection and *Trichosomoides crassicauda* infection of the urinary bladder. A variety of bacterial organisms were cultured from purulent lesions in various tissues (e.g., skin, uterus, lung) including *Staphylococcus aureus*, *Corynebacterium kutscheri*, *Bordetella bronchiseptica* and *Escherichia coli*. Given the severity of microscopic lesions and the frequency of parasitic/bacterial infections, natural disease may be an important factor contributing to urban rat mortality. There is also the potential that these co-infections and co-morbidities could influence the ecology of zoonotic pathogens carried by rats, which is an area of future investigation.

Temporal dynamics of *Trypanosoma cruzi*: an approach to wild environments

16:00 - Tuesday, 25th July, Solar Square

Diana Karina Villa-Meza

1. Universidad Nacional Autónoma de México

The American trypanosomiasis is a vector-borne neglected disease. If it isn't detected in early stages, it can damage important organs and even cause death. It is provoked by the protozoan (*Trypanosoma cruzi*). The common transmission cycle of the disease depends upon two ecological entities: vectors and reservoirs. The vector is an hematophagous triatomine bug. A great diversity of mammals can act as potential reservoirs. Especially two orders of mammals could act as key groups in the transmission cycle: rodents and bats. Both groups might have been a link between wild and domestic cycles. The knowledge about potential reservoirs into the wild is a field scarcely explored. The objectives of this work were: (1) to identify the infected hosts, (2) to assess the temporal variation of surveyed individuals (infected and non-infected) and (3) to determine if there is an association among the different temporal dynamics. We evaluated the presence of *T. cruzi* by serological methods and PCR. Then, to assess how the time series of the hosts were related, we used a CCF analysis with three different models and Cosinor's analysis as graphic representation. The prevalence of *T. cruzi* was higher in rodents by almost all the analysis. The PCR method had differences with the serological surveys. The dynamics that were significant were a) the prevalence in bugs Vs the bugs abundance; b) the abundance of bugs Vs the prevalence in bats; c) the abundance of rodents Vs the prevalence in bugs. Our results suggest that rodent's abundance in the wild might be determining the re-infestation of the parasite in the domestic cycle. Although the prevalence in bats was lower, the results hint that bat's prevalence might be shaped by bug's abundance. This work could offer hints for future researches in the transmission of the parasite between wild and domestic cycles.

Myoglobinuria in free-ranging Neotropical non-human primates attacked by dogs

16:00 - Tuesday, 25th July, Solar Square

Paloma Martins do Nascimento, Angélica Sánchez-Sarmiento, Rodrigo A. Réssio, Cinthya Cirqueira, Julia Carvalho, Silvana Mello Pereira Da Silva, Natalia A. C. Fernandes

1. Instituto Adolfo Lutz, São Paulo, SP, 2. University of São Paulo

In Brazil, the death notification of Neotropical non-human primates (NP) is mandatory, since they are sentinels for Yellow Fever. As part of the epizootics monitoring program, the Institute Adolfo Lutz receives samples from NP from São Paulo state and southern states. Due to fragmentation of forests, deaths caused by dogs' attacks have become more frequent, although no pathological data have been published in these cases. The present study describes histopathological findings with special emphasis on myoglobinuria in 16/145 (11%) NP attacked by dogs (January 2014 - June 2016). Histopathological examination was performed in all available organs, and kidney was additionally evaluated with Pearls stain and immunohistochemistry for myoglobin (Dako™, polyclonal). Fourteen animals were *Alouatta* sp. and two were *Callithrix* sp. Among animals without previous debilitating conditions, 50% were young. We found debilitating conditions in 6/16 (37.5%) animals that might have predisposed to dog attacks e.g., systemic toxoplasmosis, chronic renal disease and chronic lung disease. Fatal postraumatic sequelae included suppurative pleuritis and pulmonary hemorrhage, in 3/16 (18.7%) cases. Furthermore, 9/16 (56.2%) animals had renal myoglobin along with proteinosis, interstitial nephritis (7/9; 77.78%) acute tubular necrosis (5/9; 55.5%). Myoglobin was negative in animals that died immediately after the attack (3/16; 18.7%), but without statistical association between myoglobin detection in kidney and moment of death ($p=0.062$). There were two myoglobin immunolabeling patterns: tubular cell brush border (4/9; 44.4%) or tubular cell brush border + intratubular casts (5/9; 55.5%). Pearls stain had poor agreement with immunohistochemical analysis ($k=0.152$). Our results demonstrate acute renal changes and myoglobinuria in NP attacked by dogs. We believe acute skeletal myofiber damage together with 'stress myopathy' could explain myoglobinuria. Myoglobin immunohistochemical analysis was more useful than Pearls stain to detect myoglobin in kidney.

Estudio metagenómico de la microbiota bacteriana fecal de oso negro (*Ursus americanus*) basado en el gen 16S rRNA

16:00 - Tuesday, 25th July, Solar Square

Jesús Martínez Luna, Rogelio Carrera Treviño Antonio Guzmán Velasco, Cristina García De la Peña, Jesús Jaime Hernández Escareño

1. Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León), 2. (Laboratorio de Fauna Silvestre, Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Nuevo León), 3. (Laboratorio de Biología de la Conservación y Desarrollo Sustentable Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León), 4. (Laboratorio de Microbiología y Micología Veterinaria, Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Nuevo León.)

Los intestinos de los mamíferos albergan diversos ecosistemas microbianos que tienen importantes efectos sobre la fisiología del hospedero y juegan un papel importante en el mantenimiento de la salud y la modulación de enfermedades. La composición de la microbiota intestinal depende en gran medida de la dieta. Para las poblaciones de oso negro americano (*Ursus americanus*) presentes en México se desconoce la estructura y diversidad de la microbiota bacteriana intestinal. En el presente estudio se analizó la diversidad de la microbiota bacteriana fecal de un oso negro macho de 121kg aparentemente sano, el cual se capturo en agosto de 2016 en los límites del Parque Nacional Cumbres de Monterrey, en la Facultad de Ciencias Políticas, UANL, ingiriendo residuos sólidos urbanos; se cree que se trata de un animal habituado. Se tomaron muestras fecales del oso y se extrajo el DNA utilizando el kit Xpedition™. Se realizó metagenómica de las regiones variables V3 y V4 del gen 16S rRNA utilizando el protocolo y tecnología de Illumina®. Las secuencias obtenidas se analizaron con el programa QIIME™ para la asignación de Unidades Taxonómicas Operacionales (OTUs). Se asignaron 15,100 lecturas, las cuales se agruparon en 311 OTUs distribuidos en tres Phylum (Fusobacteria, Firmicutes, Proteobacteria) y seis géneros (*Fusobacterium*, *Clostridium*, *Peptostreptococcus*, *Romboutsia*, *Clostridium_g8*, *Cellulosilyticum*, *Faecalimonas_GL872355_g*, *Terrisporobacter*, *Paeniclostridium*, *Peptostreptococcaceae_Other*, *Agathobacter*, *Eubacterium_g4*, *Eubacterium_g23*, *Tissierella*, *Campylobacter*). Algunos de los géneros reportados en este estudio son de los más dominantes en otras investigaciones con osos, sin embargo la diversidad encontrada es baja en comparación con lo reportado para otros osos. Estos datos sientan las bases para la caracterización de la microbiota bacteriana intestinal del oso negro en México y resalta la necesidad de generar más información para poder entender el efecto de la variación de la dieta en la diversidad microbiana y la salud de estos animales.

Prevalence Of Ranavirus And Bd In Hellbender Populations In Tennessee And Arkansas

16:00 - Tuesday, 25th July, Solar Square

Rebecca Hardman¹, Debra Miller²

1. University of Tennessee 2. University of Tennessee Center for Wildlife Health

The Hellbender (*Cryptobranchus alleganiensis*), is a large aquatic salamander containing two subspecies, Ozark Hellbender (*C. a. bishopi*), and Eastern Hellbender (*C. a. alleganiensis*), from the Ozark mountains and eastern U.S., respectively. Both subspecies have seen population declines over the past 25 years, especially in *C. a. bishopi* which is federally endangered. Habitat degradation alongside other factors may lead to secondary infections with amphibian pathogens such as Ranavirus and chytrid fungus (*Batrachochytrium dendrobatidis*) or Bd. Other pathogens such as the emerging salamander chytrid (*Batrachochytrium salamandrivorans* or Bsal) are also of concern as potential primary or secondary causes of disease. Our objective was to determine prevalence of these pathogens in both subspecies to understand the role of emerging amphibian pathogens in *C. alleganiensis* declines. We collected tissue and swabs from *C. a. bishopi* and *C. a. alleganiensis* individuals from Arkansas and Tennessee respectively during the summers of 2011-2015. We used qPCR analysis to determine presence of Ranavirus and Bd from tail samples and skin swabs, respectively. In the latter two years we collected samples of microbiome and host skin secretions. Overall, for *C. a. bishopi*, we detected 32% prevalence of Bd and 8.6% ranaviral infections; for *C. a. alleganiensis*, we detected 15% prevalence of Bd and 3% prevalence of Ranavirus. We have not found any Bsal positive individuals but have discovered Bd consistently present in these populations. We are currently in our second phase of investigating morbidity and mortality in hellbenders by comparing host skin microbiomes with changes in clinical disease and host antimicrobial peptide production.

Coral diseases and their link with the affluent of Jamapa river in Veracruz Reef System

16:00 - Tuesday, 25th July, Solar Square

Jacqueline Rivera Ortega¹, Guillermo Horta-puga²

1. Posgrado en Ciencias del Mar y Limnología, UASA Puerto Morelos, UNAM, 2. Unidad de Biotecnología y Prototipos, FES Iztacala, UNAM.

In the past 40 years, as a consequence of the environmental damage of the tropical coastal zones, climate change and anthropogenic threats, the prevalence of the coral diseases have increased, due to pathogen organisms. Veracruz Reef System receive directly the affluent of Jamapa river (source of pollution and organic matter). Therefore, in this research we chose La Blanca, Chopas, and Isla de Enmedio reefs (all they have an increasing distance from the discharge and they are on the limits of the affluent).

By using linear transects, we quantitate healthy and diseased colonies, determining by visualization the disease and the percentage of damage. The sampling (2009-2014) was in the period of more and less influence of the Jamapa discharge, and we assessed the link between the discharge volume (daily volume flow: m^3/s) and the prevalence of diseases. All data belong to GM005 CONABIO project.

Of 3,766 colonies, 5.1 showed some disease, through one of those diseases: Yellow and Black Band, Tumors, White Spot, Dark Spot, White Plague and Shutdown Reaction. The prevalence at La Blanca was 9.0% ($n=134$), Chopas 2.3% ($n=42$), and Isla de Enmedio 1.2% ($n=19$), and they have significantly statistical differences (ANOVA; $F_0=6.80 > F=3.47$), La Blanca show the major difference with regard to the others (LSD; $8.57 < 11.5$ y 14.37); and a fewer correlation ($r=0.50$, $p < 0.05$), than Chopas ($r=0.52$, $p < 0.05$), and Isla de Enmedio ($r=0.66$, $p < 0.05$) between mean-prevalence/campaign/site and discharge volume (linear simple correlation). The general correlation between the total prevalence of 3 reefs and the discharge is $r=0.57$; $p=0.18$.

Thus, due to the 3 reefs showed a major proportion of diseased corals in the period of major discharge, we propose that Jamapa river do show an direct influence in the reef health, in all the campaigns 2009-2014.

Influence of host factors and seasonality on *Baylisascaris procyonis* infections in raccoons in Ontario

16:00 - Tuesday, 25th July, Solar Square

Shannon French, David Pearl, Doug Campbell, Andrew Peregrine, Claire Jardine

1. Department of Pathobiology, University of Guelph, 2. Department of Population Medicine, University of Guelph, 3. Canadian Wildlife Health Cooperative, 4. Canadian Wildlife Health Cooperative

Raccoons (*Procyon lotor*) are definitive hosts for *Baylisascaris procyonis*, the raccoon roundworm. This parasite has the ability to infect, and cause severe neurological disease, in a large range of aberrant hosts, including humans. There is conflicting information regarding the influence of demographic and environmental risk factors on the prevalence of the parasite in raccoons. Our objective was to assess the impact of host factors and seasonality on the occurrence and intensity of infection in raccoons. From 2013-2016, we recorded the number of *B. procyonis* worms present in the intestinal tracts of 1551 Ontario raccoons submitted to the Canadian Wildlife Health Cooperative for necropsy. Univariable hurdle models were fitted to simultaneously estimate associations between the presence and intensity of infection with the following independent variables: age, sex, body condition, season and year of collection. The odds of having a non-zero count were significantly greater for juveniles vs adults, being in excellent body condition vs poor condition, and being collected during the dispersal season (late summer and fall) vs all other collection seasons. For non-zero counts, the worm count was significantly higher for juveniles. No statistical differences were found between collection years. Our preliminary results are consistent with previous studies suggesting that juveniles are more likely to be infected and that infection rates are highest in the fall during the pre-denning and dispersal period. Ongoing multivariable analyses will explore interaction effects among these variables and control for potential confounding variables. This improved understanding of the risk factors influencing parasite carriage in Ontario raccoons has the potential to guide public education efforts aimed at reducing the potential for transmission of this parasite to humans.

Is migration an important factor modifying viral metacommunity structure of avian influenza?

16:00 - Tuesday, 25th July, Solar Square

Daniel Mendizabal, Ivan Castro-Arellano Gerardo Suzán, Oscar Rico-Chavez

1.Universidad Nacional Autónoma de México, 2.Texas State University

In recent years the study of symbiont communities has acquired great importance for understanding host-pathogen dynamics, as well as clinical and epidemiological factors related to it. Little is known about how viral communities related with birds are structured, as well as the ecological and phylogenetic patterns related to these associations. The current project aims to study the effect of bird migration in the structure of influenza metacommunities in different biogeographic regions. A metacommunity is composed by several communities, we considered the viral richness associated to one avian specie as a community. By using the *Influenza Research Database*, we obtained 7,187 samples of birds belonging to 34 genus and 12 families. The data was grouped in four biogeographic regions where influenza virus has been reported. Migrations patterns were obtained and a comparison was made between viral metacommunities of migratory and resident birds, and metacommunities formed only by migratory birds. Metacommunity analysis was performed in *R* free software, using the *metacom* library. No differences were found between the two groups of metacommunities, both of them presented random and quasi-clementsian structures. Our results suggest that influenza subtypes show a similar response to environmental gradients, which could be associated to ecological or phylogenetic factors. Even though migration has no direct impact in viral community structure associated to resident birds, it is an important process that can facilitate transmission and dissemination to new regions or hosts. Metacommunity analysis is an important tool that allows us to inferred ecological process on a bigger geographic range. Better sample efforts should be made, and it is fundamental that research institutions perform an adequate diagnosis and report because there's a big information gap for this type of analysis.

Interspecific transmission of feline leukemia virus and feline immunodeficiency virus between domestic cats and guignas (*Leopardus guigna*) in Chile

16:00 - Tuesday, 25th July, Solar Square

Irene Sacristan, Francisca Acuña, Emilio Aguilar, Sebastian García, Maria Jose López, Aitor Cevidanes, Javier Cabello, Ezequiel Hidalgo, Javier Millán, Elie Poulin Constanza Napolitano

1. Universidad Andres Bello, 2. Universidad de Chile, 3. Chiloé Silvestre, 4. Parque Zoológico Buin Zoo, 5. Instituto de Ecología y Biodiversidad, Facultad de Ciencias, Universidad de Chile

Human landscape perturbation facilitates the domestic-wildlife interface, increasing probabilities of interspecific pathogen transmission, thus been one of the main causes of the emergence of pathogens. In Chile, human invasion to natural habitats is increasing and may facilitate pathogen transmission between wildlife and domestic species.

Feline leukemia virus (FeLV) and feline immunodeficiency virus (FIV) are two of the most common viruses affecting domestic cats and can also affect other species of the family Felidae. The guigna (*Leopardus guigna*) is threatened small felid found in central-southern Chile and south-western Argentina. Guigna populations are extensively affected by habitat loss, being forced to inhabit forest fragments surrounded by a human matrix, which can increase their contact with domestic cats.

This study aims to understand whether an interspecific transmission of FeLV and FIV occurs between guignas and domestic cats, and also whether this is due to human landscape perturbation.

Blood and tissue samples from 80 free-ranging guignas and 140 domestic cats were collected and analyzed by nested PCR and sequencing. A total of 18 guignas and 28 domestic cats were positive to FeLV, while 5 guignas and 6 domestic cats were positive to FIV.

A high percent of nucleotide identity (PNI) of FIV and FeLV sequences between both species suggests possible interspecies transmission of these viruses, facilitated by increased contact probability through human occupation of natural habitats.

This study enhances our knowledge on the transmission of pathogens from domestic to wild animals in the global scenario of human landscape perturbation and emerging diseases.

Modeling of Avian influenza transmission dynamics through network analysis on migratory ducks – poultry interface in Lerma, Estado de México

16:00 - Tuesday, 25th July, Solar Square

Liliana Gaytán Cruz, Oscar Rico-Chavez, Rafael Ojeda Flores

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México

Wild ducks from the *Anas* genus have been consistently reported with the highest influenza A viruses prevalence in various regions of the world. It has been demonstrated that their migration facilitates dissemination of influenza viruses to great distant places. This study was performed in “Ciénegas de Lerma”, Estado de México, a Protected Natural Area that harbors migratory birds in winter seasons and regulated hunting activities are developed there. The aim was to model the influenza virus transmission dynamics from migratory ducks to poultry due to mobility of animal carcasses by local workers. Simulation models were constructed with networks at different weighted degree centrality using EpiModel package for R program based on epidemiologic information from bibliographic data and simulating the flow of hunted ducks towards backyard poultry. The results of the network analyses showed a scale-free structure, evidencing that the probability of transmission in hypothetical cases of influenza outbreaks, is higher in farms with greater contact rate with hunted wild ducks, and it could be disseminated toward far zones rather the study area. This investigation suggest that transported carcasses of hunting activities promoted by people involved in this activity, is a potential factor for influenza virus transmission to backyard poultry. This type of modeling can provide information for new large-scale research lines in Mexico. It could assist the authorities to implement sanitary and educative measures to workers and hunters as strategies to control and prevent influenza virus emergence and transmission in the wildlife – backyard animal interface with high contact rates.

Penguin bycatch: histopathologic description of drowning-related lesions in Magellanic penguins (*Spheniscus magellanicus*)

16:00 - Tuesday, 25th July, Solar Square

Carol Ewbank, Cristiane K. M. Kolesnikovas, Samira Costa-Silva, Marzia Antonelli, Janaina Rocha Lorenço Guilherme A. Nogueira, Carlos Sacristán, José Luiz Catão-Dias

1. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP, Brazil, 2. Associação R3 Animal, 3. Asso, 4. Associação R3 Animal

Fisheries bycatch, the incidental mortality caused by entanglement in fishing gear, is a significant threat to seabirds, extensively studied in albatross and petrel species (Procellariidae family). Nevertheless, penguin bycatch mortality is only anecdotally reported in coastal fishing operations in South America. We described histopathologic findings in 20 Magellanic penguins (*Spheniscus magellanicus*) (19 juveniles and 1 adult) that drowned after being caught in a gillnet in Santa Catarina state, southern Brazil. Upon necropsy, 19 birds were in good body condition and one was thin. Sexing identified 18 females and 2 males. Macroscopic findings included gastrointestinal parasitosis (100%), pulmonary edema/congestion (100%), hepatomegaly (45%), and cerebral, splenic and renal congestion (100%, 70% and 15%, respectively). Major microscopic (hematoxylin-eosin and Perls) changes were observed in the following systems: gastrointestinal (95%), neurologic (90%), respiratory (70%), lymphoid (60%), genitourinary (45%), others (20%), and cardiac (15%). All animals presented congestion in at least one system, likely caused by decreased cardiac output due to increased vascular resistance in the lungs, cardiac anoxia and acidosis. Hepatic hemosiderosis and extramedullary hematopoiesis were possibly associated with exercise and immunological challenge (migration). To our knowledge, this is the largest histopathologic study on drowning in penguins, and corroborates with drowning-related changes previously reported by our group in these birds. Drowning is considered a challenging diagnosis, due to the difficulty in differentiating drowning from *postmortem* submersion, anatomical and physiological diving adaptations of seabirds, and autolysis, predation and weather exposure of beach-cast carcasses. Drowning should be a differential diagnosis in all beach-cast seabird *postmortem* examinations and not solely based on external lesions compatible with entanglement or water in the lungs/air sacs. Further studies and public education are urgently needed to characterize penguin bycatch (e.g., fishing technique, location, season) and develop mitigation measures.

Wildlife poisoning in Kerala, South India - the canary in the coal mine?

16:00 - Tuesday, 25th July, Solar Square

*Sreejith Radhakrishnan*¹

1. Imperial College London, UK

Wildlife poisoning, intentional or otherwise, remains a constant threat to the conservation of endangered species in India. However cases of poisoning often go undetected, either because poisoning is not considered in differential diagnoses or because carcasses are often found at remote locations in advanced stages of decomposition. In this study, all cases of wildlife mortality recorded at the office of the Assistant Forest Veterinary Officer, Periyar Tiger Reserve in Kerala, South India between 2008 and 2013 were reviewed and cases of suspected or confirmed poisoning were summarized in order to understand the types of poisons detected and the extent of the problem in Kerala. During this period, four confirmed cases of wildlife poisoning were recorded, including carbofuran (a carbamate pesticide) poisoning in a bonnet macaque (*Macaca radiata*), warfarin (a rodenticide) poisoning in a mass mortality event involving several wild boar (*Sus scrofa*), endosulfan (an organochlorine insecticide) toxicity in a gaur (*Bos gaurus*) and imidacloprid (a neonicotinoid insecticide) toxicity in a wild adult Asian elephant (*Elephas maximus*). Of these, the latter two cases were expected to be instances of unintentional poisoning associated with consumption of vegetation in and around tea estates treated with endosulfan, and consumption of water from barrels used to store water mixed with imidacloprid, respectively. In a separate instance of the deaths of three wild boar exhibiting lesions of extensive systemic haemorrhages, no poisons or chemicals were detected on toxicological examination of samples. The implications of these findings, particularly the use of neonicotinoid and other insecticides in commercial agricultural estates adjoining wildlife habitats and possible ecological consequences of this use, are discussed.

First detection of *Mycobacterium avium* subsp *paratuberculosis* by different diagnostic techniques in a scimitar-horned oryx (*Oryx dammah*) in captivity in México

16:00 - Tuesday, 25th July, Solar Square

Ana Laura Hernández, Gilberto Chávez-Gris, Edith Maldonado-Castro, Luz Elena Alcaraz-Sosa, Mariela Díaz-Negrete

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. Dirección General de Vida Silvestre

Scimitar-horned oryx is a species extinct in the wild (EW) for the IUCN red list since year 2000, the conservation of this species depends on the population kept in captivity. It has been reported that the main cause of death in young and adult animals of this species are bacterial diseases. Paratuberculosis is a chronic bacterial enteropathy that affects domestics and wild ruminants. The etiologic agent is *Mycobacterium avium* subsp *paratuberculosis* (Map), an acid-fast bacilli. Transmission occurs by the fecal-oral route, the bacteria crosses the lumen of the small intestine causing a granulomatous enteritis, the clinical signs are chronic diarrhea and cachexia in cases of advanced disease. The objective of this study is to identify the presence of Map in a scimitar-horned oryx kept in captivity. The samples obtained were feces and intestine, the techniques used in the samples were culture in Herrold medium with Egg yolk, Micobactina and Pyruvate (HEYMP), PCR IS900 and multiplex DMC PCR, this multiplex technique distinguishes between C (Cattle), S (Sheep) strains, also in the intestine were performed anatomopathological studies. In feces, the specimen was culture positive after 8 weeks, both samples, feces and tissue amplified to PCR IS900 and DMC PCR to strain C (cattle). In the anatomopathological studies, macroscopically the intestine showed a thickening of the mucosa with congestion, granulomatous lesions and abundant acid-fast bacilli in the mucous were observed microscopically. In this study, it was demonstrated the ability of Map to cause granulomatous lesions and to be excreted by feces in the specie *Oryx cimatarra*, making viable the transmission of this disease. In the future it is necessary to do more research in this field, to establish strategies for the control and thus to help the preservation of the species.

Is antibiotic resistance reaching Antarctic marine mammals?

16:00 - Tuesday, 25th July, Solar Square

Josefina Gutierrez^{1 3}, *Daniel González-Acuña*², *Carlos Hernández*¹, *Claudio Verdugo*^{1 3}

1 Laboratorio de Ecología y Evolución de Enfermedades Infecciosas (E3 Lab), Instituto de Patología Animal, Universidad Austral de Chile, Valdivia, Chile. 2 Departamento de Ciencias Pecuarias, Universidad de Concepción, Concepción, Chile. 3 Programa de Investigación Aplicada en Fauna Silvestre (PIAFS), Universidad Austral de Chile, Valdivia, Chile.

Antibiotic resistance is a major issue with public health implications not only because of the consequences of treatment failure but also the emergence of resistance in non-target microorganisms living in natural environments. Although Antarctica is considered one of the most pristine and highly biodiverse ecosystem, it has been influenced by several anthropic activities. The goal of this study was to detect antibiotic resistance in Antarctic marine mammal *Enterobacteriaceae*. Swabs were taken from fresh feces of 17 Antarctic fur seals (*Arctocephalus gazella*) and 3 Wedell seals (*Leptonychotes weddellii*) from four islands of Antarctic Peninsula during the austral summer of 2017. Samples were cultivated in a BBL brain heart infusion, cultured in blood agar media, transferred to a Mueller-Hinton media, and tested against seven antibiotics discs: gentamicin (CN), florfenicol (FFC), enrofloxacin (ENR), sulphamethoxazole/trimethoprim (SXT), cefoperazone (CFP), cefuroxime (CXM) and erythromycin (E). Phenotypic antibiotic resistance was estimated measuring the exclusion halo according to CLSI standards. According to this 45% were resistant to one antibiotic and showed intermediate resistance to at least another one which was considered as multiresistant. Macrolides (E) resistance was present in 95% of the samples. 20% of the colonies were resistant to aminoglycosides (CN), one beta-lactams (CXM) or phenicols (FFC). Quinolones (ENR) resistance was determined in 25% of the samples. DNA was extracted for bacteria identification by 16S gene amplification and 16 matched with *Enterobacteriaceae*. The presence of genetic resistance cassettes was determined by PCR. To the genotypic analyses 70% of cultured strains were multiresistant. *E. coli* was the most abundant bacteria and presented 90% of multiresistant cultured strains. 98% and 81% of the samples had resistance genes against CN and ENR respectively. All genotypes presented at least one resistance cassette. To our knowledge this could be considered the first report of antibiotic resistance in pinnipeds from Antarctica.

Movement, Population Structure, and Disease Prevalence of Cattle Egrets (*Bubulcus ibis*)

16:00 - Tuesday, 25th July, Solar Square

Shannon Moore, Hanna Innocent, Claudia Ganser, Samantha Wisely

1. Department of Wildlife Ecology and Conservation, University of Florida, 2. University of Florida)

The distribution of cattle egrets (*Bubulcus ibis*) has dramatically expanded in the past two centuries. Native to central Africa, southern Portugal, Spain, and the Asian tropics, cattle egrets are now found in all continents, except Antarctica. Despite their rapid expansion, little is known about cattle egret movements including migration and dispersal, and the potential for cattle egrets to transport pathogens. The objectives of this project are to survey the genetic population structure; to estimate the movement and migration rates of cattle egrets within Florida and along the Mississippi and Atlantic flyways; and to determine cattle egrets' role in disease transmission. Live cattle egrets are trapped and sampled for blood, ticks, feathers, and morphological measurements. Dead cattle egrets are collected from USDA Bird Air Strike Hazard (BASH) control efforts and sampled for muscle, blood, ticks, feather, liver, spleen, and morphological measurements. SNP microarrays will be used to survey genetic population structure and estimate movement. PCR and gel electrophoresis will be used to determine prevalence of *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*. Positive samples will be sequenced for genetic analyses. As of April 10, 2017, 142 cattle egret have been sampled from 7 locations around Florida. In preliminary screening for *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*, 1 of 5 samples tested positive for *Leucocytozoon*. Cattle egret sample collection and screening and sequencing for Haemosporidia parasites will continue. This project will provide a better understanding of cattle egret movement and their role in disease transmission.

Infection Risk Of Canine Distemper Virus In A Domestic And Wild Carnivore Interface Within Janos Biosphere Reserve, Chihuahua, Mexico

16:00 - Tuesday, 25th July, Solar Square

Rocío Almuna Andres Lopez-Perez , Karen Moreno, André V. Rubio, Cristóbal Briceño-Urzúa , Rosa Elena Sarmiento-Silva, Gerardo Suzán

1. Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, 2. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 3. Facultad de Ciencias, Universidad de Chile

Human population growth has led to a greater interaction rate between domestic and wildlife animals. These changes have increased the spread of infectious diseases and pose a risk for wildlife conservation. For instance, several studies have found that Canine Distemper Virus may have an important role in the domestic-wildlife interface. Our objective was to determine the risk of distemper transmission between domestic dogs (*Canis lupus familiaris*) and wild carnivores in Northwestern Mexico. Two approaches were carried out: 1) questionnaires to dog owners, and 2) molecular techniques. A total of 70 questionnaires about dog ownership were completed during March 2015 in four settlements within Janos Biosphere Reserve. In addition, we sampled 90 domestic and wild carnivores during fall 2013 and spring 2014. RNA was extracted from animal blood samples and PCR was performed using the hemagglutinin primers. Finally, the sequences obtained were analyzed using MEGA6 to determine the consensus of the sequences for the amplified region. A logistic regression was used to assess the risk factors of the virus transmission. Our results showed that there is a low vaccination rate against the agent (7%), and that physical interactions between domestic and wild species exist in Janos Biosphere Reserve. Additionally, we found that rural free-ranging dogs may be an important risk factor for the virus presence in dogs ($p=0.0479$). Our findings based on molecular techniques were consistent to the qualitative approaches. Sequencing analysis of hemagglutinin identified two genetic variants in a kit fox (*Vulpes macrotis*) and in a dog. The identified strains showed a 98.8% of similarity. The results highlight the importance of prophylactic plans against Canine Distemper Virus transmission within the Janos Biosphere Reserve where many endangered species coexist, including the reintroduced black-foot ferret (*Mustela nigripes*)

Immunogenicity dose response of the *Bacillus anthracis* Sterne strain 34F2 vaccine by subcutaneous and oral administration

16:00 - Tuesday, 25th July, Solar Square

Jamie Benn, Walt Cook, Allison Rice-Ficht, Thomas Ficht

1. Texas A&M University

Anthrax (*Bacillus anthracis*) is a zoonotic disease, endemic to environments worldwide. Spores, the dormant form of the bacteria, can survive for decades in some of nature's harshest environments. Anthrax outbreaks are common in free-ranging livestock, wildlife, and even endangered species, thus making anthrax an economically and ecologically important disease. The current vaccine for livestock and wildlife, the Anthrax Spore Vaccine (ASV), is a suspension of *Bacillus anthracis* Sterne Strain 34F2 spores in saponin and is only available as a subcutaneous injection which is an impractical method of prevention for wildlife. An alternative formulation of the ASV is essential for feasible and protective oral vaccination against anthrax. Varying doses of the ASV were administered subcutaneously and orally in BALB/cJ mice to evaluate the potential for an oral vaccine against anthrax. The immunogenicity of each ASV variation was evaluated by ELISA. Antibody titers against anthrax protective antigen were measured in weekly serum samples over two months. The antibody levels of the subcutaneously administered vaccines far exceeded those of the orally administered vaccines, indicating that the ASV alone is not sufficient as an oral vaccine. The contrasting immune responses we observed between subcutaneous and oral administration of the ASV suggests that an oral vaccine against anthrax must contain a higher number of spores or a controlled release vehicle must be employed to establish a protective immune response via oral vaccination.

Widespread occurrence of hemotropic mycoplasmas in Culpeo (*Lycalopex culpaeus*) and Chilla (*Lycalopex griseus*) foxes in Chile

16:00 - Tuesday, 25th July, Solar Square

Aitor Cevidanes Sophia Di Cataldo, Bernardita Julio-Kalajzić Irene Sacristan, Carla Barría, Nicole Sallaber-ry-Pincheira, Juliana A Vianna, Javier Millán,

1. Universidad Andres Bello, 2. Pontificia Universidad Catolica de Chile

Hemotropic mycoplasmas (hemoplasmas) are epicytellar erythrocytic bacterial parasites lacking a cell wall that attach to and grow on the surface of red blood cells. Hemoplasmas are known to be the causative agents of acute and chronic infectious anemia in several mammalian species. Hemoplasma infections have been detected in a range of wild felids but rarely in free-living wild canids. In Chile, an unexpected high prevalence (57%) was found in Darwin's foxes (*Lycalopex fulvipes*) from Chiloé Island.

The way of transmission of hemoplasma is unclear, but bloodsucking arthropods are suspected to be the vectors. In addition to this, vertical transmission and infections through biting and fighting are considered another possible routes of hemoplasma transmission.

The aim of this study is to investigate the occurrence of *Mycoplasma* sp. in culpeo (*Lycalopex culpaeus*) and chilla (*L. griseus*) foxes and study differences among three different bioclimatic macro-regions of Chile: Northern (arid-semiarid), Central (mediterranean) and Southern (temperate-rainy)

Blood or spleen samples from 84 wild foxes (54 culpeo and 30 chilla; 27 from the northern, 48 from the central, and 9 from the southern regions) were analyzed by conventional PCR targeting the 16sRNA gene.

Overall prevalence was 34.5 % (29/84) (95% CI= 24.3%- 45.4%), without statistical differences between the two species. Mycoplasma was present in the three studied regions. No statistical differences were found between bioregions, although a higher prevalence was observed in arid-semiarid region (48%) when compared with the Mediterranean (27%) and the temperate (33%) regions.

To the authors' best knowledge, this is the first molecular detection of *Mycoplasma* spp. in culpeo and chilla foxes. This study revealed that hemotropic mycoplasma is widespread in foxes across Chile. No clear association between climatic condition and prevalence was observed, what prevent us to making inferences about a theoretical association between hemoplasmas and arthropod vectors.

Effects of anthropization on the ecology of rodents, reservoirs of pathogens with zoonotic potential

16:00 - Tuesday, 25th July, Solar Square

Hugo Mendoza-Gutiérrez, Gabriel E García Peña, Jesús Sotomayor-Bonilla, José Isaac Delgadillo-Gutiérrez, Paulina Álvarez-Mendizábal, María José Tolsá-García, Rosa Elena Sarmiento-Silva, Gerardo Suzán

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México

The disturbance of the landscape and ecological processes due to human activities has a marked influence on the community and metacommunity dynamics of rodents. As a result, increased coexistence between rodents and humans increases the rate of contact between humans and rodent-borne zoonotic pathogens. In this work, we investigate the changes in rodent metacommunity structure associated with the anthropization of the environment in Bahía de Kino, Sonora. We evaluate the communities Coherence, Turnover and Boundary Clumping in an anthropization gradient determined by: i) the percentage of vegetation induced, ii) the distance to the nearest human settlements, iii) the percentage of the area occupied by roads and highways, and iv) the percentage of buildings. The rodent metacommunity structure was estimated in three field samples. We ordered the presence-absence matrix of rodent species based on the anthropization of their habitats and we compared it with the meta-community structure obtained by the reciprocal averaging in a latent environmental gradient. The results indicate that, for the first two seasons of sampling (autumn-2015 and winter-2016), the metacommunity structure shows a Clementsian pattern based on anthropization of sites, while the last season (summer-2016) shows a Gleasonian metacommunity pattern. In contrast, the latent environmental gradient shows a Clumped Species Loss pattern and a Random arrangement for the first, second and third season, respectively. In general, rodent species in Bahía de Kino respond to environmental filtering derived from anthropization. From the metacommunity approach of Disease Ecology, when the distribution of potential hosts in Clementsian and Gleasonian metacommunities is limited the presence of zoonotic pathogens in the landscape, although to a lesser extent, will be given on a mostly local scale.

Trypanosoma cruzi in foxes (*Lycalopex culpaeus* and *L. griseus*) and rural free-ranging dogs in central Chile

16:00 - Tuesday, 25th July, Solar Square

Carla Tagini, Aitor Cevidanes, Catalina Muñoz, Maria Violeta Barrera, Nicole Sallaberry-Pincheira, Pedro Cattán, Javier Millán

1. Universidad de Chile, 2. Universidad Andres Bello, 3. Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile

Background: *Trypanosoma cruzi* is a zoonotic vector-borne protozoan parasite that causes Chagas disease, found in humans and other mammalian hosts with distribution throughout the Americas. In Chile, although the main vector of Chagas disease (*Triatoma infestans*), has been controlled, three other endemic species of sylvatic triatomines occupy different habitats and contribute to maintain the presence of the parasite in the country. Carnivores have great potential to be significant reservoirs due to the wide diversity in their ecological niches that might range from insectivorous to carnivorous diet in different habitats, favouring contact with different components of the *T. cruzi* transmission net. Nevertheless, very little is known about the role of carnivores in the *T. cruzi* epidemiology.

Objectives: This study aims to investigate the occurrence of *T. cruzi* in wild foxes and sympatric rural free-ranging dogs from Chile.

Methodology: We included in the study blood or spleen samples from 34 free-living foxes (21 *Lycalopex culpaeus* and 13 *L. griseus*) and blood from 33 dogs belonging to local mule drivers working in areas where foxes were captured in Región Metropolitana (central Chile). Samples were analyzed by real-time PCR and quantified.

Results: One fox (4.76%) and three dogs (9.09%) were positive to *T. cruzi*, differences in prevalence were not statistically significant. Quantification showed that the culpeo fox (a young female) presented 8.6 parasites/mL, whereas the three dogs presented < 1 parasite/mL.

Conclusions: This is the first report of *T. cruzi* in foxes in Chile and elsewhere in South America. The parasitemia presented by the culpeo fox can be considered very high. This study enhances our knowledge on the presence of this hemoparasites in wild canids and is a first approximation for future studies on the possible interspecific transmission of *T. cruzi* between foxes and rural dogs.

Modelando fenotipos de patógenos: *Pseudogymnoascus destructans*

16:00 - Tuesday, 25th July, Solar Square

Ruth Areli Gomez Rodriguez, Gabriel Gutiérrez Granados, Ángel Rodríguez Moreno, Victor Sánchez-Cordero

1. Universidad Nacional Autónoma de Mexico, 2. FES Zaragoza, UNAM, 3. Instituto de Biología, UNAM

Introducción: El Síndrome de Nariz Blanca (SNB) es una de las enfermedades más letales de la vida silvestre, matando a más de 5 millones de murciélagos en Norte América desde que se informó por primera vez en el 2006. El agente causal de la enfermedad es un hongo filamentoso psicrófilo, *Pseudogymnoascus destructans*. El hongo está ampliamente distribuido en América del Norte y Europa y recientemente se ha reportado en algunas partes de Asia, pero curiosamente, no se ha observado mortalidad en los murciélagos europeos o asiáticos.

La comparación de la dinámica del patógeno entre el fenotipo de cada región puede ofrecer una visión de qué especies y poblaciones están riesgo y se pueden identificar fuentes de dispersión e introducción del patógeno. Esto nos lleva a la necesidad de una comprensión predictiva de la distribución geográfica y el potencial de transmisión de estos fenotipos. En este trabajo, utilizamos técnicas de modelado de nicho ecológico para entender la relación entre los eventos de SNB conocidos y las características ambientales.

Métodos: Las bases se armaron con datos de la literatura publicada así como bases obtenidas de GBIF. Para construir los modelos de nicho ecológico se usó el algoritmo MaxEnt y las variables climáticas obtenidas de BioClim.

Resultados y Discusión: Los modelos mostraron una diferencia marcada entre los rangos de distribución de cada fenotipo. El Fenotipo asiático muestra una distribución más amplia mientras que el fenotipo Americano tiene la distribución más reducida.

El modelo se acerca más a la realidad cuando solo se consideran las capas climáticas de temperaturas, esto puede ser debido a que la temperatura es el factor principal que guía el crecimiento del hongo.

Conclusión: Se encontró que los fenotipos del hongo se han diferenciado ecológicamente.

Analysis of the impacts of the hunting and consumption practices of bushmeat in the regions of the Orinoquia and the Amazon of Colombia

16:00 - Tuesday, 25th July, Solar Square

Josue Hernandez, Jose Manuel Martinez, Diego Soler-tovar

1.Universidad de La Salle

In Colombia, there are few technical studies on the sustainable capacities of the exploitation of wildlife populations. Existing control and prohibition policies are not based on sustainable development objectives that help vulnerable human populations meet their food security needs by avoiding the extinction of wild species and the transmission of zoonotic diseases. The objective of this study was to analyze the environmental, epidemiological and food safety impacts of hunting and consumption practices of bushmeat in the regions of Orinoquia and Amazon of Colombia. A total of 492 surveys were conducted on women between 30 and 60 years of age, due to their direct relation with what is consumed in the households, in Leticia, Amazonas (Amazon) and Villavicencio, Meta (Orinoquia); the importance of food safety, epidemiology and environmental impact of this practice was evaluated and classified. A high rate of consumption of wild species was found, higher for vulnerable populations that do not have easy access to the family basket; among the most frequently consumed species are: Dasypodidae, Cuniculus paca, Hydrochoerus hydrochaeris, Tapirus, Cervidae and Podocnemis unifilis. There is a dependence between the decline of wild populations and the survival of communities that perform this practice. To help these communities identify abundant wild species that can be used for this practice, helping to conserve vulnerable species. The practice of hunting and consumption of bushmeat is of importance for food security in vulnerable human communities in these regions of the country, but there is little knowledge about this practice that may lead to the decline of local populations of species such as Dasypodidae or Cuniculus paca.

Plague surveillance in mammals and their fleas: An approach to explain the declining population of black-tailed prairie dogs (*Cynomys ludovicianus*) in Northwestern, Mexico

16:00 - Tuesday, 25th July, Solar Square

Andres Lopez-Perez, André V. Rubio, Rurik List, Jonathan López-Islas, Kenneth Gage, Gerardo Suzán

1. Universidad Nacional Autónoma de México, 2. Facultad de Ciencias, Universidad de Chile, 3. Universidad Autónoma Metropolitana Unidad Lerma, 4. Centers for Disease Control and Prevention

Over the last two decades the occupied active area of black tailed prairie dog in Mexico decreased more than 95%. Although black-tailed prairie dog conservation faces threats such as habitat loss and natural droughts, the decline of colonies could be a result of epizootic and enzootic plague. Plague, caused by *Yersinia pestis*, is a bacterial disease that in prairie dogs provokes mortality close to 100%. The aim of this research was to evaluate if plague epizootic events could explain the decline of prairie dog populations in Janos Biosphere Reserve, Chihuahua, Mexico. To answer this question, we collected data from four serological and molecular plague surveys in carnivores, rodents and their fleas. These surveys were conducted from 2007 to 2014 in the Janos Biosphere Reserve. Although the results were negative, when making a timeline and comparing prairie dog population dynamics with *Y. pestis* transmission cycles, we noticed that: 1) Studies on prairie dog demography report only data from 1988, 2000, 2005 and 2013 in the Reserve, therefore it is unknown the precise year of population decline; 2) The epidemiological surveys only were conducted during 2007, 2009, 2013 and 2014; 3) Enzootic cycles of plague can be detected by *Y. pestis* antibodies persistence in rodents and carnivores, about six to twelve months after exposure. In addition, the extrinsic incubation period for plague in fleas, including early transmission phase or transmission by blocked fleas, ranges from 1 to 31 days. Despite all results have been negative, plague epizootic events as a possible cause of the decrease of the prairie dog populations in northwestern Mexico are not discarded. For this reason, further studies are needed to understand the drivers of the decline of black-tailed prairie dog in Janos grasslands, including the development of systematic population survey programs as part of conservation strategies.

Genotypic identification of *Toxoplasma gondii* within bushmeat as a method to discover routes of parasite transmission into human populations and novel, potentially virulent protozoal strains

16:00 - Tuesday, 25th July, Solar Square

Emily Iacobucci, Heather Fritz, Viviana Pinedo-cancino, Robert Gilman, Robert O'connor, Massaro Ueti

1. Washington State University College of Veterinary Medicine, 2. University of California Davis School of Veterinary Medicine, 3. Universidad Nacional de la Amazonia Peruana, 4. Johns Hopkins Bloomberg School of Public Health, 5. Washington State University College of Veterinary Medicine, United States Department of Agriculture

Toxoplasma gondii is a protozoal parasite of worldwide distribution with a capacity to infect any warm-blooded animal. Throughout most of the world, infection only leads to disease among immuno-compromised animals, or pregnant females of select species, including humans. However, in the Amazon basin, atypical strains are much more common, and some capable of causing systemic illness in healthy humans have been identified. This study investigated wildlife meat as a potential route of *Toxoplasma* transmission from rainforest wildlife into human populations, both local and tourist. Peccary bushmeat (Collared Peccary, *Pecari tajacu*, and White lipped peccary, *Tayassu pecari*) was purchased from the large, famous, open market, Belén, in Iquitos, Peru. These cured skeletal muscle samples were screened for the presence of *Toxoplasma gondii* DNA via nested PCR targeting the B1 gene. *Toxoplasma* DNA was present in 8.3% (N=24) of samples. Sequencing of the amplified B1 segment revealed all positive PCR products contained a polymorphism consistent with a Type 1 or an atypical lineage, both of which are often associated with higher virulence in humans. To our knowledge, this is the first report of the use of PCR to directly examine new world bushmeat for *Toxoplasma* DNA at the point of sale before human consumption. This method, in addition to full genotypic characterization with 12 loci, represents a potential method of surveillance for novel, virulent strains of *Toxoplasma gondii*. Applied to other infectious zoonotic diseases, it can also serve as a screening tool to identify socially and geographically important locations where wild disease strains enter diverse human populations.

Identification of blood meal sources in sandflies (Diptera: Psychodidae: Phlebotominae) from San Andres Tuxtla, Veracruz, Mexico

16:00 - Tuesday, 25th July, Solar Square

Eduardo Jiménez-Girón, Yokomi Lozano-Sardaneta, Sokani Sánchez Montes, Estefania Grostieta, Pablo Colunga-Salas, Ingeborg Becker-Fauser

1. Centro de Medicina Tropical, Facultad de Medicina, Universidad Nacional Autónoma de México

Introduction: Sandflies of *Lutzomyia* genus encompass more than 400 species of small insects restricted to tropical and subtropical regions of America. Females require vertebrate blood for egg maturation and around of 50% of *Lutzomyia* species seem to be anthropophilic. Some species of sandflies have been incriminated as vectors of important tropical diseases, such as Leishmaniasis and Carrions Disease. However, little is known on the feeding preferences of many species, as well as the frequency with which they bite humans and other hosts. These factors are relevant in the epidemiology of mosquito-borne diseases.

Objective: The aim of this study was to identify blood meal sources of *Lutzomyia* species collected in San Andres Tuxtla, Veracruz, Mexico.

Method: Mosquitoes were collected using light traps, in April and May 2016 from Veracruz, Mexico. All individuals were fixed in 70% ethanol and taxonomically identified using specialized keys. DNA extraction was performed individually using the Chelex-100 protocol. For blood meal source identification, we amplified fragments of the *cyt-B* gene using specific primers to birds and mammals.

Results: A total of 25 sandflies were collected (19 ♀ y 6 ♂) and identified as (*Brumptomyia mesai*), (*L. carpenteri*), (*L. cruciata*), (*L. olmeca*) and (*Lutzomyia* sp). Eight females were positive for avian DNA (32%), but any test positive for mammalian DNA.

Discussion/Conclusion: This is the first work that identifies blood meal sources for Mexican sandflies. Some species registered here have previously been reported as having anthropophilic (*i.e. Lutzomyia cruciata*) and zoophilic eating habits (*i.e. Lutzomyia olmeca*), which are related to transmission of Leishmaniasis in mammals. Our results show that these sandflies feed on birds in the localities studied. This finding could help to develop efficient vector management programs to prevent human transmission of sandfly-borne diseases in endemic areas.

Biotic, abiotic and spatial indicators as environmental health assessment tools in Rio Grande de Comitán watershed, Chiapas

16:00 - Tuesday, 25th July, Solar Square

Jannice Alvarado-Velázquez, Alejandra Elisa Hernández-Magaña, Omar García-Suárez, Marisa Mazari-Hiriart

1.Universidad Nacional Autonoma de Mexico

Human development has induced an accelerated change in land use and increased the potential sources of pollution. These changes have an effect on the environmental conditions by allowing different contaminant to be transported modifying the ecosystems, generating ideal conditions to allow pathogen persistence and dissemination in aquatic ecosystems. Biotic and abiotic indicators have been used as environmental health assessment tools and as an approximation to pathogen evaluation. The aim of this study was to use biotic, abiotic and spatial indicators to evaluate human impact on water quality in Rio Grande de Comitán watershed. In eight sites along the river microbiological indicators were measured, including: Fecal Coliform (FC), Fecal Enterococci (FE) and Coliphages (CP) and physicochemical indicators. Potential sources of pollution and land use were geo-referenced under sub-basin delimitation by SWAT (Soil and Water Assessment Tool) to use them as spatial indicators in ArcGIS 10.1. A spearman correlation was performed with microbiological indicators, physicochemical and spatial indicators. We obtained that the highest bacteria count (FC, FE, CP; 432000, 83000, 135000 CFU respectively) were registered in the sub-basin, where municipal wastewater is discharged. A high correlation was found between microbiological indicators and water turbidity ($r^2 > 0.5$), and CP and electric conductivity ($r^2 > 0.5$). The spatial indicators (grassland and erosion) were highly correlated with FC and CP ($r^2 > 0.5$). Our results suggest that wastewater discharge and land cover modification are the main human activities which have promoted changes in water quality and have driven microbiological indicators presence, with potential implications in environmental health and therefore with a human health impact. This study represents part of the first effort towards an integral evaluation of Rio Grande watershed, incorporating several approaches to assess the human activities and their impact in aquatic ecosystems, which has an important concern on environmental health.

Molecular detection of several pathogens and endosymbionts associated with ectoparasites and small mammals in Hidalgo, Mexico

16:00 - Tuesday, 25th July, Solar Square

Mario Mata-Galindo, Diana Melissa Navarrete-Sotelo, Kevin Harnández-Vilchis, Sokani Sánchez Montes, Ali Lira-Olguin Martín Cabrera-Garrido César Ríos-Muñoz, Roxana Acosta, Pablo Colunga-Salas, Yokomi Lozano-Sardaneta, Livia León-Paniagua, Ingeborg Becker-Fauser

1. Centro de Medicina Tropical, Facultad de Medicina, Universidad Nacional Autónoma de México, 2. Laboratorio de Acarología, Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México, 3. Museo de Zoología “Alfonso L. Herrera”, Departamento de Biología Evolutiva, Facultad de Ciencias, 4. Laboratorio de Arqueozoología, Instituto Nacional de Antropología e Historia

Introduction: Ticks, fleas and sucking lice are important vectors of multiple pathogens causing several emerging infectious diseases worldwide, such as Rocky Mountain spotted fever and trench fever. However, this group of ectoparasites has been little studied in other vectors, such as mosquitoes. These hematophagous arthropods are common hosts for a wide range of largely understudied pathogens, especially several species of bacteria (e.g. *Bartonella*, *Ehrlichia*, *Rickettsia*), which can occur in co-infections and generate very severe outbreaks in human populations at risk.

Objective: The aim of this study was to identify the presence and prevalence of *Francisella*, *Anaplasma*, *Ehrlichia*, *Bartonella*, *Rickettsia* and *Wolbachia* species in ectoparasites and small mammals of Hidalgo, Mexico, with previous reports of human cases of murine typhus.

Methods: During a field trip in 2014, we collected 47 fleas and 172 sucking lice belong to six species, associated with 42 rodents of four species (*Mus musculus*), (*Peromyscus beatae*), (*Rattus norvegicus*), (*Reithrodontomys sumichrasti*) and one shrew (*Sorex orizabae*). Liver samples of hosts and ectoparasites were fixed in absolute ethanol and examined to identify the presence of selected pathogens and endosymbionts by the amplification of several fragments of the *16S-rRNA*, *gltA*, *ompB* and *wsp* genes.

Results: Only *P. beatae* and *R. norvegicus* tested positive for at least one pathogen: 11 were positive for *Anaplasma/Ehrlichia* DNA; 4 for *Bartonella* and *Francisella* and one for *Rickettsia*. In 23 specimens of two flea species tested positive for *Bartonella* and 9 for *Wolbachia*. No evidence of any pathogen or endosymbiont was detected in analyzed lice.

Discussion/Conclusion: Our findings represent the first record of several confirmed zoonotic pathogens that can cause tularemia and endocarditis in Mexico, which highlight the importance of the establishment of active entomological surveillance in wildlife.

Macroecological approach to estimate the susceptibility of birds to West Nile Virus

16:00 - Tuesday, 25th July, Solar Square

María José Tolsá-García, Gabriel E García Peña, Gerardo Suzán

1. Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México), 2. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 3. Universidad Nacional Autónoma de México)

Macroecological approaches in infectious diseases make it possible to understand patterns at local and regional scales. West Nile Virus (WNV) has negatively impacted the health and conservation of birds, and little is known about their susceptibility. Laboratory studies are concentrated in a few species, whereas field studies consider a greater diversity of species but with less detail. Thus, our objective was to investigate if it is possible to estimate epidemiological parameters obtained experimentally as reservoir competence (ability to transmit a pathogen) through field observations. We conducted a global review of studies looking for WNV in wild birds. We consider: serological prevalence (SP), molecular prevalence (MP) and death (M) as dependent variables; and the phylogeny and biogeographical origin of birds, viral genotype, space-time and sample size as independent variables. We reviewed 125 bibliographic sources, representing 34 countries and 852 species, 67.2% of birds were considered susceptible. The highest values recorded were for PS the Rock Dove (*Columba livia*), PM the Yellow-billed Magpie (*Pica nutalli*) and for M the American crow (*Corvus brachyrhynchos*). Bayesian approximations showed that sample size and time-space are important in the variability for our dependent variables. A Spearman correlation showed that PM and M are good predictors of reservoir competence. Our methodology is a highly generic approach, applicable to other diseases. We generated the first list of birds susceptible to WNV worldwide, we identified highly susceptible species such as Red-tailed hawk (*Buteo jamaicensis*) and the American White pelican (*Pelecanus erythrorhynchos*). Macroecological studies allow the identification of susceptible species and important factors for the transmission of pathogens that are not commonly considered and which are necessary to prevent infectious diseases that affect the conservation of wildlife and public health.

Hemorrhagic Disease in Florida White-tailed Deer (*Odocoileus virginianus*): A Comparison of Farmed and Wild Deer

16:00 - Tuesday, 25th July, Solar Square

Allison Cauvin, Carisa Boyce, Katherine Sayler, Samantha Wisely

1. University of Florida

Hemorrhagic disease is a common disease in white-tailed deer in the southeastern U.S. It is caused by two orbiviruses with multiple serotypes: epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV). In order to understand temporal variability in serotype prevalence, and how host density affects hemorrhagic disease prevalence, we collected blood and sera from white-tailed deer at two different densities: farmed deer at high-density and wild deer at low-density. Specimens were collected during the springs of 2016 and 2017 and were assessed via serum neutralization assays to determine exposure to EHDV and BTV. In 2016, there was an overall 89% (59/66) seroprevalence for EHDV across sampling locations, with EHDV-1 being the most prevalent serotype. In 2017, there was an observed reduction in seropositivity to EHDV-1 and -6 compared to the previous year. Preliminary data suggests that EHDV-2 prevalence was the predominant spring serotype among sampling locations in 2017. In addition, farmed animals displayed higher seroprevalence than wild cervids during the 2016 season. Farmed cervids exhibited a 98% seropositivity rate for any EHDV serotype, while 57% of wild cervids were seropositive. Analyses are currently ongoing for the 2017 season. These results imply that deer kept at artificially high densities may be more prone to EHDV exposure. Understanding when and where these viruses circulate and which factors influence prevalence can lead to more informed management practices in the cervid farming industry. Producers should consider reducing density on deer farms and implementing targeted pest management.

Species co-occurrence platform for infectious diseases in conservation biology. The case of WNV in birds from USA

16:00 - Tuesday, 25th July, Solar Square

María José Tolsá-García, Constantino González-Salazar, Jesús Sotomayor-Bonilla, Gabriel E García Peña, Gerardo Suzán, Christopher Stephens

1. Universidad Nacional Autónoma de México, 2. Centro de Ciencias de la Complejidad, Universidad Nacional Autónoma de México, 3. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 4. C3 – Centro de Ciencias de la Complejidad, Universidad Nacional Autónoma de México

Geographic co-occurrence between hosts and pathogens has been used as a strategy to predict the ecological niche of some multi-host and multi-vector pathogens. West Nile Virus (WNV) is a vector-borne disease that has been associated with the death of millions of birds in the United States and has been recognized as a threat to their conservation. The aim of our study was to evaluate if the co-occurrence between host birds and mosquito vectors is related to bird mortality by WNV infection in the United States. We collected records of dead birds associated with WNV infection and positive mosquitoes in field studies conducted in the United States. We estimated the co-occurrence (epsilon) between the presence of bird mortality and the presence of positive mosquitoes and finally we correlated our epsilon values with the presence of bird mortality. We recorded 330 bird species and 56 mosquitoes species. We found a high association between bird mortality and the presence of *Culex* ($r=0.74$), *Anopheles* ($r=0.72$) and *Culiseta* ($r=0.70$) genera. The bird species with the highest value of epsilon was the Northwestern crow (*Corvus caurinus*). Our results suggest that these mosquito genera are associated with virulent strains or are highly efficient in the transmission the virus to host birds. Using the presence of mosquitoes species, it is possible to propose strategies for the conservation of threatened bird species such the Florida Scrub-Jay (*Aphelocoma coerulescens*) and Hawaiian Crow (*Corvus hawaiiensis*).

Pathogen prevalence in American black bears (*Ursus americanus*) in areas of shared habitat use with feral hogs in southeastern Oklahoma

16:00 - Tuesday, 25th July, Solar Square

Erica Perez, Sue Fairbanks

1. Oklahoma State University

Black bears have successfully recolonized southeastern Oklahoma after their complete extirpation from the state in the early 20th century. Portions of this region include highly fragmented habitat with varying densities of feral hog populations. These two sympatric species are likely to encounter each other in areas of shared habitat use, particularly at anthropogenic food sources, increasing the likelihood for cross-species disease transmission. My objective is to assess black bear seroprevalence of certain pathogens most closely associated with feral hog populations in Oklahoma. Black bears are hunted in four southeastern counties, underscoring the importance of understanding infection rates and zoonotic risk to people within the region. From May-August 2016, blood samples from 47 black bears in four southeastern counties were collected. Rose-Bengal and agglutination tests were performed on all serum samples to detect the presence of antibodies for *Brucella* spp. and *Franciscella tularensis* respectively. Of the total samples, 6.3% tested positive for *Brucella* spp. and 4.2% tested positive for Tularemia. None of the samples were seropositive for Porcine reproductive and respiratory syndrome virus, Pseudorabies virus, and *Trypanosoma cruzi*. Preliminary analysis suggests that males are more likely to test positive as they accounted for 80% of seropositive results. These results help provide baseline data for multi-species disease transmission in Oklahoma in order to more effectively apply management plans to mitigate disease outbreaks in both wildlife and domestic animal populations. Sample collection and testing will continue in the 2017 summer field season.

Retrospective pathology survey of superorder Xenarthra from São Paulo, Brazil (1994-2017): preliminary results

16:00 - Tuesday, 25th July, Solar Square

Gislaine Taimara Dalazen, Pedro Enrique Navas-Suárez, Josué Díaz Delgado, José Luiz Catão-Dias, Eliana Reiko Matushima

1. University of Sao Paulo, 2. Laboratory of Wildlife Comparative Pathology, College of Veterinary Medicine and Animal Science of the University of São Paulo (LAPCOM/FMVZ/USP)

Restricted to the Neotropics, the superorder Xenarthra includes 13 genera and 31 species of sloths, anteaters and armadillos. In contrast to other mammalian species, knowledge on health and disease in Xenarthra members is limited and fragmented. We aimed to describe the preliminary gross and histopathological findings in Xenarthra cases archived in the tissue bank of the Laboratory of Wildlife Comparative Pathology at the University of São Paulo. Gross findings were retrieved from necropsy reports. Histological analysis was performed on 6 anteaters (*Tamandua tetradactyla* [n=3], *Myrmecophaga tridactyla* [n=3]), 14 three-toed sloths (*Bradypus variegatus* [n=5], *B. tridactylus* [n=4], and *Bradypus* sp. [n=5]) and 13 armadillos (*Dasypus novemcinctus* [n=12], *Cabassou unicinctus*[n=1]). In anteaters, the main gross findings were pulmonary edema and mitral endocardiosis, while pulmonary edema, congestion and hemorrhage were the main histopathological findings. Few cases had fibrinosuppurative bronchopneumonia and *Sarcocystis* sp. in the glossal musculature. In sloths, the main gross finding was multiorgan congestion, mainly involving animals with history of acute trauma. The main histological findings included: multiorgan congestion, multicentric lymphoid depletion, pulmonary edema and acute renal tubular degeneration. Pneumonia, hepatocellular necrosis, sepsis and massive alveolar hemorrhage were observed in few cases, and could have accounted for death in these animals. In armadillos, pulmonary edema was the most common gross finding. Histologically, severe lesions included massive hepatic necrosis, pulmonary hemorrhage, presumed systemic toxoplasmosis, sepsis and bacterial fibrinonecrotizing and ulcerative dermatitis, panniculitis, fasciitis and myositis. Incidental findings were intestinal coccidiosis and nematodiasis, and cutaneous acariasis. Despite the inherent limitations of retrospective pathology studies, a cautious interpretation may reveal a variegated spectrum of lesions that aid in future research design and widen baseline pathology knowledge on comparatively less studied species.

Retrospective Pathological Survey Of Two Neotropical Deer Species: Marsh Deer (*Blastocerus Dichotomus*) And Brown Brocket Deer (*Mazama Gouazubira*), Brazil (1995-2015)

16:00 - Tuesday, 25th July, Solar Square

Pedro Enrique Navas-Suárez, Josué Díaz Delgado, Adriana Marques Joppert, Mauricio Barbanti Duarte, Cintia M. Favero, Carlos Sacristán, Angelica Maria Sánchez Sarmiento, Eliana Reiko Matushima, José Luiz Catão-Dias

1. University of Sao Paulo, 2. Laboratory of Wildlife Comparative Pathology, College of Veterinary Medicine and Animal Science of the University of São Paulo (LAPCOM/FMVZ/USP), 3. DEPAVE, 4. São Paulo State University, 5. Laboratório de Patologia Comparada de Animais Selvagens, Departamento de Patologia, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, SP.

Neotropical deer have important functions for the sustainability and health of their ecosystem, and play an important role in the transmission and spread of infectious agents, some of them relevant to livestock, companion animals and with potential implications in public health. The present study describes the gross and histological findings and most probable causes of death (CD) in brown brocket deer (*Mazama gouazoubira*; BBD, n= 131) and marsh deer (*Blastocerus dichotomus*; MD, n= 75) from São Paulo state, Brazil, collected from 1995 through 2015. For both species combined, main gross findings were: pulmonary edema (55.6%; 89/160) and congestion (45%; 72/160); congestion (29.4%; 47/160) of the alimentary system; skin lacerations (28.8%; 46/160); inflammation in the alimentary (28.1%; 45/160) and urogenital (26.9%; 43/160) systems; pneumonia (22.5%; 36/160); bone fractures (22.5%; 36/160); and ectoparasitosis (21.3%; 42/160). Main histopathological findings were: pulmonary congestion (81.8%; 135/165); renal congestion (70.1%; 108/154); pulmonary edema (63.6%; 105/165); pneumonia (60.6%; 100/165); hepatic lipidosis (50.3%; 76/151); hepatitis (43.7%; 66/151); splenic lymphoid depletion (37%; 47/127); pulmonary hemorrhage (29.1%; 48/165); hepatic hemorrhage (28.5%; 43/151), and acute renal tubular degeneration (27.9%; 43/154). Main CD in MD were: respiratory (53.3% 40/75); alimentary (4.0%; 3/75); nutritional (4.0%; 3/75); trauma (4.0%; 3/75); and euthanasia (4.0%; 3/75). In BBD, the main CD were: respiratory (25.2% 33/131); euthanasia (12.2%; 16/131); and trauma (9.2%; 12/131). Additionally, unusual or novel pathological processes observed included: fungal myocarditis (1BBD); fungal rumenitis (1MD ovarian dysgerminoma (1BBD); pancreatic trematodiasis compatible with *Eurytrema* sp., and 7BBD cases had lesions suggestive of orbiviral hemorrhagic disease. Our results highlight the importance of the respiratory disturbances in these two species of Brazilian deer. This study establishes baseline pathology and contributes to health monitoring of these two Brazilian cervid species and provides scientific basis for future conservation policies

Vehicle-Collision Of Wild Mammals In Brazil: An Opportunity To Develop Health Studies

16:00 - Tuesday, 25th July, Solar Square

Pedro Enrique Navas-Suárez, Luciana Neves Torres, Adriana Marques Joppert, Eliana Reiko Matushima, José Luiz Catão-Dias

1. University of Sao Paulo, 2. DEPAVE

It is speculated that around 475 million of wild animals die by vehicle-collision (VC) on Brazilian roads per year. Theories associate VC with the presence of disease, however, in the Brazilian context this fact is still unknown. Many of these cases are not referred to pathological diagnosis due to factors such as advanced autolysis, long distances to laboratories and environmental conditions. Seeking to identify health status of wild mammals killed by VC, specimens received by our laboratory with history of VC from 1995 to 2015, were selected for examination. Additionally, we made a systematic review aimed to identify the main mammal taxa reported in Brazilian scientific literature. A total of 40 cases from our lab were analyzed, and most common taxonomic orders were: Artiodactyla (52.5%; 21/40), Rodentia (17.5%; 7/40) and Carnivora (15%; 6/40). Major gross findings included: skeletal fractures (67.5%; 27/40), ectoparasites (52.5%; 21/40), skin lacerations (40%; 16/40), soft tissue hematomas (32.5%; 13/40), pulmonary edema (32.5%; 13/40) and gastrointestinal tract/liver rupture (27.5%; 11/40). Major histopathological findings included pneumonia (65.0%; 13/22), hepatic vacuolar degeneration (54.5%; 12/22), pulmonary edema (50%; 11/22) and splenic white pulp depletion (50%; 11/22). Twenty-one cases were adults in good body condition, and this could be interpreted as a loss of reproductive viable and apparently healthy individuals, generating a possible population impact in terms of birth rate. For the systematic review 75 articles were selected counting 13,158 specimens belonging to 10 orders {e.g. Carnivora (4717; 35.8%), Didelphimorphia (3171; 24.1%), Cingulata (2024; 15.4%)}. Most reported species were crab-eating fox (*Cerdocyon thous*) (1550), and white-eared opossum (*Didelphis albiventris*) (1486). Four-hundred-sixty-seven records involved threatened species {giant anteater (*Myrmecophaga tridactyla*) – 333; ocelot (*Leopardus pardalis*) – 48}. Due to the high casuistic of wildlife-VC in Brazil, these samples are valuable tools to obtain data about health status of free ranging populations.

Epidemiology of *Trypanosoma cruzi* in Urban Dwelling Opossum (*Didelphis virginiana*) and Feral Cat (*Felis catus*) Populations of the Rio Grande Valley, TX

16:00 - Tuesday, 25th July, Solar Square

Italo Zecca, Lisa Auckland, Carolyn Hodo, Sarah Hamer

1. Texas A&M University

Trypanosoma cruzi is a zoonotic protozoan parasite spread by triatomine vectors and maintained by diverse wildlife species across the Americas. Some infected hosts may develop Chagas disease, a potentially fatal cardiac disease of humans and dogs. Although urban-dwelling animals have high interaction with humans, little is known about their contributions to disease risk in the southern US. In the Rio Grande Valley (RGV) of Texas where triatomine vectors are endemic, we recently described locally-acquired infections in humans and their pet dogs, and hypothesized that urban wildlife and feral animals serve as infectious reservoirs that bridge sylvatic and domestic transmission cycles. In 2017, we sampled urban-dwelling opossums (*Didelphis virginiana*) and feral cats (*Felis catus*) in the RGV. After euthanasia performed by animal control for reasons unrelated to our study, whole blood, hearts, and other tissues were collected. Through serological testing of 167 cats using immunochromatographic and indirect fluorescent antibody testing, 13.2% of cats were antibody-positive on at least two tests. Samples were subjected to qPCR for parasite detection and discrete typing unit (DTU) determination. Three cats (1.8%) tested positive for parasite DNA in various tissues including biceps femoris muscle, sciatic nerve, cardiac muscle, and/or esophagus. Seven of 100 opossums (7.0%) had infected blood, and *T. cruzi* DNA was also found in cardiac tissue, intercostal muscle, anal gland tissue, and/or anal gland secretions from a small number of opossums. Despite both parasite DTUs TcI and TcIV being found in triatomine vectors in the region, the infected cats and opossums that were typed in this study were exclusively TcI- the DTU previously associated with human disease in the US. Our data implicate feral cats and opossums as wild reservoirs in an urban focus with ongoing autochthonous human and canine disease; these species must be considered in public health interventions.

New insights on the presence of herpesvirus and poxvirus in South American cetaceans

16:00 - Tuesday, 25th July, Solar Square

Carlos Sacristán, Fernando Esperon, Carol Ewbank, Josué Díaz Delgado, Eduardo Ferreira Machado, Samira Costa-Silva, Angelica Maria Sánchez Sarmiento, Kátia R. Groch, Gustavo Henrique Pereira Dutra, Waleska Gravena, Vera Da Silva, Marta J. Cremer, Vitor L. Carvalho, Ana C.O. Meirelles, Elitieri B. Santos-neto, Alexandre Azevedo, José Jr. Lailson-brito, Pedro V. De Castilho, Fábio Gonçalves Daura-jorge, Paulo César Simões-Lopes, Juliana Marigo, José Luiz Catão-Dias

1. Laboratory of Wildlife Comparative Pathology (LAPCOM) – Pathology Department – School of Veterinary Medicine and Animal Science – FMVZ. University of São Paulo, São Paulo, SP, Brazil, 2. Centro de Investigación en Sanidad Animal (INIA-CISA), 3. Aquário Municipal de Santos. Santos, SP, Brazil. 4. Instituto Nacional de Pesquisas da Amazônia – INPA. Manaus, AM, Brazil. 5. Universidade da Região de Joinville – UNIVILLE. São Francisco do Sul, SC, Brazil. 6. Associação de Pesquisa e Preservação de Ecossistemas Aquáticos - AQUASIS, Caucaia, CE, Brazil. 7. Laboratório de Mamíferos Aquáticos e Bioindicadores “Profa Izabel M. G. do N. Gurgel” (MAQUA), Faculdade De Oceanografia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil, 8. Universidade do Estado de Santa Catarina, Departamento de Engenharia de Pesca, Laguna, SC, Brazil, 9. Universidade Federal de Santa Catarina, Florianópolis, SC, Brazil, 10. Laboratory of Wildlife Comparative Pathology (LAPCOM), College of Veterinary Medicine and Animal Science of the University of São Paulo (FMVZ/USP)

Despite being reported worldwide, the occurrence of cetacean herpesvirus (CeHV) and poxvirus (CePV) in southern Atlantic marine mammals is poorly understood. In cetaceans, herpesviruses are frequently associated with skin and mucosal lesions, whereas poxviruses are mainly associated with classic “tattoo” or “ring” skin lesions. We evaluated cutaneous and oral and genital mucosal samples from 70 free-ranging cetaceans from Brazil, belonging to five families (Delphinidae (n=38), Pontoporiidae (n=27), Iniidae (n=3), Kogiidae (n=1), Balaenopteridae (n=1)). Samples were screened by a pan-HV nested PCR and conventional CePV PCR. PCR-positive specimens were subjected to histological analysis. We identified herpesviruses and poxvirus in 4.3% (3/70) and 2.9% (2/70) of the animals, respectively. Two Alphaherpesvirus sequences were identified in the tongue of a *Stenella* sp. and ulcerated skin of a dwarf sperm whale (*Kogia sima*). Another sequence more closely related to Gammaherpesvirus was identified in a proliferative cutaneous lesion of a Bolivian river dolphin (*Inia boliviensis*). Poxviruses were identified in “tattoo” skin lesions of a common bottlenose dolphin (*Tursiops truncatus*) and a Guiana dolphin (*Sotalia guianensis*). We also identified specific amino acid motifs for all CePV, reinforcing the suggestion of a new genus. Microscopic findings in HV-positive animals consisted of multifocal, chronic ulcerative and fibrino-suppurative dermatitis and panniculitis (*K. sima*), and marked, focally extensive, chronic proliferative dermatitis (*I. boliviensis*), while CePV-positive animals (*S. guianensis* and *T. truncatus*) presented epidermal keratinocyte ballooning degeneration and occasionally small, pale eosinophilic or amphophilic intracytoplasmic inclusions,

compatible with CePV. Autolysis precluded histological evaluation of *Stenella* sp. samples. We report the first molecular identification of HV in South American cetaceans and in riverine dolphins worldwide. This study also describes the first amplification of CePV in odontocetes from South America. Two of the three novel herpesvirus sequences herein identified are possibly novel species, tentatively named *Kogiid herpesvirus-2* and *Iniid herpesvirus-1*.

Sarcocystis Sp. Associated Polymyositis In Stranded California Sea Lions (*Zalophus Californianus*)

16:00 - Tuesday, 25th July, Solar Square

Mauricio Seguel, Kathleen Colegrove, Cara Field, Elizabeth Howerth, Pdraig Duignan

1.University of Georgia, 2.University of Illinois, 3.The Marine Mammal Center

Protozoal infections are a significant cause of morbidity and mortality among marine mammals, however, little is known regarding the role of *Sarcocystis neurona* and other related protozoan species as cause of disease in California sea lions (*Zalophus californianus*). In order to characterize the spectrum of lesions caused by *Sarcocystis sp.* protozoans in California sea lions we retrospectively investigated cases with confirmed *Sarcocystis sp.* infection at the Marine Mammal Center, Sausalito, California. A total of 133 cases with diagnosis of *Sarcocystis sp.* infection through histopathology and/or ancillary testing (serology, PCR, immunohistochemistry) were assessed. In all these cases the most significant lesion associated with protozoan infection was myositis, which varied in severity from minimal to severe. In 96 sea lions protozoan myositis was considered minimal or mild, and therefore incidental. In 42 cases protozoan myositis was considered a major factor contributing to the animal death. In 27 of these cases, sea lions also presented major co-morbidities such as leptospirosis and domoic acid toxicosis, however in the remaining 15 animals severe polyphasic polymyositis was the only process that explained the animal death. These animals had multiple white streaks in the diaphragm, tongue, masseter, longissimus cervicis, intercostal and pectoral muscles. Microscopically, these areas corresponded to coagulative necrosis surrounded by neutrophils, eosinophils, macrophages and numerous CD3 positive (T-cell) lymphocytes. In some of these foci there were rare 2-3 um zoites and occasional immature protozoan cysts that had moderate immunolabeling with anti-*S. neurona* antibody. *S. neurona* antibody titers were higher in animals with severe myonecrosis when compared to animals with mild necrosis (Mann-Whitney test, p-value=0.011). In at least 10 cases with significant polymyositis the protozoan species in the skeletal muscle was molecularly identified as *Sarcocystis neurona*, however in the remaining cases cross reactivity of serology and immunohistochemistry with closely related species remain a possibility.

Landscape effects on *Cryptosporidium parvum* and *Giardia lamblia* presence in rodent communities and water bodies, in Western Mexico

16:00 - Tuesday, 25th July, Solar Square

Omar García-Suárez, Marco Antonio Tapia-Palacios, Jesús Sotomayor-Bonilla, Julio José Barron-Rodríguez, Ana Cecilia Espinosa-García, Gerardo Suzán, Marisa Mazari-Hiriart

1. Universidad Nacional Autónoma de México

Changes in landscapes configuration due to human activities degrade habitat quality at different scales, modify rodents community structure and pathogen transmission dynamics. *Cryptosporidium parvum* (Cp) and *Giardia lamblia* (Gl) are reported in a wide range of hosts, and survive in the environment, concerning public health and conservation. The objective of this study was the evaluation of the landscape configuration at different scales as drivers of the presence of CP and GI in rodent communities and water bodies in the Tropical Dry Forest (TDF) from Western Mexico. This study was carried out in the Cuitzmala River basin, during three fieldwork seasons in 2014. Three monitoring locations were set along the river, and one control zone in the Chamela-Cuixmala Biosphere Reserve. Each location had three sites to capture rodents in a habitat type gradient (forested, transformed and human settlements) and one site for water monitoring in the riverbed. Immunofluorescence microscopy was used to identify both parasites in rodent feces and water samples. Landscapes metrics were estimated for each site at various scales using GIS. A total of 1051 rodents were captured, which 164 fecal samples and nine water samples were tested. Parasites presence in rodents is associated to local changes in land cover loss not for changes in communities structure, nevertheless Cp presence has relation with landscape metrics ($p=0.005$, $R^2=0.135$). Both parasites in water samples were detected (23% Cp and 33% Gl), in low concentrations (four and eight oo/cyst/L respectively). Results suggest that human activities facilitate changes in the structure of rodents communities and the presence of both parasites in these. But TDF have mechanisms to difficult the presence in water bodies. This is a new approach in the study of both pathogens in TDF nevertheless more studies are necessary to understand complex epidemiology and what factors facilitate their dispersion.

Botulism in wintering dabbling ducks in Mexico

16:00 - Tuesday, 25th July, Solar Square

Marcela Areli Araiza Ortiz, Gerardo Suzán, Luis Zambrano

1. Universidad Nacional Autónoma de México

Avian botulism is the most important cause of mortality in dabbling ducks. Birds are intoxicated after they ingest the toxin produced for the bacteria *Clostridium botulinum*. Outbreaks have been associated with eutrophic conditions in anoxic environments. Unlike other places, where outbreaks occur mainly after the reproductive season, and stopover places, in the state of Guanajuato, México, outbreaks occurs often during the migratory season. The objective of this study was to identify factors that lead appropriate environment for toxin production and evaluate the diet of dabbling ducks as a potential risk to ingest the toxin, to suggest management strategies. The study was carried out in five reservoirs, Silva, Coyote, Purísima, Trancas and Yuriria. In order to evaluate the diet of ducks we used the stomach and esophagus content and stable isotopes of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$. Values of $\delta^{15}\text{N}$ of primary consumers were used also to identify the source of input of nutrients to the systems that can lead to eutrophic conditions. There was a significant positive relationship between values of $\delta^{15}\text{N}$ of primary consumers (zooplankton) and the percentage of agriculture present in 5 km around the reservoirs. Presa de Silva and Presa del Coyote, which have annual outbreaks, had higher values of $\delta^{15}\text{N}$ in zooplankton, which were coincident with the input of wastewater and agriculture fertilizer to aquatic systems. Stomach content and values of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ indicate that ducks in four reservoirs but Coyote, feed mainly upon macrophytes seeds. In Coyote, ducks feed mainly upon aquatic invertebrates, which is also showed by the higher values of $\delta^{15}\text{N}$ in muscles of ducks. We suggest that diet of ducks in Silva and Coyote may represent a risk to ingest the toxin. Anthropogenic activities surrounded the reservoirs make that each year Silva and Coyote have the appropriate conditions for toxin production.

Global patterns in coronavirus diversity

08:48 - Thursday, 27th July, Solar Square

Simon Anthony, Christine Johnson, Denise Greig, Sarah Kramer, Xiaoyu Che, Heather Wells, Alison Hicks, Damien Joly, Nathan Wolfe, Peter Daszak, William Karesh, W. Ian Lipkin, Steve Morse, Predict Consortium, Jonna Mazet, Tracey Goldstein

1. Center for Infection and Immunity, Columbia University, 2. University of California Davis School of Veterinary Medicine, 3. Metabiota, 4. EcoHealth Alliance, 5. Columbia University, 6. <http://www.vetmed.ucdavis.edu/ohi/predict/publications/Authorship.cfm>

Since the emergence of SARS-CoV and MERS-CoV it has become increasingly clear that bats are important reservoirs of CoVs. Despite this, only 16% of all CoV sequences in Genbank are from bats. The remaining 84% largely consist of known pathogens of public health or agricultural significance, indicating that current research effort is heavily biased towards describing known diseases rather than the 'pre-emergent' diversity in bats. Our study addresses this critical gap, and focuses on resource poor countries where the risk of zoonotic emergence is believed to be highest. We surveyed the diversity of CoVs in multiple host taxa from 20 countries to explore the factors driving viral diversity at a global scale. We identified sequences representing 100 discrete phylogenetic clusters, 91 of which were found in bats, and used ecological and epidemiologic analyses to show that patterns of CoV diversity correlate with those of bat diversity. This cements bats as the major evolutionary reservoirs and ecological drivers of CoV diversity. Co-phylogenetic reconciliation analysis was also used to show that host switching has contributed to CoV evolution, and a preliminary analysis suggests that regional variation exists in the dynamics of this process. Overall our study represents a model for exploring global viral diversity and advances our fundamental understanding of CoV biodiversity and the potential risk factors associated with zoonotic emergence.

Wildlife as a reservoir of rabies: could it happen in Australia?

08:48 - Thursday, 27th July, Solar Square

Michael Ward, Vanessa Gabriele-Rivet, Simon Johnstone-robertson Stephen Davis, Peter Fleming

1. The University of Sydney, 2. Royal Melbourne Institute of Technology, 3. NSW Department of Primary Industries

Australia is historically-free of canine rabies. However, rabies is present in Indonesia and the recent spread of this disease to some eastern islands poses an increased threat of an incursion in northern Australia. Canines in this remote region of Australia can be found in communities (mostly indigenous communities, where dogs are free-roaming) and in the wild (dingoes and their hybrids, and feral domestic dogs). An incursion of rabies directly into wild dog populations, or spillover of rabies via an incursion into domestic community dogs, would be challenging to control: the area is vast, the density of wild dogs is low, and infrastructure is not well-developed. To better plan for such an incursion, field data collection and disease spread modelling has been initiated. In one region – the Northern Peninsular Area of Cape York – the distribution of wild dogs is being described using strategic deployment of camera-traps activated by heat-in-motion in both wildlife areas and at focal sites where wild-domestic dog interactions are expected to occur, DNA analysis of scats collected near camera traps, and via surveys of local hunters. A stochastic transmission network (percolation) model of rabies spread in wild dog populations in this region has recently been developed. For the first time, model outputs have provided a foundation for disease response planning and surveillance. For example, if rabies were introduced we estimated about a 20% chance that it would become established in wild dog populations, with a rate of spread of about 67 km/year. But more importantly a global sensitivity analysis demonstrates that parameters governing dog movements and behaviour, of which there is a paucity of knowledge, explained most of the variance in model outcomes. These insights are guiding further field data collection to improve preparedness for a rabies incursion.

Pathogen-mediated selection in free-ranging elk populations infected by chronic wasting disease

08:48 - Thursday, 27th July, Solar Square

Ryan Monello, Nathan Galloway, Jenny Powers, Sally Madsen-bouterse, William Edwards, Mary Wood, Katherine O'rourke, Margaret Wild

1. National Park Service, 2. Washington State University, 3. Wyoming Game and Fish Department, 4. United States Department of Agriculture, Agriculture Research Service

Pathogens can exert a large influence on the evolution of hosts via selection for alleles or genotypes that moderate pathogen virulence. Genetic linkages, discordant interactions between parasites and the host genome, and environmental stochasticity have largely prevented observation of this process in wildlife species. We examined the prion protein gene (*PRNP*) in elk populations that have been infected with chronic wasting disease (CWD), a contagious, fatal prion disease, and compared allele frequency to populations with no history of exposure to CWD. The *PRNP* in elk is highly conserved and a single polymorphism at codon 132 can markedly extend CWD latency when the minor leucine (L) allele is present. We determined population exposure to CWD, genotyped 1018 elk from five populations, and developed a hierarchical Bayesian model to examine the relationship between CWD prevalence and *PRNP* 132L allele frequency. The predicted probability that the correlation between disease prevalence and minor allele frequency was > 0 was 0.99. Populations infected with CWD for 30-50 years exhibited L allele frequencies that were on average twice as great (range = 0.23 to 0.29) than those from uninfected populations (range = 0.04 to 0.17). Despite numerous differences between the elk populations in this study, the consistency of increase in L allele frequency suggests pathogen-mediated selection has occurred due to CWD. Although prior modeling work predicted that selection will continue, allele frequencies in uninfected populations and the potential for new prion protein strains to arise suggest that it is prudent to assume balancing selection may prevent fixation of the L allele in populations with CWD.

Niche modelling studies on Hendra virus spillover ecology

08:48 - Thursday, 27th July, Solar Square

Gerardo Martin, Carlos Yanez-arenas, Raina K. Plowright, Carla C.M. Chen, Lee F. Skerratt

1. James Cook University, 2. Universidad Nacional Autónoma de México, 3. Montana State University,
4. Australian Institute of Marine Science

Hendra virus (HeV) is a Paramyxovirus: *Henipavirus* of Australian Pteropid bats (*Pteropus sp.*) that was discovered in 1994 during an outbreak of a respiratory and neurological disease in 20 horses and one human in Hendra, Brisbane, AU. Given its seemingly high case fatality rate (50-75%), it was classified as a BSL4 pathogen making research expensive and often infeasible. In addition, the nomadic nature and very large foraging ranges of Pteropid bats makes observational studies of infection levels extremely complicated. In sight of these limitations we used ecological niche models to study pending aspects of HeV spillover ecology and epidemiology. To try and identify which of the four bat species are more likely to transmit the virus to horses, identify climatic correlates of the seasonal pattern and identify areas at risk of spillover, we used theories and methods commonly used in ecological niche modelling. We began modelling the niches of the four bat species found with antibodies against HeV and related their abundance to their niche centroids. With these analyses we found that two species *P. alecto* and *P. conspicillatus*, were more likely responsible for spillover. Then by analysing the climatic characteristics of the recorded month of transmission to horses we found that minimum temperature and rainfall seasonal amplitudes are candidates to influence the spatiotemporal pattern of spillover. In addition the biological mechanism could be driven by the effects these two variables have on each reservoir hosts. Finally, in the face of climate change we found that *P. alecto* is likely to replace *P. conspicillatus* as a reservoir host in its distribution. Climate change could also increase the horse population at risk by 175-260% according to horse population densities of 2007.

Caracterización de metacomunidades virales asociadas a quirópteros y roedores en diferentes bioregiones

10:30 - Thursday, 27th July, Solar Square

Fabiola Nieto Rabiela, Daniel Mendizabal, Maribel López Santana, Oscar Rico

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. Universidad de Guadalajara

Identificar los mecanismos que modulan la diversidad de simbioses asociados a fauna silvestre es fundamental para un mejor entendimiento de los factores que modulan los ensamblajes de sistemas multi-hospederos multi-patógenos. Los pequeños mamíferos representan un sistema ideal para explorar las estructuras de ensamblaje viral asociado a sus hospederos. El objetivo del presente trabajo fue analizar la contribución de factores filogenéticos y funcionales al ensamblaje y estructura de metacomunidades virales asociadas a roedores y murciélagos. Se realizó un meta análisis usando registros de virus reportados por métodos moleculares agrupándolos en diferentes regiones biogeográficas: Afrotropical, australiana, indonesia, neártica y paleártica. Para cada región se determinó la estructura de metacomunidad. Mediante una ordenación del análisis de redundancia se calculó la contribución de la filogenia, masa corporal, tamaño de camada, número de camadas por año y gremio trófico al ensamblaje de la metacomunidad para cada región. En roedores se detectó una tendencia hacia las estructuras clementsianas, indicando una distribución restringida de los virus a través de sus hospederos. Mientras que en murciélagos dominaron las estructuras azarosas. Los resultados indican que el ensamblaje de la diversidad viral asociada a roedores responde a características filogenéticas y funcionales, independientemente de la región biogeográfica. Debido a que la persistencia, distribución y prevalencia de las enfermedades infecciosas en fauna silvestre dependen de factores ecológicos y/o a la diversidad filogenética de sus hospederos dentro de un conjunto de comunidades, el análisis de metacomunidades de simbioses representa una herramienta integrativa para entender la ecología de enfermedades.

Primates And Sloths As Sentinels For Arboviruses In The Atlantic Forest, Bahia, Brazil

10:30 - Thursday, 27th July, Solar Square

Lilian Catenacci, Milene Ferreira, Livia Martins, Kristel De Vleeschouwer, Camila Cassano, Leonardo Oliveira, Gustavo Canale, Sharon Deem, Juan Tello, Elizabeth Travassos Da Rosa

1. Virology Graduate Program at the Evandro Chagas Institute, 2. (Evandro Chagas Institute), 3. (Royal Zoological Society of Antwerp), 4. (State University of Santa Cruz), 5. (State University of Rio de Janeiro), 6. (Federal University of Mato Grosso), 7. (Saint Louis Zoo Institute for Conservation Medicine), 8. (Center for Conservation and Sustainable Development, Missouri Botanical Garden)

Arboviruses are zoonotic and transmitted among vertebrate hosts by hematophagous vectors. Due to the emergence and re-emergence of various arbovirus infections in humans (e.g. dengue, chikungunya, Zika, West Nile, and yellow-fever virus) in Brazil, studies focused on identifying these viruses in vectors and hosts are an essential part of active surveillance. From 2006 through 2014, seroepidemiological surveys were conducted on non-human primates and sloths to investigate the possible circulation of arboviruses in Bahia Atlantic Forest, Brazil. A total of 196 samples were collected from *Leontopithecus chrysomelas*, *Sapajus xanthosternos*, *Bradypus torquatus* and *Bradypus variegatus*. Serum samples were tested using neutralization test and hemagglutination inhibition test to detect total antibodies against 26 different arboviruses. The overall prevalence of arboviruses was 36.1% (number of infected individuals = 51), with the genus *Flavivirus* having the highest prevalence (32.62%, n=46), followed by *Phlebovirus* (4.9%, n=7), *Orthobunyavirus* (4.2%, n=6) and *Alphavirus* (0.71%, n=1). Monotypic reactions and neutralization tests suggest the wild animals were exposed naturally to at least thirteen arboviruses. The animals were more likely to be exposed to *Ilhéus* (15.6%, n=22) with titers from 20 to 320, followed by *Dengue-2* (14.8%, n=20) with 20-40, *Dengue-1* (9.9%, n=14) with 20-40 and *Rocio* virus (7.1%, n=10) with 20-160. Most of the viruses were maintained in transmission cycles independent of human hosts, although antibodies against dengue virus were found in this study. The general low titer of antibodies and the absence of clinical signs in non-human primates and sloths highlight the necessity of long-term studies to evaluate the role of these species as accidental, bridge hosts or reservoirs of arboviruses, and possibility of viral isolation. Our results also highlight that the Southern Bahian Atlantic Forest has a variety of vertebrate hosts and transmission vectors, which may support the emergence or reemergence of arboviruses, including those pathogenic to humans.

Introduced alien North American Mink, Domestic Cats and dogs, and Native Endangered Southern river otter. All connected by infectious diseases in Patagonia

10:30 - Thursday, 27th July, Solar Square

Gonzalo Medina Vogel, Macarena Barros, Andrea Moreno, Fernando Dueñas, Juliana A Vianna, Barbara Ramos, Leonardo Sáenz, Lisette Lapierre, Camila Nuñez, Oscar Cabezon, Jitender Dubey, Sonia Almería, Maria Ribas, Luis Escobar

1. Universidad Andres Bello, 2. Pontificia Universidad Catolica de Chile, 3. Universidad de Chile, 4. Universidad Autónoma de Barcelona), 5. United States Department of Agriculture, 6. University of Minnesota

Domestic pets such as cats and dogs, together with introduced carnivores such as mink (*Mustela vison*) are generating important consequences in terms of diseases in native species. Blood samples were obtained for *Toxoplasma gondii*, *Leptospira* spp. CPV and CDV from 73 minks, 13 Southern river otters, 65 domestic cats and 82 domestic dogs in Chile (2009-2013). Pathogenic *Leptospira* were detected by PCR in 31/57 minks. One dog and two minks were confirmed positive to CPV by sequencing; which showed 100% identity in two minks with CPV, suggesting that CPV is transmitted between dogs and minks. Observed *T. gondii* seroprevalence in all samples were 58,9% in mink, 76,9% in otters, and 67,7% in cats. *T. gondii* DNA was detected in one mink and one otter. Our findings suggest a great pathogen pollution of aquatic environment in Patagonia. Mink has an important role in the environmental contamination with *Leptospira*, and also might have an important part in the ecology of Toxoplasmosis as minks live in aquatic environments and are important predators of rodents. Cats show no differences in Toxoplasmosis observed seroprevalences between different areas, which show that population density does not affect prevalence but population size does indeed affect prevalence in the other study species. Thus mink as a recognized rodent predator may magnify the disease by modifying the community of rodent species. Evidences of CPV, *Leptospira* and *T. gondii* infestation in mink, domestic cats and dogs are of concern for the conservation of endangered carnivores of the Patagonia.

Coronavirus Diversity In Bats From Neotropical-Nearctic Limits In Mexico

10:30 - Thursday, 27th July, Solar Square

Paola Martínez Duque, Simon Anthony, Rafael Ojeda Flores, Isamara Navarrete-Macias, Carlos Zambra-na-Torrelío, Gerardo Suzán

1. Departamento de Etología, Fauna Silvestre y Animales de Laboratorio, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, 2. EcoHealth Alliance; Center for Infection and Immunity, Mailman School of Public Health, Columbia University, 3. Center for Infection and Immunity, Mailman School of Public Health, Columbia University, 4. EcoHealth Alliance

In recent years knowledge about role played by bats in the maintenance and transmission of emerging infectious diseases has been increasing, elucidating that bats are reservoir hosts for viruses which can cross species barriers to infect humans, domestic and wild animals. Viral species within the genera Coronavirus have been identified in bat species in different countries around the world, after the outbreaks of Severe Acute Respiratory Syndrome in China (2002-03), and Middle East Respiratory Syndrome in Saudi Arabia (2012-13). Due to multiple studies suggesting that bats are the natural host-reservoir of coronaviruses, monitoring this viral group on bats has increased, becoming a major focus for modeling and predicting outbreaks. The aims of this study were to survey the presence of CoVs in Mexican bats from Nearctic-Neotropical region in Mexico and to characterize phylogenetic diversity and phylogeographic patterns within coronavirus species identified. From May to September 2014 and from January to March 2015, a total of 633 individuals of 31 different species were sampled, in 13 different refuges located in Mexico City, Puebla, Morelos and Hidalgo states. A total of 1,899 samples (oral swabs, rectal swabs and blood) were collected; and total nucleic acid was extracted from 1596 samples. Coronavirus detection was performed using PCR primers targeting the RNA-dependent RNA-polymerase. PCR products of the expected size were cloned and sequenced, the results revealed Coronavirus sequences in 39/559 (6.9%) bats of 14 different species representing three different families from eight different collecting sites. Preliminary analyses indicated the presence of 12 distinct clades at nucleotide level, nine clustered within known alpha-coronaviruses, and three within beta-coronaviruses, two of them were novel. These data represent an estimated 84% of sampling coverage for coronavirus detection in the study region and expand the knowledge on coronavirus diversity in bats from the Nearctic-Neotropical transitional region.

Potential risk assessment of Lyme disease in Mexico based on zoonotic niche modelling

10:30 - Thursday, 27th July, Solar Square

Constantino González-Salazar, Christopher Stephens

1. Departamento de Ciencias Ambientales, Universidad Autónoma Metropolitana, Unidad Lerma; C3 – Centro de Ciencias de la Complejidad, Universidad Nacional Autónoma de México

Borrelia burgdorferi, the causative agent of Lyme disease, is the most important zoonotic pathogen reported in the USA. Although, Lyme is classified as exotic for Mexico, recent studies have suggested that *B. burgdorferi* infection might be endemic. However, it has received little attention by academic and governmental institutions, with a consequent lack of information regarding Lyme disease and its transmission cycle in Mexico. Here, we aimed to assess the potential risk factors for the occurrence of Lyme in Mexico and, in particular, to identify potential vectors and reservoir hosts. Using geographic data associated with hard tick species belonging to *Ixodes* genus and migratory birds from the USA, we build a complex biotic inference network to identify potential reservoir hosts, and develop potential Lyme disease risk maps based on zoonotic niche modelling. These networks allowed us to identify the potential bird hosts based on their connectivity and interaction strength. We built a ranked bird list for predicting the most important likely hosts of hard ticks infected by *B. burgdorferi*. Additionally, we build Lyme disease risk maps for the USA based on its zoonotic niche (i.e. vector-host interaction) for species of *Ixodes* genus; thus, we identified areas with high probability of establishing enzootic cycle. The accuracy of the model to predict areas that have been reported species positive to Lyme in USA, allowed us to identify areas of greater risk. By transferring Lyme zoonotic niche to Mexico, we predict zones with high risk of becoming endemic areas of Lyme through the arrival of ticks vectors and bird hosts infected by *B. burgdorferi*. Our results allowed identifying ecological characteristics of the regions with the highest potential for establishing enzootic cycle of Lyme. These results may give a first insight about spread and range expansion of the vector-borne pathogen *B. burgdorferi* in Mexico

Co-ocurrencia y filtrado ambiental como procesos de ensamblaje de comunidades virales asociadas a murciélagos en México

10:30 - Thursday, 27th July, Solar Square

Fabiola Nieto Rabiela, Citlali C Mendoza Guevara, Oscar Rico

1. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México

La similitud entre especies juega un papel clave en los procesos que dirigen el ensamblaje de las comunidades. La co-ocurrencia de especies similares puede ser poco probable si sus requerimientos similares resultan en una intensa competencia. Por otro lado, la persistencia en un hábitat en particular puede requerir características específicas, lo que podría resultar en comunidades compuestas por especies con características similares. Hasta donde sabemos, existe poca información sobre la importancia de estos procesos en el ensamblaje de comunidades de simbiosis. Para explorar si las características del ambiente (hospederos) y/o la co-ocurrencia de los hospederos determinan el ensamblaje de comunidades virales (simbiosis), se cuantificó la asociación pareada entre 17 especies de murciélagos, usando como variables ambientales la distancia filogenética, la diferencia de masa corporal y el gremio trófico. La co-ocurrencia se calculó usando una gradilla de 20 km² obtenida de la plataforma *species* de CONABIO, tomando el número de gradillas compartidas por pares de especies. Se analizaron modelos generalizados de regresión lineal. El mejor modelo encontrado reportó que la similitud en la composición de comunidades virales asociadas a murciélagos se explica por variables ambientales como el gremio trófico, la diferencia de peso y la interacción entre estas dos variables ($LR = 13.222$, $p < 0.05$). Los resultados muestran una tendencia de que el filtrado por las características funcionales de los hospederos es el proceso que determina el ensamblaje de las comunidades virales. Nuestro estudio representa uno de los pocos en explorar los procesos de ensamblaje de comunidades de virus asociados a murciélagos y puede servir como herramienta para predicciones para los patrones de distribución de la diversidad viral en México.

Revisiting brucellosis in the greater Yellowstone area

08:48 - Thursday, 27th July, Real Room

David Jessup

1. University of California Davis School of Veterinary Medicine

The National Academy of Science was asked by USDA-APHIS to review its original 1999 report of brucellosis in the GYA. The new report will be published in mid 2017. The current cooperative interagency bison management program appears to be successful. However, it is now clear that many of the 1999 conclusions were wrong.

Elk, not bison, have been the apparent source of the 24 outbreaks in cattle and ranched bison over the last 10 years. Most outbreaks have occurred well to the northwest or northeast of YNP. Elk populations in these areas have no contact with Wyoming elk feedgrounds, and little if any with YNP bison, and appear to be sustaining high levels of infection independently.

Strain 19 vaccination of elk is ineffective for reducing herd seroprevalence and their immune response differs markedly from cattle. If wildlife vaccination is to play a role in future management of brucellosis new vaccines and delivery systems will be required

The controversial elk feedgrounds in Wyoming have support from both ranchers and wildlife groups. Any modification of them will need to be done slowly. Private land ownership patterns may make hunting a less effective tool for controlling elk numbers.

The majority of the land surrounding YNP is managed by other government agencies, much of it for cattle grazing, yet no comprehensive or cooperative program to reduce risk of contact between infected elk and cattle has been developed. The States of Montana, Idaho and Wyoming manage brucellosis in livestock (and wildlife) independently, and there is no consistent definition of 'Designated Surveillance Area' (DSA) for brucellosis.

A major investment in research, monitoring and development of tools and technology are needed. Greater coordination and cooperation between all stakeholders will be necessary to keep brucellosis from spreading. The goal of eliminating it from the USA currently seems unrealistic.

Prevalence of Anticoagulant Rodenticide Exposure in Red-tailed Hawks (*Buteo jamaicensis*) in New York State and Diagnostic Utility of Russell Viper Venom Test for Detecting Associated Coagulopathies

08:48 - Thursday, 27th July, Real Room

Cynthia Hopf, Noha Abou-Madi, Sarrah Kaye, Marjory Brooks, Mark Rishniw, Tatiana Weisbrod, Elizabeth Bunting

1. Cornell University, College of Veterinary Medicine, 2. Staten Island Zoo

Free-ranging red-tailed hawks (*Buteo jamaicensis*) are commonly exposed to anticoagulant rodenticides (ARs) through contaminated prey. Coagulation tests suitable for detecting AR-related coagulopathy in raptors are not routinely available, potentially resulting in underdiagnosed AR-related coagulopathy, and underestimation of clinical effects of repeated, sub-lethal exposure. The two objectives of this study were to assess the prevalence of AR exposure in free-ranging *B. jamaicensis* in New York State (NYS), and investigate Russell's viper venom time (RVVT) as an affordable, practical coagulation test in this species.

Blood was collected from a control group of *B. jamaicensis* housed in captivity for at least two months (n=14) and a study group of sick / injured *B. jamaicensis* presented to the Cornell University Wildlife Health Center (n=39). We performed a toxicology screen to detect AR compounds, and two clotting time tests to identify coagulopathies: prothrombin time (PT) configured with chicken brain thromboplastin, and RVVT. Livers from birds that died or were euthanized were tested for AR.

Of the 35 birds tested, 12 (34%, 95%CI: 20% to 50%) had detectable AR concentrations in liver (brodifacoum in 11/12 (92%); difethialone in 1/12 (8%)) or blood (brodifacoum in 2/35 (6%)) – only one of these two birds also had detectable hepatic concentrations). Birds with detectable AR concentrations had clotting times not different from control birds; birds without detectable concentrations had shorter PT ($P < 0.004$) but not RVVT ($P = 0.06$). The RVVT and PT correlated in the birds tested ($\rho = 0.6$). Using a reference threshold of 40sec for PT, and 50sec for RVVT, RVVT was sensitive, but non-specific for detecting coagulopathies. However, birds with markedly prolonged RVVT (> 100 sec) are likely coagulopathic.

Our results suggest that rodenticide exposure is high in *B. jamaicensis* in NYS. The RVVT might provide a practical test to rule out AR exposure, but prolonged RVVT test results warrant additional testing.

Modelling rabies in African wild dogs (*Lycaon pictus*) to inform conservation management

08:48 - Thursday, 27th July, Real Room

Thomas Smallwood, Rosie Woodroffe, Christl Donnelly

1. Imperial College London, UK, 2. Institute of Zoology, Zoological Society of London

African wild dogs (*Lycaon pictus*) are amongst the world's most endangered carnivores, with approximately 6000 adult individuals occurring in just 7% of their historic range. In addition to anthropogenic threats and limitation by other carnivores, several pathogens pose a varying degree of threat to wild dog populations. Rabies, in particular, has been implicated in the extinction of the Serengeti wild dog population, and has hindered reintroduction efforts in South Africa and Namibia.

The highly social behaviour of African wild dogs means that rabies spreads quickly within individual packs, but their large ranges and territoriality hinder transmission between packs. The threat posed by rabies is therefore contingent on the spillover of the pathogen from domestic dog populations.

There are a number of potential strategies for managing the threat posed by rabies to African wild dogs. Vaccination of African wild dogs can provide direct protection of the population, while vaccination programmes targeting local domestic dog populations may reduce the risk of outbreaks occurring. Ecological, as well as veterinary, interventions must also be considered, including strategies to reduce contact between African wild dogs and domestic dogs or reduce the sensitivity of wild dog populations to outbreaks.

However, the impact of pathogens on wildlife populations, and the efficacy of management strategies, are difficult to assess empirically. We are therefore developing a model of rabies in an African wild dog population, incorporating population dynamics and epidemiology. This model will assist in determining the extent to which rabies poses a threat to the persistence of wild dog populations, and act as a preliminary assessment of the efficacy of the strategies available to conservation managers in order to inform decision making. Furthermore, the quantitative assessment of management strategies can assist in determining their cost-effectiveness, an important consideration in wildlife management given the limited funding available for conservation.

Update on Chronic Wasting Disease (CWD), surveillance and disease management in Norway

10:30 - Thursday, 27th July, Real Room

Jørn Våge, Turid Vikøren, Petter Hopp, Carlos Das Neves, Kjell Handeland, Knut Madslie, Sylvie Benestad

1. Norwegian Veterinary Institute

Chronic Wasting Disease (CWD) is an invariably fatal neurodegenerative disease of cervids, belonging to the group of transmissible spongiform encephalopathies (TSE). The disease is endemic in some areas in North America, where natural infections occur in different cervid species. Prior to 2016 CWD had never been reported outside North America except in captive deer in South Korea, introduced by import of CWD-infected animals. The surveillance for CWD in Europe has been limited, and the European Food Safety Authority (EFSA) has stated in 2010 that the occurrence of CWD could not be excluded in cervids in Europe, especially in untested remote areas. In Norway, approximately 2,100 cervids were tested for CWD in the period 2004-2015. Less than 20 of these were free-ranging reindeer (*Rangifer tarandus tarandus*).

Norway is the last refugium for wild tundra reindeer in Europe. The species is found in fragmented sub-populations in remote alpine regions of South Norway.

In March 2016, a young adult female reindeer belonging to the Nordfjella sub-population was found dying and was diagnosed as CWD positive. This case represented the first detection of CWD in Europe and the first detection of a natural infection in reindeer worldwide. During enhanced surveillance in 2016 two additional free-ranging reindeers were diagnosed along with two cases in European moose (*Alces alces*), the moose cases being geographically separated some 300 kilometers apart from Nordfjella.

Molecular analysis suggest that the reindeer prions are similar to what is found in North America while prions found in the two Norwegian moose have characteristics never reported before, suggesting an atypical type of CWD. This raises important questions concerning the disease itself (origin, pathogenesis and transmissibility) and its future management.

Disease status, future perspectives and elucidation of current management strategies towards CWD in Norwegian cervid populations will be presented.

Chronic Wasting Disease surveillance in Sweden

10:30 - Thursday, 27th July, Real Room

Erik Ågren, Maria Nöremark, Holly Cedervind, Dolores Gavier-Widén

1. National Veterinary Institute

After the first finding ever of Chronic Wasting Disease (CWD) in Europe, in wild reindeer (*Rangifer tarandus tarandus*) in southern Norway, followed by two cases in moose (*Alces alces*) geographically separated from the positive reindeer and close to the Swedish border, CWD screening of cervids was re-initiated in Sweden. A limited screening project for CWD in Cervidae in EU-member states and Norway 2007-2010 did not find any positive cases. After 2007, Sweden did not continue testing for CWD within the wildlife disease surveillance program, but in response to the positive findings in Norway a retrospective study was done. Frozen brain tissue from 270 cervids that were in poor body condition or emaciated and necropsied 2007-2016 were retrieved from a biobank and tested with Biorad TeSeE-ELISA. All tested samples were negative. CWD has been reintroduced in the wildlife disease surveillance program in 2016 and necropsied adult cervids are now tested for CWD, all so far with a negative result. The number of sampled cervids is limited and samples are not geographically well represented, making any conclusions on the status of CWD in Sweden very unsure. More sampling and a better geographical coverage is needed. Planning for increased surveillance started in 2016, with meetings and discussion groups involving authorities, researchers, and stakeholders in hunting associations, deer farmers, and reindeer herders. Sweden is currently awaiting a EU-commission decision, based on a scientific opinion by EFSA, which will set the minimum level for the future surveillance. A management and response plan for Sweden regarding CWD is underway, in collaboration with the Environmental Protection Agency and other authorities, where practices and experiences from CWD in North America are of great value.

Designing Evidence-based National Wildlife Health Programs: An Integral Part of the One Health Approach

10:30 - Thursday, 27th July, Real Room

Tiggy Grillo, J. Paul Duff, Dolores Gavier-Widén, Hongxuan He, Hang Lee, Natalie Nguyen, Parntep Ratanakorn, Jolianne M. Rijks, Marie-Pierre Ryser-Degiorgis, Jonathan M. Sleeman, Craig Stephen, Toni Tana, Marcela Uhart, Patrick Zimmer

1. WHA, 2. Animal and Plant Health Agency, Diseases of Wildlife Scheme, England and Wales, 3. National Veterinary Institute, 4. National Research Center for Wildlife Borne Diseases, Institute of Zoology, Chinese Academy of Sciences, 5. Seoul National University College of Veterinary Medicine, 6. USGS National Wildlife Health Center, 7. Mahidol University, Faculty of Veterinary Science, 8. Dutch Wildlife Health Centre, 9. Centre for Fish and Wildlife Health, University of Bern, 10. USGS National Wildlife Health Center, 11. Canadian Wildlife Health Cooperative, 12. Ministry for Primary Industries, 13. University of California, Davis, 14. Canadian Wildlife Health Cooperative

The impacts of emerging infectious diseases, including those of wildlife origin, are global and profound. They include increased burdens on public health systems, negative impacts on the world economy, extinctions of animal species, and disruptions to ecological integrity. Thus, a national wildlife health infrastructure that complements existing public and livestock health systems is a necessary component of a multisector, or One Health approach to addressing these issues of mutual concern. A workshop of subject matter experts was conducted to define the essential functions and capabilities of a national wildlife health program (NWHP) needed to deliver a robust and reliable program, including the organizational capacity (infrastructure, workforce, information management, governance, and funding). Core functions and goals identified included: Conducting national-level wildlife disease surveillance, both general (wildlife mortality event investigation), and targeted (pathogen specific) surveillance for early detection and rapid response, supporting declarations of freedom from disease, and providing baseline information on endemic disease occurrence; gathering and maintaining national scale data on wildlife diseases for appropriate dissemination; providing expert consultation on wildlife diseases; performing wildlife disease risk analysis; maintaining and integrating networks of stakeholders; promoting harmonization and standardization of methods; maintaining a repository of biological samples; and managing diseases in wildlife populations, including emergency response. Necessary capabilities identified included applied epidemiology, diagnostic capacity, quantitative ecology and modeling, data management and bioinformatics; biological and ecological expertise; and communication and leadership skills. A variety of organizational structures were identified, including centralized, decentralized, governmental, and/or non-governmental models. The experts recognized several challenges to implementation of NWHPs; in particular, complexities related to the fact wildlife diseases cross jurisdictional responsibilities and agency authorities. The workshop concluded that a NWHP would allow a country to better enable a One Health approach to protect human, animal, and environmental health, and ensure a nation meets its societal needs and obligations.

Health Survey Of Two Subspecies Of Bent-Wing Bats (*Miniopterus Orianae Bassanii* And *Oceanensis*)

10:30 - Thursday, 27th July, Real Room

Peter Holz, Jasmin Hufschmid, Lindy Lumsden, Jo Devlin, Glenn Browning, Marc Marenda

1. University of Melbourne, 2. Department of Environment, Land, Water and Planning

This project compares the health status of two bent-wing bat subspecies to investigate the role that disease may be playing in the decline of the critically endangered southern bent-wing bat (*Miniopterus orianae bassanii*), compared to the more common eastern bent-wing bat (*Miniopterus orianae oceanensis*). Both subspecies and their environment were sampled for *Pseudogymnoascus destructans*, the fungus that causes white nose syndrome, *Histoplasma capsulatum*, a potential human pathogen associated with bat caves, and other potentially pathogenic fungi. Blood was collected to determine normal hematology and biochemistry values and smears were examined for *Polychromophilus melanipherus*, a bent-wing bat blood parasite that may be linked to anemia. Ectoparasites were collected and identified. Bats were also tested for Australian bat lyssavirus, filovirus, coronavirus, herpesvirus and paramyxovirus to determine if they could be potential reservoirs for these emerging pathogens and if the presence of these viruses could be negatively affecting the bat populations.

To date all bats tested have been negative for *P. destructans* and the RNA viruses. Approximately 25% of the bats have been positive for *H. capsulatum*. Approximately 25% of bats were positive for herpesviruses. Sequencing of herpesvirus DNA products revealed the presence of multiple novel viruses. PCR was a more sensitive method for detecting *P. melanipherus* infections than blood smears. Ectoparasites appeared to be more prevalent on southern bent-wing bats than eastern bent-wing bats.

State-wide wildlife health surveillance based at a veterinary faculty

10:30 - Thursday, 27th July, Real Room

Pam Whiteley, Andrew Stent, Anthony Chamings, Jo Devlin, Jasmin Hufschmid, Mark Stevenson, Simon Firestone, Abdul Jabbar, Marc Marenda, Rhys Bushell, Alistair Legione, Amir Noormohammadi, Joanne Allen, Paola Vaz, Rebecca Traub, Glenn Browning

1. The University of Melbourne, 2. Deakin University

Wildlife health surveillance is an essential component of One Health, improving understanding of reservoirs of zoonotic and livestock diseases and ecosystem health. Veterinary faculties provide an efficient and productive base for wildlife health surveillance, as demonstrated by the Canadian Wildlife Health Cooperative since 1990. Wildlife Health Surveillance Victoria (WHSV) is based at the Faculty of Veterinary and Agricultural Sciences (FVAS) of The University of Melbourne. The project engages directly with a wide range of stakeholders, including the public, and community and governmental organisations. Stakeholders report wildlife mortality and morbidity events to WHSV. Dead wildlife are transported to FVAS for diagnostic investigations which involves input from faculty staff in pathology, microbiology, virology, parasitology, molecular epidemiology, and epidemiology. This project undertakes field inspections and engages in important collaborations with other institutions (Agribio, CSIRO AAHL, Zoos Victoria, Museum Victoria). Approximately 100 cases are investigated annually with key cases entered into Wildlife Health Australia's electronic Wildlife Health Information System, feeding into a national surveillance program. These investigations have improved our knowledge of baseline and changing health patterns in native free-ranging mammals, birds, reptiles and amphibians. Examples include chronic phalaris toxicity in kangaroos and spill-over infections from introduced domestic and feral animals.

Chronic wasting disease surveillance in Michigan: evaluation of testing road killed deer

10:30 - Thursday, 27th July, Real Room

Julie Melotti, Thomas Cooley, Daniel O'Brien, Chad Fedewa, Chad Krumnauer, Sara Harrington, Ricki Oldenkamp, Kelly Straka

1. Michigan Department of Natural Resources, Wildlife Disease Lab, 2. Michigan Department of Natural Resources, Wildlife Division

Sampling of road killed cervids for chronic wasting disease (CWD) is often integrated into CWD surveillance programs. Road killed samples are convenient, require relatively fewer resources for collection, are less controversial than other methods of sampling, and are collected under the premise that deer infected with CWD are more likely to be involved in a vehicle strike. We analyzed data on road killed samples taken from May 2015 to present as part of Michigan's CWD Surveillance and Response plan implemented in May 2015, after identification of the first CWD-positive free-ranging white-tailed deer (*Odocoileus virginianus*) in the state. In addition to other sampling methods, large scale efforts to collect road killed deer within a 5 county CWD Management Zone were employed. In contrast to what was anticipated based on published findings, none of the over 2,000 testable road killed white-tailed deer sampled from this area tested positive for CWD. We present a summary of Michigan's response to this CWD outbreak to date, and discuss lessons learned, including some potential reasons for failure to find any positives via this surveillance stream. Collection of road killed deer can present dangers to personnel collecting samples and are costly to an agency in terms of staff and budget allocated to collection and testing. When resources are limited other methods of obtaining samples (e.g., culling, issuance of out-of-season shooting permits, and testing of hunter harvested deer) may be more advantageous in detecting and estimating prevalence of CWD.

Comparison of field research methods to characterize free-roaming cat populations in a mixed-urban environment

10:30 - Thursday, 27th July, Real Room

Emily Vincent, Andrew Yoak, Jeanette O'Quin, Rebecca Garabed

1. The Ohio State University College of Veterinary Medicine

Free-roaming cat (*Felis catus*) overpopulation presents public health, environmental, and animal welfare concerns in communities across the United States. Population control methods are often implemented without preliminary data about free-roaming cat population locations, their specific distributions, resources that may impact the presence of cats, or populations of other wildlife that may affect cat populations. To study population size and distributions of free-roaming cats on and near The Ohio State University campus, two field research methods were compared: line transect and trail cameras. Trail cameras were also used to record locations and activity patterns of other wildlife species. The locations of resources, such as uncovered trash cans, that may contribute to the presence of feral cats on campus and in the surrounding area were also mapped. Six free-roaming cats were sighted in 5/100 sampled zones using the line transect method. Ninety-two free-roaming cat photographs were recorded using the trail camera method in 9/23 sampled zones. Cats were most often sighted off campus and in urban habitats. The number of cat photographs recorded on trail cameras was significantly correlated with the density of food resources in the area. Free-roaming cats were significantly more active during the night than during daylight hours. No significant relationship was found between cat presence and the presence of other urban wildlife such as raccoons. The results of this study indicate that the trail camera method was preferable to the line transect method for studying free-roaming cat populations in a mixed-urban environment because it detected a higher number of cats in a wider variety of habitat types and also allowed for the detection of other wildlife species. Communities planning to implement a population control program for free-roaming cats should choose the trail camera method to gather baseline data and should consider programs to decrease available food resources.

Habitat fragmentation and McDonald's effect: factors and consequences of the adaptation of *Varanus salvator* (*Squamata: Varanidae*) in a fragmented landscape in the Lower Kinabatangan Wildlife Sanctuary, Malaysian Borneo

10:30 - Thursday, 27th July, Real Room

Sergio Guerrero Sanchez, Pablo Orozco-Ter Wenge, Silvester Saimin, Benoit Goossens

1. Cardiff School of Biosciences, Cardiff University/ Danau Girang Field Centre, 2. Sabah Wildlife Department

Fragmentation in the Kinabatangan floodplain, Sabah, has turned the forest and its surrounding oil palm plantations in a threat for specialist species requiring of continuous habitat. However, it has become an apparently well-fitted habitat for the Asian water monitor lizard (*Varanus salvator*) among other generalist species. Due to its abundance, resilience and natural history, we used *V. salvator* as a model to understand the factors and consequences of adaptation to this fragmented landscape. Mark-recapture methods were used to assess the population size in six different sites in both forest and crops. Stomach content was screened, and 21 biochemical markers were analyzed from blood samples (N=250) and correlated with body size parameters and prey diversity. Results showed that plantations host a high density of lizards with greater body condition values, where diet seems to be dominated by rodents, while lizards in the forest exhibited greater prey diversity. We found a negative correlation between prey diversity and biochemical markers, e.g. low-density cholesterol, gamma glutamyl transferase and proteins. A preliminary study on populations' dynamics and habitat use suggests that *V. salvator* population sizes are larger in forest/plantation boundaries, however, with a negative population health trade-off, i.e. while individuals inhabiting plantations have readily access to an abundant and easy-to-get food source (fast-food), individuals in the forest have a more diverse diet and a larger area for foraging. This results in high levels of biochemical markers associated to lower metabolic health in the plantation animals. Extrapolating this trade-off to other species, such as sun bears, wild boars, leopard cats, civets and macaques among other species that are less abundant and more cryptic, will help understanding the effects of fragmentation caused by industrial crops on population's health.

Wildlife health as a driver of One Health research: emerging threats and old problems in Norway

14:48 - Thursday, 27th July, Solar Square

Carlos Das Neves, Knut Madslie, Marianne Heum, Jørn Våge, Turid Vikøren, Kjell Handeland

1. Norwegian Veterinary Institute

Northern latitudes are vulnerable to climate changes with several pathogens extending their distributions northerly and infecting naïve animal populations. Simultaneously, human activities change habitats, reduce resources or introduce additional stresses to wild species, which leads to changes in infection patterns. More than 70% of emerging diseases have origin in wildlife species, which strengthens the importance of surveillance for up keeping wildlife health, but also as early detection of outbreaks, potentially dangerous for production animals or even humans.

The Norwegian Veterinary Institute runs a wildlife health monitoring program, which in the last years has identified pathogens/disease outbreaks, that help implement the One Health approach in the country:

Tick borne encephalitis (TBE) has been identified in cervids in several locations in Norway, even in areas where human cases of TBE have not yet been reported.

Deer ked, associated with alopecia in moose but often biting humans, continues to expand north and has been found to carry *Bartonella* spp. (zoonotic bacteria).

In 2011 classical rabies was reported in Svalbard archipelago in both wild reindeer and arctic foxes.

In 2012 large outbreaks of pneumonia with a high mortality (25-30%) occurred in muskox. The primary cause was the sheep associated bacterium *Mycoplasma ovipneumoniae*, a good example of diseases spreading from production animals to wildlife.

In 2015 European bat lyssavirus type 2 has detected for the first time in a Daubenton's bat in Norway.

In 2016 *Angiostrongylus vasorum* (French heartworm) was detected in 2 foxes in different geographic locations in Norway.

In April 2016 Chronic wasting disease (CWD) was reported for the 1st time in Europe in wild reindeer and moose (different locations).

Whether many of these agents are truly emerging due to climate, anthropogenic changes or are being identified as a result of increased surveillance remains a matter of intense discussion requiring further research.

Response to a Plague Epizootic – Wildlife, Domestic Animal and Human Health

14:48 - Thursday, 27th July, Solar Square

Mark Drew, Leslie Tenglesen, William Bosworth

1. Idaho Department of Fish and Game, 2. Idaho Department of Health and Welfare, Bureau of Communicable Disease Prevention

In 2015-2016, Idaho Department of Fish and Game (IDFG) received reports of dead Piute ground squirrels (*Urocyon mollis*) in SW Idaho. Ground squirrels tested positive for *Yersinia pestis* by multiple test modalities. Because the area is heavily used for recreation, scientific study, and military training, a multi-agency response to address plague in wildlife, pets and humans using a One Health approach was developed. Two persons reporting rodent exposure and illness tested negative for plague in 2016. One of 12 dogs was presumptive positive for *Y. pestis* in 2015 and treated successfully. In 2016, 6/12 cats tested positive for *Y. pestis* with 4 mortalities and two successful treatments. Prophylaxis was initiated for humans in canine and feline-associated high-risk occupational and household exposures. IDFG received 80 rodent mortality reports from 9 counties. CDC confirmed *Y. pestis* in 3/4 (75%) ground squirrels in 2015. IBL tested 23 rodents in 2015-2016 and confirmed *Y. pestis* in 4/4 ground squirrels. We estimated the geographic area of concern (AOC) based on mortality surveys and reports, laboratory findings, and likely *U. mollis* habitat. Public information materials about the plague epizootic for press releases, social media, agency websites, letters to homes in high risk settings, and warning signs posted at AOC access points were done. An interactive map on multiple agency websites allowed the public to ascertain their proximity to the AOC and report wildlife mortality on a web-based reporting system. Passive surveillance among physicians and veterinarians for suspected plague cases was prompted by health alerts and guidance for monitoring and prophylaxis was provided. The multi-agency response was effective for public information outreach to minimize plague transmission from wildlife or pets to humans. On-line reporting tools improved response efficiency with rapid assessment of geographic risk and timely triage of reports of rodent and domestic animal morbidity and mortality.

A multidisciplinary study of the circulation of Nipah virus at the flying-fox / human interface in Cambodia: conciliating public health and conservation

14:48 - Thursday, 27th July, Solar Square

Julien Cappelle, Hoem Thavry, Neil Furey, Vibol Hul, Steven Prigent, Jonathan Epstein, Thongchai Ngamprasertwong, Hok Visal, Veasna Duong, Sowath Ly, Raphaël Duboz, Annelise Tran, Philippe Dussart, Arnaud Tarantola, Aurélie Binot

1. CIRAD, 2. Institut Pasteur du Cambodge, 3. Fauna and Flora International, 4. Université Aix-Marseille Associated, 5. EcoHealth Alliance, 6. Chulalongkorn University, 7. Royal University of Phnom Penh

Flyingfoxes (*Pteropus spp.*) face several conservation threats in Southeast Asia. They are considered to be the main reservoir of the Nipah virus (NiV), which has caused more than 500 human cases since its emergence in Malaysia and Bangladesh. Though NiV circulation has been documented in flying foxes in Cambodia and Thailand, little is known in Southeast Asia about the risk of transmission of NiV to domestic animals and Humans.

To better assess the risk of emergence of NiV in Cambodia while taking into account the conservation threats to flying foxes, we implemented a multidisciplinary study involving researchers (in ecology, epidemiology, virology, genetics, anthropology and modelling), conservationists and local and national authorities. We monitored the population dynamics and the diet of a colony of Lyle's flying fox (*Pteropus lylei*) as well as the circulation of NiV in the urine of these bats. We investigated the perception of the bats by local communities and their practices regarding bats (such as hunting, collecting guano, harvesting fruits, harvesting and drinking palm juice). We studied the bat / human interface by deploying GPS collars on 14 bats.

Our results showed seasonal patterns in both population dynamics and virus circulation, allowing us to identify a period when local communities' practices may put them at a higher risk of infection. The telemetry study revealed areas with increased potential contacts between humans and bats. Interviews showed limited conflicts between bats and humans and the absence of perceived risk by local communities.

An integrative model is being developed and participatory approaches are being used to transfer knowledge about the risk of emergence and ecosystem services associated with the flying foxes, in order to advocate the use of prevention measures conciliating public health and conservation.

Investigations of a cattle-associated pathogen in waterfowl in the Arctic

16:30 - Thursday, 27th July, Solar Square

Jesse Klejka, Hanna Sfraga, Cristina Hansen, Elizabeth Himschoot, Danielle Lyons, Rebekah Hare, Brandt Meixell, Caroline Van Hemert, Karsten Hueffer

1. University of Alaska Fairbanks, 2. University of Alas, 3. USGS Alaska Science Center

We documented the mortality of greater white-fronted goose (*Anser albifrons*) eggs along the Arctic coast of Alaska during the 2013 and 2014 nesting seasons. We isolated numerous species of bacteria from nonviable eggs, including the cattle-associated pathogen *Streptococcus uberis*. This result was surprising because the nearest commercial cattle operations are located hundreds of miles from the nesting grounds of greater white-fronted geese. Here, we present the multi-locus sequence typing (MLST) and antibiotic sensitivity profiles of *S. uberis* isolates recovered from greater white-fronted goose eggs. We also present results from surveillance for this organism in environmental, nest, and cloacal swab samples. MLST shows that our isolates are diverse and likely resulted from multiple introductions to the Arctic. We detected resistance to gentamicin, tetracycline, erythromycin, and cefperazone. *S. uberis* DNA was detected in some cloacal swab samples, but not in nest or tundra samples, suggesting that adult geese may be the source of infection to eggs. Furthermore, greater white-fronted geese may be responsible for transporting this organism from agricultural areas to the Arctic breeding grounds. Our previous work showed that *S. uberis* is capable of causing mortality in a chicken egg model, however, it was detected in only a small proportion of wild goose eggs and therefore does not likely pose a threat at the population level.

Understanding The Effects Of Domestic Cats On Wildlife

16:30 - Thursday, 27th July, Solar Square

Sonia Hernandez, Kerrie Anne Loyd, Alexandra Newton, Clym Gatrell

1. University of Georgia, 2. Arizona State University

Domestic cats (*Felis catus*) hunt despite food subsidies, yet there is much controversy about their predation *rate*, their *effect* on populations of wildlife, and their *management*. Here we summarize the results of 4 studies: 1) we utilized KittyCams (point-of-view cameras) to quantify the hunting activities of a) free-roaming pet cats in Athens, GA and b) cats managed in Trap-Neuter-Return colonies on Jekyll Island (JI), GA; 2) we quantified non-predatory interactions between colony cats and wildlife on JI; and 3) we analyzed the data from wildlife rehabilitation centers in the USA to determine the impact of cats on the type and fate of patients. For the 2 KittyCam studies we obtained ~30 hours of video/cat in order to designate each cat as a “hunter”/“non-hunter” and describe prey type and frequency. In Athens, 42% of pet cats hunted, primarily herpetofauna, leaving more than 25% of their prey uneaten. On Jekyll Island, 65% of colony cats hunt, killing primarily invertebrates and herpetofauna, but consumed 82% of their prey. Most predation events took place during the warm season. Out of >680 hrs of video collected from cats on JI, we recorded >140 non-predatory interactions with wildlife, most frequently raccoons (*Procyon lotor*), and statistically at times when cats were provisioned food—highlighting the impact that TNR colonies can have on the aggregation and contact among wildlife and cats. Finally, the analysis of the data from 82 wildlife rehabilitation centers (the WILD-ONE database; 3.5 yr period) showed that domestic pets were responsible for 14% of admissions and the second most common identifiable cause of wildlife injury. Birds were the most frequent patient of attacks by cats, 78% of which did not survive. Together these studies illustrate the urgent need for management of cats to decrease their impact on the welfare and populations of wildlife.

Characterization Of Extended Spectrum Beta Lactamase Producing Enterobacteria In Feces Of South American Sea Lion (*Otaria Flavescens*) In An Urban Colony From The Los Ríos Region, Chile

16:30 - Thursday, 27th July, Solar Square

Ana Jara, María Paz Miró, Maria Jose Navarrete

1. Universidad Austral de Chile

The bacterial antibiotic resistance is a public health problem in the world. From the most commonly used drugs for the treatment of infections, beta lactam antibiotics are the choice, and subsequently, the production of beta lactamase enzymes are the most common resistance mechanism used by enterobacterias. The interaction between wild animals and humans facilitates the microorganism transfer from terrestrial environments to marine ecosystems and vice versa, particularly from bacteria with potential antibiotic resistance, directly affecting public health. The actual project used the South American sea lion (*Otaria flavescens*) from an urban colony from Valdivia – Chile as an animal model to characterize extended spectrum betalactamase enterobacterias (ESBL). Thirty fecal samples from South American sea lions were collected from a platform and its surroundings in Valdivia. Samples were obtained and then processed at the Animal Pathology Institute at the Universidad Austral de Chile. The bacteria isolation was made in an ESBL agar to later identify bacterial colonies and to perform DNA extraction, to characterize the main genes that encode for extended spectrum betalactamases (TEM, OXA, SHV and CTX-M) through a PCR Simplex.

As a result, 73% of the samples (n=22) showed bacterial growth in ESBL agar, isolating mostly *Escherichia coli*. From the 22 samples isolated, 68% expressed betalactamase genes, being SHV enzyme gene the most common with 46%, followed by CTXM (32%) and OXA (23%).

The present study confirms the presence of ESBL bacteria in most of the fecal samples collected. Also, enzymes that give resistance to these bacteria were identified. Furthermore, potential contamination sources were also recognized, increasing the risk of acquiring these antibiotic resistant bacteria by the human population. This information is crucial for future antibiotic resistance studies in other marine species from this area, as well as to detect this bacteria in this river and its tributaries.

Multi-scale analysis of potential drivers influencing bat-ectoparasite interaction networks in anthropogenic landscapes

16:30 - Thursday, 27th July, Solar Square

Jacqueline Hernández, Juan Biviano Morales-malacara, Sergio Amador Hernandez, Mariana Yolotl Alvarez-añorve, Luis Daniel Avila Cabadilla

1. Escuela Nacional de Estudios Superiores, Unidad Morelia, Universidad Nacional Autónoma de México, 2. Unidad Multidisciplinaria de Docencia e Investigación, Facultad de Ciencias, Universidad Nacional Autónoma de México, Campus Juriquilla

The continuous land-use changes in tropical regions – hosting more than the 50% of the terrestrial species – has created novel landscapes with implications not only for the preservation of animal communities but also for the biotic interactions and the ecological processes in which they are involved. This is especially important for ectoparasites-vertebrates host networks, which shed light about the transmission of diseases that affect directly or indirectly the structure of communities. In this study we carried out a multi-scale analysis of factors determining ectoparasites-bats host networks in one of the most diverse and threatened ecosystem in the world – the tropical dry forest (TDF). For this purpose, we carried out bat and ectoparasites (Diptera and Acari) sampling in twelve secondary forests and two old growth forests of TDF located within an anthropogenic landscape (Chame-la, Mexico). On each study site we also characterized the habitat attributes at local (vegetation composition and structure) and landscape scale (composition and configuration) regarding the dry and riparian forest – the primary vegetation types in the region. We found an idiosyncratic and epiphenomenal response of fly-bat and mite-bat host networks to variation in vegetation and landscape structure. Nevertheless, we also found an increase on the number of bat-parasite interactions in response to a reduction on vegetation structure, and in landscape coverage and connectivity. We hypothesize that the reduction on the availability of resources or the increase in their degree of dispersion across the landscape can significantly affect host health, increasing ectoparasite load and decreasing ectoparasites removal through host grooming. Our results point toward the tremendous importance of preserving remnants of the original vegetation in anthropogenic landscapes.

Monitoring mosquito populations for identifying space-temporal risk areas: an approximation in Public Health

16:30 - Thursday, 27th July, Solar Square

Josefina Ramos-Frías, Pablo Octavio Aguilar, María Dolores Osorio-Piña, Jesús A. Castillo-Valverde, María Concepción Carmona-Ramos

1. Public Health Services of Hidalgo State, 2. Universidad Autónoma del Estado de Hidalgo

Background: Vector-Borne Diseases (VBD) are a significant problem in Mexican public health. Hidalgo state gathers environmental habitat conditions for survival of transmission mosquitoes in 28 municipalities (it means near of 50% of total land surface). Nevertheless, limitations on material and human resources linked to lack of communications and challenging access to remote localities complicate carrying out control activities in complete and rural areas.

Objective: In this paper, we identify space-temporal risk areas for VBD by monitoring mosquito populations, quantification eggs in ovitraps.

Method: We installed 878 ovitraps in five localities of high risk of Hidalgo state (determined by cases number in five previous years: Huejutla Jaltocán, San Felipe Orizatlán, Chapulhuacán y Písafloras). All ovitraps were located following recommendations were given by CENAPRECE. We obtain lecture data for 52 epidemiological weeks of 2016 from Integral Vector Control and Entomological Surveillance Platform. A Cluster analysis was done for group identifying by mean Euclidean distances. Resulting groups were tested by generalized discriminant analysis. All outputs were represented by graphical way versus confirmed cases of Dengue and Zika. Key results were mapped.

Results: We identified three risk clusters (High, medium and low) with a permanent abundance of eggs in punctual sites. All groups were statistically strong. Mosquito's population were stable from January to March. In April, it becomes to grow following an exponential erratic increase phase in May. The highest point was recorded in July (27th week), followed by continuous decreasing between 32-39th weeks (September), to reach asymptotical behaviour until year ending. All sites identified in higher risk are located in Huejutla city.

Discussion and Conclusion: We identified particular areas by the abundance of mosquitoes, and the inflexion temporal point of growing curve precedent of growing phase (May). This knowledge will allow enhancing control activities head towards to decrease probabilities of catch VBD.

Identification Of Myxozoa Parasite In The Connective Tissue Of A Cascadura Fish (*Hoplosternum Littorale*) In Trinidad And Tobago

09:00 - Thursday, 27th July, Solar Square

Karelma Frontera Acevedo, Carla Ayanna Phillips

1. University of West Indies

Background: Thirty cascadura (*Hoplosternum littorale*) fish from 5 different ponds were submitted alive to the Aquatic Animal Health Laboratory of the School of Veterinary Medicine, University of West Indies as part of monitoring and quarantine procedures of a commercial aquaculture farm. Cascadura fish are commercially important in Trinidad.

Methodology: Water from the five different ponds was tested for quality. All fish were euthanized and necropsies were performed. Pooled samples from each pond were submitted for microbiology, parasitology, and histopathology.

Results: All water samples had low alkalinity, low hardness, and low pH. In general, all ponds had evidence of low to moderate ecto- and endoparasitism. A section of connective tissue from the histopathologic samples of the pond with the lowest pH contained an area of hemorrhage and numerous poorly staining oval to tear-drop shaped organisms. These organisms stained brightly acid fast, and some included two polar capsules and a polar filament. No other signs of infection were noted in these fish.

Conclusion: This is the first histopathologic description and report of myxozoan parasites in the cascadura in Trinidad. Myxozoa can be pathogenic, and should be included in the differential for causes of death in farmed cascadura, particularly when there is poor water quality which could affect the immune system of the fish.

Hallazgos Histopatológicos En Encéfalos De Crías De Lobo Fino Austral (*Arctocephalus Australis*), De Isla Guafo, Región De Los Lagos, Chile

09:00 - Thursday, 27th July, Solar Square

Francisco Muñoz, Maria Jose Navarrete

1. Universidad Austral de Chile

Introducción: El lobo fino austral (*Arctocephalus australis*), es una de las cinco especies de lobos marinos presentes en Chile. Los estudios realizados sobre el estado de salud de sus poblaciones son escasos, siendo ésta una especie clave para entender el ecosistema marino del sur de Chile.

El presente estudio describe las lesiones macro y microscópicas en el encéfalo de 17 cachorros de lobo fino austral encontrados en Isla Guafo, entre los meses de enero a marzo de 2013

Objetivos: Describir los principales hallazgos anatomopatológicos del encéfalo en cachorros de lobo fino austral. Caracterizar los principales hallazgos histopatológicos en cerebro, hipocampo, cerebelo, tronco encefálico y meninges. Relacionar los hallazgos a las diversas causas de mortalidad.

Métodos: De los 17 cachorros de lobo fino austral encontrados en Isla Guafo, a 15 se les realizaron necropsias completas y de 2 solamente se obtuvo el encéfalo.

Resultados: De los 15 cachorros a los cuales se le realizó una necropsia completa, se determinaron las siguientes causas de muerte: enteritis (26,7%), inanición (13,3), asfixia por inmersión (13,3%), trauma (20,0%), septicemia (13,3%), neumonía (6,7%) e indeterminados (6,7%).

Los hallazgos macroscópicos más importantes en el sistema nervioso central correspondieron a: hemorragia (29,4%), congestión (47,1%), autólisis (23,5%), fractura de cráneo (11,8%) y melanosis (11,8%).

Los hallazgos microscópicos más importantes correspondieron a: congestión (88,2%), edema (35,3%), hemorragia en el parénquima (23,5%), hemorragia subaracnoidea (23,5%), meningitis (23,5%), gliosis focal (41,2%), gliosis diseminada (64,7%), manguitos perivasculares (17,6%), infiltrado inflamatorio focal (70,6%), infiltrado inflamatorio diseminado (58,8%), inflamación mononuclear (82,4%), autólisis (23,5%), necrosis (11,8%), hemosiderosis (11,8%) y bacterias de putrefacción (5,9%).

Conclusión: Lesiones micro y microscópicas como congestión, hemorragia en parénquima, hemorragia subaracnoidea, gliosis focal y diseminada, inflamación mononuclear focal, diseminada y manguitos perivasculares, se presentaron en las distintas causas de mortalidad, pero no pudieron ser atribuidas a ninguna de ellas de manera específica.

Molecular detection of the 3'-UTR region of Torque Teno virus in rodents captured in México. Are the Torque Teno Virus zoonotic? Partial results

09:00 - Thursday, 27th July, Solar Square

Torres Marco, Bayron Cruz-Camargo, Rodrigo Medina-Pinto, Henry Noh-Pech, Iván Rodríguez-Vivas, Fernando I. Puerto

1.Universidad Autónoma de Yucatán

Introduction. Torque Teno virus infection has not been implicated in any disease; however, it has been shown that if it present in co-infection with other virus, it may aggravate or increase the pathogenesis of diseases. Torque Teno virus infection is not only restricted to humans, so evidence of its circulation is increasing in domestic and wild mammals. Rodents have been identified as hosts of Anellovirus, whose prototype species is Torque Teno virus. There is a hypothesis that this virus might be a zoonotic infection; so, it is possible that can be transmitted from humans to animals and vice versa.

Objective. Report the circulation, through molecular identification of a conserved region, of Torque Teno virus in rodents from Yucatán, México.

Methods. Synanthropic and wild rodents were captured in the community of Cenotillo. A liver and kidney biological samples were used in DNA extraction method. The identification of the 3'-UTR conserved region of Torque Teno virus was pretended by nested PCR whit specific primers develop for detection in humans. Two positive products (one for a synanthropic rodent, another for wild rodent) were sequenced and analyzed whit the BLAST tool.

Results. We found Torque Teno virus genome, in different percentages, in both rodent population and in both types tissues samples. The BLAST analyses showed a 100% and 95% of coverage and identity, respectively, for the synanthropic rodent isolated fragment, and 82% and 87% of coverage and identity, respectively, for the wild rodent isolation fragment.

Discussion. Torque Teno virus infection have been demonstrated in animals and wild mammals. In México, there is no information about the circulation of Torque Teno virus in animals, so maybe, this is the first molecular evidence; however, further studies are necessary to totally demonstrated that the isolated fragments of the 3'-UTR region are for human Torque Teno virus.

Occurrence of *Cysticercus fasciolaris* in rodents captured in a rural environment of Yucatan, Mexico

09:00 - Thursday, 27th July, Solar Square

Rodrigo Medina-Pinto, Torres Marco, Iván Rodríguez-Vivas, Manuel Bolio-gonzález, Bayron Cruz-Camargo, William Arcila-Fuentes, Rolando Medina, José Ortiz-Esquivel

1. Universidad Autónoma de Yucatán

Introduction. *Cysticercus fasciolaris* is the larval stage of the cestode *Taenia taeniaeformis*, whose definitive hosts are various species of carnivorous, mainly felids. This larval stage uses a wide variety of small rodents, and occasionally birds and humans as intermediate hosts. Two infection cycles can occur: an urban cycle that involves domestic cats and synanthropic rodents, and a sylvatic cycle that involves wild felines and wild rodents.

Objective. Evaluate the occurrence of the larval cestode *Cysticercus fasciolaris* in synanthropic and wild rodent populations from a rural municipality of Yucatan, Mexico

Methods. A total of 153 rodents were collected: 106 synanthropic (63 *Rattus rattus* and 43 *Mus musculus*) and 47 wild (22 *Heteromys gaumeri*, 11 *Ototylomys phyllotis*, 9 *Peromyscus Yucatanicus*, 2 *Rattus rattus*, 1 *Peromyscus leucopus*, 1 *Sigmodon hispidus* and 1 *Mus musculus*), in Cenotillo, Yucatan, Mexico. The liver of all rodents was inspected with the aim of finding metacestodes cysts. All metacestodes were collected and identified morphologically through a conventional stereoscope. The frequency of infection was calculated and a chi square test was performed to determine the association between infection and the sex and age variables of rodents

Results. All the parasites collected were classified as *Cysticercus fasciolaris*. The *Rattus rattus* synanthropic population was the only rodent species positive with a frequency of 19.47% (12/63). The chi-square test did not yield significant results for the variables sex ($P = 0.79$) and age ($P = 0.87$).

Discussion. *Cysticercus fasciolaris* infection has been reported in synanthropic and wild rodents around the world. predation of these animals is a fundamental element for infection for *Taenia taeniaeformis* in domestic and wild carnivores. In the present study, *Cysticercus fasciolaris* infection was only present in synanthropic rodents, so there is no evidence of a wild cycle of parasite transmission

Síndrome neurológico idiopático en gaviota capucho café (*Chroicocephalus maculipennis*) y gaviota cocinera (*Larus dominicanus*)

09:00 - Thursday, 27th July, Solar Square

Pablo Regner, Carla Zuccarelli, Juan Carlos Sassaroli, Melisa Unger, Laura Torres, Guillermo Wiemeyer

1. Laboratorio de Toxinopatología, Centro de Patología Experimental y Aplicada, Fac. de Medicina, Universidad de Buenos Aires / Fundación Caburé-í, 2. Reserva Ecológica de Vicente López / Fundación Caburé-í, 3. Instituto de Zoonosis Luis Pasteur, Gobierno de la Ciudad de Buenos Aires, 4. ProTenencia, Ministerio de Salud de la Nación Argentina / Fundación Caburé-í, 5. Proyecto Ecoparque Interactivo, Gobierno de la Ciudad de Buenos Aires

A partir del año 2012 comenzamos a observar, en la costa del Río de la Plata, la aparición de individuos de gaviota capucho café (*Chroicocephalus maculipennis*), y gaviota cocinera (*Larus dominicanus*) con signos neurológicos inespecíficos. Los mismos consistían en depresión, parálisis flácida de los miembros superiores e inferiores y anorexia. Debido a que el hallazgo de estos individuos fue incrementándose, se procedió en 2015 a incluirlos dentro de un proyecto para determinar la causa de los signos. El objetivo del trabajo es presentar los resultados obtenidos. Se trabajó con individuos de *Larus dominicanus* (n=17) y *Chroicocephalus maculipennis* (n=18), derivados a la Reserva Ecológica de Vicente López y al Centro de Rescate de Fauna Silvestre de la Reserva Ecológica Costanera Sur, durante los años 2015-2016. Se observó que los hallazgos se concentraban entre noviembre y abril y que más allá de los signos mencionados, algunos individuos se recuperaban sólo con dieta forzada y fluidoterapia, mientras que otros se deprimían más y fallecían. De los análisis de sangre realizados se constató una disminución en los valores de hematocrito ($27 \pm 7\%$) y un aumento de los valores de las enzimas hepáticas, siendo el resto de los valores normales. Durante las necropsias sólo se observaron los hígados levemente aumentados de tamaño y de coloración más oscura de lo normal. A partir de muestras de sangre se determinó presencia de toxina botulínica (Ensayo de neutralización), influenza aviar (ELISA/RT-PCR) y Enfermedad de Newcastle (ELISA Indirecto) también se determinó clamidiosis aviar (ELISA/PCR) y virus del oeste del Nilo (RT-PCR) a partir de hisopados cloacales y presencia de organofosforados (Cromatografía) a partir de órganos (hígado y riñón) post mortem. Todos los estudios realizados dieron resultado negativo. Habiendo descartado las principales posibles causas, durante el 2017 procederemos a determinar la presencia de micotoxinas en el tracto gastrointestinal de las gaviotas.

EpiCore: A Community of Epidemiologists and Public Health Professionals Working Together to Verify Information on Disease Outbreaks

09:00 - Thursday, 27th July, Solar Square

Nomita Divi

1. Skoll Global Threats Fund

EpiCore is a robust global community of human, animal, and environmental health professionals committed verifying disease outbreaks. EpiCore's online platform, launched in November 2015, operates under a simple premise: connecting more health professionals to a system that provides immediate access to early alerts about health threats in their area and allowing users to validate those threats as real—leads to faster, accurate outbreak verification.

Through a secure online platform, members are able to easily and quickly provide local information to expedite outbreak verification. Moderators review reports of potential outbreaks in humans or animals from disparate sources and then use EpiCore to send requests for information (RFI) to volunteers, so that signals can be verified. Volunteers combine their expertise, knowledge of on-the-ground realities, and other resources to verify or discard early indicators of an outbreak. They report back to moderators, who assimilate responses and share their findings with the global disease surveillance community. EpiCore volunteer applications are vetted to ensure that they possess the public health and epidemiologic expertise necessary to contribute to the platform. As of March, 2017 EpiCore has over 1,800 members (25% have animal health expertise) that span 136 countries. Since launch, over 500 requests for information to volunteers have been posted with a response rate of over 70%. Specifically, 24% of these requests involve animal diseases.

With its broad geographical distribution of members and high response rate, EpiCore is poised to verify potential outbreak signals faster. Looking ahead, EpiCore is focused on including more animal health practitioners to further commitment to a one health focus. By improving situational awareness and de-escalating rumors or false information, EpiCore is able to reduce the signal-to-noise ratio among disease surveillance data streams. By detecting and verifying outbreaks faster, EpiCore can enable early outbreak response efforts that curb epidemics and save lives.

Host preferences for white-tailed deer and other big game by suspected vectors of hemorrhagic disease viruses on a Florida big game preserve

09:00 - Thursday, 27th July, Solar Square

Bethany McGregor, Tanise Stenn, Katherine Sayler, Erik Blosser, Jason Blackburn, Samantha Wisely, Nathan Burkett-Cadena

1. University of Florida

Epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) cause severe hemorrhagic illness in white-tailed deer (*Odocoileus virginianus*) throughout the United States, resulting in high mortality and morbidity in wild and farmed deer populations. Big game preserves and deer farms, which constitute a rapidly growing industry throughout the United States, are often significantly affected by hemorrhagic disease outbreaks. *Culicoides* biting midges (Diptera: Ceratopogonidae), also known colloquially as no-see-ums, are the only confirmed vectors of hemorrhagic disease viruses, although the specific vectors of EHDV in Florida are not yet known. This project investigated host use of midges on a 400-acre big game preserve in north Florida with multiple species of Cervidae (n=6) and Bovidae (n=6) in order to incriminate vectors of EHDV. Blacklight traps were used to collect blood engorged *Culicoides* for PCR-based bloodmeal analysis to identify host preference of suspected vectors. Results from analysis of 1,300 individual biting midges were used to calculate forage ratios, employed to infer preference and avoidance for deer and other big game species. Six *Culicoides* species fed heavily upon birds and/or squirrels, while others fed primarily upon ruminants. The most abundant species, *Culicoides stellifer* (n=1,149), showed significant preference for *Cervus* spp. and fallow deer (*Dama dama*), while avoiding white-tailed deer. *Culicoides biguttatus* (n=60) and *C. venustus* (n=18) fed upon white-tailed deer at levels reflecting deer relative abundance. Interestingly, only *Culicoides debilipalpis* (n=60) demonstrated a significant preference for white-tailed deer over other available animals. Combined with laboratory transmission studies, these findings will be important in incrimination of vector species important in the transmission of hemorrhagic disease and determining the roles of different ungulate species in disease dynamics. These results also have implications for control of these vectors to limit the transmission of hemorrhagic disease on this and other properties throughout the southeastern United States.

An ounce of prevention: San Clemente Island fox population and disease monitoring

09:00 - Thursday, 27th July, Solar Square

Jesse Maestas, David Green, Andrew Bridges, Melissa Booker, T. Winston Vickers, Leslie Woods, David Garcelon

1. Institute of Wildlife Studies, 2. United States Navy, 3. University of California Davis School of Veterinary Medicine

The island fox (*Urocyon littoralis*) is endemic to the California Channel Islands, and their populations may be threatened by predators or disease. In the 1990s, several island fox subspecies declined dramatically and were listed as federally endangered in 2004. These populations have largely recovered and most subspecies were recently delisted. The San Clemente Island subspecies was not federally listed, but is a focal conservation species for the U.S. Navy, and is the subject of a long-term conservation program. Our program objectives were to monitor population demography and survival, and to detect potential threats by conducting disease surveillance. Demographic data was gathered annually from 12 separate 18-trap grids stratified by habitat type throughout the island. We maintained a radio-collared population of approximately 60–100 individuals to serve as disease sentinels and to gather known-fate survival data. Additional disease surveillance was conducted via necropsies and veterinary care for ill or injured foxes. We found the population grew from an estimated 431 adults in 2007 to 888 in 2015. Known-fate survival analysis from 2013–2016 suggested a high (89–95%) adult annual survival rate. Of 75 fox necropsies conducted from 2012–2017, 48% had interstitial pneumoconiosis (interstitial histiocytic refractile crystalline pneumonia), with prevalence increasing from 19% to 84% in recent years. Through a combination of population and sentinel monitoring, we have increased the likelihood of detecting threats to San Clemente foxes. While we have detected antibodies to common canine diseases in the population, there is no evidence of virulent communicable diseases. Non-communicable diseases such as interstitial pneumoconiosis, could be contributing factors to the mortalities of several necropsied foxes and warrant further investigation.

The Feasibility of Field-based Collection of Oral Fluids in Wild Pigs (*Sus scrofa*)

09:00 - Thursday, 27th July, Solar Square

Morgan Wehtje, Pauline Nol, Raoul Boughton, Bethany Wight, James Beasley, Peter Schlichting

1. United State Department of Agriculture, Animal Plant Health Inspection Agency, National Veterinary Services Lab, Wildlife Disease Investigations Team, 2. USDA/APHIS/VS/NVSL/WiLDIT, 3. University of Florida, 4. University of Georgia

Oral fluids have great potential as an efficient and cost effective remote disease detection matrix for wildlife disease surveillance efforts. Molecular and antibody evidence of pathogen exposure can be obtained from oral fluids collected via substrates attractive to certain wildlife species. North America wild pigs are host to numerous important domestic livestock diseases, such as brucellosis and pseudorabies. Additionally, in the event of an outbreak in livestock of a foreign animal disease such as foot-and-mouth disease, wild pigs have great potential to acquire and maintain such diseases, due to their increasing population size and range overlap with domestic species. We explored the feasibility of using wool balls coated with an attractive substance (termed Swineapples), so that swine chew on the ball and leave oral fluids to be extracted for testing. In pens containing captive wild pigs, Swineapples were initially tested to observe whether the animals would chew on them, and if swine-specific DNA could be extracted from the collected oral fluids. Based on positive results, Swineapples were then deployed in two study areas, Southern Florida and South Carolina, where wild pigs were already being attracted to bait sites, to see if they showed interest in them. A total of 80 Swineapples (40 at each site) were suspended from upright posts immediately adjacent to the bait site and then 100 meters from the bait site. At each study site 20 Swineapples were deployed for two weeks, collected and then replaced with new Swineapples for an additional two weeks. Cameras were placed at all Swineapple deployment sites in order to monitor usage. Camera footage was analyzed by quantifying the numbers of visits and the degree of use. Swineapple use was ranked from non-use (0) through chewed (4). Data are pending and will be reported.

The Different Roles Of Myxomatosis And Rhd In Suppression Of The Turretfield (South Australia) Rabbit Population

09:00 - Thursday, 27th July, Solar Square

David Peacock, Greg Mutze, Ron Sinclair, Peter Kerr, John Kovaliski, Lorenzo Capucci

1. Biosecurity SA, Primary Industries and Regions SA 2. Visiting Scientist, CSIRO Health and Biosecurity, 3. Biosecurity SA, Primary Industries and Regions SA, 4. Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia

Background: Myxomatosis and rabbit haemorrhagic disease virus (RHDV) have been primary biological control agents in Australia for pest European rabbits (*Oryctolagus cuniculus*) since 1950 and 1995, respectively, when both spread rapidly across the country and caused major declines in rabbit abundance and associated negative impacts. Since 1996 RHDV and myxomatosis epidemiology has been studied continuously at Turretfield, South Australia. In May 2015 RHDV2, a new RHDV related lagovirus identified in Europe in 2010, was detected in Australia. It too has spread rapidly, even though the Australian wild rabbit population had widespread immunity to RHDV.

Objectives: To assess the impacts of myxomatosis and RHDV/RHDV2 on a rabbit population and the epidemiology and interactions between these biocontrols.

Methods: Rabbits were trapped c. every 8 weeks and weighed, sexed, tagged, blood sampled and released. Carcass searches were made when outbreaks were detected, with tissue samples analysed by rt-PCR. Following the first report of RHDV2 in South Australia in December 2015, weekly searches were made at Turretfield to detect its arrival and impact.

Results: On 30th April 2016 three intact rabbits, previously seronegative for myxomatosis antibodies, were found dead showing symptoms of myxomatosis. All three tested negative by rt-PCR for RHDV or RHDV2. Four days later two adult rabbits, and another on 3rd June, with an established history of high anti-RHDV antibody titres were found dead and tested positive by rt-PCR for RHDV2. Rabbit numbers were significantly reduced compared with previous years.

Discussion and Conclusions: Both RHDV2 and myxomatosis appear to have been major influences on the Turretfield rabbit population in 2016. Their relative importance is difficult to assess without specific RHDV2-antibody serological tests but these observations support the new capacity of RHDV2 and the continuing capacity of myxomatosis to have significant population level impacts on the Australian rabbit population.

Parásitos respiratorios en pingüino de Magallanes (*Spheniscus magellanicus*) en el Centro de rehabilitación de fauna silvestre de la Universidad Austral de Chile

09:00 - Thursday, 27th July, Solar Square

Luis Miguel Flores Velazquez, Pablo Oyarzun Ruiz, Maria Jose Navarrete

1. Universidad Austral de Chile

Desde siempre nos han llamado la atención los pingüinos, ya sea por tratarse de aves que no pueden volar o por ser consideradas como poco hábiles en tierra firme. Sin embargo cuando éstas se encuentran en el agua, es una historia completamente distinta. En Chile este grupo de aves se encuentra representado por 11 de las 18 especies conocidas, esta gran variedad de pingüinos se distribuye en las costas, tanto en territorio continental como insular. Lo anterior ha despertado el interés científico nacional e internacional en el estudio de los agentes patógenos transmisibles de estos animales a nivel silvestre, como un reflejo del estado sanitario y la influencia de las actividades humanas en los ecosistemas que habitan.

En el presente estudio de patología y parasitología se estudiaron diversos especímenes de Pingüino de Magallanes (*Spheniscus magellanicus*) que llegaron al Centro de Rescate de Fauna Silvestre (CEREFAS) de la Universidad Austral de Chile. Las necropsias demostraron la presencia de nematodos, los que fueron encontrados dentro de la tráquea, sacos aéreos y pulmones. Los tejidos lesionados fueron extraídos y fijados en formalina y los parásitos adultos fueron fijados en alcohol para su identificación parasitológica. El parásito fue clasificado como *Cyathostoma phenisci*. Se encontraron lesiones patológicas asociadas tanto macroscópicas como microscópicas y que en estos casos llevaron a la muerte de los ejemplares, por la cantidad y las lesiones que provoca este nematodo en vías respiratorias. Estos resultados servirán para la mejora de la atención y medidas preventivas en estos animales, para su llegada a los centros de rescate y así poder prevenir la muerte de esta especie con problemas de conservación.

Low viral doses are sufficient to infect cottontail rabbits with influenza A virus

09:00 - Thursday, 27th July, Solar Square

Jeff Root, Susan Shriner, Jeremy Ellis, Kaci VanDalen, Heather Sullivan

1.National Wildlife Research Center

Influenza A viruses (IAV) have been reported in wild lagomorphs in environments where they share resources with waterfowl. Recent studies have conclusively shown that a North American lagomorph, cottontail rabbits (*Sylvilagus* sp.), become infected following exposures to IAVs and can shed significant quantities of virus. However, the minimum infectious dose and the efficiency of various routes of infection have not been evaluated. Thirty-six cottontail rabbits were used in a dose response study assessing both the oral and nasal routes of infection. The nasal route of inoculation proved to be the most efficient, as all cottontail rabbits shed viral RNA following inoculations with doses. The oral route of inoculation was less efficient, but still produced $\geq 50\%$ infection rates at relatively low doses. These results suggest that cottontail rabbits are highly susceptible to IAVs with low exposure doses that have been routinely observed in environments contaminated by waterfowl.

The Refugio Oil Spill: An Overview of Wildlife Effects and Response

09:00 - Thursday, 27th July, Solar Square

Michael Ziccardi, Holly Gellerman, Sarah Wilkin, Laird Henkel, The OWCN Response Team

1. Oiled Wildlife Care Network; Wildlife Health Center; UC Davis, 2. California Department of Fish and Wildlife, Office of Spill Prevention and Response, 3. National Marine Fisheries Service, NOAA Fisheries

In May 2015, oiled wildlife professionals quickly mobilized to respond to wildlife at risk from the rupture of Plains Pipeline 901 near Refugio State Beach, California. California's Oiled Wildlife Care Network (OWCN) administered by UC Davis, in concert with the California Department of Fish and Wildlife – Office of Spill Prevention and Response (CDFW-OSPR) and NOAA's National Marine Fisheries Service (NOAA-NMFS), rapidly began to search for, recover, stabilize, and transport to rehabilitation, oiled birds and marine mammals throughout the greater Santa Barbara region. Between 19 May and the conclusion of wildlife operations, 21 of the OWCN's 35 Member Organizations were activated, accounting for 5 different facilities for stabilization and primary care and the mobilization of more than 180 staff and volunteers. In all, more than 260 birds and 160 marine mammals were collected during this effort. This presentation will provide an overview of California's oiled wildlife response program, the activities of the Wildlife Branch for this incident (including mobilization and activation of staff and facilities), and an overview of effects noted both during the spill and based on data collected through post-release survival studies on pelicans and sea lions.

Spontaneous infections of *Mycobacterium marinum* in Japanese original amphibians

09:00 - Thursday, 27th July, Solar Square

Tokuma Yanai, Mari Yamauchi, Misato Tanaka, Mohie Haridy, Hiroki Sakai, Shiomi Yoshida, Takayuki Wada

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Background: *Mycobacterium (M.) marinum* is a slow-growing environmental mycobacterium, which is associated with granuloma formations in aquarium and wild fishes, and is a zoonotic agent causing granulomatous lesions often occurred in the hands and feet following exposure of abraded skin to infected water. Outbreaks of *M. marinum* was reported in a commercial breeding farm of bullfrogs (*Rana catesbeiana*) in Brazil with skin lesions and disseminated granulomatous lesions which were observed in both symptomatic and asymptomatic frogs (Ferreira et al., 2006).

Results: Total 13 Japanese green tree frogs (*Rhacophorus arboreus*) which were exhibited in an aquarium were sporadically found dead or moribund from 2012 to 2016. Grossly, various degrees of tan-yellow multiple nodular foci were observed in the liver and spleen, heart, lungs, ovaries and kidneys, as well as splenomegaly and hepatomegaly. Histologically, two major types of lesions were observed: one was multifocal necrotic foci with numerous acid-fast bacilli in the vicinity of the necrotic center, and another type was granuloma dominant lesions in the liver, spleen, kidneys, lungs, intestine and ovaries. *Mycobacterium* spp. was cultured from 3 dead or moribund frogs. They were identified as *M. marinum* by colony growth rate and photochromogenicity and DNA sequencing. A Japanese fire belly newt (*Cynops pyrrhogaster*) in the Salamandridae family endemic to Japan, and maintained in the same aquarium with infected frogs, was found dead. Grossly, the two newts had various degrees of visceral nodular lesions. Histologically, there were various degrees of granulomas correlated with various densities of acid-fast bacilli.

Discussion and conclusions: These findings indicated possible fatal mycobacteriosis of *M. marinum* in some endangered species of amphibians like Japanese green tree frogs, as well as concern of zoonotic infection to aquarium keepers. It is necessary to clarify the route of transmission via watering systems in the aquarium.

Tick-borne encephalitis virus in wild cervids in Norway: sentinels for human and production animals' health in a ONE HEALTH approach

09:00 - Thursday, 27th July, Solar Square

Carlos Das Neves, Katrine Mørk Paulsen, Faisal Suhel, Eriq Granquist, Kjell Handeland, Knut Madslie, Åshild Andreassen

1. Norwegian Veterinary Institute, 2. Norwegian Institute of Public Health, 3. Norwegian University of Life Sciences

Tick-borne encephalitis virus (TBEV) is among the most important emerging vector-borne diseases in Europe, transmitted by the hard tick *Ixodes ricinus*. Factors like climate change, human behaviour and migrating animals are involved in the distribution of both the tick and the virus. The main route of disease transmission to humans is through tick bites, but wild- and production animals are also susceptible to infection. One theory is that wild animals can serve as sentinels/ early warning systems for virus transmission to humans and production animals. 653 serum samples were collected in 15 of the 19 counties in mainland Norway from wild reindeer, moose, roe deer and red deer. Several thousand nymphs and adult ticks were collected from multiple locations all over Norway, and more than 100 milk- and serum samples were collected from dairy farms in areas where ticks are abundant.

The TBEV seroprevalence (IgG) in cervids shows that 32 of 653 tested sera had antibodies. The seropositive animals originated in different areas of the country, including areas where human TBE cases have not yet been reported.

The Estimated Pooled Prevalence (EPP) and the minimum infection rate (MIR) were calculated, with MIR ranging from 0 to 21% in adults and from 0 to 3% in nymphs (EPP up to 4% in nymphs). Of the approximately 100 analysed bovine milk samples (individuals), preliminary PCR results reveals some TBEV positive samples from all farms and the impact of these findings requires further studies.

These results seem to indicate that TBEV is circulating in wild- and production animals, and further studies should be conducted to evaluate the importance of these animals in the maintenance and transmission dynamics of TBEV in Norway and elsewhere.

Perfil metagenómico 16S rRNA de las comunidades bacterianas del ácaro *Ornithodoros turicata* y su potencial como vector de la tortuga *Gopherus flavomarginatus*

09:00 - Thursday, 27th July, Solar Square

Karla Nohemí Villa Vázquez, Cristina García De la Peña, Veronica Ávila Rodríguez, Felipe Vaca Paniagua, Clara Díaz Velasquez, Luis Valenzuela-Núñez

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3. Laboratorio Nacional en Salud: Diagnóstico Molecular y Efecto Ambiental en Enfermedades Crónico-Degenerativas, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México,
4. Laboratorio de Biología y Ecología Forestal, Facultad de Ciencias Biológicas, Universidad Juárez del Estado de Durango

Ornithodoros turicata es una garrapata argásida de importancia médica y veterinaria que se reconoce como vector de bacterias causantes de diversas enfermedades en fauna silvestre y en humanos. Su distribución abarca regiones áridas del sur de los Estados Unidos y en América Latina. Es una especie que ha sido reportada como ectoparásito de la tortuga *Gopherus flavomarginatus* en la Reserva de la Biosfera Mapimí (RBM) en Durango, México. Para este trabajo se planteó el objetivo de determinar las comunidades bacterianas que alberga esta garrapata y su relación con las bacterias encontradas en sangre de *G. flavomarginatus*. En 2016 se realizó un análisis metagenómico de las regiones V3-V4 del gen 16S rRNA de 30 garrapatas colectadas en la RBM, se secuenciaron con MiSeq Illumina® y para el análisis de los datos se usó el software QIIME con la referencia de EzBioCloud. Se obtuvieron 97,192 secuencias correspondientes a 13 phyla (Proteobacteria 64%, Actinobacteria 23.5%, Firmicutes 10%) y 325 géneros siendo el más abundante el género *Midichloria* con 56%, seguido por *Streptomyces* (7%), *Anaplasma* (6%), *Novcardioides* (5%) y *Clostridium* (4%). En un estudio previo se analizó sangre de *G. flavomarginatus* y se identificaron 340 géneros entre los cuales se encuentran los mismos que en *O. turicata* a excepción del género *Midichloria*. Con estos resultados se infiere que existe una relación simbiótica vector-hospedero entre *Ornithodoros turicata* y *G. flavomarginatus*, lo cual coincide con lo reportado por diversos autores que señalan a esta garrapata como vector potencial de bacterias en reptiles y que la reportan como ectoparásito de *G. flavomarginatus* en la RBM. Este es el primer estudio que determina las comunidades bacterianas de *O. turicata* a nivel metagenómico, siendo ectoparásito de *G. flavomarginatus*; estos resultados serán considerados en un análisis posterior del estado general de salud de esta tortuga.

Microbiota bacteriana fecal del coyote (*Canis latrans*) por secuenciación 16S rRNA en la Reserva de la Biosfera Mapimí, México

09:00 - Thursday, 27th July, Solar Square

Sergio Barraza-Guerrero, Cristina García De la Peña, Karla Nohemí Villa Vázquez, Felipe Vaca Paniagua, Clara Díaz Velasquez, Amorita Ivonne Salas-Westphal, Veronica Ávila Rodríguez, Luis Valenzuela-Núñez

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El uso de técnicas moleculares como la secuenciación masiva del gen 16S rRNA está incrementado el conocimiento de las bacterias que componen la materia fecal de los vertebrados sin necesidad de aislamientos. El coyote (*Canis latrans*) es un carnívoro oportunista cuya su dieta es extremadamente variada. Han sido capaces de ocupar una gran cantidad de hábitats ampliando su área de distribución y ocupando casi toda América del Norte. Para esta especie se han realizado estudios de bacterias fecales mediante técnicas tradicionales (medios de cultivo) pero no por metagenómica 16S rRNA. En el 2016, se colectaron muestras fecales de coyote en la Reserva de la Biosfera Mapimí. Se extrajo el DNA bacteriano y se amplificó la región V3-V4 del gen 16s rRNA; los amplicones fueron secuenciados con MiSeq de Illumina®. Se utilizó QIIME para el análisis de unidades taxonómicas operacionales (OTUs), con EzBioCloud como referencia. En promedio se obtuvieron 25,602 secuencias; nueve phyla (Fusobacteria 67%, Firmicutes 26%), 19 ordenes (Fusobacteriales 67%, Clostridiales 26%), 27 familias (Fusobacteriaceae 67%, Lachnospiraceae 9%, Clostridiaceae 7%) y 91 géneros (*Fusobacterium*, *Clostridium*, *Collinsella*, *Blautia*, *Anaerobiospirillum*, *Helicobacter*, *Sporobacter*, *Faecalibacterium*, *Paeniclostridium*, *Eubacterium*, *Eisenbergiella*, *Slackia*, *Butyricoccus*, *Oribacterium*, *Hydrogenoanaerobacterium*, *Pseudoflavonifractor*, *Coprococcus*, *Acholeplasma*, *Ruminococcus*, *Campylobacter*, *Lachnospira*, *Oscilibacter*, *Succinivibrio*, *Caproiciproducens*, *Sphingomonas*, *Olsenella*, *Dorea*, *Akkermansia*, *Adlercreutzia*, *Anaerofilum*, *Parvimonas*, *Cellulosilyticum*, *Marvinbryantia*, *Rubellimicrobium*, *Novosphingobium*, *Microcoleus*, *Eggerthella*, *Paraclostridium*, *Nocardioides*, *Anaerotruncus*, *Hydrogenispora*, *Tepidisphaera*, *Brevundimonas*, *Methylobacterium*, *Terrisporobacter*, *Murimonas*, *Romboutsia*, *Paracoccus*, entre otros). El perfil taxonómico de las bacterias fecales del coyote obtenido en este estudio amplía significativamente lo ya reportado por algunos autores mediante aislamientos. El género más abundante fue *Fusobacterium* (67%), organismos zoonóticos de gran importancia al estar relacionada con enfermedades como el síndrome de Lemierre e infecciones producidas por mordidas de animales.

Molecular investigations on piroplasm species in sika deer (*Cervus nippon yesoensis*), Japan

09:00 - Thursday, 27th July, Solar Square

*Mohamed Moustafa, Elzahara Elbaz, Kyunglee Lee, Wessam Mohamed, Ryo Nakao, Michito Shimozurua,
Mariko Sashika, Toshio Tsubota*

1. Hokkaido University, 2. Mansoura University, 3. National Institute of Fisheries Science

Babesia and *Theileria* species are apicomplexan tick-borne hemoprotozoan parasites that have a veterinary and zoonotic importance. In order to investigate the prevalence and genetic diversity of these parasites, a total of 269 sika deer blood DNA samples collected from Hokkaido, Japan, were examined for *Babesia* and *Theileria* species by touch-down PCR targeting the 18S rRNA gene. Reverse line blot (RLB) hybridization was then used to detect 16 piroplasm species. The results revealed that 95.5 % (257/269), 94.1 % (253/269), 14.1 % (38/269), 87.7 % (236/269) and 11.5 % (31/269) of the examined PCR products hybridized with the probes which were designed to detect all *Babesia* and *Theileria* spp., all *Theileria* spp., all *Babesia* spp., *Theileria* sp. Thrivae and *Babesia divergens*-like, respectively. The 18S rRNA partial gene sequences were divided into *Theileria* sp. Thrivae, *T. capreoli*, *B. divergens*-like and an undescribed *Babesia* species. This study showed the first detection of *T. capreoli* and the undescribed *Babesia* sp. from Japan. Therefore, more studies are required to understand the ecology of the newly detected tick-borne pathogens in Hokkaido.

Garrapatas (*Acari: Argasidae, Ixodidae*) Como Vectores De Patógenos En Chile

09:00 - Thursday, 27th July, Solar Square

Daniel González-Acuña, Sebastián Muñoz-Leal, Lucila Moreno

1. Universidad de Concepción, 2. Universidad de Sao Paulo

Las garrapatas son ectoparásitos hematófagos obligados de los vertebrados que además de provocarles un daño mecánico, causan dermatitis y estados de anemia, pueden además ser vectores de enfermedades que pueden llegar a provocar la muerte de sus hospedadores. Se describen en el mundo hasta la fecha 208 especies de la familia Argasidae (garrapatas blandas), y 722 de la familia Ixodidae (garrapatas duras). En el neotrópico, se han documentado 208 especies de garrapatas, 92 blandas y 116 duras. En Chile, el conocimiento biogeográfico y taxonómico de las garrapatas ha aumentado notoriamente gracias a dos proyectos de investigación de nuestro grupo que ha permitido realizar colectas en las 14 ecoregiones descritas para el país, incluyendo el territorio antártico, todo esto en 360 días de campaña incluidos en siete años de estudio. Hemos desarrollado ciclos biológicos completos de cuatro especies de garrapatas blandas, además identificado cinco nuevas especies y una serie de nuevas localidades para diferentes especies de garrapatas. Por medio de estas investigaciones, la diversidad de garrapatas para Chile ha aumentado en más del 30% en los últimos 10 años, llegando a ser actualmente no menos de 31 especies para Chile. En relación a patógenos, para Chile se describen a *Otobius megnini* como potencial portador de *Coxiella burnetii* y produce otitis en humanos; *Argas neghmei* que causa eritema, prurito y decoloración de la piel; *Rhipicephalus sanguineus* sensu lato ha sido registrada en humanos y es una especie abundante en animales domésticos, principalmente en perros. Hallazgos importantes corresponden a la descripción de las bacterias *Borrelia chilensis* en *Ixodes stilesi* en los bosques del sur y *Rickettsia* sp. en *Amblyomma parvitarsum* en el altiplano del norte de Chile. Finalmente, estudios en desarrollo contribuirán al entendimiento del rol de las garrapatas nativas de Chile como vectores de microorganismos. Financiamiento Proyecto Fondecyt 1130948 e INACH T-12-13.

Carcinoma De Células Escamosas En Lagarto Verde Europeo (*Lacerta Viridis*)

09:00 - Thursday, 27th July, Solar Square

Pablo Regner, Andrea Schapira, Francisco Zapata, Leonardo Minatel

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El lagarto verde europeo es criado en cautiverio tanto para investigación como para animal de compañía. La información obtenida a partir de estos planteles, podría ser de utilidad para el trabajo con animales en vida libre. El objetivo de este trabajo es describir un caso de carcinoma de células escamosas en un ejemplar de esta especie. El individuo, un macho reproductor de 6 años, presentó una deformación en más en la zona labial izquierda. Había recibido tratamiento antibiótico y antiinflamatorio por 15 días sin obtener respuesta. Se le realizó una punción con aguja fina sin un resultado concluyente. Por tal motivo, se procedió a intervenirlo quirúrgicamente. Se lo premedicó con tramadol 5 mg/kg y meloxicam 0,5 mg/kg e indujo con ketamina 20 mg/kg y midazolam 1,5 mg/kg, posteriormente se lo mantuvo intubado con isoflurano al 3,5%. Finalmente se procedió a extraer el tejido afectado tomando el mayor margen de seguridad que su localización permitía. La tumoración nodular poseía 1,5 cm de diámetro, superficie irregular y consistencia firme-elástica. La observación microscópica evidenció que estaba formada por una proliferación de células epiteliales formando islas y cordones en la dermis. Las células presentaban abundante cantidad de citoplasma acidófilo, con núcleos redondeados y grandes, cromatina laxa y nucléolos evidentes. Varias islas exhibían, en el centro, queratina, en muchos casos conservando los núcleos. Se observaron entre 1 a 2 figuras mitóticas por campo de 400X. El grado de pleomorfismo y anaplasia fue elevado. Entre las células neoplásicas se encontró baja cantidad de tejido conectivo. El crecimiento fue infiltrativo, no encontrándose áreas libres de células neoplásicas en los bordes ventrales. El diagnóstico definitivo fue carcinoma de células escamosas. No se observaron recidivas durante al menos 6 meses. Siendo escasa la información publicada sobre patologías oncológicas en esta especie, la información obtenida es de suma importancia.

Registro de *Mycoplasma* spp. en la cavidad oral de la tortuga *Gopherus flavomarginatus* por secuenciación 16S rRNA en la Reserva de la Biosfera Mapimí, México

09:00 - Thursday, 27th July, Solar Square

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Las bacterias *Mycoplasma agassizii* y *M. testudineum* son causantes de la enfermedad del tracto respiratorio superior en las tortugas terrestres *Gopherus agassizii* y *G. polyphemus*. Este padecimiento ha mermado drásticamente las poblaciones de estas tortugas en EUA, provocando preocupación en cuanto a su conservación. La tortuga del Bolsón, *G. flavomarginatus* habita en el Desierto Chihuahuense, es endémica y se encuentra en peligro de extinción. Debido a su estatus de vulnerabilidad se caracterizó su perfil bacteriológico oral en la Reserva de la Biosfera Mapimí para determinar la presencia de bacterias potencialmente patógenas como *Mycoplasma* spp. En el 2015-2017, se colectaron muestras orales de 12 individuos de *G. flavomarginatus*. Se extrajo el DNA bacteriano, se amplificó la región V3-V4 del gen 16s rRNA y los amplicones fueron secuenciados con MiSeq de Illumina®. Las unidades taxonómicas operacionales (OTUs) se analizaron con QIIME y EzBioCloud como referencia. En promedio se obtuvieron 146,164 secuencias: 34 phyla (Proteobacteria 63%, Actinobacteria 14%), 99 clases (Gammaproteobacteria 44%, Alphaproteobacteria 14%), 194 órdenes (Pasteurellales 25%, Pseudomonadales 10%), 436 familias (Pasteurellaceae 25%, Moraxellaceae 10%), 1,410 géneros (*Chelonobacter*, *Acinetobacter*, *Citrobacter*, *Paracoccus*, *Rothia*, *Bergeyella*, *Rubellimicrobium*, *Kocuria*, *Enterococcus*, *Staphylococcus*, *Corynebacterium*, *Sphingomonas*, *Hymenobacter*, *Petrimonas*, *Facklamia*, *Aerococcus*, *Microcoleus*, *Modestobacter*, *Streptococcus*, *Pseudomonas*, *Roseomonas*, *Brachybacterium*, *Chryseobacterium*, *Geodermatophilus*, *Escherichia*, *Clostridium*, *Kineococcus*, *Tepidiphraera*, *Exiguobacterium*, *Methylobacterium*, *Deinococcus*, *Microvirga*, *Actinoplanes*, *Neisseria*, *Sphingobacterium*, *Craurococcus*, *Micromonospora*, *Pasteurella*, entre otros). Se registró *Mycoplasma* spp. con una media de abundancia relativa de $9.42 \times 10^{-6}\%$. Este género mostró una prevalencia en las tortugas del 25%. Este registro es importante para la conservación de *G. flavomarginatus*, ya que se sabe que *Mycoplasma* es oportunista en condiciones de inmunosupresión. Actualmente, esta tortuga se enfrenta a cambios climáticos globales negativos (años de sequía extrema) que al generar estrés fisiológico puede ocasionar vulnerabilidad a este tipo de infecciones bacterianas. Este registro debe ser considerado en las estrategias de conservación de esta tortuga.

Vasectomy In Patterson's Elands (*Taurotragus Oryx Pattersonianus*) As A Tool Of Population Control

09:00 - Thursday, 27th July, Solar Square

Waseem Ashraf, Abid Mehmood, Mubarak Hesseb Elrasol, Bilal Kabeer, Muhammad Jawad Jilani, Muhammad Arslan Asadi, Iftikhar Raza, Ibrahim Al Nassan, Buthaina Al Qubaisi, Pavla Hejmanova

1. Barari Forest Management, 2. Barari Forest Management; Czech University of Life Sciences, Prague, 3. Barari Forest Management; Czech University of Life Sciences, Prague, 4. Tourism Development and Investment Company, 5. Czech university of Life Sciences

Taurotragus oryx pattersonianus is one of the charismatic game species and Sir Bani Yas Island holds a population of 1500 free ranging individuals of which 700 are males; sharing the habitat of 4200 hectares with 18 other ungulate species including oryx, gazelles, giraffes and deer. They are breeding very well under semi-captive conditions of Sir Bani Yas Island, leading to over population. Culling or castration of dominant males disrupts complex social structure of elands in which the dominant males are involved in most of the mating and protect their harem from other males. Vasectomy was experimented as viable tool to minimize unwanted population increase. Vasectomy is a safe and quick surgical procedure with comparatively less complications for male sterilization. Anesthesia was achieved by using combination of Thiafentanyl hydrochloride at a dose of 0.01 mg/kg, Xylazine hydrochloride 0.2 mg/kg, and ketamine hydrochloride 0.14 mg/kg via dart. A total of 42 males were vasectomised by casting them on left lateral recumbency. Vas deferens was located by palpation and a small incision was made at neck of the scrotum. Vascular and avascular portions were separated via blunt dissection, vas deferens were clamped with 2 artery forceps then severed in between and ligated with No.1-0 polyglycolic acid sutures at both ends. Incision site was closed by No. 1-0 polyglycolic acid sutures. An injection of Naltrexone at a dose of 30 mg for every 1 mg thiafentanyl and Yohimbine 0.1 mg/kg given as a antagonists to recover from sedation.

Lyssavirus polyhostality: criteria for reservoir capacitation in wildlife disease emergence and perpetuation?

09:00 - Thursday, 27th July, Solar Square

Charles Rupprecht, Ivan Kuzmin

1.LYSSA LLC, 2.UTMB

Lyssaviruses are single-stranded, negative-sense, non-segmented, bullet-shaped RNA viruses and the etiological agents for rabies, a major but neglected zoonotic disease. Plans for the global elimination of canine rabies by 2030 are well underway. Will such large-scale elimination of dog rabies in the Americas, Eurasia and Africa open niches for other hosts, especially with the probability for re-establishment of canine rabies? If so, are there informative criteria for enhanced epidemiological surveillance that may allow early identification of suitable species that are, or may become, functional lyssavirus reservoirs? Considering the options of polyhostality, several fundamental anatomical, physiological virological and ecological attributes were reviewed from the recent peer reviewed literature (including case reports, outbreaks and primary research studies) and selected as appearing critical for reservoir establishment. These characteristics included: a complex central nervous system (excluding all non-animals); homeothermy/heterothermy (excluding all invertebrates and cold-blooded vertebrates); functional teeth (largely excluding all extant birds); relative distribution and abundance (excluding all highly endangered mammals); and sociality (excluding large apex predators and typically solitary species). Currently, all known wild reservoirs are also vectors, but not all vectors are also reservoirs. Relevant host contact and exposure parameters, with viral replication and excretion are primary criteria for success. Using Australia as an insular example, realistic representation among the marsupials appears remote. Potential explanations for exclusion of other groups, such as certain representatives among the insectivores, rodents, non-human primates, hoofed stock, felids, mustelids, viverrids, pinnipeds, etc., are less clear. Given the global distribution of rabies, establishment of clear surveillance criteria and improved laboratory methodology will allow wildlife disease professionals to better participate in current disease prevention plans as well as to identify novel viral species, hosts and cycles in a One Health context.

Field and lab studies to investigate the role of avian malaria in modulating West Nile virus transmission

09:00 - Thursday, 27th July, Solar Square

Gabriel Hamer

1. Texas A&M University

Multiple extrinsic and intrinsic factors drive the ability of mosquitoes to transmit arboviruses of public health concern. One such intrinsic factor is the presence of symbiotic organisms or pathogens that are capable of modulating the infection, dissemination, and transmission of viruses. Our long-term research studying West Nile virus transmission and amplification demonstrates that the *Culex* mosquito vectors and wild avian amplification hosts are infected with a suite of other pathogens, including viral symbionts, Haemosporida, trypanosomes, and helminths. Most notable is the high prevalence of avian malaria (multiple lineages of *Plasmodium* spp.) which co-occur with WNV but the consequences of mosquitoes ingesting *Plasmodium* concurrently with WNV or prior to a WNV infectious blood meal is unknown. We have established *Plasmodium relictum* in a Canaries and *Culex* mosquitoes and are conducting experimental co-infections to evaluate the effect of *Plasmodium* infection on WNV dissemination, salivary gland infection, and transmission. Our long-term goal is to derive empirical data from these laboratory infection experiments combined with our field prevalence studies to parameterize mathematical models such as vectorial capacity and R_0 to see if these within host interactions scale-up to have population level consequences.

Bat Ectoparasites As Potencial Vectors Of Pathogens To Humans

09:00 - Thursday, 27th July, Solar Square

María Magdalena Ramírez Martínez, Will Reeves, María Orlova, Martha Pilar Ibarra López, Thomas Yuill

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Recently, there are more studies in bat ectoparasites related to taxonomy and abundance in different species, unfortunately they are poorly studied as vector of pathogens to humans. Mexican bats are not the exception; recently done work in the south coast of Jalisco shows the big diversity of this group of ectoparasites. Streblidae are rarely studied as vectors, but there are some reports about the *Trichobius major* positive for *Bartonella* sp. However, they are unlikely to infect humans. In this work we want to report those species that can be vectors of some pathogens that may cause a diseases, which can be found in México. We have collected bats from 2011 to 2015 with mist nets in different sites of southwestern Jalisco, México. We have different types of vegetation as *Quercus* forest, disturbed areas, deciduous forest, riparian vegetation, farmland (sugarcane, corn, banana, pineapple, coffee). Ectoparasites were collected using tweezers and placed in vials with 70% of alcohol. We found three families of ectoparasites, Acari (Argasidae, Laelapidae and Spinturnicidae) and six species of mites. With these results we extend the known range for some species into Jalisco. Although the taxonomy of mammal's mites is well understood, there are reports of Anaplasmataceae and *Bartonella* spp in bat mites. Actually some bat mites can be vectors of filarial nematodes of bats in the genus *Litomosoides*. With our results, we found species of bat ectoparasites that can potentially be vectors of some pathogens to humans. In this area we have a high diversity of flying mammals and ectoparsites, there are reports of filarial worms in *Glossophaga* sp, but we don't know anything about the vectors. It's necessary to make an effort to understand the importance of bat ectoparasites as vectors of some pathogens that could be a risk for humans and natural fitness for bats.

Estado Actual Del Conocimiento De Los Piojos (*Phthiraptera*) En Aves Silvestres De Chile

09:00 - Thursday, 27th July, Solar Square

Daniel González-Acuña, Armando Cicchino

1.Universidad de Concepción, 2.Universidad de Mar del Plata

Los Piojos (Insecta: Phthiraptera), además de provocar un daño mecánico a sus hospedadores, adquieren importancia sanitaria por ser vectores de diferentes agentes bacterianos y además ser hospedadores intermediarios de parásitos tales como las Filarias. Actualmente, los estudios de piojos se están abocando al estudio del proceso evolutivo entre aves y ectoparásitos, pudiendo vivir varias especies distintas en un mismo hospedero, mientras cada Phthiraptera tiene su hospedador específico. Esto, cobra gran interés en Chile ya que la información referente a la diversidad de este tipo de organismos ha sido limitada, sin embargo este hecho se ha revertido durante el último decenio.

Realizamos una revisión sistemática de los trabajos referenciados hechos hasta ahora en piojos en Chile y de esta forma ordenar la información de este grupo en el país. Recopilamos un total de 73 referencias publicadas entre los años 1849 y 2017. En relación a la diversidad de este grupo de insectos, se han registrado hasta la fecha 196 especies de piojos en 105 especies de aves hospedadoras representadas en 20 órdenes y 46 familias. Al clasificar taxonómicamente los piojos descritos en Chile, 69 corresponden al suborden Amblycera, 127 al suborden Ich-nocera. Las familias más representadas corresponden a Philopterae y Menoponidae con 143 especies.

En aves los grupos de hospedadores más representados corresponden a las familias Tinamidae, Procellariidae, Phalacrocoracidae y Columbidae. Las especies con mayor cantidad de registros han sido: *Gallus gallus domesticus*, *Larus dominicanus*, *Fulmarus glacialis*, *Puffinus griseus* y *Zenaidura macroura*.

La mayor parte de los estudios de piojos en Chile han sido de tipo descriptivos y/o han tratado aspectos taxonómicos. El conocimiento de la ecología de este grupo de artrópodos es reducido y ha sido limitado. Estudios preliminares muestran una relación de las intensidades de infestación con el sexo de hospedador y localidades donde estos viven.

Haemosporidios (*Haemoproteus*, *Plasmodium* y *Leucocytozoon*) en aves del Norte de Chile: variaciones de prevalencia ecorregionales y estacionales

09:00 - Thursday, 27th July, Solar Square

L. Gonzalo Torres-fuentes, Lucila Moreno, Daniel González-Acuña

1.Universidad de Concepción

Los Haemosporidios son protozoos endoparásitos que infectan en su estado inmaduro a anfibios, reptiles, mamíferos y aves, utilizando artrópodos (Insecta: Díptera) como sus hospedadores definitivos. En aves son el grupo de hemoparásitos más estudiados en cuanto a ecología y evolución, siendo detectados en todos los continentes, excepto Antártica. En Chile los estudios referidos a hemoparásitos en fauna silvestre han sido escasos, mas aún aquellos que evalúen conceptos ecológicos de localidad y estación. El objetivo de este estudio fue determinar la prevalencia de Haemosporidios en aves del Norte de Chile y determinar sus variaciones de prevalencia según ecoregión y estación. Para esto, entre Marzo 2010 y Agosto 2012 se visitaron 14 localidades (18°11'S, 31°32'S) del norte de Chile, abarcando 6 ecorregiones (Desérticas de litoral y de interior; Tropical marginal y de altura; Mediterráneas árida y per-árida). Fueron capturados un total de 1035 aves (59 especies, 13 familias) mediante el uso de redes niebla. De cada ave se obtuvo un frotis sanguíneo el cual fue fijado con metanol, teñido con solución Diff-Quick y posteriormente observado al microscopio. Mediante el Software Quantitative Parasitology 3.0 se determinó prevalencia y se realizaron comparaciones de estas, considerando un valor de $p < 0.005$ como significativo. Se obtuvo una prevalencia general del 14,4% (149/1035; IC: 0.1231 – 0.1669). Los géneros de Haemosporidio registrados fueron *Haemoproteus*, *Leucocytozoon* y *Plasmodium* con prevalencias de 13,8%, 0,5% y 0,1% respectivamente. Las prevalencias se diferenciaron significativamente entre ecorregiones, estaciones del año y especies de ave. Solo se registró infección por *Leucocytozoon* en *Sephanoides sephanioides*. La gran dominancia de *Haemoproteus* respecto a los otros géneros podría ser explicada por las características del ambiente que favorecen la transmisión de este parásito en particular.

Estado Actual del Conocimiento de los Patógenos en Antártica: Identificación de Vacíos y Oportunidades para Investigar

09:00 - Thursday, 27th July, Solar Square

Daniel González-Acuña, Michaela Blyton, Erli Costa, Meagan Dewar, Rachael Gray, Robert Harcourt, Gary Miller, Michelle Power, Ralph E.T. Vanstreels, Andrés Barbosa

1. Universidad de Concepción, 2. Sydney University, 3. Universidad Estadual do Rio Grande do Sul, 4. Deakin University, 5. Macquarie University, 6. University of Tasmania, 7. University of Sao Paulo, 8. Museo Nacional de Ciencias Naturales

Los patógenos, juegan un activo rol en la regulación de las poblaciones de sus hospedadores. Pueden provocar muertes masivas y afectar rasgos de su historia de vida. Además, pueden aumentar la vulnerabilidad a las toxinas, otros patógenos oportunistas y también parásitos, o aún reducir la capacidad de los animales para soportar cambios ambientales extremos. La información sobre el estado de salud de aves y mamíferos marinos en la Antártida es crucial para evaluar el riesgo de brotes de enfermedades y posibles eventos de mortalidad en la población, de los cuales se han presentado pocos en este continente, sin embargo con el aumento de la actividad humana y los cambios ambientales en curso durante los últimos años, existe un aumento en el riesgo de epidemias de enfermedades. Además, las especies migratorias pueden contribuir a la propagación de organismos patógenos en la Antártida (ej. reciente caso de ingreso de virus influenza H5). Por lo tanto, la información de referencia sobre qué patógenos y parásitos están presentes en la Antártida, su prevalencia e intensidad de la infección, es necesaria. Esta información es hasta ahora escasa y fragmentada a pesar de algunas recientes revisiones. Como tal, los esfuerzos deben dirigirse hacia el aumento del conocimiento sobre no sólo la presencia / ausencia de enfermedades o parásitos dentro de la fauna antártica, sino sobre su potencial para causar enfermedad clínica y mortalidad. En esta presentación revisamos toda la información publicada sobre patógenos y enfermedades en la fauna antártica y entregamos una visión general del conocimiento actual de las enfermedades y la presencia de patógenos en la fauna antártica. También analizamos la distribución espacial y temporal de los estudios por el hospedador, el patógeno y el método de análisis y analizamos las lagunas de conocimiento sobre este tema y las oportunidades futuras de investigación.

Momificación de fetos y adenocarcinoma papilar ovárico en *Boa constrictor constrictor*

09:00 - Thursday, 27th July, Solar Square

Pablo Regner, Alberto Vartabedian

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La información sobre enfermedades reproductivas en reptiles se centra principalmente en patologías como distocias, prolapsos de hemipenes, oviducto o cloaca o celomitis producidas por caída de contenido del tracto reproductivo (folículos, huevos, secreción del oviducto) en el celoma. La descripción sobre otro tipo de patologías reproductivas es escasa. Este trabajo busca describir un caso de momificación de fetos en forma conjunta con un adenocarcinoma ovárico en *Boa constrictor constrictor*. Una hembra reproductora, de 10 años, con historia de parición de 12 crías, 8 meses antes, había fallecido hacía 6 horas sin presentar ningún signo aparente de enfermedad. Se procedió a realizar la necropsia. Al ingreso al celoma se observó gran cantidad de líquido libre, con pequeños coágulos y de color borraivino. Ambos ovarios estaban aumentados de tamaño y repletos de líquido serohemorrágico, quedando poco tejido sólido. El ovario derecho estaba perforado. Dentro del oviducto derecho se encontraron dos deformaciones en más, de consistencia sólida de unos 9.5 cm por 5 cm de tamaño y de coloración amarronada. Al corte estaban compuestos por los tejidos momificados de los fetos, visualizándose material de consistencia terrosa circundando la columna vertebral, costillas, cabeza, restos de escamas y algunos órganos poco diferenciados. Los oviductos se encontraban edematosos y con líquido en su interior. Los pulmones se encontraban con gran cantidad de secreción purulenta en su extremo craneal. El diagnóstico definitivo fue neumonía y adenocarcinoma papilar ovárico. La causa probable de muerte fue la ruptura del adenocarcinoma derecho, siendo las momificaciones un hallazgo. En la bibliografía consultada sólo se encontraron dos descripciones de adenocarcinoma papilar ovárico en serpientes y sólo una sobre momificaciones. Por tal motivo, consideramos que la unión de estas dos patologías en un paciente, es un caso raro y que su descripción podría contribuir al conocimiento de la medicina de reptiles.

Retrovirus associated with ethmoidal tumors in moose (*Alces alces*)

09:00 - Thursday, 27th July, Solar Square

*Erik Ågren, Mikhayil Hakhverdyan, Kjell Handeland, Turid Vikøren, Henrik Uhlhorn, Dolores Gavier-Widén,
Mikael Leijon*

1.National Veterinary Institute

Ethmoidal tumors in moose (*Alces alces*) always originate in the nasal mucosa adjacent to the ethmoidal bone causing a typical midline hole-in-the-head lesion in the frontal bone as the tumor erodes bone tissue of the in the upper nasal cavity. Penetration of the ethmoidal bone is followed by tumor masses compressing the frontal aspects of the brain, causing clinical CNS symptoms. The disease has been noted as sporadic cases since at least a century in Sweden, and appears to have been found in moose only in Sweden and Norway. The tumors are predominantly adenocarcinomas, but are occasionally classified as carcinosarcomas or sarcomas at histopathology. Viral etiology as a cause for this tumor growth has previously been suggested, due to similarities with nasal tumors of sheep and goats. Illumina MiSeq high-throughput sequencing technology was used to search for virus in archived frozen tumor tissue samples from 24 necropsied moose cases from Sweden and Norway. Nucleotide sequences related to the enzootic nasal tumor virus of goats, ovine enzootic nasal tumor virus, or Jaagsiekte sheep retrovirus were identified in all samples. These results suggest that a virus, tentatively named moose ethmoidal tumor retrovirus, is associated with the ethmoidal tumors of moose. If this virus causes the tumors leading to moose hole-in-the head-disease, it seems to be endemic in the moose population of the Scandinavian peninsula, as this specific type of tumor has not been reported in moose from other countries or continents. Further characterization of the tumors and immunohistochemical studies using retroviral antibodies are to be done, and attempts at virus isolation are ongoing.

High occurrence of incisor breakage in muskoxen (*Ovibos moschatus*) in the Canadian Arctic

09:00 - Thursday, 27th July, Solar Square

Fabien Mavrot, Sanchit Chopra, Samuel Sharpe, Ann Gunn, Mary Gamberg, Matilde Tomaselli, Lisa-Marie Lelerc, Stephanie Behrens, Susan Kutz

1. Faculty of Veterinary Medicine, 2. University of Calgary, Salt Spring Island, British Columbia, 3. Gamberg Consulting, Yukon, 4. Faculty of Veterinary Medicine, University of Calgary, 5. Government of Nunavut, 6. Government of the Northwest Territories, 7. University of Calgary

Dental health is crucial for wild ruminants as it is directly associated with food intake and is thus a determining factor for the nutritional condition and survival of an individual. Recent anecdotal observations of dental abnormalities in muskoxen (*Ovibos moschatus*) on Victoria Island, Nunavut, in the Canadian Arctic led us to initiate a study on muskox dental health.

In this pilot study, we aimed to investigate jaw health in hunted muskoxen from Victoria Island and on the Canadian mainland. We recorded cracked, broken and misaligned teeth, molar wear pattern, incisor height and jaw width as well as soft tissue and bone abnormalities.

In a total of 41 samples (eight incisor bars, 33 whole mandibles) collected between 2015-17, the most common findings were incisor cracks (34/41) and breakage (26/41). In contrast, premolar and molar breakage occurred only in 10/33 individuals. Incisor breakage in our sample set differed from normal tooth wear in that it affected predominantly central incisors and did not occur uniformly along the occlusal surface of the incisors. Our results also indicate that individuals from Victoria Island tended to have more broken incisors when compared with animals from the mainland ($p=0.002$). This is in contrast with results from a similar study conducted in the same areas in 1989-91 where incisor breakage and cracks was more frequent on the Canadian mainland. Finally, there was a strong association between occurrence of misaligned incisors and incisor breakage ($p<0.001$).

Causes of incisor breakage are still unclear but may be associated with vitamin or mineral deficiencies, genetic predisposition or mechanical wear due to changes in diet such as an increase in browsing on willow shrubs. This pilot study will establish a basis for a continued long-term monitoring of dental health in muskoxen of the Canadian Arctic.

Las enfermedades de *Acropora palmata* y su relación con fuentes de contaminación en el Caribe Mexicano

09:00 - Thursday, 27th July, Solar Square

Eduardo Navarro Espinoza, Lorenzo Alvarez Filip

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El coral cuerno de alce (*Acropora palmata*) es el principal formador de arrecifes en el Caribe. En décadas recientes sus poblaciones han disminuido rápidamente. Estos cambios se atribuyen a eventos epizoóticos de gran magnitud, protagonizadas por causados por las enfermedades de la banda blanca en la década de 1980s y la viruela blanca en 1990s. El aporte de patógenos y la reducción de la resistencia de los hospederos ocasionada por el exceso de nutrientes y aumento de la turbidez del agua se han descrito entre las principales causas de la aparición de enfermedades en los corales. El presente estudio evaluó la prevalencia de enfermedades del coral *A. palmata* en el Parque Nacional Arrecifes de Puerto Morelos (PNAPM) en relación con la cercanía a una fuente de contaminación puntual y el desarrollo costero. Para lo cual, se realizó un censo de las colonias de *A. palmata* en el PNAPM. Además, para evaluar el efecto de la fuente puntual de contaminación, se tomó como referencia la desembocadura de la laguna de Nichupté. La prevalencia de enfermedades de *A. palmata*, fue del 9.61%, siendo la enfermedad de la viruela blanca la que tuvo una mayor presencia con el 5.86% de colonias enfermas, mientras que la banda blanca se registró en el 3.82% de las colonias, valores más altos que los registrados en el resto del Caribe Mexicano. Asimismo, se encontró que existe una relación negativa entre la distancia a laguna de Nichupté y la prevalencia de la enfermedad de la viruela blanca, la cual podría estar sirviendo como transporte para los contaminantes y sedimentos contenedores del patógeno. Nuestros resultados son una muestra de los efectos adversos del desmesurado desarrollo costero del norte del estado de Quintana Roo sobre los arrecifes coralinos.

Aislamiento de espiroquetas intestinales del género *Brachyspira* de anseriformes que llegan a presas de agua de Guanajuato, México

09:00 - Thursday, 27th July, Solar Square

Enrique Corona-barrera, Marcela Areli Araiza Ortiz, Magda Hernández-rosales, Brenda Toledo-flores

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Espiroquetas intestinales (EI) del género *Brachyspira* han sido asociadas con trastornos intestinales en animales domésticos y el humano. Hay varias especies de EI de importancia veterinaria (p. ej., *B. hyodysenteriae*, *B. pilosicoli*, *B. intermedia*, *B. hamptonii*) y otras de importancia en medicina humana (*B. aalborgi*, *B. pilosicoli*). En reportes recientes se ha encontrado a las Anseriformes (aves migratorias) como reservorio natural de EI (Jansson *et al.*, 2011; Martínez-Lobo *et al.*, 2013). El objetivo de este trabajo fue determinar la presencia de EI (*Brachyspira* spp.) en aves migratorias que llegan a presas de agua del estado de Guanajuato, México. Mediante hisopos rectales (*Amies Charcoal Transport Swabs*, COPAN, Brescia, It) se colectaron 90 muestras de heces de aves migratorias Anseriformes (Anatidae) que llegan a algunas presas de agua de Guanajuato, México. Las muestras fueron sembradas en medio selectivo BSM, *Brachyspira Selective Medium* e incubadas en jarra anaeróbica usando GasPak (Oxoid, UK), a 42 °C durante 7 días. Una proporción de 38.8 % (35/90) de muestras produjeron crecimiento característico (actividad hemolítica y crecimiento en avanzada) de EI en cultivo (primoaislamiento), el cual fue confirmado por la observación de cuerpos espiroquetales Gram negativos en microscopio óptico. Aislamiento de EI de animales domésticos (de producción) y en humanos de comunidades rurales de Guanajuato en México se ha reportado (Corona-Barrera *et al.*, 2016). Sin duda la epidemiología de EI es compleja, ya que estos patógenos tienen la capacidad de colonizar a varios hospederos sean animales domésticos, de vida libre y al humano. Encontrar a las aves migratorias como reservorio de *Brachyspira* spp., abre la posibilidad de su transmisión a otras especies animales y al humano. Este trabajo representa el primer reporte en México de la presencia de EI (*Brachyspira* spp) en aves migratorias Anseriformes (Anatidae) que llegan a las presas de Guanajuato, México

The African (*Cape*) buffalo (*Syncerus caffer*) is a reservoir of important zoonotic diseases

09:00 - Thursday, 27th July, Solar Square

Elizabeth Cook, Eric Fèvre, Alice Kiyong'a, Velma Kivali, Francis Gakuya, David Ndeereh

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African buffalo (*Syncerus caffer*) have long been recognised as reservoirs of livestock pathogens including foot and mouth disease virus, *Theileria* sp. and *Trypanosoma* sp. Buffalo are also considered maintenance hosts of zoonoses such as *Mycobacterium* sp. and *Brucella* sp. This study investigated the seroprevalence of zoonotic pathogens in serum collected from buffalo in different regions of Kenya.

One hundred and seventy buffalo serum samples collected from different locations in central and southern Kenya were available for testing. Sera were tested for antibodies to *Brucella* sp using the Rose Bengal test; for antibodies to *Coxiella burnetii* by immunofluorescence antibody test and for antibodies to Rift Valley fever virus (RVFV) by competitive ELISA.

The apparent seroprevalence of antibodies to *Brucella* sp in the buffalo samples was 7.1% (95% CI 4.1-11.9); *C. burnetii* 54.1% (95% CI 46.6-61.4); and RVFV 22.1% (95% CI 15.9-29.7). The brucellosis seropositive animals were located in the southern semi-arid parts of Kenya; there were no brucellosis positive buffalo on private ranches where cattle were routinely vaccinated against brucellosis. The proportion of *C. burnetii* seropositive buffalo was high in all areas surveyed. RVFV seropositive buffalo were distributed across the surveyed areas with higher proportions of positive animals in central Kenya.

This is the first study to report a range of zoonoses in buffalo in Kenya. Further research identifying the epidemiology of zoonoses in buffalo needs to be conducted particularly with regard to the transmission of diseases between buffalo and domestic livestock.

Epizootic hemorrhagic disease in deer: using molecular analysis of no-see-um (Diptera: *Culicoides*) bloodmeals to incriminate vector species in Florida

08:00 - Friday, 28th July, Solar Square

Nathan Burkett-Cadena, Kristin Sloyer, Jason Blackburn, Erik Blosser, Bethany McGregor, Katherine Saylor, Samantha Wisely

1. University of Florida

In Florida USA Epizootic Hemorrhagic Disease virus (EHDV) has caused extensive mortality in wild and farmed white-tailed deer (*Odocoileus virginianus*) in recent years. Currently, no specific treatments or vaccines are available to protect white-tailed deer from this devastating virus. In addition, the specific no-see-um (Diptera: *Culicoides*) species that transmit EHDV in Florida are not yet known. Each of the 46 *Culicoides* species found in Florida have specific larval habitat and host affinities, which severely limits the use and efficacy of vector control for preventing EHDV transmission. Evidence of direct contact (blood-feeding) between the suspected vector species and the host animals is one of three major criteria for incriminating vectors of a pathogen. The current study represents PCR-based bloodmeal analysis of eighteen *Culicoides* spp. sampled from deer and cattle ranches in five Florida counties. *Culicoides* were trapped using blacklight traps and individual blood-engorged specimens were processed for host identification using PCR assays targeting amplification of vertebrate cytochrome b and 16s RNA genes, followed by Sanger sequencing. Results indicate that birds are preferred hosts of four species (*C. arboricola*, *C. crepuscularis*, *C. edeni* and *C. haematopodus*), while mammals are preferred by all other species. Ruminants were dominant hosts of six species (*C. venustus*, *C. pallidicornis*, *C. insignis*, *C. floridensis*, *C. edeni* and *C. debilipalpis*) of which only three species (*C. venustus*, *C. insignis*, and *C. debilipalpis*) took more than half of bloodmeals from deer and were also abundant at sampling sties. Identifying the larval habitats of these putative vector species should enable the development of biological, chemical and/or physical control strategies to reduce vector populations below thresholds that can maintain EHDV transmission. Ultimately, this information can be used to provide best management practices for land managers to protect white-tailed deer from EHDV.

Multispecies infection dynamics can have an important influence on Rift Valley fever epidemiology

08:00 - Friday, 28th July, Solar Square

Melinda Rostal, Noam Ross, Louise Matthews, Daniel Haydon, Sarah Cleaveland, William Karesh

1. EcoHealth Alliance and University of Glasgow, 2. EcoHealth Alliance, 3. Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow

Background: Rift Valley fever (RVF) outbreaks have severe economic and animal health impacts, yet they occur periodically (every 5-10 years). There is mounting evidence of low-level circulation of the virus in livestock during these inter-epidemic periods.

Objectives: This study investigates the impact of having slower-reproducing, less susceptible (buffalo) and faster reproducing, more susceptible (springbok) ruminants in a natural system on RVF disease dynamics.

Methods: Two host, two vector, deterministic, compartmentalized ODE models were developed to simulate the dynamics of an outbreak of RVF in a region with a flock of springbok and herd of buffalo.

Results: In the springbok, the virus quickly infects nearly all animals and becomes extinct, whereas the virus persists longer in the buffalo population. Combining both systems changes the dynamics and the persistence of the virus in the system, within the given timeframe.

Discussion: The results indicated that interactions between ruminant host species during an RVF outbreak can significantly modify the stability of the disease dynamics within the system. Given the livestock-wildlife interface throughout the entire African range of RVFV, consideration of these interactions is vital to our understanding of RVFV.

Conclusions: Wildlife have been neglected in much of the RVF literature, yet the studies that have been conducted on ruminants indicate that they may be affected similarly as livestock. This study indicates that a multi-host system likely plays a key role in understanding the dynamics of RVFV.

Simulation modeling approach in wild animal- backyard pigs interface: The case of influenza in Estado de Mexico

08:00 - Friday, 28th July, Solar Square

Jéssica Paola Mateus Anzola , Rafael Ojeda Flores , Oscar Rico

1.Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México)

The wildlife - livestock interface plays a key role in the transmission of infectious diseases, for example influenza. Wild aquatic birds are well known to be the natural reservoir of influenza viruses, and pigs are important agents in the disease ecology due to their capacity to replicate viruses from swine, avian and human origin. In Mexico, high percentage of rural population raise backyard animals, specially poultry, turkeys, ducks and pigs. Moreover, the informal trade in living animal markets constitutes a risk for the emergence, maintenance and spread of diseases. The aim was to generate a simulation model of transmission of influenza in Lerma, Estado de Mexico, where there are 260 backyard pig productions near to Lerma wetlands, a natural protected area and bird conservation zone with the presence of migratory birds. A SIR-network model was implemented using the Epi-model package available in the free software R, in which the 260 farms were considered as nodes and 3 different scenarios of connectivity mediated by trade: high, medium and low were generated and compared. We detected that the scenarios with more connectivity are key in the dynamic of influenza virus transmission between wild and domestic animals. The high connectivity due to the informal trade channels constitutes a significant risk for human and animal health. Therefore, the model represents a plausible overview of the national reality; it highlights the necessity of implement active epidemiological surveillance in wild animals, backyard productions and living animal markets. This approach may constitute a helpful tool providing a better understanding of disease transmission and developing of prevention and control dynamics.

Batrachochytrium Salamandrivorans Pathology In Susceptible Species

09:42 - Friday, 28th July, Solar Square

Debra Miller, E. Davis Carter, J. Patrick Cusaac, Rebecca Hardman, Laura Reinert, Lori Williams, Louise Rollins-smith, Matthew Gray

1. University of Tennessee Center for Wildlife Health, 2. University of Tennessee Comparative and Experimental Medicine, 3. Vanderbilt University School of Medicine, 4. North Carolina Wildlife Resources Commission

Batrachochytrium salamandrivorans (*Bsal*) is a recently discovered pathogen that is of global concern because of its potential to cause high mortality in amphibians, especially salamander species. Within North America, the Appalachia region is one area of particular concern because of the high diversity of salamander species and suitable environmental conditions for *Bsal*. An outbreak in this area could potentially result in a devastating loss of species. Thus, experimental challenges are underway to determine species susceptibilities in order to calculate risk and develop disease mitigation strategies to minimize the possibility of *Bsal* emerging in North America. To date, 19 amphibian species (15 salamander and 4 anuran) have been tested. For each challenge, individuals were exposed to *Bsal* in a water bath at one of five concentrations (0, 5×10^3 , 10^4 , 10^5 , 10^6) for 24 hours then their condition monitored for six weeks; swabs to test for *Bsal* infection were collected every six days. In general, positive qPCR results begin appearing 1-2 weeks after exposure. Clinical signs of disease varied by host and in some cases only increased skin sloughing was noted. Although discrete ulcerations were occasionally seen, often sparse multifocal to diffuse distribution was noted on histologic examination, suggesting that the gross lesions are not always obvious. Our results reinforce that histopathology is necessary to determine the severity of the infection, and PCR is necessary to verify the identity of the pathogen. Additionally, our results demonstrate that suitable hosts for *Bsal* exist in North America, hence the pathogen may represent a significant conservation risk.

Ophidiomyces ophiodiicola and snake fungal disease detected in wild European snakes

09:42 - Friday, 28th July, Solar Square

Lydia Franklinoš, Jeff Lorch, Elizabeth Bohuski, Julia Rodriguez-Ramos Fernandez, Owen Wright, Liam Fitzpatrick, Silviu Petrovan, Chris Durrant, Chris Linton, Vojtech Baláž, Andrew Cunningham, Becki Lawson

1. Institute of Zoology, Zoological Society of London, 2. U.S. Geological Survey–National Wildlife Health Center, 3. Froglife, 4. Public Health England, 5. Department of Ecology and Diseases of Game, Fish and Bees, University of Veterinary and Pharmaceutical Sciences Brno

Background: *Ophidiomyces ophiodiicola* is the causative agent of snake fungal disease (SFD), an emerging disease of conservation concern of wild snakes in eastern North America. Whilst *O. ophiodiicola* has been isolated from captive snakes outside North America, the pathogen has not been reported from wild snakes elsewhere.

Objectives: Our study objective was to investigate the occurrence of *O. ophiodiicola* and SFD in wild snakes in Europe.

Methods: We utilised a convenience sample of opportunistically collected wild snake skin sheds and conducted scanning surveillance through pathological examinations. We screened 303 moulted skins and 33 carcasses collected from 2010–2016 in Great Britain (n=335) and the Czech Republic (n=1) for the presence of macroscopic skin lesions and used real-time PCR to test for *O. ophiodiicola*. Fungal culture and histopathology were performed on a subset of PCR-positive cases. Culture characterisations and phylogenetic analyses (ITS, actin, translation elongation factor genes) were conducted on *O. ophiodiicola* isolates.

Results: The fungus was detected using real-time PCR in 26 (8.6%) specimens from multiple species across the period of collection, with a widespread distribution in Great Britain and a single specimen from the Czech Republic. Culture and microscopic examination confirmed that both *O. ophiodiicola* and SFD occur in wild European snakes. The severity of lesions varied, being mild in most cases, but were sometimes severe and considered likely to have contributed to mortality. Colony expansion rates were, on average, 4.8 times slower for the European than US *O. ophiodiicola* isolates. The GB and Czech isolates formed a single, well-supported phylogenetic clade that was distinct from isolates of *O. ophiodiicola* from eastern North America.

Conclusions: Phenotypic and genetic differences indicate that the European isolates represent novel strains of *O. ophiodiicola*. Further research is required on the impact, if any, of *O. ophiodiicola* infection on wild snake populations in Europe.

Snowy Owl (*Bubo scandiacus*) Health and Mortality Investigations With Project SNOWstorm During the Great Irruption of 2013- 2015 and Beyond

09:42 - Friday, 28th July, Solar Square

Cindy Driscoll, Erica Miller, Sherrill Davison, Lisa Murphy, Perry Habecker, Elizabeth Bunting, Mark Pokras, Julie Melotti, Ginger Stout, Fiep De Bie, David Green, Susan Knowles, Julia Lankton, Marcos Isidoro-Ayza, Valerie Shearn-Boschler, Jason Weckstein, Ellen Bronson, Allison Wack

1. Maryland Department of Natural Resources, 2. Brandywine Zoo, 3. University of Pennsylvania, 4. Cornell Wildlife Health Lab, 5. Tufts University, 6. Michigan Department of Natural Resources, Wildlife Disease Lab, 7. Biodiversity Research Institute, 8. Canadian Wildlife Health Cooperative, 9. Drexel University, 10. Maryland Zoo

An irruption of snowy owls (*Bubo scandiacus*) began in December 2013 in the northeastern United States and Canada and was the largest influx into the region in 50 years. To take advantage of this rare opportunity, a few key biologists and veterinarians contacted colleagues throughout the region to place bands and transmitters on owls, and collect health and disease samples from live and dead owls. Project SNOWstorm (www.projectSNOWstorm.org), an online crowd-funding event, launched in early January 2014 in an effort to provide resources to purchase transmitters, and conduct necropsy exams and other diagnostic tests.

This report presents the findings from biologists and veterinarians of Project SNOWstorm that continued through 2016. The team conducted gross necropsies, morphometrics and diagnostic sampling on 153 birds from nine states, the District of Columbia, and three Canadian provinces. Sixty birds were female, 82 were male, and 11 were undetermined. Diagnostics included toxicology, histopathology, parasitology, microbiology, limited virology and radiology. During the first winter, most birds (55-60%) were in fairly good body condition with the majority of mortalities associated with trauma. During the subsequent two winters, more birds were in poor body condition or emaciated, and many had secondary fungal, bacterial or internal parasitic infections. Nearly all birds, were infested with external lice of the genus *Strigiphilus*, regardless of body condition. Data analysis shows that while many birds had been exposed to rodenticides, heavy metals and organochlorines, levels were not likely a contributor to mortality. Additionally, blood was collected from a small number of live birds and these findings will be presented as the beginning of a baseline health summary.

This collaboration was possible due to the willingness and cooperation of all Project SNOWstorm partners involved in wildlife conservation. Manuscripts will be developed to describe snowy owl irruption demographics, pathology, toxicology, diet, genetics, and migratory movements.

Prevalence and intensity of *Amblyomma helvolum* (Acari: Ixodidae) infesting the water monitor lizard (*Varanus salvator*) within a fragmented landscape in Borneo

09:42 - Friday, 28th July, Solar Square

Anya V. Tober, Sergio Guerrero Sanchez, Joanne Cable, Benoit Goossens

1. Cardiff School of Biosciences, Cardiff University, 2. Cardiff School of Biosciences, Cardiff University/ Danau Girang Field Centre

Amblyomma helvolum (hard-shell tick) is a vector for the Spotted Fever Group Rickettsiae (SFGR) and is widely distributed across tropical Asia. Yet, little is known about this vector in Sabah, Malaysian Borneo. The water monitor lizard (*Varanus salvator*), one of the largest predators in Southeast Asia that is well adapted to anthropogenic-fragmented habitats, has been considered one of the most common hosts for this species of tick. Here, we assessed the prevalence and intensity of *A. helvolum* on *V. salvator* in different habitats within the Kinabatangan floodplain. During the period between July 2013 and October 2016, we set 12 transects of 1.6 km long spread in three forested and three oil palm plantation areas, with 5 cage traps placed every 400m in each transect. All ticks on each lizard (n=730) were removed, counted and identified morphologically: *A. helvolum* was the only tick species present. Prevalence and intensity differed significantly between habitat types and boundary/interior sites. Tick intensity was positively correlated with lizard's body size and population density. The highest tick's intensity occurred in the oil palm plantation with the highest density of lizards. This site also hosts a population of domestic goats and cattle; meanwhile, in the other 2 plantations we just recorded the presence of domestic chickens. Although we can conclude that abundance of monitor lizards is a relevant factor for the presence of *A. helvolum*, it is important to understand how the habitat features (i.e. forest structure and presence of other potential host species) and land management drive the dynamics of both host and parasite in order to get a better understanding of the ecology and zoonotic risk of *A. helvolum* within this fragmented landscape.

Urban-agricultural malaria infection patterns of a successful urban exploiter bird

09:42 - Friday, 28th July, Solar Square

Diego Santiago Alarcón, Pilar Carbó Ramírez, Ian Macgregor Fors, Carlos A. Chávez Zichinelli, Pamela Yeh

1. Instituto de Ecología, A.C. - CONACYT, 2. El Colegio de Puebla, 3. University of California Los Angeles

Urbanization affects the ecology of wildlife diseases. Little is known of the ecological dynamics of bird-parasite interactions in urban and sub-urban areas, particularly for invasive species. In this study we compared haemosporidian infections of one urban and one non-urban populations of the successful invader House Sparrow (*Passer domesticus*). We subjected males from these populations to a stress experimental treatment and used microscopy and PCR to determine haemosporidian infection prevalence and relative intensity. We measured total leucocyte counts, leucocyte differentials, and calculated the H/L ratio and the Polychromatic Index as measures of stress and condition, respectively. We found significantly higher prevalence in non-urban House Sparrows compared to those inhabiting the highly urbanized area in Mexico City. We also found significantly higher prevalence in the non-urban males both before and after experimental treatment, and a significant increase in parasite relative intensity only in the non-urban individuals after experimental treatment. Furthermore, a non-significant positive trend in prevalence was detected after experimental treatment for both urban and non-urban House Sparrows, indicating the relapse of chronic infections, likely due to stressful conditions during captivity. The H/L ratio was significantly higher for non-urban compared to urban male sparrows before experimental trials, and it remained similar throughout the experiment for urban sparrows, indicating higher stress in non-urban birds. We recorded a total of eight lineages in House Sparrows, seven are new records for the species (MALERY01, PIPUB01, MYITYR01, TROAED18, AFR094, and ICTLEU01), six of which are restricted to the American continent and only AFR094 originally detected in Africa. Our study suggests that highly built areas of cities represent lower haemosporidian infection risk compared to non-urban areas and to greenspaces within cities in the case of other bird species (e.g., *Arremon brunneinucha*); this can be one factor behind the successful invasion of House Sparrows in the American continent.

Detección molecular de *Plasmodium malariae*/*Plasmodium brasilianum* en primates no humanos en cautiverio de Costa Rica

09:42 - Friday, 28th July, Solar Square

Alicia Fuentes Mauricio Jimenez Ruth Castro, Juan José Romero-Zuñiga, Gaby Dolz

1. Posgrado Regional en Ciencias Veterinarias Tropicales, Universidad Nacional de Costa Rica, 2. Universidad Nacional de Costa Rica 3. Escuela de Medicina Veterinaria, Universidad Nacional Costa Rica

La malaria es una enfermedad vectorial ocasionada por protozoos del género *Plasmodium*. En el año 2012 se diagnosticaron casos humanos ocasionados por *Plasmodium malariae* en Costa Rica, especie que no había sido reportada desde 1959, mientras que *Plasmodium brasilianum* fue encontrado en sangre de monos en el 2006. Los monos sudamericanos son naturalmente infectados por *P. brasilianum*, y la elevada identidad genética encontrada entre *P. malariae* y *P. brasilianum* sugiere una transferencia reciente entre huéspedes. El objetivo del presente trabajo fue determinar la presencia de especies de *Plasmodium* en monos autóctonos (*Saimiri oerstedii*, *Ateles geoffroyi*, *Cebus imitador*, *Alouatta palliata*) y no nativos (*Callithrix jacchus*) de Costa Rica. Se recolectaron 158 muestras sanguíneas en 13 Centros de Rescate, las cuales se analizaron mediante gota gruesa, reacción en cadena de la polimerasa (PCR), clonación y secuenciación. En gota gruesa se determinó la presencia del parásito *P. malariae*/*P. brasilianum* en dos muestras, mientras que por PCR multiplex semi-anidado un total de cinco muestras (3.3%) resultaron positivas. Mediante amplificación del gen 18S rDNA, clonación y secuenciación se logró obtener un producto de 860 pb (GenBank KU999995) de una muestra de *A. palliata*. El análisis Blast determinó que esta muestra es nucleotídicamente idéntica (100%) a *P. malariae* (GenBank KJ934251), obtenida de humano ocurrido en el 2012. El árbol filogenético construido confirmó que nuestra secuencia se agrupa con otras secuencias de humanos y primates. El hallazgo de *P. malariae*/*P. brasilianum* en diferentes especies de primates en cautiverio (*A. palliata*, *A. geoffroyi* y *C. jacchus*) y en diversas regiones del Sur de Costa Rica, refuerza la hipótesis de que los primates no humanos podrían estar actuando como reservorios de *Plasmodium*, por lo que es importante incluirlos en los programas de control y erradicación de malaria, además de realizar más investigaciones en el ciclo ecológico.