67th Annual International
Wildlife Disease Association Conference

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St. Augustine, Florida, USA

www.conference.ifas.ufl.edu/wda2018

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Welcome Letter

Dear Attendees,

Welcome to St. Augustine, the First Coast of Florida, home of the oldest colonial city in the United States, and venue for the 67th International Conference of the Wildlife Disease Association. We have a wonderful scientific program that includes workshops, special sessions and a symposium. In addition to the amazing science that you will see showcased, we have planned plenty of time for networking, reconnecting with old friends and making new friends. The Wednesday afternoon break offers you the opportunity to enjoy the sites of northern Florida on your own or on one of the scheduled field trips.

The theme for this year's conference is "Connecting Wildlife Health, Conservation, and Management in a Changing World." The theme was inspired by the Florida Interagency Wildlife Disease Working Group, an informal assembly of wildlife veterinarians, ecologists, disease biologists, and epidemiologists from state and federal agencies and academia, which meets quarterly to discuss pressing issues in wildlife diseases in our state. The individuals that comprise this group have different goals and varied perspectives on wildlife populations and the diseases that they carry, yet the working group provides a professional milieu in which people can connect. They ultimately came up with the crazy idea that they could host a conference!

This meeting would not have been possible without the time and contributions of many institutions and people. The organizing committee is grateful to our platinum sponsors, the University of Florida Institute of Food and Agricultural Sciences' Cervid Health Research Initiative and the Florida Fish and Wildlife Conservation Commission, as well as to our many other sponsors who helped keep conference registration costs down. The US Fish and Wildlife Service, UF Department of Wildlife Ecology, UF College of Veterinary Medicine, UF student chapter of the WDA, UF/IFAS Office of Conferences and Institutes and others have contributed time and effort to making this conference a reality. We thank all of the professionals and students who have volunteered their time before, during and after this conference to make the workshops, field trips, auction, photo contest, mentor event and symposium possible.

We have over 350 registered attendees from 27 countries and 44 US states. We have 104 oral presentations and 124 posters including our student showcase on Tuesday. Our scientific program has special sessions on outbreak investigations and response, global wildlife health capacities, marine health and emerging diseases of herpetofauna, just to name a few. Our workshops include vampire bat management, diagnostic sample handling and processing, and crocodilian health. On our final day, we have a Cervidae Health Science Symposium focused on farmed deer health. Please take advantage of these innovative science opportunities, and be sure to get out and explore the gorgeous surroundings of St. Augustine, Florida, USA!

Enjoy the conference and have a wonderful time in Florida!

Your Organizing Committee:

Mark Cunningham, Samantha Gibbs, Lisa Shender, Thomas Waltzek, and Samantha Wisely

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Abstract Compilation

Listed alphabetically by presenting author last name.
Presenting author names appear in **bold**.

MODELING APPROACHES FOR PROMOTING HEALTH IN FREE-LIVING ORNATE BOX TURTLES (*TERRAPENE ORNATA ORNATA*)

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Modeling is a powerful tool for extracting information from complex systems. It is frequently used to target mitigation efforts for wildlife diseases. However, controlling disease is challenging and strategies, which focus on supporting robust population health instead, may improve conservation outcomes. The objective of this study was to model predictors of health in free-living ornate box turtles (*Terrapene ornata ornata*) and identify factors, which support positive health status. We hypothesized that physical examination (PE) abnormalities and protein electrophoresis (EPH) values would best predict poor health. Turtles (N=168) from an Illinois prairie restoration site were evaluated using PE, hematology, plasma biochemistry, EPH, and hemoglobin-binding protein in May 2016 and 2017. DNA from oral/cloacal swabs and blood was assayed for four ranaviruses, three *Mycoplasma* spp., three herpesviruses, two *Salmonella* spp., *Terrapene* adenovirus, intranuclear coccidiosis, *Borrelia burgdorferi*, and *Anaplasma phagocytophilum* using qPCR. Health was modeled as a categorical outcome using structural equation modeling and Bayesian network modeling, followed by information-theoretic model ranking. “Healthy” turtles had 1) no significant PE abnormalities, 2) no pathogens affecting clinical condition, and 3) fewer than three abnormal bloodwork values. Turtles violating these criteria were classified as “Unhealthy”. Many turtles examined (51-59%) had shell damage from suspected predator trauma. Pathogen detection (adenovirus, Terrapene herpesvirus 1) was not related to health status. Predictors of “Unhealthy” classification from the most parsimonious model included the presence of shell abnormalities and deviations from population median values for total leukocyte count, eosinophils, basophils, and heterophil:lymphocyte ratios ($p<0.05$). Modeling demonstrated that PE and hematology sufficiently predict health within this population, and that commonly-identified pathogens do not significantly impact individual health. Mesopredator control was recommended to support overall population wellness. This study reveals the feasibility of modeling health in wildlife and illustrates its use for identifying clinically useful diagnostic tests and informing practical conservation interventions.

<u>Presenter Bio:</u> Laura received her DVM from the Virginia-Maryland Regional College of Veterinary Medicine in 2012. She completed internships in companion and exotic animal medicine before starting a PhD in epidemiology in 2015. Her research involves modeling health in sympatric populations of herptiles to promote the development of effective conservation strategies.

VENOUS BLOOD GAS IN FREE-LIVING EASTERN BOX TURTLES (*TERRAPENE CAROLINA CAROLINA*) AND THE EFFECTS OF PHYSIOLOGIC, DEMOGRAPHIC, AND ENVIRONMENTAL FACTORS

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Blood gas analysis facilitates the clinical assessment of acid-base status, oxygenation, and ventilation. It also serves as a useful adjunctive test for health assessment in wildlife, but is infrequently utilized in reptiles. The objectives of this study were to model blood gas analytes in wild eastern box turtles (*Terrapene carolina carolina*) as a function of demographic, environmental, and physiologic parameters in order to characterize expected normal variation and enhance our ability to identify pathologic changes. The hypotheses were that blood gas parameters would be non-directionally influenced by season, air temperature, and packed cell volume (PCV). iSTAT blood gas panels including pH, partial pressure of oxygen (pO_2), partial pressure of carbon dioxide (pCO_2), total carbon dioxide (TCO_2), bicarbonate (HCO_3^-), base excess (BE), and lactate were evaluated in 102 wild turtles from May-September 2014. Candidate sets of general linear models were constructed for each blood gas analyte and ranked using an information-theoretic approach (AIC). Season, PCV, and attitude were the most important predictors for all blood gas analytes ($p<0.05$). Elevations in PCV were associated with increases in pCO_2 and lactate, and decreases in pH, pO_2, HCO_3^-, TCO_2, and BE. Turtles with quiet attitudes had lower pH and pO_2 and higher pCO_2 than bright individuals. pH, HCO_3^-, TCO_2, and BE were lowest in the summer, while lactate was highest. Overall, blood pH was most acidic in quiet turtles with elevated PCVs during summer. Trends in the respiratory and metabolic components of the blood gas panel tended to be synergistic rather than antagonistic, demonstrating that either 1) mixed acid-base disturbances are common or 2) chelonian blood pH can reach extreme values prior to activation of compensatory mechanisms. This study shows that box turtle blood gas analytes depend on several physiologic and environmental parameters, and the results serve as a baseline for future evaluation.

Presenter Bio: Laura received her DVM from the Virginia-Maryland Regional College of Veterinary Medicine in 2012. She completed internships in companion and exotic animal medicine before starting a PhD in epidemiology in 2015. Her research involves modeling health in sympatric populations of herptiles to promote the development of effective conservation strategies.

HEALTH ASSESSMENT OF AFRICAN LAND TORTOISE *GEOCHELONE SPECIES* USING MORPHOMETRY AND BODY CONDITION INDEX

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The body condition index (BCI) of 120 (56 Males and 64 females) African land tortoises *Geochelone species* sourced from local markets in Ibadan, Oyo state Nigeria were evaluated, based on the linear relationship between body mass and linear measurement of the body. The body mass (M), height (H), straight carapace length (SCL), Straight plastron length (PL), and plastron width (PW) of the tortoises were measured. Compared with other linear measurement, the Mass-SCL established the strongest linear association. In addition, the Mass-SCL was highly significant in both sexes ($F_{1,54}$= 437.2, P< 0.001, R^2 (adj)= 0.89 for the males and $F_{1,62}$ = 173.8, P< 0.001, R^2 (adj)= 0.73 for the females). The females were significantly taller and wider that the males (58.52 ± 7.87mm, 55.46 ± 7.09 mm, t = -2.22, p = 0.03) and wider than the males (106.00 ± 9.12mm, 101.61 ± 10.37 mm, t = -2.47, p = 0.02) respectively. The mass linear association was used to generate an equation which was used in calculating the expected mass m using these equation for the females $^{\log (m) = -2.21 + 2.33 \log (SCL)}$, and for males $^{\log (m) = -2.86 + 2.62 \log (SCL)}$, where log (m) is the expected mass. The linear-mass equation was used to calculate the BCI (LogM/m). Loss of body mass was observed in 21(38%) males and 31(48%) females. It was concluded that the body mass index could serve as a valuable noninvasive, less stressful method of health assessment in captive chelonians by the zoo veterinarians.

Presenter Bio: Dr. Veronica Adetunji is a lecturer from the University of Ibadan, Nigeria. She teaches wildlife ecology and diseases to the DVM students and her research works focus on blood parasites of reptiles with particular interest on chelonians, wildlife health management and diseases of public health importance.

EFFECTS OF THE ILLEGAL CONSUMPTION OF SEA TURTLES ON ENVIRONMENTAL SECURITY AND HUMAN HEALTH IN NORTHWESTERN MEXICO

***A. Alonso Aguirre*[1]*, Kathryn Jacobsen*[2]*, Lila C. Fleming*[2]*, Alexander J. Robillard*[1]*, Cesar P. Ley-Quiñónez*[3]*, Alan A. Zavala-Norzagaray*[3]

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Human consumption of endangered sea turtles remains prevalent throughout Mexico even though laws restricting trade in threatened and endangered species have been in place for several decades. Our prior research has found that the majority of sea turtle mortality in Baja California is due to human consumption. While demand for sea turtle meat has reportedly decreased in some regions, turtle trafficking and illegal harvesting continue to threaten environmental security in the region. Besides being a threat to animal and ecological health, poaching may be a threat to human health. People who consume turtle meat may be exposed to bacteria, parasites, and other pathogens as well as organochlorine compounds and heavy metals such as cadmium and mercury. In 2017, we conducted a knowledge, attitudes, and practices (KAP) survey with a convenience sample of more than 200 residents of 14 fishing communities in northwestern Mexico. We asked participants about their nutritional and health status, dietary and risk behaviors, and perceptions of local ecological issues, and we collected hair samples that could be tested for heavy metals. About one-quarter of the participants reported consuming sea turtle in the past month. Laboratory tests showed a high prevalence of elevated levels of arsenic, lead, and mercury. Preliminary analyses show that people who eat sea turtle meat are more likely than their neighbors to have high levels of mercury in their hair. Conservation efforts may be more successful when they appeal to people's self-interest rather than merely focusing on ecological benefits. Concerns about toxins in sharks, tuna, and other types of deep-sea fish have reduced human consumption of some species. Sea turtle conservation efforts may benefit from awareness campaigns that emphasize the adverse health outcomes associated with eating turtle meat while continuing to affirm the economic benefits of healthy ecosystems. Transdisciplinary research that draws on diverse fields such as ecology, epidemiology, toxicology, environmental law, and public policy provides a valuable foundation for solving planetary health issues. Creative reframing of biodiversity concerns in countries around the globe will be necessary for promoting environmental health and public health in a time of accelerating environmental change.

FECAL BACTERIAL COMMUNITIES OF WILD-CAPTURED AND STRANDED GREEN TURTLES (*CHELONIA MYDAS*) ON THE GREAT BARRIER REEF, AUSTRALIA

***Md. Shamim Ahasan*[1,2]**, *Thomas B. Waltzek*[1], *Roger Huerlimann*[3] *and Ellen Ariel*[2]
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Chelonia mydas are primarily herbivorous long-distance migratory sea turtles that contribute to marine ecosystems. Extensive research has been conducted to restore the populations of green turtles. Little is known about their gut microbiota, which plays a vital role in their health and disease. In this study, we investigated and compared the fecal bacterial communities of wild-captured green turtles to stranded turtles by PCR amplification of a hypervariable region (V1-V3) of the bacterial 16S rRNA gene for each sample followed by sequencing on an Illumina MiSeq platform. At a phylum level, Firmicutes predominated among wild-captured green turtles, followed by Bacteroidetes and Proteobacteria. In contrast, Proteobacteria (*Gammaproteobacteria*) was the most significantly dominant phylum among all stranded turtles, followed by Bacteroidetes and Firmicutes. In addition, Fusobacteria was also significantly abundant in stranded turtles. No significant differences were found between the wild-captured turtles from two different locations. At a family level, 25 of the 53 families were identified in both the wild-captured and stranded green turtles, while 14 families were found only in stranded turtles. At the OTU level, 256 (48.7%) of the total OTUs (>1% abundance) were shared between the wild-captured groups of turtles, while absent in stranded turtles. The predominance of *Bacteroides* in all groups indicates the importance of this bacteria in turtle gut health. In terms of microbial diversity and richness, wild-captured green turtles showed the highest microbial diversity and richness compared to stranded turtles. The marked differences in the bacterial communities between wild-captured and stranded turtles suggest the possible dysbiosis in stranded turtles in addition to potential causal agents.

Presenter Bio: Mr. Ahasan is currently working as a postdoctoral associate in the department of infectious diseases and immunology under the University of Florida. His research is focused on investigating gut microbiome of white-tailed deer. Recently, he has completed his PhD from James Cook University, Australia focusing on gut microbiome of green turtles.

ISOLATION AND MOLECULAR CHARACTERIZATION OF A NOVEL MAMMALIAN ORTHOREOVIRUS TYPE 2 FROM FLORIDA WHITE-TAILED DEER

Md. Shamim Ahasan[1,2], *Kuttichantran Subramaniam*[1], *Katherine A. Sayler*[3], *Julia Loeb*[4,5], *Vsevolod L. Popov*[6], *John Lednicky*[4,5], *Samantha M. Wisely*[3], *Thomas B. Waltzek*[1], *Juan Campos Krauer*[7]

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The family *Reoviridae* is a diverse group of viruses with segmented double-stranded RNA genomes enclosed within a multi-layered icosahedral capsid. *Mammalian orthoreovirus* (MRV) is the type species of the genus *Orthoreovirus* and it causes a range of respiratory or enteric diseases of importance in human and veterinary medicine. In 2017, a farmed white-tailed deer (*Odocoileus virginianus*) fawn became ill displaying lethargy, dehydration, and profuse foul smelling diarrhea. A necropsy was performed after the three-week-old fawn succumbed and samples were submitted to the University of Florida's Cervidae Health Research Initiative for diagnostic evaluation. Aliquots of homogenized spleen were inoculated onto Vero E6 (*Cercopithecus aethiops* [African green monkey] kidney, ATCC CRL 1586) cells grown as monolayers at 37°C. The Vero culture displayed cytopathic effects (CPE) and was submitted for transmission electron microscopic evaluation. Numerous icosahedral viral particles (approximately 75nm in diameter) were observed within the cytoplasm of Vero cells. RNA was extracted from Vero cells displaying CPE using a QIAamp viral RNA minikit (Qiagen). A cDNA library was prepared using a NEBNext Ultra RNA library prep kit and sequenced using a V3 chemistry 600-cycle kit on a MiSeq platform (Illumina). *De novo* assembly of the paired-end reads in SPAdes followed by BLASTX searches of the assembled contigs against a proprietary viral database in CLC Genomic Workbench recovered all 10 segments that displayed highest nucleotide identities to MRV type 2 (MRV-2). A Maximum Likelihood (ML) analysis based on the outer capsid protein sigma-1 supported the Florida white-tailed fawn isolate as a strain of MRV-2 branching as the sister group to a MRV-2 strain isolated from a moribund lion in Japan. To our knowledge, this is the first occurrence of MRV-2 infection in a white-tailed deer. Continued surveillance efforts are needed to determine the threat of this MRV-2 strain may pose to health of farmed white-tailed deer populations.

<u>Presenter Bio:</u> Mr. Ahasan is currently working as a postdoctoral associate in the department of infectious diseases and immunology under the University of Florida. His research is focused on investigating viral pathogens in Florida white-tailed deer. He is also looking at gut microbiome of white-tailed deer.

RISK ASSESSMENT FOR THE INCURSION AND ESTABLISHMENT OF ORBIVIRUSES IN ONTARIO CANADA: SEROSURVEILLANCE IN WILDLIFE AND LIVESTOCK AND CHARACTERIZATION OF CURRENT VECTOR COMPOSITION AND DISTRIBUTION

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Epizootic hemorrhagic disease (EHDV) and bluetongue viruses (BTV) are midge-borne orbiviruses presenting imminent threats to Ontario's wildlife and livestock populations. They are spreading northward in North America, which may be facilitated by changing climatic conditions. Recent detection of BTV-seropositive cattle and documentation of *Culicoides sonorensis* midges suggest that Ontario is at risk for the incursion and establishment of EHDV and BTV. Ontario ruminants are immunologically naïve to these viruses; thus, their introduction may lead to negative impacts on wild cervid populations and livestock (farmed cattle, sheep and deer) through morbidity, mortality and production loss. We sought to characterize *Culicoides* vector biology and assess for recent and/or ongoing transmission of EHDV and BTV in wild cervids and livestock in Ontario for two spring-summer field seasons (2017-2018). During the 2017 field season, CDC-type LED light traps were placed on farms and in natural areas across southwestern Ontario, and *Culicoides* vectors were taxonomically and molecularly identified. Blood from wild cervids and livestock were screened for antibodies to EHD and BT viruses by ELISA and virus neutralization assay. After one completed field season, we have collected 1460 *Culicoides*, including individuals of the following species: *C. variipennis*, *C. biguttatus*, *C. crepuscularis*, *C. stellifer*, *C. travisi*, *C. haematopotus* and *C. venustus*, with the most commonly identified species being *C. stellifer*. Data will be statistically analyzed to investigate regional and temporal patterns in vector distribution and disease associations with age, sex, seasonality, and weather. Furthermore, during the 2017 season, we identified two white-tailed deer that died of EHDV (serotype 2), these being the first EHDV cases reported in Ontario, Canada. In addition, 33 *Culicoides* spp. midges were collected at the same location to assess potential vector activity. Collectively, these results will help improve current policies and practices for safeguarding Ontario livestock and wild cervid populations.

Presenter Bio: Dr. Allen, DVM, M.Sc, is a PhD candidate at the University of Guelph. Her PhD research focuses on vector-borne viruses and wildlife diseases at the livestock and human interfaces. She has years of experience working with wildlife diseases in the realm of public and animal health.

THE CHANGING EPIDEMIOLOGY OF SNAKE FUNGAL DISEASE OVER THE LAST 10 YEARS

***Matthew C. Allender*[1]**, *Ellen Haynes*[1], *Laura Adamovicz*[1], *Houston Chandler*[2], *Kristin Stanford*[3], *Marta Kelly*[1], *Sarah J. Baker*[1,4]

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Snake fungal disease (SFD), caused by the fungus *Ophidiomyces ophiodiicola,* has emerged as a wildlife disease over the last 10 years and may threaten the conservation of free-ranging snakes. Historical records and museum collections have now indicated that SFD was present in some populations at least a decade before its description in the literature. The disease syndrome involves clinical signs ranging from minor raised and thickened scales to severe crusts or ulcers on the head and body and can cause death in severe cases. The current range of this pathogen includes the eastern United States with scattered reports west of the Mississippi River and in Canada and Europe. The disease has been found to affect at least 31 snake species. As part of ongoing surveillance for SFD, the Wildlife Epidemiology Lab routinely tests samples for the presence of *O. ophiodiicola* using qPCR. Since 2013, we have tested over 2000 snake samples from 69 species. In total, 616 positive samples have been recorded across 31 species in 11 states. Despite the apparent sensitivity of pit vipers, only 12.5% (n=99/693) of Eastern massasaugas (*Sistrurus catenatus*) were positive, whereas nearly 60% (n=218/365) of water snakes (*Nerodia* sp.) were positive for *O. ophiodiicola*. Males (28.9%; n=138) and females (n=29.4%; n=173) were similarly positive (p=0.456). Adults (29.6%; n=300) were the most common age class testing positive, followed by juveniles (20.3%; n=39), and subadults (12.6%; n=12) (p<0.001). Characterizing the epidemiology of this disease can improve future surveillance and management efforts that may mitigate its effects on snake populations worldwide.

EXPERIMENTAL INFECTION OF EGYPTIAN ROUSETTE BATS (*ROUSETTUS AEGYPTIACUS*) WITH SOSUGA VIRUS

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In August 2012, a wildlife biologist became ill after a six week field work trip to South Sudan and Uganda, where she caught and processed several species of bats and rodents. After returning to the United States, she was admitted to the hospital with multiple symptoms including fever, malaise, headache, generalized myalgia and arthralgia, stiffness in the neck, and sore throat. Deep sequencing and metagenomic analyses identified a novel paramyxovirus related to fruit bat-borne, rubula-like viruses. RT-PCR analysis of tissues taken from bats collected by the biologist during the three week period just prior to the onset of symptoms, as well as archived tissues collected from multiple marburgvirus investigations in Uganda, revealed several Egyptian rousette bats (*Rousettus aegyptiacus*) to be positive for the recently described Sosuga virus (*Paramyxoviridae*). To further investigate the dynamics of Sosuga virus infection in these bats and determine if the virus replicates in a manner consistent with expectations for Egyptian rousettes being a Sosuga virus natural reservoir, we performed an experimental infection study in which we infected 12 captive-bred Egyptian rousette bats with a recombinant Sosuga virus genetically identical to the isolate obtained from the human patient. The bats were inoculated subcutaneously and daily samples of blood, fecal, oral and rectal swabs were collected. Serial euthanasias were performed at pre-determined time points. The samples were analyzed using ELISA, qRT-PCR, and/or IFA, depending on sample type. All 12 bats became infected with Sosuga virus, as evidenced by multiple qRT-PCR- and virus isolation-positive oral swab, rectal swab, fecal and/or tissue samples, suggestive of systemic infection without any evidence of overt morbidity or mortality. These results are consistent with what would be expected of a natural reservoir of a virus and suggest Egyptian rousette bats may be the reservoir for Sosuga virus in Uganda.

<u>Presenter Bio:</u> Brian Amman received his PhD in Zoology from Texas Tech University in 2005 and is currently employed as a Disease Ecologist for the Viral Special Pathogens Branch, Virus Host Ecology Unit, at the Centers for Disease Control and Prevention in Atlanta, GA.

TOXOPLASMA GONDII PREVALENCE IN RAPTORS FROM FLORIDA AND EAST TENNESSEE

***Sawsan Ammar**[1,4], Chunlei Su[2], Maria Spriggs[3] , Richard Gerhold[1]*

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Toxoplasma gondii is an important zoonotic protozoan parasite that can infect all warm-blooded animals including mammals and birds. Raptors are an excellent indicator of environmental contamination of *T. gondii* given their predatory and scavenging behavior. We investigated the seroprevelance of *T. gondii* in several raptor species from Florida and East Tennessee followed by parasite bioassay on select seropositive samples. From a total of 49 raptors, we found 8 (16%) to be seropositive via the modified agglutination test (MAT). The seropositive raptors consisted of five red-shouldered hawks, two eastern screech owls, and one barred owl. Seronegative raptors consisted of 13 red shouldered hawks, eight barred owls, seven eastern screech owls, five Cooper's hawks, three red-tailed hawks, two Great-horned owls, two ospreys, and one sharp-shinned hawk. Five of the seropositive raptors were from Florida, while the other three were from Knox County in Tennessee. Mice bioassay attempts using fresh brain and/or heart tissue was performed on 5 of the 8 seropositive birds. We successfully isolated *T. gondii* tachyzoites from one red-shouldered hawk. Further research is still needed to investigate the prevalence of *T. gondii* in the raptors in the U.S. and to obtain a better understanding of the parasite life cycle, wildlife population impacts, and transmission dynamics.

Presenter Bio: Sawsan Ammar is a graduate PhD student at the University of Tennessee. She graduated from Veterinary school at Egypt (2008). She got her masters on Tuberculosis from Egypt (2012) and she is currently working on toxoplasmosis in birds. She would like her future research to be on protozoal diseases.

FECAL ENDOPARASITE PREVALENCE AND INTENSITY IN A DYNAMIC UNGULATE COMMUNITY IN YUKON TERRITORY, CANADA

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Community-level studies of endoparasites among ungulates are uncommon. In response to concerns by local people, and to provide a baseline for future monitoring, we examined the prevalence and intensity of endoparasites in archived fecal samples from (re)-introduced and resident ungulate species in southwestern Yukon, Canada. The ungulate community in this region is particularly dynamic: bison (*Bison bison*; *n*=184) are reintroduced after historical extirpation; elk (*Cervus canadensis*; *n*=9) are introduced; mule deer (*Odocoileus hemionus*; *n*=5) are naturally colonizing; while Dall sheep (*Ovis dalli*; *n*=32), Woodland caribou (*Rangifer tarandus*; *n*=35), and moose (*Alces alces*; *n*=117) are resident to the area. We used centrifugal fecal flotation for eggs of gastrointestinal helminths and oocysts of coccidians (in all host species), Baermann examination for protostrongylid lungworms (in cervids and sheep), and immunofluorescence antibody techniques for detection of protozoans (*Giardia and Cryptosporidium*) (in a sub-sample of bison and moose). We will present and compare data on the diversity, prevalence and intensity of endoparasites among these species. While molecular characterization would be needed to determine species and origin of endoparasites in this ungulate community, our data provide a survey from which to establish a baseline for this dynamic community of ungulates.

<u>Presenter Bio:</u> Cassandra is a Doctor of Veterinary Medicine candidate at the WCVM with a particular interest in the impacts of climate change on wildlife and public health. As a strong proponent of One Health, she is passionate about enhancing mutually beneficial inter-species interactions and mitigating those, which are harmful.

CHANGES IN THE BAT MICROBIOME DURING HIBERNATION AND FUNGAL INFECTION

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The influence of the microbiome (the micro-organisms that live in and on their hosts) on host health is a rapidly growing area of research in both human and animal disease research. For hibernating animals, such as bats, one gap in our understanding concerns how the downregulation of host metabolism and immune system during hibernation affects the microbiome. Hibernation induces a cascade of chemical and physical changes to the body of the bat, and the disturbance to the gut and skin during these bouts of metabolic inactivity are expected to induce changes in the associated microbial communities. A greater understanding of the bat microbiome and its role in bat health is particularly important in light of the dramatic declines in North American bat populations due to white-nose syndrome (WNS), caused by the emerging fungal pathogen *Pseudogymnoascus destructans* (*Pd*)*.* This pathogen thrives in cold hibernacula and is able to infect bats when the immune system is suppressed during hibernation. Diseased animals tend to arouse multiple times from hibernation, have reduced fat stores, are dehydrated, and have *Pd* conidia on exposed epidermis. Using a cohort of captive little brown bats (*Myotis lucifugus*), we tracked the gut and skin microbiome of healthy and *Pd* infected bats before and after hibernation. Results indicate that both hibernation and *Pd* infection were associated with significant changes in the bat microbiome. We found that *Pd* infection load was correlated with distinct changes in the beta diversity of skin communities. Lastly, we found a significant loss of microbial diversity and biomass in the bat gut during hibernation. Overall, this research suggests that hibernation and disease events have a large effect on the bat microbiome, and further investigation may yield novel tools that incorporate the microbiome into treatments that improve the disease outcome for bats affected with WNS.

Presenter Bio: Christine Avena is a Ph. D. candidate in Ecology and Evolutionary Biology at CU-Boulder. Before starting as a student in Boulder, she completed an M.S. degree in Conservation Medicine from Tufts Cummings School of Veterinary Medicine. Her work focuses on the effect of disease on host-microbe interactions, particularly in wildlife.

SOUTHEASTERN U.S. SONGBIRDS AND THEIR SUSCEPTIBILITY TO LOW VIRULENT (LENTOGENIC) NEWCASTLE DISEASE VIRUS

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Newcastle disease virus is closely associated with poultry, and increasingly recognized as a virus of wild birds. We have previously shown that live NDV vaccine viruses can escape and transmit into pigeons and other wild bird species. Therefore, under controlled conditions, we tested the susceptibility of wild song birds to infection with the live Newcastle disease LaSota vaccine. We further evaluated the effect of the infection on the humoral response of these birds. NDV-antibodies-free House Finches, Brown-headed Cowbirds, Northern Cardinals, and American Goldfinches were inoculated by the oculo-nasal route with 0.1 ml ($10^{6.7}$ EID_{50}/ml) with the LaSota vaccine. In addition, adult SPF chickens were inoculated similarly, and co-housed in separate isolators with two to five wild birds of the species listed above. This design resulted in three treatments: wild bird direct inoculation (5 groups), and wild bird exposure to one (2 groups) or two inoculated chickens (6 groups), respectively. Blood, oropharyngeal and cloacal swab samples were collected after inoculation with the live vaccine. All directly inoculated birds were actively shedding the vaccine virus as demonstrated by virus isolation. Cardinals were the most susceptible species based on shedding from 1 to 11 days post inoculation (dpi) with titers up to $10^{3.9}$ EID_{50}/ml. Although live viruses were shed by all inoculated chickens and were present in the drinking water, all non-inoculated wild birds co-housed with these chickens remained uninfected for 14 days. However, one transmission House Finch tested positive for NDV by rRT-PCR at 13 dpi. Only one directly inoculated cowbird (out of three) and two cardinals (out of two) developed detectable humoral responses with specific HI antibody levels of 16 and 128, respectively. Interestingly, wild birds co-housed with chickens had poorer body condition indices than directly inoculated birds housed only with conspecifics.

Presenter Bio: House Finches, Northern Cardinals, American Goldfinches, Brown-headed Cowbirds, Newcastle disease virus, live vaccines, backyard poultry, agricultural-wildlife interface.

EXPERIMENTAL INFECTIONS AND SEROLOGY PROVIDE EVIDENCE FOR INCLUDING WHITE IBIS (*EUDOCIMUS ALBUS*) AMONG THE TYPE A INFLUENZA VIRUS NATURAL RESERVOIR SYSTEM

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The American White Ibis (WHIB; *Eudocimus albus*) is a nomadic wading bird common to many coastal habitats in the southeastern United States. In South Florida, habitat encroachment has driven a large number of WHIBs to become highly urbanized. While they forage in neighborhood parks, artificial wetlands, backyards, and golf courses, the majority continue to nest and roost in natural wetlands, often in dense colonies. Adults and juveniles commonly disperse thousands of kilometers to other breeding colonies in the Southeast, resulting in frequent contact with humans, waterfowl, domestic poultry, and other urbanized and non-urbanized avian species throughout their range. Historically, wading birds were not considered significant hosts for influenza A virus (IAV), yet as WHIBs now regularly move among various human, domestic animal, and wildlife interfaces, their potential to be exposed or infected with IAV deserves attention. To investigate this, we experimentally challenged wild-caught, captive-reared WHIBs with three low pathogenic IAVs and serologically tested wild WHIBs for antibodies to IAV. Ibis were highly susceptible to experimental challenge with H6N1 and H11N9 IAVs with cloacal shedding lasting an average of six days for most birds. Nine of thirteen infected birds seroconverted by 14 days post infection as determined by blocking enzyme-linked immunosorbent assay (bELISA). In contrast, no WHIBs challenged with H3N8 were infected. We tested 330 serum samples from WHIBs captured in southeastern Florida in 2015-2017 for antibodies to IAV. Fifty-nine percent of wild birds were antibody-positive by bELISA, indicating that exposure to IAV is common in WHIBs. The highest antibody prevalence was detected in the spring (64%) while the lowest prevalence was detected in the summer (51%). These results provide compelling evidence that WHIBs are susceptible and naturally infected with IAV and may represent a component of the IAV natural reservoir system.

Presenter Bio: Charlie Bahnson is a third year graduate student at the Southeastern Cooperative Wildlife Research Study. His research concerns drivers of influenza a virus in the natural reservoir. In addition, he serves as a veterinarian on the SCWDS diagnostic service.

SUSCEPTIBILITY OF LAUGHING GULLS AND MALLARDS TO RUDDY TURNSTONE-ORIGIN TYPE A INFLUENZA VIRUSES

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Delaware Bay remains the only location where influenza A virus (IAV) is consistently detected in a shorebird species, the Ruddy Turnstone (RUTU; *Arenaria interpres morinella*). Although this disease system has been well studied over the past few decades, the importance of other species and the annual source of IAVs that infect RUTUs each spring remains unclear. We assessed the role of Mallards (*Anas platyrhynchos*) and Laughing gulls (*Larus atricilla*), two species that are commonly observed cohabitating the beaches at Delaware Bay. Captive-reared gulls were challenged with RUTU-origin H6N1, H10N7, H11N9, H12N4, and H13N6 IAV; as well as Mallard-origin H6N1 and H11N9. We challenged captive-reared Mallards with the same viruses, with the exception of H13N6. At a biologically plausible challenge dose (10^4 EID_{50}/0.1ml), one of five gulls challenged with either H6N1 IAV briefly shed virus. The remaining gulls were resistant to infection with all challenge viruses. In contrast, all Mallards shed virus, with the exception of the H12N4 challenge group, in which no birds were infected. There was no difference in viral shedding or seroconversion between the RUTU vs Mallard-origin virus groups. These results indicate that if Laughing gulls contribute to IAV dynamics at Delaware Bay, behavioral factors within this species (feeding strategies, high density roosting, etc.) and interspecies interactions must overcome a substantially higher threshold of exposure dose as compared to Mallards.

Presenter Bio: Charlie Bahnson is a third year graduate student at the Southeastern Cooperative Wildlife Research Study. His research concerns drivers of influenza a virus in the natural reservoir. In addition, he serves as a veterinarian on the SCWDS diagnostic service.

MEDICAL AND SURGICAL MANAGEMENT OF PECTORAL ENTANGLEMENT IN THE FLORIDA MANATEE *(TRICHECHUS MANATUS LATIROSTRIS)*

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Entanglements from marine debris are a significant morbidity event for the Florida manatee (*Trichechus manatus latirostris*). From 2008 to the end of 2017, 220 manatee rescues have been conducted due to entanglements. Entanglement of the pectoral limbs with crab traps or monofilament is most common. If the status of an injury is questionable, or the overall health of the manatee has been compromised, veterinarians are consulted or the manatee is taken to a critical care facility. Therapy often consists of systemic antibiotics, wound cleaning, surgical debridement, or in some cases, partial or complete amputation of the pectoral limb. Often surgical amputation entails general anesthesia and may require up to 2 hours. Follow up care can involve bandaging and cleaning the wound, and overall hospitalization of 6-8 weeks minimum. Conservative management due to stress of animal restraint and related welfare concerns demonstrated healing without direct intervention. This realization has led to a few pectoral amputations in field conditions. In all cases, the overall health of the manatee was deemed to be good and laboratory results analyzed in the field or later have confirmed no systemic concerns. Most field amputations have involved only soft tissue dissections, but all resulted in bone exposure post-operatively, usually the humerus and/or radius. In some cases, granulation tissue was already noted on these bones at the time of rescue. The pachyostotic bones allow a ready blood supply that support granulation beds, and exposed bones may not be at a higher risk for bacterial infection than other exposed tissues in manatees. To date, none of the manatees having field amputations have required follow up or been found dead. Given the limited capacity for manatee rehabilitation and stress involved in hospitalization of wild animals, field amputation of manatee pectorals should be given serious consideration based on veterinary evaluation.

Presenter Bio: Senior Veterinarian at Tampa's Lowry Park Zoo

EVALUATING BAT GUANO AT SUMMER ROOSTS AS AN ALTERNATIVE SAMPLING STRATEGY FOR SURVEILLANCE OF *PSEUDOGYMNOASCUS DESTRUCTANS*

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Surveillance strategies for detection of *Pseudogymnoascus destructans* (*Pd*), the causative agent of white-nose syndrome, consist primarily of collecting skin swabs from bats during hibernation when the fungus is most prevalent among affected bat populations. However, hibernacula are not always accessible, and locations where susceptible species overwinter are not always known. Alternative strategies for early detection of *Pd* are warranted. Guano was collected from underneath bat roosts in Wisconsin (n =3) and Washington (n =1) at 7- and 28-day intervals between May and August 2017. Molecular analyses indicated the presence of *Pd* DNA in accumulated guano at all roost locations for nearly every time point sampled throughout the summer with 28-day collection intervals demonstrating more reliable *Pd* detectability during mid-summer in regions where *Pd* had occurred for at least one year. Skin swabs and guano from individual Little Brown Bats (*Myotis lucifugus*) captured at the three Wisconsin maternity roosts were also positive for *Pd* as long as 15 weeks post-hibernation with overall *Pd* prevalence ranging from 10% to 38% into early August and involving juvenile bats (24%). One source of *Pd* exposure in Wisconsin during the summer appeared to be the roost structures which tested positive for the presence of *Pd* DNA. As expected, all sample types (community guano, skin swabs, and guano from individual bats) showed a trend of increasing cycle threshold (Ct) values as the summer progressed, indicating decreased amounts of detectable *Pd* DNA. Fungal cultures to assess the viability of *Pd* contamination found at summer roosts are ongoing. Recommendations for the collection of community bat guano are being developed as are laboratory protocols for efficient sample processing. While bat guano at summer roosts shows promise as a surveillance tool, additional evaluation is necessary to assess its reliability for early detection of *Pd* dispersal into new areas.

Presenter Bio: Anne joined the USGS National Wildlife Health Center (Madison, WI) as a wildlife disease specialist in 2008 after completing a PhD at North Carolina State University (Raleigh). She coordinates a nationwide surveillance project for Pd/white-nose syndrome and serves as the lead of the WNS Diagnostic Working Group.

CAUSES OF DEATH IN FLORIDA FARMED WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) DURING 2017

Hannah M. Barber[1,2], *Olivia Goodfriend*[2,3], *Katherine A. Sayler*[2,3], *Julia Loeb*[2,4], *Jeremy Orange*[2,5], *John A. Lednicky*[2,4], *Kuttichantran Subramaniam*[2,6], *Heather Walden*[2,7], *Thomas Waltzek*[2,6], *Jason K. Blackburn*[2,5], *Samantha M. Wisely*[2,3], *and Juan M. Campos Krauer*[1,2,3]

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Farmed white-tailed deer (*Odocoileus virginianus*) breeding operations, commonly referred to as deer farms, are an emerging agricultural industry in Florida. A major challenge to this industry is the high mortality rate in breeding stock, especially fawns and yearlings, caused by various bacterial infections and viral hemorrhagic diseases (HD). Before management can be improved and properly implemented, the cause of death in the farmed herds must be determined. Using the diagnostic program provided by the University of Florida Cervidae Health Research Initiative (CHeRI), we determined the proportion of farmed white-tailed deer that have died from bacterial infections, hemorrhagic disease-causing viruses, or other causes. Participating ranches throughout the state provided deceased, farmed white-tailed deer to be necropsied on-site or sent-in sampled organs to be analyzed throughout the 2017 calendar year. Samples from both collection methods were each tested for hemorrhagic disease using molecular methods, in addition to microbiological and histopathology methods. Parasite identification was also performed when applicable. A total of 121 deceased farmed white-tailed deer were sampled in the year 2017. Of the animals submitted, 76 were born in the year 2017, 19 were born in 2016, and 25 were born in 2015 or before, with one animal's age being unknown. The cause of death was reported as hemorrhagic disease in 43% (52/121) of the animals, while 42% (51/121) of the deer deaths were attributed to bacterial infection. For the remainder, 11 animals died of other causes, and seven had too little information provided to determine a cause of death. HD and bacterial infections are a significant sources of mortality in farmed white-tailed deer. This data provides farmed white-tailed deer breeder's insight on how to improve management practices that can significantly improve the health of present and future herds.

Presenter Bio: Hannah Barber is a graduate student at the University of Florida, College of Veterinary Medicine pursuing a Masters of Science through the College of Veterinary Medicine under the advisement of Dr. Juan Campos Krauer.

PATHOPHYSIOLOGICAL EFFECTS OF HYPOTHERMIA IN AQUATIC WILDLIFE

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Warmer ambient temperatures encourage expansion of habitat, resulting in animal range enlargement and increased risk of exposure to sudden drops in temperature when seasonal change occurs. The antithesis to increased atmospheric and sea surface temperatures are cyclical cold fronts observed in unusual locations. These extreme hypothermic temperatures can shift the paradigm of species relying on warm water such as the Florida manatee (*Trichechus manatus latirostris*) or affect the migratory patterns of species such as marine turtles. Cold stress syndrome in the manatee is defined as morbidity and mortality resulting from prolonged exposure to water temperatures <20°C with a multifactorial pathophysiology. Cold-stunning in sea turtles is a frequent natural cause of mortality, defined as a hypothermic state due to exposure to water temperatures < 12ºC. This study examined the pathophysiological effects of hypothermia on these two taxa identifying the effects on coagulation. Thromboelastography was performed on both healthy and hypothermic individuals to compare changes in coagulation. Statistically significant differences in R (reaction time), K (kinetics), α (angle), and MA (maximum amplitude) parameters in sea turtle species demonstrated that the time taken for blood clot formation was prolonged and the strength of the clot formed was reduced by cold-stunning. In contrast thromboelastography in cold stressed manatees found a hypercoagulable state increasing the risk of thromboembolic disease. Increased incidence of cold stunning and cold stress syndrome could be attributed to an increase in overall population sizes, but exposure to sudden or prolonged periods of hypothermic conditions may also be playing a role.

Presenter Bio: Dr. Ashley Barratclough graduated from the Royal Veterinary College in 2009. She spent three years in mixed animal practice in Yorkshire before undertaking a Masters in Wild Animal Health at the Zoological Society of London, followed by a Master's of Science at the University of Florida in conservation.

PARASITES OF CONCERN IN NORTH AMERICAN RIVER OTTERS (*LONTRA CANADENSIS*)

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North American river otters (*Lontra canadensis*) may have a variety of parasites that can have an impact on health, especially in a rehabilitation setting. *Dirofilaria lutrae* and *Dirofilaria immitis* have been reported in NA river otters with the former species considered otter-specific. In-house ELISA tests for heartworm disease may be positive with both infections because female antigens are conserved. Confirmation of a positive result, either by an echocardiogram or examination of blood for microfilaria, is needed. Adult *Di. lutrae* worms are found subcutaneously and the microfilaria in the blood are much larger than those of *D. immitis*. The subcutaneous abscesses that can develop due to *Di. lutrae*, may be lanced and the worm gently removed. The wound should be flushed and the animal treated with doxycycline and ivermectin. Otters in an outdoor rehabilitative setting should ideally be placed on monthly heartworm preventative. Another differential for worms found subcutaneously in NA otters is *Dracunculus lutrae* (or Guinea worm). When these worms or nodules are lanced, larvae with long taping tails will be detected vs. the microfilaria that would be present with *D. lutrae* infections. Also, no *Dr. lutrae* larvae enter circulation. Local hair loss and skin damage due to self-inflicted trauma (scratching) may occur with *Dr. lutrae*. There is no treatment other than physical removal and because *Dracunculus* have no evidence of *Wolbachia* endosymbionts, treatment with doxycycline would probably not be indicated. Animals with evidence of pneumonia should be checked for an eosinophilia on CBC. If present, this may indicate a high probability for *Crenosoma goblei* (lungworm). Although *C. goblei* larvae may be found on a fecal exam, bronchoscopy or bronchoalveolar lavage may be more sensitive. In our hands, treatment with fenbendazole (50 mg/kg PO q24h x3d) appeared to be more effective than ivermectin (0.3 mg/kg PO) in treating several individuals.

Presenter Bio: Hospital director at CROW. Residency then faculty in Zoological Medicine at UGA CVM. Department Head of Clinical Medicine at SMU SVM in the Cayman Islands and veterinarian for Cayman Wildlife Rescue. Wildlife/exotics consultant for IDEXX and Antech Imaging Services; former president of Association of Avian Veterinarians & ABVP Avian Vice Chair and boarded avian specialist.

SEABIRDS WITH BREVETOXICOSIS: CLINICAL FINDINGS, TREATMENT, AND PROGNOSTIC INDICATORS

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Brevetoxicosis, a condition resulting from ingestion of toxins produced by *Karenia brevis* algal blooms, has been shown to cause mass morbidity and mortality events worldwide in sea birds. These toxins cause neuronal and muscle cell depolarization, leading to neurologic signs in affected animals, but other clinical signs may also be seen and appear to vary to some degree across species lines. Brevetoxins are metabolized by the liver and excreted by the kidneys, potentially leading to disease in these organs. ELISA testing of 23 serum samples from four species of commonly affected seabirds showed positive brevetoxin concentrations ranging from 0.15ng/ml to greater than 2ng/ml. Uric acid levels were abnormally high in 74% of avian patients (17/23), whereas bile acids were only elevated in ~34% (8/23). A regenerative anemia was frequently demonstrated. In a retrospective study at CROW, 78% of cormorants were hypoproteinemic (73/93) and 38% were anemic (35/92). These findings were consistent with the brevetoxin possibly causing a protein losing enteropathy (PLE) or nephropathy (PLN); liver disease causing a decrease in albumin production, or GI ulceration leading to blood loss. Effective treatment protocols should be individualized to patient needs and include a variety of medications and support. Birds that were positive for both anemia and hypoproteinemia had only a 32% chance of surviving unless blood or plasma transfusions were given. Targeted treatment based on clinicopathologic findings resulted in an overall 54.6% release rate of affected birds (n=319) at CROW. Birds given appropriate treatment that were able to survive the first 24 critical hours after admission to the hospital had release rates of 77%. Using a logistic regression model, it was found that in double-crested cormorants, total protein concentration had a significant effect on survival ($P < 0.001$). The probability of survival was only 50% at total protein levels of 2.3 g/dL.

Presenter Bio: Hospital director at CROW. Residency then faculty in Zoological Medicine at UGA CVM. Department Head of Clinical Medicine at SMU SVM in the Cayman Islands and veterinarian for Cayman Wildlife Rescue. Wildlife/exotics consultant for IDEXX and Antech Imaging Services; former president of Association of Avian Veterinarians & ABVP Avian Vice Chair and boarded avian specialist.

INCIDENCE OF CYATHASTOMA MICROSPICULUM IN DOUBLE-CRESTED CORMORANTS (*PHALACROCORAX AURITUS*) AND TREATMENT APPROACHES

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Double-crested cormorants (*Phalacrocorax auritus*) admitted to CROW are occasionally parasitized by *Cyathostoma microspiculum* as determined by either endoscopy and/or fecal exam. Results of hemogram, fecal exam for presence of ova, physical and endoscopic exam findings, and subsequent treatment of 708 double-crested cormorants were analyzed from 2014-2017. Prevalence of tracheal worm infestation was 11.2% and infection was correlated with lower total protein values. The release rate and survival times post treatment were also analyzed for various treatment/response options once a patient was diagnosed with *Cyathostoma* infection. Out of the 24 *Cyathostoma*-infected patients who survived longer than 1 day in the clinic, five were treated by mechanical removal of adult worms via endoscopy and they had a mean survival of 5 days post treatment with a 20% release rate. Four were treated by mechanical removal of adult worms by endoscopy in conjunction with administering an anthelminthic (either ivermectin, fenbendazole or pyrantel) after full recovery from general anesthesia. These cormorants had shorter mean survival post treatment (2.25 days) and a 0% release rate. The most successful treatment group was treated with only fenbendazole (20 mg/kg PO) for three days, resulting in a mean survival time of 7.45 days post treatment and a 73% release rate. Four patients that were untreated after diagnosis had a mean survival of six days post diagnosis and 50% release rate. Adjunctive treatment with antihistamines and anti-inflammatory drugs had no effect on survival. Interactive effects of brevetoxicosis and *Cyathostoma* were noted as the release rates of a control group of brevetoxicosis-diagnosed/*Cyathostoma*-negative birds was significantly higher (65.6%, 21/32) than cormorants that were brevetoxicosis-diagnosed and also infected with *Cyathostoma* (39.3%, 11/28). Thus, tracheal parasitism may have an impact on survival of cormorants admitted to rehabilitation centers regardless of the primary admitting problem; however, treatment modalities may impact survival and/or release success.

Presenter Bio: Hospital director at CROW. Residency then faculty in Zoological Medicine at UGA CVM. Department Head of Clinical Medicine at SMU SVM in the Cayman Islands and veterinarian for Cayman Wildlife Rescue. Wildlife/exotics consultant for IDEXX and Antech Imaging Services; former president of Association of Avian Veterinarians & ABVP Avian Vice Chair and boarded avian specialist.

ADENOVIRUS HEMORRHAGIC DISEASE IN MOOSE (*ALCES ALCES*) AND SURVEILLANCE IN CERVIDS IN ALASKA

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An epizootic episode of adenovirus hemorrhagic disease (AHD) in 1993 caused the death of at least 1,000 mule deer (*Odocoileus hemionus*) in California. Since then, numerous cervid species in the United States have had AHD confirmed mortalities. In 2015, the death of two captive moose (*Alces alces*) calves marked the first AHD-caused deaths in Alaska. Both cases were characterized by systemic vasculitis with endothelial cell intranuclear inclusion bodies, pulmonary edema, petechial hemorrhages and enterotyphlocolitis. Possible pathways of transmission from wild cervids or from cross species transmission at the facility were investigated. Nasal and conjunctival swabs as well as respiratory associated tissues collected from captive and wild cervids were tested for cervid adenovirus by virus isolation and polymerase chain reaction. Four hundred thirty-three samples were tested from caribou (N=219), moose (N=207), elk (N=4), and Sitka black-tailed deer (N=2). Cervid adenovirus was not detected in surveillance samples of swabbed surfaces from live free-ranging and captive animals. Tissues were also negative, except from the two moose calves diagnosed with AHD based on necropsy findings and intranuclear inclusion bodies observed by histopathology. Virus from the positive cases was genotyped using DNA extracted from multiple tissues or swabs. Genotype B was identified based on genetic sequence of the variable region. Virus isolation attempts were negative. This supports the hypothesis that AHD does not establish prolonged infections with shedding, or that persistently infected animals do not shed virus at detectable levels under most circumstances. Further work is needed to address how the virus persists in the environment between disease outbreaks, including the potential for undetected persistent infections with rare intermittent shedding. In the meantime, management techniques such as limiting the potential for interaction between wild and captive animals, facility quarantine and additional surveillance have been employed to mitigate potential future outbreaks of AHD in Alaska.

<u>Presenter Bio:</u> Dr. Beckmen is a wildlife health veterinarian for the state of Alaska. She specializes in health assessment, disease surveillance and anesthesia of free-ranging marine mammals and big game species.

INFECTIOUS CANINE HEPATITIS-LIKE LESIONS IN AN ALASKAN BLACK BEAR CUB

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In October 2015, a free-ranging brown bear (*Ursus arctos*) found dead in Katmai, Alaska tested positive for canine adenovirus type 1 (CAV-1), known as infectious canine hepatitis. CAV-1 serum antibody prevalence in Alaskan bears has been documented but until 2015 there had been no known clinical cases. In June 2017, an estimated six-month-old female black bear (*Ursus americanus*) cub was found dead in Juneau, Alaska and submitted for necropsy. Gross necropsy revealed severe jaundice. The gallbladder was bright yellow and severely thickened with prominent vasculature. The liver was swollen with pin-point white foci. The spleen was markedly enlarged, turgid, and had pin-point white foci. Preliminary differentials included CAV-1, canine distemper virus (CDV), and leptospirosis. Fresh and fixed tissues were initially sent to Colorado State University Veterinary Diagnostic Laboratories. Brain, lung, and spleen tested negative for CDV by real-time polymerase chain reaction (PCR). Kidney tested negative for leptospirosis by PCR. Liver, brain, lung, spleen, and kidney tested negative for CAV-1 and canine adenovirus type 2 (CAV-2) by PCR. Histopathologic lesions included severe multifocal necrosis with mineralization and a few intranuclear inclusion bodies within the liver and severe edema within the connective tissues between the gallbladder and liver. These are highly suggestive of infectious canine hepatitis. In addition, several gram-negative protozoal cysts were identified in the liver, compatible in size and shape with *Toxoplasma gondii*. Previously frozen liver samples were subsequently sent for CAV-1 and CAV-2 PCR testing and immunohistochemical staining at Athens Veterinary Diagnostic Laboratory and CAV-1 and CAV-2 PCR testing at Wisconsin Veterinary Diagnostic Lab. All tests were negative. Pan-adenovirus PCR and sequencing at the University of Illinois is pending. If positive for CAV-1 this would be the first documented clinical case of infectious canine hepatitis in a free-ranging black bear.

Presenter Bio: Class of 2018 graduate of the University of Wisconsin, School of Veterinary Medicine. I plan to pursue an anatomic pathology residency with particular interest in wildlife disease.

DETECTION OF *ECHINOCOCCUS GRANULOSUS* AND *ECHINOCOCCUS MULTILOCULARIS* POSITIVE CANIDS IN EASTERN OREGON

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Surveys for *Echinococcus multilocularis* and *E. granulosus* tapeworms have not been conducted in Oregon. The recent reintroduction of wolves to the state, plus a growing recognition of an expanded geographic range for *E. multilocularis* in North America, make identification of prevalence rates for these parasites important from a public health viewpoint. An opportunistic survey, utilizing carcasses involving hunter-killed (predator removal) and natural mortality events was undertaken to document the prevalence of *E. granulosus* and *E. multilocularis* in Oregon wild canids. A total of 67 coyotes, 6 foxes and 3 wolves were sampled by sieving of previously frozen intestinal tracts to isolate worms. Sieve contents were assayed using PCR techniques specific to each of these *Echinococcus* species, with subsequent sequencing and BLAST analysis of positive products. *Echinococcus granulosus* was identified in four animals from eastern Oregon: one wolf and three coyotes. *Echinococcus multilocularis* was discovered in six coyotes. One coyote harbored both species. To our knowledge, *E. multilocularis* has not been previously documented in Oregon. Given the ability of coyotes to range over considerable distances, and to adapt to semi-urban settings, domestic dogs in Oregon are at risk of infection with *Echinococcus* species. Public health education to emphasize the risks associated with these infections in both the canid population and in intermediate host species may be needed.

<u>Presenter Bio:</u> Rob Bildfell is a faculty member at the Carlson College of Veterinary Medicine, Oregon State University and longtime member of WDA. Kathryn Gaub undertook this research as DVM student and is currently pursuing a PhD in the field of Public Health.

DEVELOPMENT OF AN ELISA SEROLOGICAL TEST FOR *ODOCOILEUS* ADENOVIRUS 1

Ling Jin, Wendy Black and ***Rob Bildfell***
Oregon State University, Carlson College of Veterinary Medicine

Serodiagnostic testing for Odocoileus Adenovirus 1 (OdA-1), an important cause of disease in cervids, has been challenging. Virus neutralization (VN) tests require the maintenance of stocks of suitable cell lines susceptible to the virus infection while fluorescent antibody-based tests present a different set of limitations. We were able to clone OdA-1 spike protein gene into a pET6xHN-N vector and produce sufficient quantities of this unique, highly antigenic protein to use as a diagnostic tool. The protein expressed from pET6xHN-N was suspended in xTractor buffer and used as antigen to coat ELISA plates. Positive control material consisted of archived serum from confirmed OdA-1 infected deer (via virus isolation or histologic observation of typical inclusion bodies). Sera from deer that had no evidence of OdA-1 infection and were VN negative served as negative controls. Cut-off optical density values were based on the average reading from negative sera. Sensitivity and specificity values of the test are based on comparison to indirect FA results.

Presenter Bio: Rob Bildfell is a faculty member at the Carlson College of Veterinary Medicine at Oregon State University.

GAMMAHERPESVIRUS INFECTION IN FREE-RANGING BLACK BEARS (*URSUS AMERICANUS*)

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In 2013, three cases of neurological disease in black bears (*Ursus americanus*) were identified in Reno, Nevada. The lesion identified in the brains of these bears was a nonsuppurative encephalitis. As a component of the investigation, brain tissues were tested for herpesvirus infection with a nested PCR method that uses pan degenerative primers specific for the DNA polymerase gene. Positive detections were observed on brain tissue from bears with and without encephalitis and from a variety of other ursine tissues. Phylogenetic analysis of PCR products amplified from DNA samples isolated from the brain, spleen and lymph node suggested that they were closest to Ursid gammaherpesvirus 1 (UrHV-1). To our knowledge, UrHV-1 had previously only been demonstrated via PCR testing of tissue from sun bears (*Ursus malayanus*). Using tissue samples from numerous Nevada ursid mortalities, a wide array of cell lines were inoculated during the following three year period without successful viral isolation until (Human Rectal cell line) HrT-18G cell line was employed. Supernatant from inoculated culture examined by electron microscopy revealed herpesvirus-like particles. Sequencing of the DNA polymerase gene from these virions confirmed a gammaherpesvirus. When this isolation protocol was applied to archived frozen tissue samples, a similar virus was recovered from the three encephalitis cases and from 11 other black bear mortalities between 2013 and 2017, including animals from Nevada, California and Oregon. These results strongly suggest that UrHV-1 is widespread in the black bear population throughout western United States. Given the ubiquitous nature of many host-specific gammaherpesviruses, and the results from sun bear testing, this agent may even be present in most ursine species. At this time, no link to clinical disease is apparent in black bears. An UrHV-1 specific PCR test has been developed and further characterization of the virus is planned.

Presenter Bio: Rob Bildfell is a faculty member at the Carlson College of Veterinary Medicine, Oregon State University and longtime member of WDA.

REGIONAL SURVEILLANCE OF PARASITIC INFECTIONS IN NORTHERN BOBWHITE QUAIL (*COLINUS VIRGINIANUS*) UTILIZING A MOBILE RESEARCH LABORATORY PLATFORM

***Kendall R. Blanchard**, Aravindan Kalyanasundaram, Cassandra Henry, Matthew Brym, and Ronald J. Kendall*
The Wildlife Toxicology Laboratory at Texas Tech University, Lubbock, TX

Northern bobwhite quail (*Colinus virginianus*), a popular gamebird among hunters, have been declining over recent decades in the Rolling Plains ecoregion in the United States. Investigations in recent years have revealed a high prevalence of eyeworms (*Oxyspirura petrowi*) and caecal worms (*Aulonocephalus pennula*) in this ecoregion, prompting a need to better understand their host-parasite interaction and other factors that influence infection. In this study, the efficiency of a mobile laboratory in comparison to the Wildlife Toxicology Laboratory (WTL) as a reference laboratory was tested by deploying it to three field sites in the Rolling Plains between July and August of 2017. Cloacal swabs were collected from bobwhites at each location. DNA was extracted from swabs for quantitative PCR (qPCR) and ran in the mobile and reference laboratories to detect *A. pennula* and *O. petrowi* infection. Methods for extraction and qPCR utilized a multiplex qPCR protocol developed by WTL for highly accurate and non-lethal detection of *A. pennula* and *O. petrowi* eggs in bobwhite feces. When compared to the reference laboratory, the mobile lab had a 97% ($\hat{p} = 0.967$) and 99% ($\hat{p} = 0.993$) agreement for *A. pennula* and *O. petrowi* detection, respectively. Due to its efficiency, it is proposed that the mobile laboratory would be an effective way to monitor infection levels for future treatment methods in addition to factors that may influence infection such as climate, diapause, and intermediate host populations.

Presenter Bio: I am a Master’s student in Environmental Toxicology at Texas Tech’s Institute of Environmental and Human Health. My research interests include wildlife biology, parasitology, ecotoxicology, disease ecology, and biotechnology.

BURNS, BATS, AND BUGS: SPATIAL AND TEMPORAL EFFECTS OF FIRE ON BATS AND THEIR PREY SPECIES

Cristina M. Blanco *and Jorista Garrie*
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Due to the recent spread of white nose syndrome, and its effects on the energetic costs of bats during winter, it is necessary to understand how prescribed fires affect both the site-occupancy of bat species, and their prey availability before hibernation. Our research aims to determine the availability of insect prey, and spatial and temporal variation in occupancy of bat species native to the Ozark Mountains of northwestern Arkansas. The effects of prescribed fire on bat species can be used as a model to determine potential effects of catastrophic wildfires on those same species, their prey, and their habitats. To determine the effects of prescribed burns on bat species including *Nycticeius humeralis, Perimyotis subflavus,* and *Myotis grisescens*, and their nocturnal flying insect prey species, acoustic monitors and insect traps were deployed at 20 burned and 20 unburned sites, that were visited twice, between April and November of 2017. We used single-season occupancy modeling to determine that the probability of detection increased with higher ambient temperature for all three species, (ex. *N. humeralis*, β=0.106). The most supported model of occupancy probability included the interaction between burn status and forest basal area, with occupancy increasing with lower basal area at sites that were previously burned. Although both Coleopteran and Lepidopteran biomass estimates were similar during the summer season, both orders had biomass over 50% higher at unburned sites than burned sites during the fall foraging period before bat hibernation. These data indicate that fires may cause a decrease in food availability in the period leading up to hibernation, which could exacerbate the effects of white nose syndrome on populations suffering from the disease.

Presenter Bio: Cristina Blanco is pursuing her Master’s degree in Fisheries and Wildlife (August 2018). She received her Bachelor’s degree in Biology from the University of South Florida and has diverse experience with animals including wildlife husbandry, handling, and preventative medicine. She is interested in wildlife conservation, epidemiology, and host-pathogen interactions.

BLOOD NUTRITIONAL MARKERS REVEAL EFFECTS OF REHABILITATION DIET ON GREEN SEA TURTLE HEALTH

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Threatened and endangered green turtles (*Chelonia mydas*) are unique because hatchlings and pelagic juveniles are carnivorous, while later life-stages are primarily herbivorous. This makes mimicking dietary requirements during rehabilitation of sick or injured turtles challenging. In such settings, green turtles are often fed non-herbivorous high-protein, low-fiber diets to counteract poor appetite and emaciation, even when they are at a size consistent with the herbivorous life-stage. This can result in gastrointestinal pathology and obesity, thus delaying recovery and release. The objective of this study was to use hematology, plasma chemistry, and nutritional parameters to determine the effect of diet on health and recovery of green turtles in rehabilitation. We compared turtles undergoing rehabilitation at the Georgia Sea Turtle Center in Jekyll Island, Georgia (n = 34) to healthy, free-ranging turtles captured in St. Lucie County, Florida (n = 34). Blood was collected from free-ranging turtles at a single time point. Rehabilitation turtles were sampled at admission (primarily seafood diet), mid-rehabilitation (mixed seafood and herbivorous diet), and upon recovery (primarily herbivorous diet). Duration of rehabilitation ranged from 25 - 233 days (mean = 100). Changes to blood nutritional parameters during rehabilitation and differences between rehabilitated turtles and free-ranging turtles were analyzed with linear mixed effects models and MANOVA. Several analytes improved during rehabilitation, including total protein, uric acid, potassium, and vitamins A and E. Cholesterol, triglycerides, and phosphorus were significantly higher in rehabilitated turtles at recovery compared to free-ranging animals, while calcium, vitamin D, and magnesium were significantly lower (all $p < 0.01$). A diet that more closely mimics the wild diet is clearly important for green turtles during rehabilitation. Formulation of a novel, nutritionally complete gel diet based on our findings should enhance recovery of green turtles in rehabilitation and help maintain the nutritional health of animals held long-term in captivity.

Presenter Bio: Jennifer is a dual-degree DVM-PhD student at the University of Georgia. She finished her PhD research under Dr. Sonia Hernandez in 2016, and is currently in the third year of the DVM curriculum. She hopes to work in wildlife medicine and continue doing research on wildlife health when she graduates.

IDENTIFICATION AND GEOGRAPHIC DISTRIBUTION OF *BABESIA* SPP IN MESOCARNIVORES (PROCYONIDAE AND MUSTELIDAE) IN SOUTHEASTERN MASSACHUSETTS

***Nancy C. Boedeker*[1], *Victoria Riggs*[2], *Henry Marr*[3], *Brian Bjorklund*[4], *Ryan Bevilacqua*[4], *and Adam Birkenheuer*[3]**
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Tick-borne diseases are of increasing concern due to human encroachment into wildlife habitats, increased contact with urban wildlife, and effects of climate change with subsequent alteration in the ranges of ectoparasites and their hosts. Raccoons (*Procyon lotor*) act as hosts for Ixodes tick species that also feed on humans and domestic animals. *Babesia microti-like* infection, though generally subclinical, has been associated with disease in wildlife. The *B. microti-like* strain of foxes has been found to cause hemolytic anemia in European dogs, raising concern for the potential of *B. microti-like* organisms infecting wildlife to cross species and pose a health risk. Our study aim was to assess the prevalence of *Babesia* spp infections in mesocarnivores in southeastern Massachusetts. Blood was collected from over 500 mesocarnivores, primarily raccoons (n=451), between 2014 and 2016 as part of Massachusetts rabies oral vaccination program surveillance. Samples came from raccoons both on (n=197) and off (n=254) Cape Cod, a hotspot for human tick-borne disease separated from the mainland by a canal. *Babesia* spp DNA was amplified by PCR to assess the prevalence in raccoons from both locations. Prevalences of both *B. sensu stricto* and *B. microti-like* were significantly higher in mainland than Capeside raccoons. No significant differences in *Babesia* spp prevalence were found between sexes or age classes of raccoons. The sample size for other mesocarnivores precluded statistical evaluation, but *Babesia* spp were identified in striped skunks (*Mephitis mephitis*) and fishers (*Martes pennanti*). To our knowledge, this is the first report of Babesia infection in fishers. This study confirms prevalent *Babesia* spp infections in wild mesocarnivores and expands our understanding of potential host species and wildlife reservoirs. Further surveillance of wildlife species is warranted to obtain genetic sequences for comparison to future human and domestic animal cases to inform public education, management, and preventive health plans.

Presenter Bio: Nancy Boedeker works as the Indiana Department of Natural Resources' first wildlife veterinarian. She previously worked at the Smithsonian's National Zoo in Washington DC and the Cape Wildlife Center in Massachusetts. This study is part of her dissertation for her master's degree in Conservation Medicine through the University of Edinburgh.

REFINEMENT OF METHODOLOGIES FOR SUSCEPTIBILITY CHALLENGES WITH THE EMERGING FUNGAL PATHOGEN *BATRACHOCHYTRIUM SALAMANDRIVORANS*

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[3]Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee Institute of Agriculture, Knoxville, TN, USA

The emerging chytrid fungus *Batrachochytrium salamandrivorans* (*Bsal*) has caused declines of wild European Fire Salamanders (*Salamandra salamadra*). Initial susceptibility trials by European scientists suggest that *Bsal* is primarily pathogenic to salamanders in the family *Salamandridae*. For example, they reported that the North American Eastern Newt (*Notophthalmus viridescens*; 'NOVI') is hyper-susceptible to *Bsal*, with 100% mortality within 12-18 days at one low 5000-zoospore dose. We tested the susceptibility of NOVI using six wild populations and four zoospore doses ($5 \times 10^{3-6}$) and found that mortality was moderate (21%) among doses and populations. Mortality at the highest zoospore dose (5×10^6) was about 40%. Our results could reflect greater host genetic diversity and immunological competence of wild NOVI. However, we also followed standard protocols for *Bsal* experimental exposures outlined by the North American *Bsal* Task Force, which differ partly from the exposure methods used by the European scientists. In particular, we used water bath exposure compared to directly inoculating zoospores on the dorsum of the newts. The Europeans also used zoospores from liquid culture and we used agar plates. Lastly, both laboratories used terrestrial husbandry containers (despite aquatic life history of the adults) and swabbed animals every six days to estimate infection, which could affect infection dynamics of the *Bsal* skin pathogen. Therefore, we designed a series of follow-up experiments to test how differences in the design of pathogen challenge experiments could lead to different outcomes. Results from these additional experiments will be shared, and we will propose a modified set of standard procedures for *Bsal* exposure experiments.

Presenter Bio: Markese Bohanon received a BA in biology from Lubbock Christian University and is a research technician in the UTIA Center for Wildlife Health where his primary responsibility is performing diagnostic tests for amphibian pathogens.

HEALTH OF BOREAL CARIBOU IN A PERIOD OF UNUSUALLY HIGH MORTALITY IN NORTHEASTERN BRITISH COLUMBIA, CANADA

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Although boreal caribou populations are declining across Canada and are listed as threatened, little is known about their health. From May to July 2013, an unusually high number of adult boreal caribou were found dead with no signs of predation in northeast British Columbia, Canada. In response, the BC Boreal Caribou Health Program was created to assess multiple health indices for boreal caribou in this region. From December 2012–April 2016, blood, fecal, and hair samples were collected from 239 adult female boreal caribou across seven herds that were live-captured for a radio-collaring monitoring project in northeastern BC. Health indices measured included infection with parasites (e.g., helminth larvae/eggs and winter tick *Dermacentor albipictus*), exposure to selected bacterial (e.g., *Brucella* spp. and *Erysipelothrix rhusiopathiae*), parasitic (e.g., *Besnoitia tarandi*, *Neospora caninum*, and *Toxoplasma gondii*) and viral (e.g., alphaherpesviruses and pestiviruses) pathogens, measures of inflammation (haptoglobin, serum amyloid A), trace mineral status, and chronic stress (hair cortisol concentration). Key findings include: 1) a significant increase in exposure to the emerging bacterial pathogen *E. rhusiopathiae* from 2012/13 to 2013/14, 2014/15, and 2015/16, 2) a new syndrome of hair loss associated with winter tick infestations found in 72% (74/103) and 86% (117/136) of caribou in early (Dec. 1-Feb 15) and late winter (Feb. 16-Apr. 30), respectively, 3) low trace mineral levels for copper and selenium, and 4) a significant positive linear association between hair cortisol concentration and mortality within the next year. We discuss how *E. rhusiopathiae* may have played a role in the high mortality observed in 2013 and propose a health assessment monitoring strategy, exemplified in this study, that provides a framework for establishing herd health status and investigating disease outbreaks in other caribou and wild ungulate populations.

PARASITE AND INFECTIOUS DISEASE SURVEY OF LESSER PRAIRIE CHICKENS IN TEXAS AND NEW MEXICO

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[4]Department of Fisheries and Wildlife, Oregon State University, Corvallis, OR

Habitat loss is cited as the primary cause of population declines of Lesser Prairie Chickens *(Tympanuchus pallidicinctus)*. However, parasites and infectious agents can also contribute to population declines via regulating host abundance or extirpating small, isolated populations. Little is known about how parasites and infectious agents impact Lesser Prairie Chicken populations and if new pathogens have emerged since the last surveys were conducted in the late 1990's. From March-April 2018, we will live-capture Lesser Prairie Chickens in Sand Shinnery Oak Prairies in Texas and New Mexico and conduct a parasitological and serological survey of various pathogens. We will focus on pathogens that have been previous identified to potentially impact Lesser Prairie Chickens or other North American grouse species. Fecal samples will be collected to determine prevalence and intensity of parasitic nematodes (e.g., cecal worms, roundworms, eyeworms), cestodes (e.g., tapeworms), and protozoa (e.g., *Eimeria spp.*). Blood samples will be collected to determine infection with parasitic helminths (microfilaria) and hematozoa (malarial agents) as well as exposure to various bacteria (e.g., *Salmonella* Typhimurium and Pullorum and *Mycoplasma spp.*) and viruses (e.g., infectious bronchitis, West Nile virus and avian influenza). Birds will be examined for ectoparasites (e.g., ticks, mites, and lice), and feathers will be collected and tested for cortisol and corticosterone, which have been found to be measures of integrated chronic stress in other species. The results from these tests will be discussed in relation to demographics of the birds, a changing climate, and management of this species.

CHIKUNGUNYA VIRUS TRANSMISSION USING TERRAFORMA ARTIFICIAL ECOSYSTEMS

Angela Bosco-Lauth, *Airn Hartwig, Paul Gordy, Richard Bowen*
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Vector-borne and zoonotic diseases comprise the majority of emerging infectious diseases that impact human and animal health. These pathogens are part of a complex system of multifaceted and deeply integrated components that, when certain criteria are met, can lead to epidemics that are often poorly understood and difficult to contain. Our approach to elucidating some of the factors related to disease emergence is to integrate ecological pressures into controlled laboratory settings to tease out the drivers of an emergent event. The system we have designed, referred to as TerraForma, uses models in a BSL3 laboratory that mimic barnyards, wet markets, or terrariums where different animal species intermingle and abiotic factors can be altered to investigate causation of emergent events. Here we report using Chikungunya virus, a known human pathogen with an undetermined enzootic cycle, to answer the question of whether reptiles and amphibians can serve as reservoir hosts for viral maintenance. Previous studies have demonstrated that Chikungunya viremia develops in garter snakes, leopard frogs, and common toads following needle inoculation; in this experiment, we allowed these animals to comingle, and then introduced infected *Aedes albopictus* mosquitoes into the environment. Twenty eight days following the mosquito introduction, one toad seroconverted; viremia was not detected. In a follow up experiment, naïve mosquitoes were released into the ecosystem with infected snakes, toads, and frogs. While all of the animals were viremic at the time of exposure, none of the mosquitoes that were harvested from the system developed disseminated Chikungunya infections following extrinsic incubation. While this model did not provide substantial evidence regarding the potential of these ectothermic vertebrate hosts to source an infection, it does provide the basis for any number of similar experiments to be performed utilizing a variety of hosts, including birds, rodents and bats, with varying vectors and pathogens.

Presenter Bio: Dr. Bosco-Lauth has a DVM and a PhD in microbiology with a focus on virology. Her primary research interests include zoonotic disease transmission modeling and her clinical field is laboratory animal medicine.

PROTOZOA IN THE CITY: CHARACTERIZING THE ROLE OF URBAN INVASIVE MONK PARAKEETS AS A PUBLIC HEALTH THREAT IN SANTIAGO, CHILE

***Cristóbal Briceño*[1,2]**, *Daniela Marcone*[1,2], *Karina Yévenes*[1,2], *Héctor Hidalgo*[3], *Valeria Alcayaga*[3], *and Fernando Fredes*[1]
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Invasive species are not only one of the major threats to biodiversity; further they are also linked with emerging diseases for animals and even humans. The monk parakeet (*Myiopsitta monachus*) is a successful and widely distributed invasive species, unique in its ability to build communal nests among psittacids. Up to date, little is known on its impact as a synanthropic species on urban health. As part of a FONDECYT 11160852 project, we have conducted three consecutive sampling periods of nestlings from different parts of Santiago (2015 to 2017), during breeding seasons in austral spring. Intestinal content of 213 chicks (each belonging to a different tree) have been analyzed microscopically using the Ziehl-Neelsen technique for *Cryptosporidium* spp. and modified Telemann for *Giardia* spp. obtaining, roughly, a 20% infectious rate for both protozoa, independently. Polyparasitism has been described for both parasites, being *Giardia* spp. considered the most common gastrointestinal parasite in animals, which depending on its species and lineage, may have a zoonotic potential given its wide range of hosts. Spatial analyses of sampled trees are aiding to understand which territorial variables shape the distribution of these protozoa in Santiago. Further, ongoing molecular characterization and phylogenetic analyses will allow to trace reservoir species, the role of the parakeets, and risks for human and animal health in urban Santiago, Chile.

Presenter Bio: At Conserlab we are interested in wildlife conservation and understanding threats to biodiversity, with a focus on anthropic pressure and how it contributes, not only to impoverish nature heritage but its role on emerging infectious diseases.

DEFINING THE IMPACTS OF WEST NILE VIRUS ON RUFFED GROUSE (*BONASA UMBELLUS*) IN PENNSYLVANIA

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West Nile virus (WNV) was detected throughout Pennsylvania by 2002, which temporally was associated with precipitous population declines in ruffed grouse (*Bonasa umbellus*). Statewide, grouse populations have not since recovered. The present study assessed the potential impacts of WNV on Pennsylvania ruffed grouse populations through integrating laboratory- and field-derived data. Methods included both experimental infections of juvenile grouse and serology on field-collected blood samples. Grouse were susceptible to experimentally-induced WNV morbidity and mortality. Forty percent (4/10) of naïve inoculated grouse were euthanized on 7-8 days post-inoculation (DPI) due to severe clinical disease; lesions in these birds included severe myocarditis and mild encephalitis. Subclinically-infected grouse that survived to the end of the trial at 14 DPI (6/10) had moderate myocardial and more widespread neurologic lesions. These results suggest encephalitis is more likely a chronic manifestation of WNV in grouse, and that longer-term survival may have been compromised in some of these surviving birds. No in-contact sham-inoculated controls had evidence of infection. Nobuto filter strips collected from hunter-harvested Pennsylvania ruffed grouse during the 2015-2016 and 2016-2017 seasons revealed statewide WNV seroprevalence of 14% (28/202) and 22% (48/217), respectively. Seropositive birds were detected in every region of the state and in the majority of sampled counties. Collectively, experimental challenge data and field-derived serologic data provide insight into the distribution and extent of WNV prevalence and the potential impacts of WNV on Pennsylvania ruffed grouse.

Presenter Bio: Justin Brown is the veterinarian for the Pennsylvania Game Commission. He received his D.V.M. from Virginia-Maryland Regional College of Veterinary Medicine in 2004 and his Ph.D. in Pathology from the University of Georgia in 2008. From 2008-2013, he was a diagnostician and researcher at the Southeastern Cooperative Wildlife Disease Study.

MOSQUITO SURVEILLANCE FOR WEST NILE VIRUS IN RUFFED GROUSE (BONASA UMBELLUS) HABITAT

Justin Brown[1], *Lisa Williams*[1], *Matt Helwig*[2], *Mike Hutchinson*[2], *and Andy Kyle*[2]
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West Nile Virus (WNV) is increasingly implicated in population declines of Ruffed Grouse (*Bonasa umbellus*) in Pennsylvania; however, little is known about the WNV transmission cycle in the remote woodland habitat occupied by this species. Nearly all mosquito surveillance efforts for WNV occur in urban, suburban, and other peri-domestic environments for the primary purpose of monitoring risks for human or domestic animal health. These peridomestic surveillance efforts may not provide accurate information on the timing, vector(s), and prevalence of WNV in forested settings. The objectives of this pilot study were to identify potential vectors of WNV in grouse habitat and evaluate whether existing surveillance data from peridomestic habitats reflect WNV viral activity in woodlands. Mosquito surveillance was conducted at 8 sites on forested state game lands for 12 weeks from mid-June through mid-September. Paired gravid traps (baited with hay, lactalbumin and water) and basic light trap (baited with CO2) were used to capture a wide array of mosquito species on each site. Weekly mosquito collections from each trapping location and trap-type were sorted by species, and pools of each species were tested for WNV using reverse transcriptase polymerase chain reaction. More than 15,000 adult mosquitoes representing 25 species were captured and identified. Eight recognized WNV-vectors were identified, with *Culex restuans* being the predominate of these species and representing 22% of the adult mosquitos. Three pools of *C. restuans* tested positive for WNV beginning in mid-July. All other mosquito pools were negative for WNV. These preliminary data suggest that *C. restuans* may be an important vector of WNV in woodland habitats.

Presenter Bio: Justin Brown is the veterinarian for the Pennsylvania Game Commission. He received his D.V.M. from Virginia-Maryland Regional College of Veterinary Medicine in 2004 and his Ph.D. in Pathology from the University of Georgia in 2008. From 2008-2013, he was a diagnostician and researcher at the Southeastern Cooperative Wildlife Disease Study.

WILDLIFE RESEARCH COMPLIANCE AND OVERSIGHT: AN OVERVIEW

John A. Bryan, II
American Society of Mammalogists (ASM), Ila, GA, USA

Traditional institutional animal care and use committees (IACUCs) charged with the oversight of animal use projects often struggle with appropriate applications of their mandate regarding activities involving free-ranging species (wildlife) in their natural habitats. Moreover, the traditional sources upon which conventional, biomedically-oriented IACUCs rely to review animal use activities; e.g. the Animal Welfare Act (AWA: USC; Title 7, Chapter 54, sections 2131 - 2159) and its Regulations (AWA&R: CFR; Title 9, Chapter 1, Subchapter A, parts 1 - 4), and the *Guide for the Care and Use of Laboratory Animals* (*The Guide*; National Institutes of Health, 8th Edition), are woefully insufficient to the task of appropriate, efficient, and timely review of wildlife activities. This inequity frequently results in project approval delays, incomplete/insufficient oversight, burdensome and inappropriate demands upon principle investigators (PIs), and systemic IACUC frustration. However, despite these challenges, PIs engaged in wildlife activities and their reviewing IACUCs do indeed have recourse to a variety of appropriate sources and techniques to facilitate the welfare compliance process. The proposed presentation will focus on the aforementioned resources and techniques to foster appropriate, timely, and legal oversight of wildlife activities. Perceptions and expectations of PIs and IACUCs engaged in wildlife activities and their review also will be discussed, and audience participation in the form of a question and answer session will be encouraged.

Presenter Bio: John A. Bryan, II, is the Chair of the ASM IACUC. He is also the primary author and architect of the U.S. National Park Service Animal Welfare Policy, and currently serves on the Board of Trustees of the Association for Assessment and Accreditation of Laboratory Animal Care, International.

SURVEILLANCE FOR OTHV1 AND UROGENITAL CARCINOMA IN MALE CALIFORNIA SEA LIONS (*ZALOPHUS CALIFORNIANUS*) AT BONNEVILLE DAM

Julia Burco Speten*[1]*,* *Alissa Deming[2,3], Kathleen Colegrove[4], Frances Gulland[3], and Bryan Wright[1]

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Urogenital carcinoma (UGC) is the most commonly diagnosed cancer in California sea lions (*Zalophus californianus*) that strand at The Marine Mammal Center (TMMC; Sausalito, CA) and is known to be associated with OtHV1 infection. A recent study showed a 23% prevalence of UGC in sea lions necropsied at TMMC, with adult males having the highest prevalence (33%). This aggressive and eventually fatal cancer arises from penile and cervical mucosal surfaces and spreads rapidly to other organs with sea lions typically stranding in end-stage disease. This study estimates UGC and OtHV1 infection prevalence in healthy male sea lions (removed at Bonneville Dam, OR, under Section 120 Authorization under the Marine Mammal Protection Act). Consequently, these samples may better reflect the “true” prevalence in the free-ranging population. In the Spring of 2017, 24 adult male sea lions were euthanized, full necropsies were performed, and penile tissue (formalin fixed and frozen) was collected for identification of UGC (histologic examination) and OtHV1 (PCR). UGC was confirmed via gross and histologic findings in nine animals (37.5%), with all confirmed cases presenting with visible gross penile abnormalities ranging from slight discoloration to raised pink to beige, roughened, plaque-like lesions. Upon internal examination, none of these animals had gross evidence of widespread metastases indicating early stages of the cancer. PCR results on abnormal and healthy penile tissue are pending and will provide an estimate of OtHV1 prevalence in apparently healthy male sea lions that carry the OtHV1 virus and have not yet developed cancerous lesions. Our prevalence estimate in apparently healthy sea lions coming up the Columbia River is consistent with that found in the stranded TMMC males, suggesting that their sampling effort may not have been biased and their findings in adult males may be reflective of the dynamics in the free-ranging population.

Presenter Bio: Julia Burco Speten received her DVM from Oregon State University in 2000 and then an MPVM and PhD working with the Wildlife Health Center at University of California, Davis in 2009. She is now a state wildlife veterinarian with Oregon Department of Fish and Wildlife in Corvallis, Oregon.

CASCADING IMPACTS OF THE INVASIVE BURMESE PYTHONS ON THE TRANSMISSION OF EVERGLADES VIRUS

Nathan Burkett-Cadena[1]*, Isaiah Hoyer*[1]*, Erik Blosser*[1]*, Carolina Acevedo*[1]*, Annie Loggins*[2]*, Bob McCleery*[2]
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Invasive apex predators have profound, almost universally negative impacts on natural communities, yet the consequences of these impacts on the transmission of zoonotic pathogens is virtually unexplored. Invasion of southern Florida by the Burmese python, *Python bivittatus*, for example, has been linked to the collapse of large- and medium-sized mammal populations in that region, however, the indirect effects of these changes on zoonotic pathogens is not known. We used historic and current data to investigate potential impacts of the Burmese python on contact between the rodent reservoir hosts (*Sigmodon hispidus* Say and Ord, and *Peromyscus gossypinus* (Le Conte)) and vector (*Culex cedecei* Stone and Hair) of Everglades virus, a zoonotic mosquito-borne pathogen. Mosquitoes were sampled from python-impacted (Everglades National Park and Big Cypress National Preserve) and adjacent natural areas (Fakahatchee Strand State Preserve and Florida Panther National Wildlife Refuge). Between 1979 and 2017, the percentage of blood meals taken from the reservoir hosts of Everglades virus increased by more than 400% in Burmese python-impacted areas. In these same areas blood meals from northern raccoon, *Procyon lotor* (Linnaeus), Virginia opossum, *Didelphis virginiana* Kerr and white-tailed deer, *Odocoileus virginianus* (Zimmermann) decreased by nearly 99%. Outside of python-impacted areas, a far greater diversity of hosts was fed upon by *Cx. cedecei*, including native mammalian apex predators such as Florida panther, *Puma concolor coryi* (Bangs, 1899), and black bear, *Ursus americanus* (Pallas, 1780). Predictions based upon the dilution effect theory suggest that increased relative feedings upon reservoir hosts translate into increased abundance of infectious vectors, and a corresponding increased prevalence of Everglades virus exposure, although this was not tested in the current study. This work constitutes the first indication that an invasive predator can increase contact between vectors and reservoirs of a zoonotic pathogen and highlights unrecognized indirect impacts of invasive predators.

Presenter Bio: Nathan Burkett-Cadena is Assistant Professor of Entomology at the Florida Medical Entomology Laboratory in Vero Beach Florida. His research interests focus on the ecology of vector-borne zoonotic disease, including viruses, protozoa and helminths transmitted by mosquitoes, no-see-ums and blackflies.

EVALUATING THE THREAT OF *BATRACHOCHYTRIUM SALAMANDRIVORANS (BSAL)* TO NORTH AMERICAN AMPHIBIAN SPECIES INCLUDING UNKNOWN ANURAN HOSTS

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[6]Association of Fish and Wildlife Agencies, Washington, DC, USA

Batrachochytrium salamandrivorans (*Bsal*) is a recently discovered fungal pathogen that has caused declines of wild Fire Salamander (*Salamandra salamandra*) populations across Europe. Risk models based on environmental suitability suggest that *Bsal* poses high risk to North American amphibian biodiversity, especially in the southeastern USA. Our goal was to estimate the susceptibility of 26 North American amphibian species to *Bsal* infection and chytridiomycosis. Experimental animals were exposed to one of four *Bsal* zoospore doses ($10^{3\text{-}6}$), and their condition monitored for at least six weeks. We swabbed animals every six days to estimate *Bsal* infection intensity. Susceptible species that developed clinical chytridiomycosis and mortality included *Aquiloeurycea cephalica*, *Chiropterotriton* sp. *Eurycea wilderae, Pseudotriton ruber, Notophthalmus viridescens, N. meridionalis, N. perstriatus* and *Taricha granulosa*. Tolerant species that maintained low intensity *Bsal* infections over several successive swabs include eight caudates: *Ambystoma opacum, A. mexicanum, Aneides aeneus, Cryptobranchus alleganiensis, Desmognathus aeneus, D. ocoee, E. lucifuga* and *Plethodon metcalfi.* Four anurans were also tolerant of *Bsal* infection, including *Anaxyrus americanus, Hyla chrysoscelis, Lithobates chirichahuensis,* and *Scaphiopus holbrookii,* Resistant species which did not maintain *Bsal* infections after exposure include *A. latarele, D. monticola*, *Hemidactylium scutatum*, *Necturus maculsosus, L. sylvaticus,* and *P. shermani* x *teyahalee.* Our results indicate that ample amphibian hosts exist in North America to facilitate the emergence and spread of *Bsal*. Moreover, some species likely will experience declines due to their high susceptibility. We recommend that natural resource and wildlife health agencies deem the introduction of *Bsal* to the USA, Canada or Mexico as a serious conservation threat, and proactively establish regulations to prevent emergence, and evaluate disease intervention strategies that could eliminate spread upon introduction.

Presenter Bio: Davis Carter is a MS student in the Center for Wildlife Health at the University of Tennessee, Knoxville where he is mentored by Drs. Matthew Gray and Debra Miller. His research interests include unraveling the epidemiology of emerging amphibian pathogens.

SUSCEPTIBILITY OF SPECIES IN THE SUBFAMILY SPELERPINAE TO *BATRACHOCHYTRIUM SALAMANDRIVORANS*

***E. Davis Carter*[1]*, Joseph P. W. Cusaac*[1]*, Debra L. Miller*[1,2]*, Jenny A. Spatz*[1]*, Louise Rollins-Smith*[3]*, Laura Reinert*[3]*, Lori A. Williams*[4]*, Andrea English*[5]*, Markese Bohanon*[1]*, and Matthew J. Gray*[1]

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The emerging fungal pathogen *Batrachochytrium salamandrivorans* (*Bsal*) has gained notoriety because of its role in declines of Fire Salamander (*Salamandra salamadra*) populations in Europe. Previous controlled experiments suggest a strong phylogenic signal with host susceptibility to *Bsal* chytridiomycosis, with several species in the family Salamandridae developing clinical disease upon exposure to *Bsal* zoospores. Although risk models for *Bsal* invasion suggest that the southeastern USA is a region of high risk, little information is available on the susceptibility of North American salamander species to *Bsal*. Because of their endemism, high species richness, and general conservation risk ranking of high concern, we investigated the susceptibility of the subfamily Spelerpinae to *Bsal*. We conducted experimental challenges with captive-raised and wild (2 populations) Blue Ridge Two-lined Salamanders (*Eurycea wilderae*), and captive-raised Cave Salamanders (*Eurycea lucifuga*) and Red Salamanders (*Pseudotriton ruber*). We exposed individuals to *Bsal* in a water bath at one of four zoospore concentrations ($5x10^{3-6}$) and monitored their condition for at least six weeks. Captive and wild *E. wilderae* from Georgia and North Carolina, respectively, experienced dose-dependent mortality (100% in the highest dose) and had signs of disease consistent with *Bsal* chytridiomycosis. Additionally, *P. ruber* experienced high mortality (100%) when exposed to high concentrations of *Bsal*. In contrast, limited disease or mortality was observed in *E. wilderae* from Mt. Rogers, VA and in *E. lucifuga*, but infection occurred. Our results indicate that several Spelerpinae species can be infected with *Bsal*, and some are highly susceptible to development of *Bsal* chytridiomycosis. Additional experimental challenges are needed to fully assess the conservation risk of *Bsal* to Spelerpinae, but our preliminary evidence suggest this subfamily could play a significant role in *Bsal* epidemiology if this pathogen emerges in the USA.

Presenter Bio: Davis Carter is a MS student in the Center for Wildlife Health at the University of Tennessee, Knoxville where he is mentored by Drs. Matthew Gray and Debra Miller. His research interests include unraveling the epidemiology of emerging amphibian pathogens.

A REVIEW OF THE CURRENT CHALLENGES FACING SALMONID MANAGEMENT IN WASHINGTON STATE

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The salmonid industry in Washington contributes approximately a billion dollars annually to the state's economy impacting a diverse group of stakeholders. In Washington, approximately 150 hatcheries that raise coldwater finfish species are managed by a variety of entities including treaty Indian tribes, public utility districts, the state's department of fish and wildlife, and the United States Fish and Wildlife Service. There are seven species of Pacific salmon which are further subdivided in stocks based upon run timing and watersheds. These distinctions are essential for determining a threatened and endangered species listings. These anadromous species have complex life histories including migratory routes that cover thousands of miles that complicate fisheries management strategies and monitoring activities. In recent years salmonid populations and returns have declined. The objective of this review is to highlight specific reasons for these declines and to make intervention recommendations. Three major factors contributing to the decline in salmonid returns were identified: environment, predation, and disease. Increasing inland water temperatures, anthropogenic habitat degradation and loss, and water pollution make it difficult for salmonid populations to thrive. Additionally, an abundance of marine mammals (specifically pinnipeds) along the West Coast has contributed to significant salmonid mortality due to predation. Similarly, piscivorous waterbirds nesting in colonies along salmon out-migration routes have shown to significantly limit salmon survival. Wild and domestically-raised populations of salmonids are also continually threatened by diseases, especially when subjected to hatchery conditions. Here we provide recommendations to address these areas of concern: 1) improving production efficiency and investing in preventive medicine, 2) mitigating effects of predation through various control programs, 3) developing an consensus statement regarding hatchery fish genetic programs, 4) supporting research on disease diagnostic and surveillance methods and implementing evidence-based medicine in hatcheries, and 5) expanding current education programs and planning for climate change impacts.

Presenter Bio: The author received a BS in Wildlife Biology from the University of Vermont and an MS in Veterinary Biomedical Sciences from University of Georgia (UGA). She is currently completing a duel DVM/MPH program at UGA. Her research interests include investigating infectious diseases at the human, domestic animal, and wildlife interface.

THE NASAL MICROBIOME OF WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) IN THE PRESENCE AND ABSENCE OF A DISEASE STATE

***Allison Cauvin**, Katherine Sayler, Samantha M. Wisely*
Cervidae Health Research Initiative, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL, USA

Microbiome analysis is a rapidly-growing field in disease ecology. The microbiome is the collection of microorganisms that live on or within another organism, particularly at a specific body site. Little work has been done thus far to characterize the microbiome of any cervid species. Cervid farming is a rapidly-growing industry in Florida that suffers significant economic loss from hemorrhagic disease (caused by epitzootic hemorrhagic disease or bluetongue virus) and/or pneumonia. This study sought to establish a baseline for the normal nasal microbiome in white-tailed deer and study how that community structure shifts in response to upper respiratory tract infection or hemorrhagic disease. Nasal swabs were collected from white-tailed deer weanlings (n=27) in September of 2016. Healthy animals were considered clinically normal upon presentation (n=11). Sick animals (n=16) were designated either due to the presence of non-specific respiratory illness (n=11) or testing positive for EHDV/BTV by qPCR (n=5). DNA was extracted from these nasal swabs and amplified by 16S PCR, then purified and indexed following Illumina protocol. High-throughput sequencing was run on an Illumina MiSeq. Analyses are currently ongoing. We hypothesize that the respiratory microbiome in healthy white-tailed deer will be dominated by the phyla Firmicutes, Bacteroidetes, and Proteobacteria, as seen in other ruminants, and that sick white-tailed deer will have reductions in α- and β-diversity in their nasal microbiome. In-depth microbiome analysis might help us identify “sentinel microbes” for white-tailed deer respiratory health, which could lead to the development of early diagnostics and therapies for these animals.

<u>Presenter Bio:</u> Allison is a graduate student with the Cervidae Health Research Initiative at the University of Florida. She is highly interested in disease ecology, pathology, and microbiome analysis. She is the current president of the WDA student chapter at UF and hopes to get her PhD and continue in academia.

ARTHROPODS AND VECTOR-BORNE PATHOGENS IN ANDEAN AND CHILLA FOXES INHABITING THE MEDITERRANEAN BIOREGION IN CENTRAL CHILE

***Aitor Cevidanes*[1]**, *Sophia Di Cataldo*[1], *Claudia Ulloa*[2], *Andrea D Chirife*[4], *Carla Barría-Loaiza*[4], *Irene Sacristán*[1], *Nicole Sallaberry-Pincheira*[4], *Juliana A. Vianna*[3], *Javier Millán*[4]

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Among globally distributed agents, canine vector-borne pathogens (CVBP) compromise a relevant group of agents transmitted by arthropods. Very little is known about the presence of these CVBP in Chile, and no information exist for foxes. The presence of arthropod vectors and selected vector-borne pathogens [hemotropic *Mycoplasma* (aka hemoplasmas), *Ehrlichia*/*Anaplasma* and *Hepatozoon* sp.] were evaluated in 79 Andean (*Lycalopex culapeus*) and 14 chilla foxes (*L. griseus*) in central Chile, an area with a typical Mediterranean climate. Detection of CVBP was performed in blood or spleen samples by conventional PCR and sequencing of the PCR product. Sixty-four wild-caught foxes were also examined in detail for ectoparasite presence. Thirty-four percent of the Andean foxes and 21% of the chilla foxes were infected with hemoplasmas (68% of the obtained sequences corresponding to *M. hemocanis/hemofelis*, 14% to *Candidatus* M. haematoparvum, and 18% to other species). Only one Andean and one grey fox were infected with *Anaplasma platys*. *Heptazoon* sp. was detected in 66% and 80% of Andean and grey foxes, respectively. Prevalence of hemoplasma was significantly higher in adult Andean foxes (37%) when comparing with juveniles (11%). A total of 103 ixodid ticks were found, belonging to two species: *Amblyoma tigrinum* (85% of the specimens, 21% of prevalence, 4.4 of mean intensity) and *Rhipicephalus sanguineus* (15%, 11%, 1.6). A total of 589 fleas were retrieved, chiefly *Pulex* sp. (84%, 64%, 9.1). *Ctenocephalides canis*, *C. felis* and *Equidnophaga gallincea*, among other species, were less frequent. This is the first large survey for pathogens and ectoparasites with vectorial capacity in Chilean foxes, confirming the presence of previously undetected vector-borne pathogens.

Presenter Bio: Degreed in Veterinary Medicine and MSc in Terrestrial Ecology and Biodiversity Management. PhD student in Conservation Medicine at Universidad Andres Bello, Chile. Currently carrying out field and labwork for his PhD project about canine vector-borne diseases shared between dogs and foxes in Chile under the advise of Dr. Javier Millán.

DISTRIBUTION AND PREVALENCE OF RACCOON ROUNDWORM (*BAYLISASCARIS PROCYONIS*) IN A SEMI-URBAN LANDSCAPE IN NORTHWEST MISSOURI AS DETERMINED BY FECAL FLOTATION ANALYSIS

Bridgette French-Harbison, ***Cary D. Chevalier****, Bethany Bolander, Cassie Daldrup, Rachael Domann, and S. Malone*

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Raccoons are the only member of the raccoon family to naturally occur in Missouri, and are very adaptable to life around humans. Their proximity to humans can cause some health concerns as they can carry diseases and parasites that could be transmitted to humans. One such parasite is raccoon roundworm (*Baylisascaris procyonis*). Raccoon roundworm larvae can infect the central nervous system of humans, causing disease and in rare cases death. Since raccoons live in urban and suburban environments, there is increasing awareness of the possibility of human infection from raccoon roundworm. Roundworm eggs are shed in raccoon feces, and can remain viable in the environment for long periods of time. We surveyed the Missouri Western State University campus (approximately 670 acres) for raccoon feces and latrine sites during the summers of 2014-2017 to determine the distribution and prevalence of raccoon roundworm. We divided the campus into 100 x 100 m grids systematically searched each grid once for raccoon feces. We recorded the location of each fecal sample and latrine using mapping grade global positioning systems (Trimble Navigation, Ltd., Sunnyvale, CA). From each fecal sample we made 5 subsamples from which we applied standard fecal floatation technique. A slide was made from each floatation episode and carefully scanned for raccoon roundworm eggs. We collected and analyzed 517 feces and found raccoon roundworm eggs in 38; an approximately 7.4% infection rate.

CONCERNS, CONFLICTS AND CONSERVATION: WHEN VAMPIRE BATS COME BACK HOME TO ROOST

Richard B. Chipman
National Rabies Management Program. USDA, APHIS, Wildlife Services, Concord, NH, USA

The common vampire bat (*Desmodus rotundus*) and vampire bat-transmitted rabies has a significant impact on human and animal health and results in considerable economic costs to agriculture producers and local communities. Fossil records indicate that the vampire bat range included the USA from 30,000 to 5,000 years ago, before the species was extirpated locally. Contemporary records from Mexico document vampire bats within 50 km of the Texas border. Recent modeling to predict future range expansion of vampire bats suggests current suitable habitat exists in extreme southern Texas and southern Florida. A unique opportunity exists for wildlife, public health and agriculture experts to proactively begin a discussion on an “entrance strategy” for a unique wildlife species and novel rabies virus variant becoming established in the southern USA. The goal of these strategic discussions would be to explore ways to avoid spreading fear and panic among the public and negatively impacting the critical progress made in bat conservation to date, while exploring ways to reduce future human-bat conflicts. Applied disease management options should be investigated that are effective, selective and humane as possible in reducing risk to public health and livestock. To this effect, since 2016, a vampire bat surveillance pilot project has been conducted by the USDA, APHIS, Wildlife Services in Texas, Arizona and Florida, targeting livestock sales barns, dairy barns and feedlots to survey cattle for evidence of vampire bat bites. A total of 561 surveys examining 132,932 cattle were conducted over the two years with no evidence of bat-inflicted wounds. In addition, an ad-hoc survey of wildlife professionals regarding the introduction of vampire bats to the USA has been conducted, including collaboration and communication strategies, perceived impacts to human and animal health, alternate options for surveillance, potential status as a listed or protected species, jurisdictional issues associated with vampire bat management and potential disease abatement strategies.

Presenter Bio: Richard Chipman is a Certified Wildlife Biologist and Coordinator of the USDA, Wildlife Services, National Rabies Management Program. He received his MS in Wildlife Biology from UVM and a MBA from the State University of New York. Professional interests focus on the management of human-wildlife conflicts including wildlife rabies.

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STAMMTISCH AND THE ART AND SCIENCE OF RABIES MANAGEMENT IN A CHANGING WORLD

Richard B. Chipman
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The ability to adapt and thrive in a changing world is essential for organisms that pose disease threats as well as for programs tasked with reducing or eliminating these threats. Implementing effective programs in today's white water environment requires an appetite for risk taking, resiliency and hyper-communication that promotes benefits and casts a wide net to secure strategic partnerships. Despite significant public and animal health impacts and costs, rabies remains a globally neglected disease lacking adequate prevention, control, applied research and sustained commitment of resources. However, a dedicated group of researchers and managers collaborating across agency and organizational lines are focused on managing rabies at its source with methods that make it feasible to control and eliminate rabies in dogs and specific wildlife populations. Rabies management at the landscape scale requires coordination and collaboration, new or improved oral and injectable rabies vaccines, enhanced surveillance and monitoring that leads to real-time adaptive management. Early detection/response combined with a clear understanding of the economic benefits of preventing rabies spread and eventual elimination is essential. Effective rabies management is possible through oral rabies vaccination in terrestrial mammals as illustrated by the elimination of rabies in foxes in several countries in Europe and southern Ontario. The annual application of 9-11 million oral rabies vaccine-baits across 17 states by the National Rabies Management Program and cooperators has contributed to canine rabies elimination, near elimination of gray fox rabies in Texas and prevented appreciable spread of raccoon rabies. Success is due in part to clearly defined goals and objectives outlined in the North American Rabies Management Plan and U.S. National Plan for Wildlife Rabies Management. The art and science of rabies management revolves around creativity and skilled bureaucratic boxing that promotes patience, applied scientific knowledge and managing expectations required for long-term planning for landscape-level disease management.

Presenter Bio: Richard Chipman is a Certified Wildlife Biologist and Coordinator of the USDA, Wildlife Services, National Rabies Management Program. He received his MS in Wildlife Biology from UVM and a MBA from the State University of New York. Professional interests focus on the management of human-wildlife conflicts including wildlife rabies.

LEATHERBACK SEA TURTLE (*DERMOCHELYS CORIACEA)* EMBRYO AND HATCHLING PATHOLOGY IN GRENADA

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Leatherback sea turtles (*Dermochelys coriacea*) have a global hatch success rate of around 50%, the lowest of all the sea turtle species in the world, and a reflection of embryo mortality rather than non-fertilized eggs. Yet there is a paucity of literature describing the pathology affecting embryos and non-emergent hatchlings. In St. Kitts, hatch success is <10% with late stage embryos and dead-in-nest hatchlings often impacted by muscle necrosis, renal mineralization, or bacterial pneumonia. The goal of this study was to describe the pathology of embryos and hatchlings in Grenada, where hatch success more closely approximates the global average at 25-35%. Dead hatchlings (n=7), pipped (n=6), late stage embryos (n=29), and early stage embryos (n=5) were sampled from 17 leatherback nests excavated on Levera Beach, Grenada in August 2017 at 77-105 days post lay. Heart, liver, gallbladder, lungs, gastrointestinal tract, fetal membranes, kidneys, gonads, and cranium were collected for histopathology. Pathology was identified in 21/47 (44.7%) individuals and 8/17 (47.1%) nests. Lesions included inflammation of the fetal membranes (n=5, 10.6%), pneumonia (n=3, 6.4%), muscle degeneration (n=7, 14.9%), epidermal necrosis (n=2, 4.3%), renal tubular degeneration (n=3, 6.4%), and renal gout (n=2, 4.3%). Histological features of 45 gonads evaluated were all consistent with female sex, similar to that observed in St. Kitts and raising concern for high nest temperatures. Muscle necrosis and pneumonia appear to be problematic for Caribbean perinatal leatherbacks because they were also seen in Floridian hatchlings. Further investigation into their etiology would seem warranted. Renal mineralization was not observed in Grenada, suggesting that this lesion may be related to environmental or maternal factors unique to St. Kitts. Studies of the nest environment, including temperature, moisture, pH, and gas partial pressure may help explain the large proportion of perinatal deaths that showed no pathology.

Presenter Bio: Esther Choi is a fourth year veterinary student at Ross University School of Veterinary Medicine and is currently working on her master’s degree through an integrated program with the veterinary curriculum. She is interested in aquatic animal medicine and pathology.

MICROBIOME AND ANTIMICROBIAL RESISTANCE IN REHABILITATED HARBOR SEALS (*PHOCA VITULINA*) OF BRITISH COLUMBIA

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The use of marine mammals as sentinels of environmental and human health has been proposed in the scientific literature. Harbor seals (*Phoca vitulina*), in particular, are a model species due to their nearshore coastal habitat, relatively long life span, and documented history of sharing many common bacterial isolates with humans. This study aimed to establish the expected flora and antimicrobial resistance (AMR) levels in free-ranging harbor seals, and to better understand the nearshore marine environmental prevalence of AMR where there is high human activity. During June and July 2017 at Vancouver Aquarium's Marine Mammal Rescue Centre, nasal and rectal swabs were obtained from 54 rescued harbor seal pups for culture and sensitivity testing upon admission to the facility and again at release (depending upon survival). The most common bacteria isolated upon admission were: *Vibrio sp.* (13.48% nasal), *Escherichia coli* (20.77% rectal) and *Klebsiella sp*. (20.77% rectal). The most common bacteria isolated upon release were: *Plesiomona shigelloides* (20% nasal) and *Escherichia coli* (39.53% rectal). Multiple antimicrobial resistance (MAR) index values were determined for each cultured isolate, and a categorical level of resistance was assigned (No resistance: MAR index = 0; Low resistance: MAR index <0.2; High resistance: MAR index ≥0.2). 68.82% of the isolates cultured demonstrated some level of antimicrobial resistance, with 31.56% demonstrating high levels of resistance (MAR index ≥0.2). *Citrobacter freundii* and *Klebsiella sp*. were the most resistant species identified overall, with the highest mean MAR indices. Overall resistance, measured by mean MAR index, was higher at admission versus release. Possible reasons for the change in flora between admission and release include: change in diet from milk to fish, co-housing with other patients, and antibiotic exposure through either treatment or environmental exposure.

Presenter Bio: Abby Clayton is a senior student at Tufts University in the dual-degree DVM / MPH program, as well as a candidate for the International Veterinary Medicine Post-Graduate Certificate Program. Her research interests include wildlife conservation, exploring wildlife as sentinels for human and environmental health, and strategic health communications.

HIGH-THROUGHPUT SEQUENCING FOR DIAGNOSIS OF ONCOGENIC PAPILLOMAVIRUSES IN BREEDING FACILITIES

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[5]Animal Health, Disney's Animals, Science, and Environment, Bay Lake, FL, USA

Papillomaviruses are small non-enveloped dsDNA epitheliotropic viruses. Some of the early papillomaviral genes (E5, E6, E7, and E8) are potentially oncogenic. These viruses may have significant impacts on breeding populations. Papillomaviruses lack some genes that are more conserved in larger viruses, limiting primer design for broad range papillomaviral PCR for use in viral discovery. Our first case corresponds to a male Somali wild ass (SWA), *Equus africanus somaliensis*, with equine sarcoid identified on his penis. Equine sarcoids are usually self-limiting and caused by Bovine papillomaviruses (BPV1, BPV2, and BPV13). The second case corresponds to a female large flying fox (*Pteropus vampyrus*) with genital wart-like lesions that progressed to squamous cell carcinoma. In both cases, histology was consistent with papillomaviral etiology, but molecular confirmation with PCR was not possible. Next Generation Sequencing (NGS) with the Illumina MiSeq platform was used to obtain full papillomavirus genomes from each case. BPV-1 was confirmed in the SWA. An unusual, possible case of integration into the host genome was seen, with 129 bps missing in the L2 gene. A novel papillomavirus was detected in th e fruit bat (PvPV1). PvPV1 had a 57.9 % nucleotide identity with *Sus scrofa* Papillomavirus 1 which is consistent with a new genus in the Papillomaviridae. The PvPV1 E7 gene in this case may promote progression to squamous cell carcinoma. Papillomaviruses may potentially present significant risk to endangered species under human care. Captive settings may increase the risk of pathogen transmission, especially in breeding facilities. Full sequence analysis is encouraged for diagnostics and of these potentially oncogenic viruses. NGS is a useful tool for diagnosis and prognosis of papillomaviruses in wildlife.

<u>Presenter Bio:</u> Galaxia Cortes-Hinojosa obtained her veterinary degree at the Universidad de Chile in 2006. She then obtained a master's degree in Marine Science at UCN, Chile in 2009. In 2014 she completed a PhD at UF working in adenoviruses and other viruses in marine animals. She is currently a Postdoctoral Associate at Dr. Milner's comparative oncology laboratory; working in osteosarcoma and melanoma comparative research and wildlife viral oncology.

PATHOGEN SURVEILLANCE IN TRANSLOCATED GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*) IN NORTHWEST FLORIDA

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Gopher tortoises (*Gopherus polyphemus*) are listed as threatened throughout most of their range and face population declines due to direct habitat fragmentation and loss. Translocation of tortoises from lands slated for development has become an important tool for conserving the species and minimizing losses of individuals. However, pathogens may reduce translocated tortoise survival and threaten recipient tortoise populations. *Mycoplasma* spp. has been widely studied in gopher tortoises, yet other pathogens have rarely been documented in wild or translocated populations. We present results from two years of pathogen surveillance efforts at Nokuse Plantation in Florida. Surveillance was initiated in 2016 for previously translocated tortoises and was expanded in 2017 to also include tortoises prior to release (n=29), recaptured individuals (n=20), and tissues from tortoises from a mortality event. Whole blood, oral/cloacal swabs, and additional tissues from dead tortoises, were tested for nine chelonian-associated pathogens using Fluidigm qPCR assays. Whole blood samples were negative for all pathogens. We found a 52% prevalence of *Mycoplasma* spp. in swabs in 2016. In 2017, prevalence decreased to 15% and 31% for previously translocated and pre-release tortoises respectively. Fifteen of the 48 tortoises sampled in 2016 (31.2%) were positive for Frog Virus 3 (ranavirus strain). Ranavirus prevalence in 2017 was 0%, with a change in infection status for seven resampled tortoises. We also detected ranavirus in the gastrointestinal tract of three dead tortoises, yet no histopathological evidence for it as a cause for mortality. In other chelonian species, infections with ranavirus present as explosive outbreaks with mortality rates that approach 50–100% with very low prevalence between outbreaks. Change in ranavirus prevalence in these tortoises over time may suggest the same epidemiological pattern, and the absence of clinical signs further supports their potential as reservoirs. These results indicate the importance of pathogen surveillance in translocated animals.

PREDICTING SHIFTS IN IMMUNITY FOR THE URBAN-ADAPTING WHITE IBIS (*EUDOCIMUS ALBUS*) IN SOUTH FLORIDA

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White Ibis (*Eudocimus albus*), a wetland species, are recently abundant in developed Palm Beach County, Florida (PBC) and may be adapting physiologically to urban habitats. Ibis in more developed areas experience altered exposure to stressors and pathogens (both environmentally and via contact with reservoir species including gulls and peridomestic ducks). Increased stress may suppress ibis immunity and increase infection risk. However, some studies in other species demonstrate adaptation to urban stressors, with resultant decreased stress and mitigation of immune suppression. We assessed whether innate immunity differs in ibis using more developed sites, via related changes to baseline stress and *Salmonella* spp. infection. We identified 12 sites around PBC that ranged from 0% to 91% surrounding developed land cover. We captured 62 ibis at these sites from July 2016–July 2017, divided across three seasons relevant to ibis ecology and wetland hydrology. We evaluated multiple parameters relevant to pathogen infection: innate immunity (plasma bactericidal capacity), baseline stress (plasma corticosterone hormone at capture), and *Salmonella* spp. infection (fecal bacterial shedding). We also recorded the season of capture, and determined ibis age (juvenile or adult), ibis sex, and percent developed land surrounding the capture site. We used AIC to compare generalized linear models predicting ibis innate immunity based on all variables. Results suggest that age, sex, and season are most important in predicting immunity. Results from pairwise comparisons demonstrate significantly lower baseline corticosterone in ibis captured in summer versus fall or spring ($F_{2,59}$=8.501, p<0.001). We found no other significant correlations between pathogen parameters (immunity, stress, *Salmonella* infection) and predictive variables (urbanization, season, age, sex). Ibis across urban sites have increased exposure to pathogens of wildlife and public health concern (e.g., avian influenza, paramyxoviruses, *Salmonella* spp.), so better contextualizing shifts in immunity is critical in managing pathogen transmission between wildlife, domestic animals, and people.

<ins>Presenter Bio:</ins> Shannon received her BA (Anthropology) and PhD (Forestry/Wildlife Ecology) from the University of Georgia (UGA). Her doctoral research addressed motivations for public bird feeding, and physiological impacts of bird feeding on urban avian health. Shannon is currently a postdoctoral researcher at UGA interested in how anthropogenic activities alter pathogen dynamics.

EPIDEMIOLOGY OF DERMATOPHYTOSIS IN FREE RANGING FLORIDA PANTHERS

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Commonly referred to as ringworm, dermatophytosis is an infection of keratinized tissue (e.g. skin, hair, and claws) by one of three genera of fungi (*Epidermophyton, Microsporum*, and *Trichophyton*). Species of *Microsporum* and *Trichophyton* are the most important animal pathogens and *M. canis* is the most common species reported in domestic felids. Though dermatophyte fungi are commonly found on wildlife species, reports of clinical disease from dermatophyte infection in free-ranging wildlife are less common and infections are often self-limiting. The Florida (FL) panther (*Puma concolor coryi*) is an endangered subspecies of puma with a breeding population restricted primarily to southwest FL. With an estimated population of only 120-230 animals, this population is at continued risk due to habitat loss, inbreeding depression, and disease. First diagnosed in a FL panther in 1995, dermatophytosis (*Microsporum* and *Trichophyton* species) has since been documented in multiple juvenile and adult animals. Clinical disease in FL panthers seems to parallel that seen in domestic species, with some animals clearing the infection and others, particularly kittens, being severely affected. Two adult panthers have died as a result of the disease, with one severely affected male being emaciated and completely alopecic at the time of death. Potential population effects of this disease are multiple, including direct effects on individuals (immunosuppression and life-threatening disease), mortality and loss of entire litters, and loss of breeding females, resulting in subsequent loss of future litters. A review of risk factors associated with this disease in FL panthers suggests an increased risk of dermatophytosis in canonical panthers. Selective targeting of panthers of direct descent from the original population of FL panthers may increase the loss of genetic diversity and poses an additional threat to this already vulnerable population.

Presenter Bio: A graduate of the Atlantic Veterinary College, Dr. Cusack has completed specialty training in aquatic and terrestrial wildlife health and is currently the veterinarian for the Florida panther project with the Florida Fish and Wildlife Conservation Commission.

INVESTIGATIONS INTO AN UNUSUAL MORTALITY EVENT OF MANATEES IN THE INDIAN RIVER LAGOON, FLORIDA

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The Indian River Lagoon (IRL) on Florida's east coast is one the most biologically diverse estuaries in the nation, and an important habitat to the threatened Florida manatee (*Trichechus manatus latirostris*). Since 2012, the Florida Fish and Wildlife Conservation Commission and partners have been investigating an unusual mortality event (UME) of manatees in the IRL. This event followed a dramatic reduction of seagrass (the manatee's primary food) in the area due to long-term, non-toxic phytoplankton blooms. At least 186 manatee deaths were attributed to the event between 2012 and 2017, and mortality peaked in 2013 when 111 deaths that fit the UME case definition were recorded. The case definition includes carcasses in good nutritional condition, with multi-organ congestion and/or wet lungs indicative of drowning. A common observation among carcasses is gastrointestinal filling with varied species of macroalgae and more fluid than usual. Microscopic lesions include enteritis or colitis lymphoplasmacytic, heterophilic, eosinophilic) with submucosal edema and small intestine villous and submucosal lymphatic lacteal dilation. A multidisciplinary approach involving environmental and carcass sampling found no causative evidence through testing of algal biotoxins (brevetoxin, domoic acid, saxitoxin, okadaic acid, polycavernoside A), trace metals, general toxin gas chromatography/mass spectrometry, vitreum biochemistry, fungal culture, and viral sequencing. Currently, the role of toxin-producing gastrointestinal bacteria is being studied through culture, histology, cytology, immunohistochemistry, and molecular diagnostics in archived samples; however, carcass decomposition and limited baseline on manatee carcass gut flora complicate consistency and interpretation of results. While the investigation is still ongoing, most results to date suggest that a diet-shift to macroalgae could possibly be correlated with a lethal change in gut flora in a proportion of manatees in the IRL.

Presenter Bio: Martine de Wit graduated from the Faculty of Veterinary Medicine at Utrecht University in the Netherlands. Since 2005, she has worked at the Marine Mammal Pathobiology Laboratory of the Florida Fish and Wildlife Conservation Commission, where she oversees the statewide manatee necropsy program and health research.

MOLECULAR IDENTIFICATION OF HUNTER-REPORTED WILDLIFE SPECIES IN THE BUSHMEAT TRADE IN NORTHERN UGANDA

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Spillover of zoonotic diseases from hunted wildlife to humans occurs most frequently from contact with primates and bats in sub-Saharan Africa. In Northern Uganda, consumption of bats and primates is not widely culturally accepted; however, baboons are often hunted, butchered, and then sold as culturally desirable species such as antelope. Hunters report misrepresenting animal species routinely at the point of sale. This deception in the market subverts the ability of community members to make informed choices about the risks involved in consuming bushmeat. We collected 228 bushmeat samples from 21 communities adjacent to Murchison Falls National Park. The reported species at sale was recorded for each sample, and PCR targeting the mammalian *cyt b* gene and sequencing were performed to identify each sample to the lowest taxonomic unit by performing BLAST analysis on resultant sequences. Questionnaires were administered to community members to gauge disease awareness as well as perception of hunting and selling activities. Our preliminary dataset shows that 38% of samples had disparate results between species reported and NCBI BLAST analysis. The predominant species detected were antelope species (48%), common warthog (15%), black rat (9%) and hippopotamus (9%). Furthermore, the level of species deception in the communities is greatly underperceived by women, with 50.2% of women reporting that they believe meat is never disguised as another kind of meat; however, 95% of hunters report usually disguising bushmeat at the point of sale. This data indicates a public health risk for bushmeat consumers in Northern Uganda. If consumers cannot accurately assess risk when purchasing bushmeat, they may be at an increased chance of exposure to zoonotic pathogens. This data also provides insight into hunting behaviors and prey preference of hunters in this region.

Presenter Bio: Bree is a PhD student in Comparative and Experimental Medicine at the University of Tennessee (UT). She received her DVM in 2017 and MPH in 2015 from UT. Her current research investigates the diversity of pathogens found in bushmeat in northern Uganda and community perceptions surrounding the bushmeat trade.

RETROSPECTIVE INVESTIGATION OF TRANSLOCATED ELK IN TENNESSEE (USA) AND EXAMINATION OF CANID DEFINITIVE HOSTS FOR *ECHINOCOCCUS GRANULOSUS*

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Echinococcus granulosus is a zoonotic cestode parasite that maintains a life cycle in wildlife in North America between ungulates and canids. *E*. *granulosus* has been described in wildlife in Canada with few reports in the Unites States; however, the geographical distribution of *Echinococcus* species in wild hosts is increasing consequent to human activities. In 2000, the Tennessee Wildlife Resource Agency reintroduced elk sourced from Elk Island National Park in Canada to the North Cumberland Wildlife Management Area in the southeastern US. From 2000 to 2008, 201 elk were released, and the population continues to increase. We investigated the prevalence of *Echinococcus* spp. in the re-established elk and wild canid populations in an area with no previous reports of this disease in wildlife. We performed a retrospective search of elk necropsies at the University of Tennessee College of Veterinary Medicine (UTCVM) from 2002 to 2017 to identify elk with lesions consistent with echinococcosis. Archived paraffin blocks were sectioned, stained with H&E and examined microscopically to identify characteristic lesions. Subsequent PCR and sequencing targeting the parasite mitochondrial COX1 gene were performed on sections of paraffin blocks with corresponding lesions. In addition, from January to March 2018 we necropsied and performed complete helminth exams on 11 coyotes killed in areas surrounding the elk relocation zone. In total, 4 elk were PCR positive for *E*. *canadensis*. Each sequence had at least 98% coverage and identity to multiple *E. canadensis* genotypes in Genbank. Adult *E*. *granulosus* were not detected in any of the coyotes examined in this study. Continued surveillance of this disease in susceptible species in this area is warranted and these data further underscore the risk of pathogen introduction due to wildlife translocation.

Presenter Bio: Bree is PhD student in Comparative and Experimental Medicine at the University of Tennessee (UT). She received her DVM in 2017 and MPH in 2015 from UT. Her current research investigates the diversity of pathogens found in bushmeat in northern Uganda and community perceptions surrounding the bushmeat trade.

RETROSPECTIVE ANALYSIS OF THE PREVALENCE OF UROGENITAL CARCINOMA OVER A DECADE IN STRANDED CALIFORNIA SEA LIONS (*ZALOPHUS CALIFORNIANUS*)

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A high prevalence of urogenital carcinoma has been observed in California sea lions (*Zalophus californianus*) along the Pacific coast of the US since the 1980s. This carcinoma of urogenital origin has been associated with a sexually transmitted herpesvirus, Otarine herpesvirus 1, as well as high levels of PCBs, DDTs and a possible genetic predisposition. This study provides a retrospective overview of medical, necropsy and histology reports from January 1, 2005 to December 31, 2015 of juvenile, subadult and adult California sea lions that died or were euthanized at The Marine Mammal Center. In this 10-year period 1,917 juvenile, subadult and adult sea lions were necropsied. Fourteen percent (263/1,917) were diagnosed with cancer, of which 90% (237/263) were urogenital carcinoma. Prevalence of urogenital carcinoma was 10-fold higher in adults (211/932), compared to juvenile and subadults (26/985). Adult male sea lions were the age/sex class with the highest prevalence at 33% (37/111), closely followed by adult females at 21% (174/821). Advanced stage disease was present in 78% (182/232) of cases, with widespread metastases and poor body condition in these animals. Metastases were most commonly observed in the sublumbar lymph nodes and lungs. Hydronephrosis, secondary to ureter obstruction by metastases, was identified in 62% (114/185) of animals with advanced stage disease. No significant temporal change in prevalence was detected over this decade compared to previous years, and this highly aggressive, fatal cancer remains common in stranded California sea lions.

Presenter Bio: Alissa Deming received her MS from Florida Atlantic University in 2008 and her DVM from the University of Florida in 2012. She is now the Geoffrey Hughes Research Fellow at The Marine Mammal Center and completing her PhD at University of Florida studying urogenital carcinoma in California sea lions.

ASSESSMENT OF WILDLIFE HEALTH CAPACITY IN NEPAL

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Improving wildlife health capacity in developing countries elevates wildlife conservation efforts in places of high biodiversity and can improve human and domestic animal health. Recently, we used a semi-structured interview to elicit expert opinion on wildlife health needs in Nepal, specifically to identify perceived diseases of importance for wildlife and domestic animals and to understand facility and capacity needs to improve wildlife health. The survey was completed by 22 Nepali nationals and 7 foreigners with experience working in Nepal. The top four diseases identified in wild animals were tuberculosis (45%), foot and mouth disease (38%), rabies (35%) and avian influenza (28%). The top four diseases identified in domestic animals were foot and mouth disease (identified by 62% of people), tuberculosis (55%), rabies (45%), and avian influenza (41%). Zoonotic diseases of top concern identified included tuberculosis (55%), rabies (41%), avian influenza (31%) and brucellosis (24%). While numerous other diseases of importance were also identified, the results from the experts surveyed highlighted the interconnectedness of human, domestic animal and wildlife health in Nepal and the multifactorial benefit of addressing these diseases. Some priority actions identified for addressing wildlife medicine gaps in Nepal included creating new wildlife veterinary positions in National Parks, training of veterinary students in wildlife medicine, and providing post-graduate short courses for licensed veterinarians. Improving and increasing veterinary training facilities, animal holding facilities and wildlife transportation capacity were other important needs identified. Increasing wildlife health capacity in Nepal will greatly benefit wildlife conservation and have the added benefit of improving domestic animal and human health.

Presenter Bio: Professor I.P. Dhakal is a veterinarian and the Vice-Chancellor for the Agriculture and Forestry University in Nepal.

MOLECULAR AND HISTOPATHOLOGICAL CHARACTERIZATION OF *SPIROCERCA LUPI* IN CULPEO FOX (*LYCALOPEX CULPAEUS*) IN CHILE

***Sophia Di Cataldo*[1]**, *Mario Alvarado*[1], *Aitor Cevidanes*[1], *Andrea Chirife*[2], *Carla Barría*[2], *Javiera Consanzo-Chávez*[3], *Javier Millán*[2]

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Spirocerca lupi is a heteroxenous nematode parasitizing dogs and other carnivores. It forms nodules in the walls of the esophagus and the stomach and can migrate through the aorta causing ossifying spondylitis of the thoracic vertebrae and aneurisms. In South America, it was described in domestic dogs in Brazil and in a bush dog (*Speothos venaticus*) in Argentina. In this work, two male adult culpeo foxes (*Lycalopex culpaeus*) from central Chile were necropsied revealing the presence of nodular structures in the wall of their stomachs. Eleven and three intact worms were respectively recovered and identified by light microscopy. Histological examination of the cysts revealed multiple foci of lymphoplasmacytic inflammatory infiltrate in the mucosa and a dense fibrous connective tissue surrounding the nodule. These pathological observations are consistent with those previously reported in dogs and wild carnivores. Nine parasites were analyzed by a set of primers targeting the *cox1* gene. PCR amplicons were sequenced, confirming the presence of five haplotypes that showed around 95% identity with sequences of *S. lupi* from the GeneBank. This is the first report of *S. lupi* in Chile both for domestic and wild carnivores. The presence of this parasite in foxes should rise awareness among parasitologists, wildlife researchers, and veterinary practitioners in the country. The abundant population of free-ranging dogs may be acting as a source of parasites for wildlife.

<u>Presenter Bio:</u> Sophia Di Cataldo is a veterinarian and currently is a PhD student of the Conservation Medicine doctorate program at Andrés Bello University in Santiago, Chile. Her interest focuses on carnivore diseases and the epidemiology of vector-borne diseases shared by dogs and foxes.

SEROLOGICAL SURVEY OF CANINE INFLUENZA VIRUS SUBTYPES H3N8 AND H3N2 IN FREE-RANGING CANIDS IN PENNSYLVANIA, USA, 2017

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Influenza A virus is a pathogen of global importance. Although carnivores are susceptible to spillover infection and intra-specific transmission of several influenza virus subtypes, there are few, sporadic reports of influenza viruses in free-ranging carnivores. Canine influenza virus (CIV) subtypes H3N8 and H3N2 are enzootic among domestic dog populations in the northeastern United States. Coyotes and foxes are generalist mesocarnivores that exploit anthropogenic and peri-urban habitats creating a wide interface with domestic dogs and high potential for transmission of infectious disease. To investigate the potential exposure of free-ranging canids to CIV in Pennsylvania, plasma samples were obtained from freshly killed coyotes (*Canis latrans*, *n*=67), grey fox (*Urocyon cinereoargenteus*, *n*=8), and red fox (*Vulpes vulpes*, *n*=5) from 24 counties in Pennsylvania harvested during the January-February 2017 hunting season. Hemagglutination inhibition antibody titers against subtypes H3N2 and H3N8 were measured using assays validated for domestic dogs. All titers were <8, inconsistent with exposure and immune response to CIV. Results suggest that CIV is not endemic in coyote and fox populations in PA or that prevalence is too low to be detected by the limited sample size. This is the first investigation of CIV spillover to free-ranging carnivores in PA. As this emerging infectious disease becomes more prevalent in domestic carnivore populations, surveillance of free-ranging carnivores should be more strongly considered.

Presenter Bio: Rebecca Revay earned a B.S. in biology from Stockton University in 2015 having completed minors in chemistry and marine science. She is a fourth year student at the University of Pennsylvania School of Veterinary Medicine and looks forward to a career as an exotic animal and wildlife veterinarian.

A DEER WALKS UP TO A BITING MIDGE: SITE FIDELITY DIFFERENCES BETWEEN FLORIDA WILD AND FARMED WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) CAN AFFECT ARBOVIRAL EXPOSURE RISK

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Epizootic hemorrhagic disease virus (EHDV), vectored by *Culicoides* midges, causes significant economic loss in the cervid farming industry. There is no efficacious vaccine for the virus and its ecology is poorly understood. Studying space use by EHDV ruminant hosts during the risk period may help elucidate EHDV ecology by determining when and where transmission events can occur. Here, we tested whether free-ranging white-tailed deer (WTD) in a high-fenced, private hunting preserve (farmed) and native WTD from a nearby state-managed properties (wild) exhibited differences in home range (HR) size and usage, and EHDV exposure. Over the two years of our study, there were no significant differences in HR sizes, except for large wild male activity space (95% HR). Site fidelity was significantly different between farmed and wild deer. Farmed deer of both sexes tended to revisit sites more often but stay for shorter periods than wild deer. Virus exposure during the 2015-2016 hemorrhagic disease (HD) season was predominantly to EHDV serotype 1 (EHDV-1) and was associated with a single mortality that season in the farmed population. EHDV-1 seroprevalence was higher in farmed deer. In the 2016-2017 HD season, EHDV-2 was the predominant serotype and was associated with higher rates of mortality in farmed deer. Farmed deer had a significantly higher seroprevalence than wild deer for EHDV-2 during the 2017 sampling period. Overall, farmed deer had significantly higher exposure levels to whichever EHDV serotype was predominant for the immediately-preceding HD season. Each year, the EHDV serotype that was predominant in farmed deer was also the serotype most prevalent in wild deer, suggesting that serotype-specific exposure is similar between groups. Findings suggest more site revisitations of short duration may increase virus exposure and therefore disease risk in farmed WTD.

DYNAMICS OF STRESS AND IMMUNE COMPETENCE DURING REHABILITATION OF DEBILITATED SEA TURTLES

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Chronic debilitation, characterized by near-terminal starvation of any cause, is a grave problem for stranded and rehabilitating loggerhead sea turtles (*Caretta caretta*). Although chronically debilitated turtles are common patients in rehabilitation facilities and are presumably stressed and immunosuppressed, to date little is known about fluctuations in the stress and immune responses during the rehabilitation and recovery process. This study aims to provide a better understanding of the role of stress and immune function in chronically debilitated loggerhead turtles by investigating the dynamics of various biomarkers throughout the duration of rehabilitation. For up to 100 loggerhead turtles, we will analyze blood/plasma samples for various biomarkers of immune system health (e.g., PCV, complete blood count [CBC], H/L ratio, haptoglobin); and chronic and oxidative stress (e.g., plasma glucose, corticosterone, superoxide dismutase [SOD] and lysozyme activities, and ROS concentrations). We retrospectively analyzed blood health data for 48 cases of chronically debilitated loggerhead turtle patients in rehabilitation facilities during 2013 – 2017, and found that pre-release values were significantly higher than entry values for PCV, total protein, total WBC counts, and glucose. These results point to the critical role of nutritional and supportive care in re-establishing normal immune capacity, and emphasize the need to expand upon these data to include more specific biomarkers of chronic and oxidative stress and multiple time points. We predict that biomarkers of stress will decrease as turtles' health improves over time, and that levels of biomarkers of acute/chronic stress and biomarkers of oxidative stress are positively correlated. We also expect to identify certain stress biomarkers that are reliably predictable for rehabilitation outcome. Prognostic indicators identified in this study will be valuable to rehabilitators by helping to direct triage and clinical decision-making, thereby helping to steer hard-won resources towards cases more likely to have high survivorship.

Presenter Bio: Grace Dodillet received her Bachelor's degree in Environmental Science from Northwestern University. She is currently pursuing her Master's degree in Marine Science and Oceanography at Florida Atlantic University's Harbor Branch Oceanographic Institute where she is a member of Dr. Annie Page-Karjian's Marine Wildlife and Veterinary Medicine Research laboratory.

THE RELATIONSHIP BETWEEN AVIAN INFLUENZA VIRAL LOAD AND SIALIC ACID RECEPTORS IN WILD DUCKS

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Individual heterogeneity in viral shedding can impact disease transmission dynamics; therefore, identifying intrinsic factors responsible for variation in viral load is necessary for determining which individuals are prone to be most infectious. Low-path avian influenza (LPAI) viruses in wild ducks (*Anas* spp.) preferentially bind to alpha-2,3 sialic acid receptors (SA-α2,3-Gal) in the host intestines and bursa of Fabricius for replication; therefore, we investigated the relationship between viral load and receptor quantity in both mallards (*Anas platyrhyncos*) and blue-winged teals (*Anas discors*). Birds were raised in captivity after being collected as eggs from free-ranging birds' nests, then infected with LPAI H5N9 between the ages of eight and twelve weeks old. We sacrificed birds at different time points during the infection period, collected sections of the intestines and bursa of Fabricius, and analyzed each tissue via lectin histochemistry. Using the lectin *Maackia Amurensis* I (MAAI), which stains SA-α2,3-Gal, we assessed the quantity of sialic acid receptors with a visual scoring system. We used RT-qPCR to quantify individual viral load in cloacal swabs, ileum, and bursa. In both species, we observed broad individual variation in viral load. In mallards, we observed large SA-α2,3-Gal individual variation in all sections of the intestine, but little variation in the bursa. In blue-winged teals, we observed little SA-α2,3-Gal individual variation in the jejunum, ileum, and colon, but moderate variation in the duodenum, cecum, and bursa. In mallards, the quantity of SA-α2,3-Gal in the villi enterocytes of the ileum and crypts of the colon were positively correlated with viral load. Overall, our findings suggest that inherent variation in availability of SA-α2,3-Gal could be an important intrinsic factor responsible for variation in LPAI viral load.

Presenter Bio: Amanda Dolinski, DVM, is a PhD candidate in the Fisheries and Wildlife Department at Michigan State University. Her research interests are in disease ecology and emerging zoonotic diseases. Her other interests include One Health, wildlife disease surveillance, and influencing government policy.

ELEVATED BODY TEMPERATURE ASSOCIATED WITH KETAMINE MIXTURES DURING CAPTURE OF WOLVES, CANIS LUPUS, IN IDAHO, 1997-2018

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Since reintroduction in 1995-96, 884 gray wolves, *Canis lupus*, were captured and handled in Idaho for management purposes. Two wolves died of hyperthermia during aerial darting in 2015. A retrospective analysis of data from these captures indicated that ketamine combinations appeared to be associated with higher body temperatures irrespective of season or method of capture (foothold trap or aerial darting). Data from 443 capture events met the analysis criteria with 268 summer captures (May-Nov) and 175 winter captures (Dec-Apr). Most summer captures used foothold traps and one of three drug combinations (Ketamine and Xylazine, n=52, Ketamine and Medetomidine, n=46, and Telazol, n=161). Most winter captures used aerial darting from a helicopter with one of two drug combinations (Ketamine and Medetomidine, n=70 and Telazol, n=105). Irrespective of season and method of capture, Ketamine combinations were associated with higher maximum body temperatures than Telazol. Mean maximum body temperatures of summer captures were 103.9 F, 103.9 F, and 103.1 F for Ketamine/Xylazine, Ketamine/Medetomidine, and Telazol, respectively. Mean maximum body temperatures of winter captures were 104.8 F and 102.8 F for Ketamine/Medetomidine and Telazol, respectively. The cause of the higher body temperatures with Ketamine is unknown. The higher body temperatures with Ketamine combinations could not be explained by differences in ambient temperatures or snow water equivalents from SNOTEL data. Ketamine, especially when combined with Medetomidine for winter aerial captures, appears associated with increased body temperatures over Telazol. Higher dosages of Ketamine may allow quicker onset of anesthesia to avoid excessive muscle exertion. Reversible sedatives provide muscle relaxation, but the inhibition of cooling mechanisms may be detrimental to wolves anesthetized with Ketamine.

Presenter Bio: Mark Drew is the wildlife veterinarian for the Idaho Department of Fish and Game. He has a DVM from University of Minnesota (1987), MSc from University of Alberta (1984). He is a diplomat of the American College of Zoological Medicine. Mark is the president of the American Association of Wildlife Veterinarians and a member of the Wildlife Disease Association Council.

MARYLAND BLACK BEAR HEALTH AND DISEASE INVESTIGATIONS DURING DEN VISITS AND NUISANCE ANIMAL RESPONSES

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Maryland has a rebounding American black bear *(Ursus americanus)* population. After decades of few sightings, black bears now thrive in the western counties of the state. They prefer forested areas but are increasingly found where they occasionally encounter humans and pets. The population once thought to be under 300 is now estimated at 2000. The increase in the bear population is primarily due to improved habitat conditions throughout the Mid-Appalachian region. Den investigations began in the 1980s and continue today. To begin to examine the health of this population, from 1999-2011 we collected 84 serum samples from 63 black bears (18 males; 45 females) in five Maryland counties and tested them for normal blood values and exposure to select infectious diseases. No antibodies to *Brucella canis* or *Ehrlichia canis* were detected. Low antibody prevalences to zoonotic agents such as rabies virus and to infectious agents of carnivores including canine adenovirus and canine parvovirus were documented. A larger number of bears had antibodies to canine distemper virus and *Toxoplasma gondii*. Bears also had antibodies to vector-borne pathogens common to bears and humans such as West Nile virus, *Borrelia burgdorferi, Rickettsia rickettsii,* and *Anaplasma phagocytophilum*. Antibodies were detected to *Leptospira interrogans* serovars *Pomona, Icterohaemorrhagiae, Canicola, Grippotyphosa,* and *Bratislava.* Low levels of clinical disease indicate that Maryland black bears living at the human-domestic-wildlife interface may be a spillover host, but they may also serve as sentinels ecosystem health and for pathogens of concern for humans and domesticated animals. This and other One Health issues in Maryland are being addressed through regular meetings of state departments of agriculture, health and natural resources and through our MD One Health Bulletin.

<u>Presenter Bio:</u> Dr. Driscoll is the Maryland State Fish & Wildlife Veterinarian monitoring health and diseases of natural resources. She also teaches Wildlife Diseases at the University of MD, and provides lectures for AQUAVET, MarVet, UPENN, U. Vermont, and others. She is also a contractor for the federal government on biological terrorism.

RANAVIRUS DISTRIBUTIONS IN THE HERPETOFAUNA OF THE USA: EXAMINING THE UTILITY OF DATABASES AND THE LITERATURE

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Ranaviruses are globally emerging infections of amphibians, fish, and reptiles. They are wide spread in the continental United States and are responsible for many morbidity and mortality events each year. Despite being defined as a reportable infection in amphibians by the World Organization for Animal Health (OIE), there are few tools that actively track *Ranavirus* infection. In the USA, there are three widely available resources used to report and track *Ranavirus* infections. One way to track infections is by searching scientific literature, which is cumbersome to navigate and may not be accessible. Another method to track infections is by using the Wildlife Health Information Sharing Partnership event reporting system (WHISPers) database run by the USGS National Wildlife Health Center. WHISPers is an online searchable database that is populated with wildlife morbidity and mortality events of all sorts from across the USA that have been studied by USGS. The third way to track infections is by using the Global Ranavirus Reporting System (GRRS), which is an online searchable database that is currently specific to *Ranavirus* infections in all affected species. The GRRS is a new tool with data populated by scientists and predominantly based on published accounts of *Ranavirus* infection, morbidity, and mortality events around the globe. Currently, the majority of reports in the GRRS appear to come from the USA. Here we compare the relative utility of each data source for tracking amphibian and reptilian *Ranavirus* infections in the USA. A major failing of the online databases is that they typically are a few months behind when compared to the more cumbersome task of sorting through the literature. However, they provide a quick reference and starting point for more in depth questions.

Presenter Bio: Amanda Duffus is an Associate Professor of Biology whose predominant research interests are *Ranavirus* biology and amphibian ecology. While her current position is dominated by the instruction of undergraduates, she still tries to be active in research pursuits. She is currently the Secretary/Treasurer of the Global Ranavirus Consortium Inc.

EVALUATING FUNGAL EXTRACELLULAR SERINE PROTEASES (PDSPS) AND A FUNGAL METALLOPROTEASE (ASP F 2) AS VIRULENCE FACTORS OF WHITE-NOSE SYNDROME IN BATS

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Pseudogymnoascus destructans (Pd) is the etiological agent of white-nose syndrome (WNS) in hibernating bats. Since 2006, this emerging disease has caused dramatic mortality, leading to a decline in multiple bat species. Pathognomonic lesions are severe erosion and ulceration of the skin epidermis, especially on the patagium, muzzle and ears. Typical fungal skin infections initiate when fungal conidia adhere to host tissues and after germination, hyphae start to invade and digest skin epithelium using secreted proteases. Studies of Pd secretomes and transcriptomes reveals two possible families of secreted proteases that could be involved in this process; serine proteases (PdSPs) and a metalloprotease (Asp f 2). The objectives of this study were to further characterize and investigate the roles of PdSPs and Asp f 2 in Pd pathogenesis. Protease activities from *in vitro* fungal cultures were studied using gel zymography and western-blot analysis. Differential gene expression of *PdSPs* and *Asp f 2* during Pd infection on bat patagium versus *in vitro* culture were analyzed using qRT-PCR. To localize PdSP1, one isoform of PdSPs, immunostaining using rabbit polyclonal anti-PdSP1 was performed on fungal conidia. The expression of PdSP1 on infected skins was detected by immunohistochemistry and western-blot analysis. The results showed that proteases derived from different culture media showed distinct profiles and activities. During Pd infection, both serine and metallo- proteases were highly upregulated, interestingly *Asp f 2* was the most upregulated protease. On Pd conidia, PdSP1 was localized on fungal cell wall. During Pd infection, PdSP1 was actively produced in bat tissues. This study provides evidences that PdSPs and Asp f 2 are involved in Pd virulence. Ongoing experiments are focusing on the mechanism(s) in which PdSPs and Asp f 2 help Pd colonizes and causes infection on bat skin epithelium. This information could provide a treatment option for WNS in bats.

<u>Presenter Bio:</u> Piyaporn Eiamcharoen is a PhD candidate in Integrative Pathobiology at UC Davis. She obtained her DVM from the faculty of Veterinary Medicine, Kasetsart University, Thailand in 2013. In the Keel Lab, she is studying secreted proteases of *Pseudogymnoascus destructans*, the fungal pathogen of White-nose syndrome in bats.

EFFECTS OF ANTHROPOGENIC HABITAT MODIFICATION ON CHRONIC STRESS AND SIN NOMBRE VIRUS PREVALENCE IN DEER MICE (*PEROMYSCUS MANICULATUS*)

Angela Luis and ***Andreas Eleftheriou***
Wildlife Biology Program, the University of Montana-Missoula, MT, USA

Sin Nombre virus (SNV) can cause hantavirus cardiopulmonary syndrome (HCPS) in humans. The wildlife reservoir is the deer mouse (*Peromyscus maniculatus*), which when infected does not exhibit any overt clinical signs. In this host-pathogen system, we see higher SNV prevalence in deer mice at peridomestic settings, which are typically anthropogenically modified habitats. Such habitat modification may be associated with chronic stress in wildlife leading to immunosuppression and increased infection prevalence. Chronically stressed individuals may have elevated baseline glucocorticoids (GCs) and an altered stress response. GCs are called fecal glucocorticoid metabolites (FGM) when excreted in feces and can be used to evaluate stress. We tested whether higher SNV prevalence in peridomestic settings may be due to chronic stress in deer mice. We compared 3 chronic stress measures (i.e. baseline FGM, stress-induced FGM, body condition score) in deer mice from 1 peridomestic and 1 sylvan setting over 2 months. Deer mice were captured using Sherman traps. They were ear tagged, weighed, sexed, sampled for feces and blood, and were evaluated for reproductive and body condition before release. Blood samples were analyzed for presence of anti-SNV antibodies and feces were evaluated for FGM. Overall, we found higher deer mouse numbers at the sylvan grid. We did not identify any infected peridomestic deer mice but we did identify 2 infected individuals from the sylvan grid. There were no differences in FGM between peridomestic and sylvan populations. However, sylvan deer mice had overall higher body condition. We conclude that higher SNV prevalence in anthropogenically modified habitats may not be due to chronic stress in deer mice. Even though peridomestic mice had overall lower body condition, this may not have been due to chronic stress since there were no differences in FGM levels. Further studies across time and space are needed to expand on our findings.

Presenter Bio: Dr. Andreas Eleftheriou graduated from Cummings School of Veterinary Medicine at Tufts University. After graduation, he completed a clinical veterinary internship at the University of Pennsylvania's Matthew J. Ryan Veterinary Hospital for Small Animals. He is now a Ph.D. Candidate in the Wildlife Biology Program at the University of Montana-Missoula.

LEAD AND MERCURY PREVALENCE IN BALD EAGLES (*HALIEETUS LEUCOCEPHALUS*) IN THE MID-ATLANTIC UNITED STATES

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Environmental contamination with heavy metals remains a critical health problem. In particular, lead and mercury are known to affect avian health. Predatory birds (e.g. bald eagles) become exposed to these metals through their diets. In the mid-Atlantic United States, some studies found a decreasing trend in lead contamination but no trend for mercury. Chesapeake Bay was found to have higher mercury contamination than Delaware and Barnegat Bays, but similar lead contamination. We evaluated the prevalence of blood lead levels (BLL) and blood mercury levels (BML) in bald eagles across time (2004 -2013) and space (state county level) in 3 mid-Atlantic states (Delaware, New Jersey, Maryland). Blood samples from bald eagles presenting at the Tristate Bird Rescue and Research Inc., (TSBRR) in Delaware, were analyzed for lead and mercury using atomic spectrometry at PADLS Toxicology Laboratory of the University of Pennsylvania. Threshold detection limits for lead and mercury were reported as 0.05ppm, and 0.3ppm, respectively. We categorized BLL > 0.6ppm, and BML > 1ppm, as clinically significant. Wilcoxon rank sum tests for censored data were used to detect trends in BLL and BML prevalence over time. State counties of origin for birds with clinically significant BLL and BML were identified. There were no significant trends in lead and mercury prevalence over time. We found that bald eagles with clinically significant BLL originated from counties near Chesapeake and Delaware Bays, whereas most bald eagles with clinically significant BML originated from counties near Delaware, and Barnegat Bays. The study's findings suggest that lead and mercury contamination in the environment continues to persist in the mid-Atlantic USA. By routinely monitoring bald eagles presenting for rehabilitation for these contaminants, we can ensure that they do not negatively impact their populations and gain knowledge of the degree and trend of heavy metal contamination in the environment.

Presenter Bio: Dr. Andreas Eleftheriou graduated from Cummings School of Veterinary Medicine at Tufts University. After graduation, he completed a clinical veterinary internship at the University of Pennsylvania's Matthew J. Ryan Veterinary Hospital for Small Animals. He is now a Ph.D. Candidate in the Wildlife Biology Program at the University of Montana-Missoula.

EFFECT OF EPIZOOTIC HEMORRHAGIC DISEASE VIRUS SEROTYPE 2 ORAL INFECTION ON SURVIVAL AND REPRODUCTION OF THE VECTOR, *CULICOIDES SONORENSIS* (DIPTERA: CERATOPOGONIDAE)

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Biting midges in the genus *Culicoides* transmit bluetongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV) to ruminants, which causes significant economic losses in animal agriculture worldwide. Despite their importance, very little is known about the fundamental life history traits of midge species associated with BTV/EHDV transmission. In this study, we examined the effect of EHDV-2 infection on midge longevity, fecundity (number of eggs deposited), and subsequent egg hatch in *Culicoides sonorensis* Wirth and Jones, a confirmed vector of BTV and EHDV in North America. *Culicoides sonorensis* females (Ausman strain) were allowed to feed on defibrinated bovine blood inoculated with EHDV-2 (5.5 $\log_{10}$ PFU/mL [treatment group]) or blood without virus (control group) using a Hemotek membrane feeding apparatus. Individual blood-fed females were housed in 175 ml cardboard cups and provided with moist cotton as an oviposition substrate. Adult longevity, fecundity, and hatch rate of the eggs deposited by individual females in each group were monitored for two weeks. Survival of midges past the extrinsic incubation period (5 days post feeding), percentage of females that deposited eggs, and overall fecundity were not significantly different between the infected group and the uninfected group. However, egg hatch rates were significantly lower in the EHDV infected group (32.3 ± 10.2%) than in the control group (68.8 ± 7.7%). These findings suggest that EHDV-2 infection has no major impact on survival or oviposition of *C. sonorensis* females that feed upon infected host blood, but virus infection has a significant negative affect on midge reproduction as it reduces the hatch rate of deposited eggs. It is currently unknown whether reduced egg hatch rate is due to virus infection of embryos or due to unknown physiological effects in gravid females. Further studies will be needed to examine the mechanisms behind EHDV associated reproductive cost in biting midges.

<u>Presenter Bio:</u> Dinesh Erram, PhD, focuses on understanding various biological aspects of arthropods of medical and/or veterinary significance to develop IPM strategies against target species. Our research on *Culicoides* species associated with BTV/EHDV transmission in North America provides valuable information on the potential cost of an infectious blood meal in biting midges.

EVALUATION OF ENZOOTIC ABORTION EVENTS IN THE PERUVIAN POPULATION OF SOUTH AMERICAN FUR SEALS (*ARCTOCEPHALUS AUSTRALIS*) AT PUNTA SAN JUAN, PERU

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The Punta San Juan (PSJ) marine protected area in Peru protects one of the largest breeding colonies of the endangered Peruvian subspecies of South American fur seals (SAFS, *Arctocephalus australis*). At PSJ, second term abortions in female SAFS are routinely observed annually between July and August. Since 2014, these abortions have been systematically recorded at 12 of the 20 PSJ beaches. In addition, detailed records of abortions in the main reproductive colony located at beach S3 have been collected using direct surveillance methods at consistent scheduled times encompassing seven hours per day. Since reproduction in this species is highly synchronous, with >90% of parturitions occurring between November and December, the presence of either a fetus or placenta between June and September was considered an abortion event. We report a total of 38, 71, 43 and 112 abortions in the years 2014, 2015, 2016, and 2017, respectively, occurring at S3 rookery, which produces 366 ±85 live pups annually (ten-year average). Demographic and temporal variation in abortion rates have been observed, but we estimate abortion rates of up to 26% of total pregnancies for this rookery in certain years based on live pup count data. Serologic evidence of abortogenic diseases (e.g. *Brucella*, *Leptospira*, *Toxoplasma*.) has been reported in SAFS at PSJ, but a pilot study in 2016 testing tissues from aborted pups has not revealed a causative relationship for any pathogen. The El Niño Southern Oscillation produces profound changes in this marine ecosystem and food availability may play a role in maternal fitness and abortion prevalence. It is recommended that continued efforts aim to clarify the cause of these abortions and their impact in the population dynamics of this endangered marine mammal.

Presenter Bio: Fernando Vilchez and Leticia Escobar are Peruvian veterinary students with a passion for health research in marine mammals. They started their research in 2015, during their third year of college. With support from the Chicago Zoological Society, they have been able to complete several projects and present at international congresses.

MESOCESTOIDES IN QUAIL FROM TEXAS: WHAT WILDLIFE DISEASE SPECIALISTS, WILDLIFE BIOLOGISTS, AND HUNTERS SHOULD KNOW ABOUT THIS POTENTIALLY ZOONOTIC CESTODE

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A Northern Bobwhite (*Colinus virginianus*) and a Scaled Quail (*Callipepla squamata*) harvested during the 2016–2017 hunting season in Texas were infected with numerous *Mesocestoides* sp. tetrathyridia, representing the first report of *Mesocestoides* found in birds from North America. Molecular analysis indicated an undescribed species, which also was recently found in a Ground Skink (*Scincella lateralis*) from Oklahoma. Our finding of *Mesocestoides* in quails from Texas serves to alert wildlife disease specialists, wildlife biologists, and quail hunters to the existence of this zoonotic parasite; therefore, appropriate precautions can be taken to minimize risk of infection when handling, processing, and eating quail.

FROG VIRUS-3 OUTBREAK INVESTIGATION IN FLORIDA BOX TURTLES

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A mortality event was recognized by a wildlife rehabilitation group on Captiva and Sanibel Islands in Florida that affected Florida box turtles (*Terrapene carolina bauri)*. Clinical signs included facial swelling, stomatitis, open-mouth breathing, mucopurulent nasal discharge, bilateral chemosis, dehydration, emaciation, and skin sloughing over the head and neck. The animals were either dead or euthanized upon presentation to the clinic. Post mortem findings in all carcasses examined included buphthalmos, oronasal discharge, fibrinonecrotizing stomatitis, glossitis, and red-tinged fluid and blood within the coelomic cavity. Histologic findings included fibrinonecrotizing and heterophilic stomatitis and glossitis, as well as marked skeletal muscle degeneration. *Ranavvirus*-specific polymerase chain reaction (PCR) amplifying a conserved region of the coding region of the major capsid protein was done on blood samples and oral swabs when available, from all turtles (n=8) examined. Sequencing and phylogenetic analysis confirmed FV3 in 4/7 oral swabs and 3/8 blood samples. Virus isolation was successful in only one individual despite characteristic lesions being present in all four carcasses. Immunohistochemical staining for Ranavirus sp confirmed the presence of antigen in the oral mucosa and peri-oral skin (3 turtles) and in the kidney (1 turtle). This mortality investigation details the pathologic findings of an epizootic in southern Florida and emphasizes that diagnosing ranavirus infection in free-ranging box turtles can be challenging in chronic stages of disease.

POST-RELEASE SURVIVAL AND MOVEMENT OF OILED AND REHABILITATED BROWN PELICANS (*PELECANUS OCCIDENTALIS*) AFFECTED BY THE 2015 REFUGIO OIL SPILL IN CALIFORNIA

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Enormous amounts of financial and human resources are devoted to oiled wildlife rehabilitation, but there remains a paucity of information on post-release survival and behavior of most affected species. Brown pelicans (*Pelecanus occidentalis*) are near-shore seabirds that are frequently impacted by oil spills. In a previously published study of brown pelicans that were oiled, rehabilitated, and released in California in 1990-91, oiled birds disappeared at a higher rate than control birds, showed movement patterns typical of nonbreeding birds, and did not demonstrate any evidence of breeding activity. In May 2015, Plains Pipeline 901 spilled >100,000 gallons of oil near Refugio State Beach, California. Fifty oiled pelicans were captured and underwent rehabilitation. Forty-six survived and were released following rehabilitation. Of these, 12 adults (6M, 6F) were fitted with solar-powered GPS satellite transmitters and released in June. In early July, 8 adult, unoiled pelicans (3M, 4F, 1U) near Ventura, California were similarly instrumented and released for comparison. Four months after release, transmitters from 11 of 12 oiled and all 8 control pelicans were still transmitting. After one year of tracking, transmitters from 2 rehabilitated and 2 control birds were still active. On average, rehabilitated birds survived 2 weeks longer than control birds. Rehabilitated pelicans traveled significantly greater total and average daily distances than controls. Individual birds traveled as far as the central Oregon coast and Baja California. Neither rehabilitated nor control birds were documented breeding, although some did visit known breeding areas. One limitation of the study was the unreliability of the technology; 5 birds that stopped transmitting were later observed alive, indicating transmitter failure or loss. Despite this and the limited sample size, these data demonstrate that pelicans can survive long-term after oiling and rehabilitation, and that the timing and scope of their movements are comparable to those of unoiled pelicans.

PACIFIC AVIFAUNA CONSERVATION HEALTH PROGRAMS: GUAM AND COMMONWEALTH OF THE NORTHERN MARIANAS ISLANDS (CNMI)

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The avifauna of Guam and the CNMI region are in critical decline due to the accidental introduction of the brown- tree snake (*Boiga irregularis*)[1] Disney's Animals, Science, and Environment has a strong presence in the Mariana's regional repatriation and translocation programs for the Guam rail (*Hypotaenidia owstoni*), Micronesian kingfisher (*Todiramphus cinnamominus*), Rufous fantail (*Rhipidura rufifrons*), Marianas fruit dove (*Ptilinopus roseicapilla*), Tinian monarch (*Monarcha takatsukasae*), and both Golden (*Cleptornis marchei*) and Bridled white eye (*Zosterops conspicillatus*) partnering with other Association of Zoos and Aquarium (AZA) institutions, Pacific Bird Conservation, and the Guam Department of Aquatic and Wildlife Resources and CNMI Department of Fish and Wildlife.[2,3] Pre-release and translocation health surveillance show minimal health concerns to individual and population risk. Surveillance populations under managed care ex situ and in situ with in situ- pre-release and translocation population surveillance from 2011- 2017 show the following findings: Gastrointestinal (GI) pass-through of Mycobacterium avium complex (MAC) is noted with no evidence of systemic mycobacteriosis for in situ and ex situ managed care populations of Guam rail[4]; no evidence of MAC, pass through or systemic, in the managed care in situ kingfisher population; however, ex situ populations have reported systemic avian mycobacterosis; *Campylobacter spp.* has not been recovered for in situ managed care populations of rails or kingfishers despite asymptomatic shedding reported in captive ex situ populations in AZA institutions; characterization of protozoal enteric and hemoparasites is currently underway in translocated populations of white-eyes, fantails, and monarchs; nematodes and coccidian species have been noted sporadically on fecal surveillance; and validation of fecal[5] and methodology for feather[6] corticosterone (enzyme-immunoassay) have been conducted in the surveillance of the fantail, white-eye, monarch, and fruit dove populations. Health surveillance results guide pre-release and translocation testing criteria and release fitness for future veterinary programs for conservation of these in situ extinct and at risk Pacific avifauna species.

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Presenter Bio: A graduate of the University of Georgia in 1996, Deidre completed her post- graduate training in exotic companion and wildlife medicine and surgical internship at UGA as well as a two-year clinical internship at Riverbanks Zoo. She then completed a contract clinical position for the Zoological Society of San Diego prior to becoming a cast member for Disney's Animals, Science, and Environment in 2000. She is currently an animal health team operations manager at Disney and lives in the metro Orlando area with her husband Scott; two sons, Dylan and Tyler, and a rescue menagerie including dogs, severe macaw, sulcata tortoise, and fresh water fish tanks.

NESTING SEASON MORTALITY OF ADULT EASTERN BLUEBIRDS, *SIALIA SIALIS*, DUE TO NECROTIZING ENTERITIS

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Increased mortalities of adult Eastern bluebirds, *Sialia sialis*, breeding in artificial nesting boxes were recorded in populations subject to long-term monitoring in New York State, United States. A total of 46 dead bluebirds were reported from early April to mid-August 2017. In 23 instances carcasses were available for examination by a wildlife pathologist. The most common cause of death was necrotizing enteritis, found in 56% of birds that could be examined histopathologically. Lesions consisted of foci of hypereosinophilic debris and inflammation rich in Gram (-) bacteria that yielded unrewarding culture results. *Plagiorhynchus cylindraceus* acanthocephalids were often but not invariably present in affected birds. Additional lesions found occasionally and considered incidental included foreign-body microgranulomas in the wall of the gizzard and occasional intravascular nematodiasis.

Traumatic injury to the intestinal wall from acanthocephalid attachment to the mucosa and secondary bacterial infection was proposed in similar cases of necrotizing enteritis of Western bluebirds, *Sialia mexicana*. The parasite is not uncommonly present in healthy passerine birds, however, and the bacteria involved in previous reports are Gram (+) *Clostridium* sp. The originating cause of sporadic necrotizing enteritis in breeding bluebirds remains undetermined and warrants further investigation.

Presenter Bio: M. J. Forzán is a wildlife pathologist with a special interest in infectious diseases of wild birds and all topics relating to health and disease of amphibians.

THE INFLUENCE OF DEMOGRAPHIC AND ENVIRONMENTAL FACTORS ON *BAYLISASCARIS PROCYONIS* INFECTION IN ONTARIO RACCOONS

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Raccoons (*Procyon lotor*) are definitive hosts for *Baylisascaris procyonis*, the raccoon roundworm. Since the larval form of this parasite is capable of causing neurological disease in more than 150 species of birds and mammals, including humans, understanding factors that influence carriage of the parasite by raccoons is important for mitigating risk. Our objective was to assess the impact of host factors (i.e., age, sex, fat stores) and environmental factors (i.e., season, human land use, urbanization and year of collection) on the occurrence of infection in raccoons. From January 2013 to December 2016, we recorded the number of *B. procyonis* worms present in the intestinal tracts of 1534 Ontario raccoons submitted to the Canadian Wildlife Health Cooperative for necropsy. In total, *B. procyonis* was found in 531 individuals (34.6%) across Ontario and the median intensity of infection was 4.6 worms (range: 0 - 326). Using a mixed multi-variable logistic regression model, we identified significant interactions between age and season, season and host fat stores, and host sex and human land use, indicating that there are complex relationships between host and environmental factors that influence parasite carriage in Ontario raccoons. These complex interactions may explain differences among previous studies. As such, this knowledge may inform public education programs aimed at reducing the transmission of *B. procyonis* to humans.

<u>Presenter Bio:</u> Shannon French is a veterinarian and PhD candidate at the Ontario Veterinary College. With a strong interest in zoonotic disease and the human-animal interface, she is currently investigating the ecology of *Baylisascaris procyonis*, a zoonotic roundworm, in Ontario.

EVALUATION OF GONACON, A CONTRACEPTIVE VACCINE, TO STOP TRANSMISSION OF BRUCELLOSIS IN BISON

***Rebecca Frey*[1]**, *Ryan Clarke*[1], *Pauline Nol*[2], *Matt McCollum*[2], *Doug Eckery*[3] *and Jack Rhyan*[2]
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[3]USDA APHIS Wildlife Services, Fort Collins, CO, USA

Immunocontraception has been proposed as a management tool to reduce transmission of *Brucella abortus* in bison. The purpose of this study was to determine if a single intramuscular injection of GonaCon (gonadatropin releasing hormone vaccine) would decrease shedding of *B. abortus* in a group of *Brucella*-seropositive bison as compared to a similar group of untreated *Brucella*-seropositive bison. Two cohorts of treated bison (n=35) and untreated bison (n=30) were monitored for 5 and 3 calving seasons (by cohort) after vaccination. Overall, 75/105 pregnancies occurred in the control groups (71%) and 37/148 pregnancies occurred in the treated groups (25%). Total efficacy of one dose of GonaCon over 5 years of pregnancy was 64.7%. Efficacy was highest in year one (81%) and dropped to 52% by year five. *Brucella abortus* shedding events occurred at a much higher rate in controls versus treatments (Controls: 2.57 abortions and 1.43 infectious live births/year; Treatments: 0.125 abortions and 0.125 infectious live births/year). In addition, we observed 29 shedding events in 17 controls, confirming that an abortion event does not induce full immunity in the dam, and these seropositive bison continue to pose a risk to the population via infectious abortions/parturitions. Also, 15/17 (88%) GonaContreated bison had non-shedding births when becoming pregnant after treatment, only 1 animal aborted. These data suggest that one dose of GonaCon in seropositive female bison is effective in reducing *B. abortus-related* shedding events and thus transmission of the disease in this species.

Presenter Bio: Rebecca Frey is currently a Wildlife Biologist for USDA APHIS Veterinary Services in Montana, working for 16 years on management and research related to Brucellosis in the Greater Yellowstone Area. Ms. Frey received her BS from Montana State University and her MS from the University of Idaho

NONNATIVE FISH AND WILDLIFE IN FLORIDA: AN OVERVIEW

Sarah Funck
Florida Fish and Wildlife Conservation Commission

The Wildlife Impact Management Section (WIM) within Florida Fish and Wildlife Conservation Commission (FWC) strives to minimize adverse impacts of conflict wildlife in Florida, which includes nonnative *invasive species*. Response to problematic wildlife, including invasive wildlife, is one way that citizens of Florida interact with our natural resources. Invasive species include wildlife that may cause harm to the environment, economy, or human health and safety. Although invasive species are not a problem unique to Florida, the subtropical climate has been conducive to the establishment and expansion of certain nonnative species of wildlife, including Burmese pythons, large lizards, such as the Argentine black and white tegu, many freshwater fish, lionfish, and even some mammals, such as Rhesus macaques. Over 58,000 observations of nonnative wildlife have been recorded in Florida since 1924, representing almost 600 species. The Nonnative Fish and Wildlife Program within FWC WIM determines which of these introduced species may become established and cause a problem. Health and safety concerns may elevate the need for the FWC to respond to reports of nonnative wildlife. Disease transmission to humans through wildlife bites, scratches, and other means is a serious component to determining the level of conflict a species may have on the citizens of Florida and how we respond. Three high priority health concerns from invasive wildlife include Herpes B transmission from non-human primates, ectoparasites, such as screw worm, and vectors of chytrid fungus, such as African clawed frogs. This presentation will provide an overview of nonnative species in Florida and highlight these three case studies.

HUMAN EXPECTATIONS AS A CRITICAL DETERMINANT OF HEALTH FOR THE VERVET MONKEYS OF ST. KITTS

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[2]Canadian Wildlife Health Cooperative and the Western College of Veterinary Medicine, University of Saskatchewan, Canada

Emerging conceptual models of wildlife health define health as capacity for individuals or populations to cope with stresses and changes and continue to thrive. This contrasts with historic models that focus on health as the absence of disease. Newer models see health as a multifactorial outcome of interacting biotic, abiotic and social variables. Incorporating human dimensions into wildlife conservation has been shown to be a useful approach but in practice wildlife health pays comparatively little attention to the determinant of health known as "human expectations." This presentation explores how human-vervet interactions in St. Kitts has spawned significant social conflict among local stakeholders with strong divergent perspectives and values. We show how the resolution of these conflicts will be the principle determinant of the capacity of the vervets to thrive and thus the major determinant of population health. We used participatory methods that adapt the health belief model, theory of planned behaviour, and transtheoretical model from human health promotion to: (i) find shared community expectations for healthy human-vervet interactions; (ii) identify critical control points that can reduce social harms (impacts on agriculture, tourism and emerging diseases) while maintaining a healthy vervet population and (iii) help those empowered to act see the unintended consequences of possible management options on vervet health or on the nature and magnitude of human-vervet conflict. Knowledge gained by exploring spatial and temporal variations in expectations, determinants of health and capacity to act, will help to develop collective plans for action that are locally adaptive and concomitantly consider the implications of actions for vervet population and human community health. The outcomes will help to integrate wildlife health information into community risk reduction and preparedness. This presentation will highlight the marked influence that human social dimensions can have on the health and resilience of wildlife species.

Presenter Bio: Christa Gallagher is an Assistant Professor of Public Health and Epidemiology. J. Wittrock is a PhD candidate in the Department of Veterinary Microbiology at the University of Saskatchewan. C. Stephen is the director of the Canadian Wildlife Health Cooperative and Professor in Population Health.

PREVALENCE OF ANTIBODIES TO ORTHOPOXVIRUS IN WILD CARNIVORES OF NORTHWESTERN CHIHUAHUA, MEXICO

***Nadia F. Gallardo-Romero*[1], *Clint N. Morgan[1], Andrés M. López-Perez[2], Paola Martínez-Duque[2], Felix R. Jackson[1], Gerardo Suzán[2*]*

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The distribution of orthopoxviruses (OPXV) across the North American continent is suggested to be widespread based on previous serosurveillance studies; additionally, OPXV seroprevalence have been observed in a wide range of mammalian hosts. To address the question of whether carnivores in northwestern Mexico are exposed to naturally-circulating OPXVs, 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, sampled within four different habitat types. Blood samples were collected for diagnostic testing (n=51). Anti-OPXV immunoglobulin G Enzyme-Linked Immunosorbent Assay (ELISA), Western Blot (WB) and Rapid Fluorescent Focus Inhibition Test (RFFIT) assays were conducted. Results showed that 24/51 (47.1%) of the carnivores tested were seropositive for anti-OPXV binding antibodies and had presence of immunodominant bands indicative of OPXV infection. All samples tested were negative for rabies virus neutralizing antibodies (RVNA) by RFFIT, thereby suggesting the OPXV antibodies are due to circulating OPXV, and not by potential exposure to oral rabies vaccine (vaccinia vectored rabies glycoprotein vaccine) bait distributed along the USA-Mexico border. These results indicate that there is an endemic OPXV circulating within six species of carnivores in northwestern Mexico.

FACTORS ASSOCIATED WITH RELEASE OF MARINE ANIMALS PRESENTED TO A WILDLIFE REHABILITATION CENTER IN NEW JERSEY, USA: 1978-2016

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[3]Marine Mammal Stranding Center, Brigantine, NJ, USA

Marine animals occupy high trophic levels and serve as sentinels of ecosystem health. Due to their cryptic habitat, presentation to wildlife rehabilitation facilities provides an opportunity to assess the health of these species. To determine stranding patterns in the mid-Atlantic region of the United States, records of animals presented to the Marine Mammal Stranding Center (MMSC) in Brigantine, New Jersey from 1978-2016 were collected for analysis. 4,811 records from pinnipeds (*n*=1,478), cetaceans (*n*=1,408), and chelonians (*n*=1,926) were available. Factors analyzed included taxa, age, sex, season, and final disposition. Final disposition included natural death, euthanasia, transfer, or successful release. Binary logistic regression was employed to identify predictors associated with release of the stranded animal. A multivariate logistic regression model was developed to evaluate whether the association between taxa and chance of release persisted after adjustment for the other animal and environmental characteristics. Chelonians and pinnipeds had respectively 7 times (OR: 6.7; 95% CI: 4.6 to 9.8) and 16 times (16.1; 10.6 to 24.4) the odds of being released compared to cetaceans. Age, season and sex were all significantly associated with the probability of release. A ROC curve built based on the model had an AUC of 0.88 (95% CI: 0.87 to 0.89). The results of this study provide a reference for pinniped, cetacean, and chelonian stranding patterns in the mid-Atlantic region. Understanding these patterns is useful for rehabilitators and veterinarians to anticipate seasonal strandings and prognosticate outcomes and for the early identification of unusual mortality events in the species described.

Presenter Bio: Stefan Gallini earned his Bachelor of Arts and Science degree in Anthropology and Organismal Biology at McGill University. He is currently a VMD candidate at the University of Pennsylvania School of Veterinary Medicine. He looks forward to a career in zoo and exotic companion animal medicine.

A NOVEL *BABESIA* SPECIES IN THE VIRGINIA OPOSSUM (*DIDELPHIS VIRGINIANA)*

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Over 100 species of *Babesia* have been reported across the animal kingdom, including a number in wildlife, although the majority of species studied are in domestic animals and humans. *Babesia* spp. in wildlife can either be host-specific or found in closely related domestic animals. Virginia opossums are ubiquitous in North America and common patients at wildlife rehabilitation centers. They have adapted to living in close proximity to humans and domesticated animals in urban and suburban settings. Because of this relationship, the study of vector-borne illnesses in this species can be extremely valuable. Although *Babesia* spp. have been described in monodelophid opossums in Brazil and in several species of Australian marsupials, there are no reports of the parasite in Virginia opossums to date. An adult Virginia opossum was treated at the South Florida Wildlife Center in Fort Lauderdale, Florida, for anemia that worsened despite supportive treatment. Post-mortem diagnostic testing revealed *Babesia* spp. in peripheral blood films and bone marrow cytology. Standard PCR with reverse line blot hybridization confirmed the presence of *Babesia* spp. and genetic sequencing confirmed that it was a novel species. Subsequently, blood and/or spleen samples were collected from nine additional opossums presented to the wildlife center and sent for PCR; of these nine two were positive for the same novel *Babesia* sp. Both of these patients were symptomatic, one with severe anemia and the other with icterus and hematuria; neither survived. The morbidity and mortality of this novel *Babesia* sp. appears significant, as subclinical infection is more common in wildlife. More work is needed to study this parasite in opossums in the wild and in rehabilitation, in order to further characterize this *Babesia* taxonomically and to determine its clinical and epidemiological implications for Virginia opossums in Florida and elsewhere.

Presenter Bio: Dr. Antonia Gardner graduated from the University of Florida in 2004 then completed a small animal rotating internship. In 2005 she began working at the South Florida Wildlife Center (SFWC), and In 2014 Dr. Gardner accepted the role of medical director at SFWC.

VISUAL ASSESSMENT AND EPIDEMIOLOGY OF SKIN DISEASE IN SOUTHERN RESIDENT KILLER WHALES

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Southern resident killer whales (*Orcinus orca*) are small population of endangered salmon-eating killer whales. Since being federally listed as ‘endangered’ this population has not recovered and currently numbers 76 animals. Biologists conducting photo ID work often note skin lesions in these animals; however the significance of skin disease as an indicator of individual, population or ecosystem health is unknown. In endangered North Atlantic right whales, bottlenose dolphins, Guiana dolphins, minke whales, and other cetacean species, skin disease has been reported as a putative indicator of health. Without attempting to identify etiology, we evaluated photographs collected by the Center for Whale Research for photo-identification population monitoring from 2004 through 2016 for evidence of skin disease. Of the 141 whales that were alive for some portion or all of the study, 125 animals (88%) had photographic evidence of skin lesions. Serial, follow up photographs through the study interval demonstrated resolution with occasional recrudescence or progression of signs. The high prevalence noted is similar to a decade-long study of bottlenose dolphins (*Tursiops truncatus*) off of California that found skin disease in 79% of study animals. We identified ten syndrome types: calf epithelial sloughing, gray patches, gray target lesions, orange on gray coloration, pinpoint black discoloration, black erosions on the saddle patch, bull's eye target lesions, erosions, and red patches. Lesion classes will be evaluated using a multivariate model including age, sex, pod, and matriline across time to determine if there are lesion types that can be used as an indicator of individual or population health.

Presenter Bio: Joe Gaydos is a veterinarian and science director for the SeaDoc Society, a place-based marine conservation program of UC Davis' Karen C. Drayer Wildlife Health Center. He likes wild things: wildlife, wild place, and wild people.

EMERGENCE OF THE ARTERIAL WORM *ELAEOPHORA SCHNEIDERI* IN MOOSE (*ALCES ALCES*) AND TABANID FLY VECTORS IN NORTHEASTERN MINNESOTA, USA

Caroline M. Grunenwald[1], Erika Butler[2], Arno Wünschmann[3], Anibal G. Armien[3], Michelle Carstensen[4], Erik Hildebrand[4], Roger D. Moon[3] and ***Richard W. Gerhold[1]***

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[2]Nor-West Animal Clinic, Ontario, Canada
[3]University of Minnesota, St. Paul, MN, USA
[4]Minnesota Department of Natural Resources, Forest Lake, MN, USA

Moose (*Alces alces*) are a culturally and economically valued species in Minnesota. However, the moose population has experienced a sudden, marked decline in their range, including extirpation in the northwest and a 58% decline in the last decade in the northeast portions of the state. Although the exact cause of this decline is unclear, parasitic metastrongylid and filarioid nematode infections are known causes of morbidity and mortality in moose across North America. To determine if these parasitic nematodes could be contributing to the Minnesota moose population decline, we molecularly examined banked tissues obtained from moose that died of known and unknown causes for the presence of nematode DNA. Extracted brain DNA of 34 individual moose was amplified utilizing primers targeting the 18S rRNA gene and internal transcribed spacer regions of nematodes. DNA sequencing revealed that PCR products obtained from 15 (44.1%) of the moose were 99% identical to *Parelaphostrongylus tenuis,* a metastrongylid known to cause neurological disease and death. Additionally, brain tissue from 20 (58.8%) individuals yielded sequences that most closely aligned with *Elaeophora schneideri,* a parasite associated with neurological impairment but previously unreported in Minnesota. *Setaria yehi*, a common filarioid parasite of deer, was also detected in the brain tissue of 5 (14.7%) moose. Molecular screening of 618 captured tabanid flies from four trapping sites revealed *E. schneideri* was present (6%) in the Minnesota environment and transmission could occur locally. Prevalence rates among the flies ranged between 0-100% per trapping site, with *Chrysops* spp. and *Hybomitra* spp. implicated as the vectors*.* Together, these data confirm that *P. tenuis* is widespread in the Minnesota moose population and raise the question of whether *E. schneideri* may be a contributing factor to morbidity and mortality in moose.

Presenter Bio: Richard Gerhold is an assistant professor at the University of Tennessee College of Veterinary Medicine. His research focus is parasitic diseases of wildlife, avian diseases, and vector-borne diseases. Caroline Grunenwald is currently a Post-doctoral fellow at Vanderbilt University investigating pathogen/host interactions.

HISTOMONAS MELEAGRIDIS (BLACKHEAD DISEASE) TRANSMISSION FROM COMMERCIAL POULTRY LITTER TO WILD TURKEY (*MELEAGRIS GALLOPAVO*) IN MIDDLE TENNESSEE

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There is a perceived decline of wild turkeys (*Meleagris gallopavo silvestris*) in multiple adjacent counties in south central Tennessee; however, the cause of the decline is unknown. To determine if diseases are associated with the decline, a bioassay study was conducted consisting of healthy wild turkeys housed on discarded commercial poultry litter from a poultry farm in the region of the turkey decline. Two (8.3%) turkeys developed Blackhead disease due to *Histomonas meleagridis* during the bioassay trial, but it was unclear whether *H. meleagridis* was contracted directly from the litter or from ingestion of the numerous arthropod pests found within the litter. To determine the route of transmission of *H. meleagridis* from poultry litter to turkeys, we molecularly tested 387 adult and seven larval darkling beetles (*Alphitobius diaperinus*) recovered from the poultry litter used in the bioassay trial. Twenty (5.1%) beetles were PCR and sequence positive for *H. meleagridis*. These results indicate that the beetles originating from the poultry litter used in the bioassay study harbored *H. meleagridis*. While previous research has demonstrated that darkling beetle larvae can be infected *with H. meleagridis,* to our knowledge this is the first report of adult darkling beetles being infected with the protozoa. The greater mobility and visibility afforded to the adult stage of the darkling beetle suggests that they may play a role in the transmission of *H. meleagridis*. Given the pervasiveness of darkling beetles in poultry facilities in the southeastern United States, these results suggest that modifications of the handling and disposing of poultry litter is warranted to protect both commercial poultry flocks and wild turkey populations from *H. meleagridis* infection.

Presenter Bio: Rick Gerhold is an assistant professor at the University of Tennessee College of Veterinary Medicine. His research focus is parasitic diseases of wildlife, avian diseases, and vector borne diseases.

COMPARISON OF AN ACTIVE AND PASSIVE SURVEILLANCE SYSTEM FOR DETERMINING THE DISTRIBUTION AND INFLUENCE OF HOST AND ENVIRONMENTAL FACTORS ON CANINE DISTEMPER VIRUS IN ONTARIO RACCOONS

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Canine Distemper Virus (CDV) has a broad and expanding mammalian host range. In Ontario, CDV is frequently encountered in wild carnivores and is the most common infectious cause of death for raccoons; raccoons are considered an important maintenance host of CDV in Ontario. The recent isolation of CDV strains genetically distinct from vaccine strains in North America highlight the importance of studying epidemiological patterns of this virus in raccoons and their role in its evolution. However, wildlife surveillance is challenging and often requires a combination of active and passive surveillance methods with aggregation of data from multiple sources. Our objective was to compare CDV data obtained through passive and active surveillance of Ontario raccoons using a retrospective evaluation of 1079 raccoons submitted to the Ontario-Nunavut node of the Canadian Wildlife Health Cooperative between 2007 and 2017. Passive surveillance produced 495 raccoons between 2007 and 2017 while another 584 raccoons were obtained through active surveillance conducted between 2012 and 2017. For each dataset univariable logistic regression was used to identify associations between the occurrence of CDV infection and the following independent variables: age, sex, season, and year. Additionally, coordinates from each raccoon submission were mapped in QGIS to compare the areas represented by each surveillance method. Geographical data demonstrated that CDV infection was present throughout Southern Ontario and the areas captured by active and passive surveillance were overlapping and similarly clustered. The risk factor analyses produced statistically significant associations between the presence of CDV and age, season and year of collection which were discordant between the two datasets and at times indicated opposite relationships. This study illustrates the impact that a surveillance strategy can have on the types of data that are obtained and our interpretation of the epidemiology of disease.

Presenter Bio: Jolene Giacinti graduated from the Ontario Veterinary College in 2016. After gaining clinical experience she returned to the OVC to complete a Master's of Science in wildlife disease ecology.

ENHANCING WILDLIFE SURVEILLANCE IN ONTARIO: DEVELOPMENT AND EVALUATION OF THE WILDLIFE HEALTH TRACKER

*Mark Reist[1,2], **Jolene Giacinti**[2], E. Jane Parmley[2], Colin Robertson[3], Lenny Shirose[2], David Cristo[2], Claire Jardine[2]*
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Wildlife surveillance allows us to detect new or emerging diseases which can have important impacts on human and domestic animal health. The goal of the Canadian Wildlife Health Cooperative (CWHC) is to monitor the health of wild animals and to inform decision makers and the public about wildlife health issues. Currently, the CWHC core surveillance efforts rely on email or phone reports of dead or diseased wildlife followed by submission of carcasses for examination. While effective, this approach requires a large investment of human and financial resources. The objectives of this project were to develop, pilot, and evaluate the utility of a citizen science, web-based reporting tool to enhance wildlife surveillance in Ontario. The Wildlife Health Tracker (WHT) was launched in October 2016 and individuals identified as having an interest in wildlife (e.g., hunters, biologists) were engaged via email. An increased focus on engagement occurred between May and October 2017. Data were extracted from the WHT and CWHC databases between October 2016 and October 2017 for comparative analysis. An online survey was also administered to registered WHT users to gain feedback. Overall, the 107 observations reported to the WHT were more localized, dominated by mammals, and more likely to be trauma related when compared to the CWHC submissions. Communication via email played a role in increasing the number of new users and in the future, should target both new and current users. Survey responses re-enforced that frequent communication is required for continued engagement and ongoing technical management is needed to improve the user interface and accessibility. It was encouraging that most respondents felt that they were contributing to wildlife conservation in Ontario. The WHT has the potential to augment current wildlife health surveillance activities and moving forward, it will be operated nationally under the CWHC.

Presenter Bio: Jolene Giacinti graduated from the Ontario Veterinary College in 2016. After gaining clinical experience she returned to complete a Master's of Science in wildlife disease ecology. Along with her own research, Jolene is currently employed as a graduate student researcher with the CWHC where she collaborated on the WHT initiative.

ABANDONED, LOST AND DISCARDED FISHING GEAR RECOVERY AS AN OCEAN HEALTH STRATEGY IN CALIFORNIA

Kirsten V. Gilardi*, Jennifer Renzullo and Shannon McDiarmid*
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Lost, abandoned and discarded fishing gear (ALDFG) impacts ecologically and economically important living marine resources: target and non-target species suffer entanglement and ingestion, and seafloor and rocky reef habitats are altered and damaged. In order to reduce the threat that ALDFG poses to California coastal marine wildlife, the California Lost Fishing Gear Recovery Project has been conducting ALDFG recovery since 2006. To date, the Project has retrieved 100+ tons of lost commercial nets, pots, traps and fishing-related equipment (and other debris, e.g. automobile tires). Data collection has documented impacts to marine mammals, sea birds, sharks, fish and invertebrates, and elucidated gear loss “hotspots.” Key to the success of the project has been close coordination with the commercial fishing industry in California: urchin harvesters are contracted for all in-water (SCUBA-based) gear retrieval work, and the project has implemented partnerships with commercial fishermen’s associations to run Dungeness crab gear recovery operations themselves. Project activities have been instrumental in inspiring new legislation lobbied for by commercial Dungeness crab fishermen to require a permanent gear retrieval program for all ports. Gear retrieval activities have also helped build scientific evidence for the regional and global impact of ALDFG on marine wildlife. As both a research and mitigation endeavor, lost fishing gear recovery presents opportunities for scientists, fisheries managers, and the fishing community to join forces for improving ocean health.

<u>Presenter Bio:</u> Kirsten V. Gilardi, DVM, DACZM is Co-Director of the Karen C. Drayer Wildlife Health Center at the UC Davis School of Veterinary Medicine, and Clinical Health Sciences Professor in the Department of Medicine & Epidemiology. She is the Founding Director of the California Lost Fishing Gear Recovery Project (lostfishinggear.org)

A MOVING TARGET: RESEARCH INSIGHTS FOR THE MANAGEMENT OF VAMPIRE BAT RABIES

Amy T. Gilbert
USDA, APHIS, WS, NWRC, Fort Collins, CO, USA

Vampire bats have an extensive geographic range throughout Latin America, and can vary locally from rare to highly abundant. Rabies virus circulation in vampire bats has been recognized for the better part of the last century due to associated livestock and public health morbidity and mortality, yet disease management outcomes resulting from localized depopulation practices are poorly described. Beyond rabies, enhanced surveillance has uncovered a variety of pathogens that may be associated with vampire bats, although realized impacts to livestock and public health are not clearly defined for many of these pathogens. Ecological studies have shed light into the movements and behaviors of these fascinating creatures, revealing novel insight into anthropogenic influences on bat population dynamics and health. Improved assessment of management strategies, and identification of research gaps, will be necessary to achieve lasting outcomes for prevention and control of vampire bat rabies in Latin America.

Presenter Bio: Dr. Gilbert earned a Ph.D. in Ecology and Evolutionary Biology at the University of Tennessee studying bat rabies virus ecology. Her current research focuses on rabies virus ecology in wild carnivores, evaluation and development of oral rabies vaccine baits, and enhancing methods for disease surveillance and management in target wildlife.

ELUCIDATING PATHOGEN DYNAMICS WITH SEROLOGIC DATA FROM MINNESOTA GRAY WOLVES (*CANIS LUPUS*)

***Marie L.J. Gilbertson*[1]**, *L. David Mech*[2], *Shannon Barber-Meyer*[2], *Ellen Brandell*[3], *Andy Dobson*[4], *and Meggan E. Craft*[1]

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Pathogen screening via serologic assay is a commonly used tool for assessing pathogen prevalence and impacts in wildlife systems. However, serologic data can be limited by the fact that serology simply indicates exposure, not active infection, often making temporal dynamics more difficult to elucidate. With the addition of high-quality host age estimates, however, serologic data can shed light on pathogen dynamics; for example, discerning between epizootic versus enzootic pathogens. This information can subsequently identify pathogens or populations at greatest risk for population-level impacts due to disease, and help guide management and animal health decisions. Here, we utilize serologic data and high-quality host age estimates from gray wolves (*Canis lupus*) in northeastern Minnesota from 2010 to 2013. We examine age-based seroprevalence of up to nine different pathogens, which vary in their modes of transmission, morbidity, and mortality. With this age-based seroprevalence, we then fit age-dependent force of infection models which can suggest key age classes important for the dynamics of each pathogen. Results indicate that the wolves of northeastern Minnesota show high levels of exposure to some important canine pathogens (canine parvovirus, canine adenovirus), with the youngest age classes experiencing the highest force of infection, a pattern consistent with enzootic pathogens. However, in the case of canine distemper virus, another important canine pathogen, overall prevalence is much lower, with older age classes showing higher risk of being exposed; in this case, a pattern more consistent with epizootic pathogens. While these results cannot determine mortality rates due to each pathogen, they do shed light on the dynamics of a wide range of pathogens in Minnesota's wolves, and can provide valuable information for the long-term health and management of this iconic species.

<u>Presenter Bio:</u> Marie Gilbertson is a veterinarian and PhD student at the University of Minnesota. Her research interests are in disease dynamics, particularly at the interface of wildlife, domestic animals, and humans. Her PhD research is focused on using mathematical models to better understand the dynamics of feline retroviruses in puma.

CHRONIC WASTING DISEASE BEST MANAGEMENT PRACTICES FOR STATES AND PROVINCES: AN ASSOCIATION OF FISH AND WILDLIFE AGENCIES INITIATIVE

***Colin M. Gillin*[1]*, Jonathan R. Mawdsley*[2]*, and John R. Fischer*[3]

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Chronic wasting disease (CWD) is the most important disease impacting North America cervids and more recently has been found in wild cervids in northern Europe. The susceptibility of all native North American cervid species to this fatal transmissible disease agent and its environmental persistence greatly confound CWD management. In 2017, the Association of Fish and Wildlife Agencies appointed a working group to draft recommendations for state, provincial, and federal wildlife agency administrators and managers in order to assist them in the development and implementation of their own suite of CWD management practices. The group comprised more than 30 wildlife health specialists, veterinarians, biologists, and agency leaders in the management of CWD across North America. The working group approached its task with the objective of presenting best management practices (BMPs) to prevent, detect, respond to, and manage CWD, as well as selected alternatives for addressing CWD prevention, surveillance, and response actions. The CWD BMPs are dynamic and will be adapted as advances are made in the science and practice of CWD management. Best management practices and guidelines are presented for both publicly owned, free-ranging and captive cervids including sections on planning, management, surveillance, monitoring, transport, disinfection, research, human dimensions, and regulatory issues, among others. An overview of these guidelines will be reported in this presentation.

Presenter Bio: Colin Gillin serves as the state wildlife veterinarian and manager of the Wildlife Health and Population Laboratories for Oregon. He previously worked as veterinary research faculty for Tufts University and the Consortium for Conservation Medicine. He is the Chair of the US Animal Health Association's Wildlife and Zoo Committee.

SUSCEPTIBILITY OF NORTH AMERICAN NEWT SPECIES TO *BATRACHOCHYTRIUM SALAMANDRIVORANS*

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The recently discovered fungal pathogen *Batrachochytrium salamandrivorans* (*Bsal*) has caused population declines of wild fire salamanders (*Salamandra salamandra*) in Europe, and preliminary controlled experiments suggest that *Bsal* is highly pathogenic to species in the family Salamandridae (i.e., newts). Our goal was to robustly estimate the susceptibility of four North American newt species (*Notophthalmus viridescens*, *N. perstriatus*, *N. meridionalis*, and *Taricha granulosa*) to *Bsal* infection and chytridiomycosis. For *N. viridescens*, we were able to test the susceptibility of six populations from four U.S. states. Animals were exposed to one of four zoospore doses ($5x10^{3-6}$) at 15^oC for 24 hours, and their condition and fate were monitored for at least six weeks. In general, the greatest mortality, infection prevalence, and *Bsal* loads were in the following order: *N. meridionalis* (greatest), *N. perstriatus*, *Taricha granulosa*, and *N. viridescens* (least). In addition, susceptibility differed among *N. viridescens* populations, with the greatest occurrence of *Bsal* chytridiomycosis occurring in the Michigan population and least in the Blue Ridge physiographic region, Tennessee (100% vs. 20% mortality at the highest zoospore dose, respectively). Interestingly, mucosome inactivation of *Bsal* zoospores by Michigan newts was lower than Tennessee newts. *N. viridescens* efts also had higher susceptibility than adult *N. viridescens* populations. Our results indicate that newt species could play a significant role in the epidemiology of *Bsal* if it emerges in North America. Moreover, *Bsal* represents a significant conservation risk to *N. meridionalis* and *N. perstriatus*, which are species of greatest conservation need in the southern United States.

<u>Presenter Bio:</u> Matthew J. Gray, B.S., M.S., Ph.D. I am a disease ecologist that studies the epidemiology of amphibian pathogens. I serve as chair of the Research Working Group of the North American *Bsal* Task Force and co-chair of the National Disease Task Team for the Partners in Amphibian and Reptile Conservation.

SAN CLEMENTE CHANNEL ISLAND FOX DEMOGRAPHY AND ECTOPARASITE DISEASE MONITORING

***David A. Green*[1]**, *Jesse Maestas*[1], *Andrew Bridges*[1], *Nathan Nieto*[2], *Winston Vickers*[1, 3], *and David Garcelon*[1]

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The island fox (*Urocyon littoralis*) is a keystone species that is particularly susceptible to novel disease and predators, both of which have nearly extirpated subspecies from islands. The San Clemente Island fox (*U. l. clementae*) an island-endemic, is a focal taxa for conservation by the U.S. Navy, and the subject of an intensive long-term management and monitoring program. Our primary objectives were to monitor population demography and detect potential threats by conducting disease surveillance. Monitoring protocols have been adapted through time, and we currently gather annual demographic data from 11 separate 18-trap grids stratified by habitat type and location throughout the island. We have radio-collared approximately 60-100 adult foxes which serve as disease sentinels and gather known-fate survival data. From 2014-2017, we conducted ectoparasite sampling. Our results indicate a healthy population that grew from an estimated 431 adults in 2007 to a high of 990 in 2014, the most recent estimate is 770 in 2017. The known-fate analysis yielded an adult annual survival rate of 94%. Ear mites were documented in every fox tested and otisis was associated with infestation; however, we have not documented the ceruminous gland tumors found in similarly infested Santa Catalina Island Foxes (*U. l. catalinae*). We found that ectoparasite abundance was greater post rain for fleas by 86.6% and ticks by 98.1%, with no relationship between ectoparasite load and fox age or sex. Assays were run for *Borrelia burgdorferi, Anaplasma phagocytophilum* and, *Borrelia miyamotoi* on 159 ticks collected from 40 individual foxes. None of these pathogens were detected. Through a combination of population monitoring and disease surveillance, we have determined the population currently is stable and the tick-borne diseases we have tested for do not currently appear to be a threat; however, mite-associated otitis and corresponding potential for ceruminous tumors development could warrant further investigation.

<u>Presenter Bio:</u> David completed his bachelor's degrees in biology and secondary education from Northern Arizona University. He has been working with the island fox for the last three years, carrying out population and disease monitoring, as well as providing veterinary care.

IDENTIFICATION OF *HETERAKIS* SPECIES IN GAME BIRDS IN PENNSYLVANIA

Denver Greenawalt[1]*, Justin Brown*[2]*, Lisa Williams*[2]*, Mary Jo Casalena*[2]*, Robert Boyd*[2]*, Eva Pendleton*[3]*, Patricia Dunn*[3]*, Michael Yabsley*[4]

[1]Department of Veterinary and Biomedical Sciences, Penn State University, University Park, PA, USA
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[4]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA

Histomoniasis, caused by the protozoan *Histomonas meleagridis,* is a significant disease of wild and domestic gallinaceous birds. Transmission of this parasite is dependent on utilization of the cecal nematode *Heterakis gallinarum* as an intermediate host. Due to the critical role that *H. gallinarum* plays in the introduction, transmission, and maintenance of *H. meleagridis*, it is important to define the host range and distribution of this nematode. From 2015, 2016, and 2017, ceca were collected from 260 wild and propagated game birds from Pennsylvania, representing eight species and 44 counties that were either submitted as diagnostic cases or harvested by hunters. Cecal contents were examined for *Heterakis* nematodes using a 1–mm sieve and preserved in 70% ethanol. All *Heterakis* spp. present were counted and species identified based on morphologic characteristics of the male worms. The prevalence and intensity of infection were determined. *Heterakis* nematodes were detected in five of the eight game bird species examined, including ring-necked pheasants (*Phasianus colchicus*; 52/53 (98%)), ruffed grouse (*Bonasa umbellus*; 48/64 (75%)), wild turkeys (*Meleagris gallopavo*; 49/65 (75%)), domestic chickens (*Gallus domesticus*; 3/8 (38%)), and chukars (*Alectoris chukar*; 4/38 (11%)). Nematodes in all species were identified as *H. gallinarum*, except for ruffed grouse, which harbored *H. isolonche*. No infections with multiple *Heterakis* species were identified in any examined birds. No *Heterakis* nematodes were identified in ducks (*Anas* sp.; n=50), American woodcock (*Scolopax minor*; n=27), or domestic turkeys (*M. gallopavo,* n=10). The results presented herein indicate that *H. gallinarum* is common in wild and domestic upland game bird species. Future research is needed to determine the prevalence of *H. meleagridis* infection in these species and determine the potential for *H. isolonche* to serve as a paratenic host for *H. meleagridis*.

Presenter Bio: Denver Greenawalt is a fourth year undergraduate student studying Veterinary and Biomedical Sciences with a minor in Poultry and Avian Sciences at The Pennsylvania State University. He is interested in the wild and domestic animal interface and avian parasitology.

ANTHROPOGENIC DISTURBANCE MODULATES THE MAMMAL HOST COMMUNITY AND INFECTIOUS DISEASE RISK

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Emerging zoonoses represent a significant threat to human health, and identifying factors responsible for the emergence of particular pathogens is an urgent priority. The linkage between biodiversity and epidemiology underpins the modulatory effect of host community assemblage on disease dynamics. To this end, empirical data integrating host community composition, life histories, and zoonotic diversity is fundamental to building a predictive framework for evaluating the impacts of land use change and biodiversity loss on the potential for emerging infectious disease outbreaks. Here, we examined how land use—more generally, anthropogenic disturbance—impacts tick-borne pathogen risk in small mammal communities in the Greater Yellowstone Ecosystem, one of the most pristine ecosystems remaining in the Northern hemisphere. We combined a high–resolution block experimental design to sample naturally occurring rodent community assemblages across land–use gradients of paired pristine versus degraded habitats with comprehensive pathogen screening of rodents hosts through a sensitive DNA–based reverse line blotting technique. Using this approach, we describe the effects of anthropogenic change on reservoir assemblage shifts and the risk of pathogen infection. We show that disturbance dramatically increased overall density of infected individuals, not because a particular focal host species became more abundant, but rather due to 50% greater relative abundance of the remaining host species across the rodent community assemblage. Further, disturbed environments supported higher overall rodent density, likely owing to reduced predator pressure and abundant food. These empirical findings highlight the key role of host community assemblage in density-dependent and frequency-dependent disease dynamics in the context of ecosystem-disturbance. By disentangling the ecosystemic nexus between ecosystem biodiversity and community assemblage, our results emphasize the importance of a comprehensive framework to recognize the factors influencing the risk of zoonotic disease to humans at the wildlife-environment-human interface.

Presenter Bio: Dr. Leticia Gutiérrez Jiménez, field veterinarian and disease ecologist for the PREDICT-2 program at the EcoHealth Alliance, is responsible for implementing field-based research under a variety of global programs related to pandemic risk reduction. Her work directly tackles a paramount goal in public health: Zoonotic disease prevention through a holistic approach – One Health.

UNTANGLING SUCCESS STORIES OF ONE HEALTH: CAPACITY BUILDING

Leticia Gutiérrez-Jiménez*, Carlos Torrelio-Zambrana, Leilani Francisco, Jonathan H. Epstein*
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Capacity building under the One Health framework is essential to preventing pandemics. Improving emerging infectious disease surveillance skills in "hot spots" translates not only to preventing pandemics, but also improves outcomes for conservation, ecosystem health, wildlife and human well-being. EcoHealth Alliance under the PREDICT USAID program has trained hundreds of One Health professionals across eleven countries. Trainees are routinely subject to theoretical and hands-on training comprising animal surveillance, human surveillance and behavioral risk, biosafety, emergency preparedness, and cold chain assurance, among other topics. However, workforce participation in training program opportunities is often at the discretion of local stakeholders. As a result, training participation based on gender or affiliated institutions may change over time in ways that might affect wildlife conservation. In this study, we examined a data set of nearly 7,000 training events administered to over 680 trainees. We discuss how participation in the training programs changed over time. Specifically, we explore whether different organization types (e.g., host country government, NGOs, universities, research institute) are more persistent in these programs over time. We also explore whether gender dynamics evolve over time, and whether women are gaining increasing access to these training opportunities. Preliminary results indicate that each cumulative implementation year translates to an increase in governmental agency employee participation, suggesting that host country government staff require longer programs to first engage and then persist as sustainable long-term major contribution for national capabilities. Further, we find that the proportion of women involved in the training programs increases over time. The latter result suggests that beyond intrinsic male-biased access to these training opportunities, there is a potential to foster workforce gender equality through longer-term initiatives. These data and preliminary results have far-reaching implications for wildlife health, diversity conservation, as well as gender equity implications in "hot spot" countries where these trainings are commonly administered.

Presenter Bio: Dr. Leticia Gutiérrez Jiménez, field veterinarian and disease ecologist for the PREDICT-2 program at the EcoHealth Alliance, is responsible for implementing field-based research under a variety of global programs related to pandemic risk reduction. Her work directly tackles a paramount goal in public health: Zoonotic disease prevention through a holistic approach – One Health.

NEBULIZATION TREATMENT OF A BROWN WATER SNAKE *(NERODIA TAXISPILOTA)* FROM GLADES COUNTY, FLORIDA, FOR SNAKE FUNGAL DISEASE

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Snake Fungal Disease (SFD) was first recorded in the eastern United States in 2006. In 2013, the disease was associated with an emerging fungal pathogen, *Ophidiomyces ophiodiicola*. This fungus persists in the environment, and although physiologically stressed snakes may be more susceptible, SFD can also manifest in healthy snakes. We describe a case report of SFD in Glades County, Florida. On January 30, 2016, a U.S. Army Corps of Engineers Natural Resource Specialist, recently educated on SFD, recognized signs of disease in a cluster of six brown water snakes (BRWS; *Nerodia taxispilota*). Five snakes were collected for evaluation by the Florida Fish and Wildlife Conservation Commission. Diagnostic specimens were submitted to the Southeastern Cooperative Wildlife Disease Study. All snakes tested positive for *O. ophiodiicola* via PCR and/or culture of swabbed skin lesions or sheds, and fungal hyphae were seen on histology in four deceased snakes. Treatment of the surviving snake was initiated with a new protocol. After a shed on April 4th that reduced visible signs of SFD, a consecutive 25-day treatment regime of 30-minute, 2mg/mL Terbinafine nebulization was begun. The snake gained 80 grams and was released at the site-of-capture on May 5th, at which time clinical signs had resolved. This is the first recorded case of SFD in Glades County. Although FWC's mission generally excludes wildlife rehabilitation, this case presented a serendipitous opportunity to test the treatment protocol on a yet untested species. Despite being unable to assess its post-treatment survival, the snake's clinical response suggests this treatment method is a viable alternative to euthanasia for rehabilitators receiving BRWS with mild cases of SFD. Due to uncertain effects of climate change on the range and severity of fungal pathogens, field recognition and reporting of diseased wildlife is critical to understanding fungal disease ecology. Enhanced disease surveillance is benefited by cross-discipline education.

Presenter Bio: Veronica is a wildlife disease technician at the Florida Fish & Wildlife Conservation Commission primarily assisting with responding to avian mortality events, disease surveillance, and research projects. She has a keen interest in herpetology and hopes to do further research on fungal pathogens affecting reptiles and amphibians.

EFFECTIVENESS OF TWO CAPTURE TECHNIQUES FOR JAGUARS (*PANTHERA ONCA*) IN THE DRY FOREST OF COSTA RICA

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The jaguar (*Panthera onca*) is the largest feline in the Americas, since 1973 is included in CITES Appendix I, due to the effects of human intervention on the decline of its populations. To contribute to the reduction of the risk of extinction of jaguars in the dry forest of the Guanacaste Conservation Area (ACG) by generating information on the status of their populations, their habitat and health, a project was carried out for the capture and anesthesia of free ranging jaguars in the ACG. This is the second study in Costa Rica, which capture and marked jaguars in the wild, the first was done 20 years ago in Corcovado National Park in the southern part of the country. Both projects investigate the movements and habitat use patterns throughout telemetry, however the type of forest and climate are different. Due to the success of the first project with the use of the cage type trap, the same technique was replicated in the dry forest during the years 2012 to 2014. There were 33 cage trap nights, of which two were successful, due to this, at the end of 2014 the foot snare technique began to be used, it has been used in other countries where jaguars are present, with which four trap nights were made, for a total of two successful. Both types of trap were baited with sea turtles hunted by jaguars the previous night and camouflaged with the surrounding vegetation. The monitoring of the traps was constant from its placement until the next day through remote alarms. Finally concluding that the foot snare technique is more successful for capturing jaguars in the dry forest of Costa Rica, as long as a previous training has been carried out for the proper placement for safety of the animals and success.

Presenter Bio: Professor of internal medicine courses of small animals, collaborator in research projects of wild animals *in situ* and *ex situ*, doctor treating free-range wild animals and zoo. Technical advisor of different zoos and rescue centers, NGOs and government agencies.

DETECTION OF EMYDID *MYCOPLASMA* SP. IN WILD-CAUGHT CRITICALLY ENDANGERED VIETNAMESE BOX TURTLES, *CUORA BOURRETI*

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Four wild-caught, recently imported specimens of the critically endangered Asian box turtle, *Cuora bourreti*, were presented to the M.J.R. Veterinary Hospital of the University of Pennsylvania for non-specific clinical signs including malaise, anorexia and poor body condition. Complete blood cell counts, plasma biochemistry panels, blood cultures and ocular-choanal-cloacal swabs were collected from 3 of the 4 specimens. In 2 of the 3 animals tested, *Mycoplasma* sp. was detected by polymerase chain reaction. Subsequent DNA sequencing was homologous with a novel *Mycoplasma* sp. previously detected only in three free-ranging North American turtle species (*Clemmys guttata*, *Glyptemys muhlenbergii*, *Terrapene carolina carolina*) of the family Emydidae in which it is suspected to cause ocular and oral mucosal disease. It is unknown whether this organism caused disease in these individuals, however its detection suggests active shedding. Poor biosecurity in wholesale exotic animal retailers and in international reptile trafficking are suspected to have exposed the turtles to this organism. This is the first report of emydid *Mycoplasma* sp. detected in a species of the family Geoemydidae and suggests Vietnamese box turtles may serve as competent hosts of emydid mycoplasma.

Presenter Bio: Colin Hansen earned a B.S. in Biology from Millersville University. He is currently a second year student at the University of Pennsylvania School of Veterinary Medicine and is preparing for a career in zoological companion animal and wildlife medicine.

HELLBENDER SKIN ANTIMICROBIAL PEPTIDES SHOW VARIABLE INHIBITION AGAINST CHYTRID FUNGUS, BATRACHOCHYTRIUM DENDROBATIDIS

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Hellbenders (*Cryptobranchus alleganiensis*) are large aquatic salamanders from the eastern United States and have experienced considerable population declines in both Ozark and Eastern subspecies, *C. a. bishopi* and *C. a. alleganiensis*, respectively. Furthermore, ulcerative non-healing lesions have been observed with frequency in *C. a. bishopi*. *Batrachochytrium dendrobatidis (Bd)* is a fungal skin pathogen of concern as it is present in wild hellbender populations and is known to cause mortality in captivity during times of stress. Factors such as environmental degradation and genetic bottlenecking may negatively affect host immunity with subsequent manifestation of disease in a population. Antimicrobial peptides (AMPs) secreted on the skin are an important component of amphibian innate immunity and may be a factor in manifestation of *Bd*-related disease (chytridiomycosis). In frogs, purified AMPs have demonstrated growth inhibition of *Bd* in vitro and, in some species, have been linked to variable resistance. Our objective was to determine if hellbender AMPs exhibited anti-*Bd* activity and if inhibition correlated to subspecies. We challenged *Bd* growth against purified AMPs comparing effects of subspecies, site, and infection status. Assays measured zoospore growth via change in optical density in culture wells of serial AMP concentrations of 6 to 1000 ug/mL over seven days. We found significantly higher Bd-inhibition from Eastern Hellbenders (*C. a. alleganiensis*) compared to Ozark Hellbenders (*C. a. bishopi*) with an MIC50 of 250 and 2500 ug/mL, respectively. Although we were unable to evaluate effects of *Bd* infection status on AMP activity, AMPs from Ranavirus negative animals had significantly higher inhibition than those from Ranavirus positive individuals within Tennessee, (MIC50 75 and 400 ug/ mL, respectively). Our study is the first to show that hellbenders harbor skin peptides with inhibition against *Bd* and that factors such as infection status and subspecies can affect AMP quality and risk for chytridiomycosis.

Presenter Bio: Rebecca Hardman is a PhD student at the University of Tennessee Knoxville Comparative and Experimental Medicine Program. She is a veterinarian that focuses on wildlife health issues in herpetological conservation. Her primary research focuses on amphibian disease complicated by habitat degradation and anthropogenic disturbance.

PERMETHRIN SEQUESTERING IN THE SERUM OF FARMED WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*)

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Two important pathogens transmitted to white-tailed deer are blue-tongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV), both of which are transmitted by *Culicoides* Latrielle biting midges. To reduce the transmission of these pathogens, deer farmers use insecticides to manage *Culicoides* populations. Of these insecticides, pyrethroids, especially permethrin, are the most commonly used, due to perceived low mammalian toxicity, the effectiveness of these insecticides at low doses, their relatively low cost, and a good environmental safety record. However, there have been studies linking pyrethroid exposure in mammals to multiple toxicities, including neurotoxicity, cardiotoxicity, and cytotoxicity, as well as a syndrome expressed in the offspring of parents that were previously exposed to pyrethroids, and the effect these insecticides may have on deer health is not well understood. The objective of this research was to determine if, following permethrin exposure of farmed deer, the insecticide would be absorbed through the skin and be sequestered. Serum samples were collected from animals in three areas of varied permethrin exposure levels and during low (spring) and high (fall) pesticide application seasons. Samples were extracted via solid phase extraction in dichloromethane and analyzed by gas-chromatography mass-spectrometry (GC-MS), and the cis- and trans- isomers of permethrin were analyzed. Sample sizes consisted of 16 individuals (8 males, 8 females) for each application season. GC-MS analysis showed higher levels of cis-permethrin in deer serum from penned deer extracted during the fall application season. No trans-permethrin was detected by GC-MS in any of the samples, likely due to the higher metabolism rate of the trans-isomer. Studies into the sequestering of permethrin have previously been conducted on small mammals and humans, however, this study represents the first investigation into potential insecticide sequestering in farmed white-tailed deer.

Presenter Bio: Laura Harmon is a second year Master's student at the University of Florida, in the Entomology and Nematology department. Her research focuses on determining insecticide resistance in *Culicoides* biting midges, if insecticides are sequestering in farmed deer, and the perception and utilization of insecticides by deer farmers in Florida.

ADDRESSING THE THREAT POSED BY AFRICANIZED HONEY BEES TO SOUTH FLORIDA WILDLIFE AND AGRICULTURE

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Africanized honey bees (*Apis mellifera scutellata*) (AHB) have been observed in Florida since 2001, when first sighted near the port of Tampa. Since that time, they have become firmly ensconced in urban and agricultural settings south of the I-4 corridor. Africanized honey bees exhibit a more defensive behavior and swarm 4 to 8 times more frequently than *Apis mellifera*, the common European honey bee used for commercial pollination and honey production. For this reason, Africanized honey bees pose a serious threat to outdoor workers, wildlife, and livestock that may accidently disturb their cryptic hives. These may include holes in the ground, tree cavities, building partitions, old tires, shipping pallets, culverts, or even equipment such as tractors and harvesters. A safety program has been formulated to educate wildlife specialists, growers, and outdoor workers about AHB behavior and the risks they pose. The program addresses: 1) awareness and recognition of potential AHB nesting sites, 2) how to react if an AHB hive is accidently disturbed, and 3) how to mitigate or eliminate the threat once an AHB nest is discovered. The program also involves a "push-pull" integrated pest management strategy using encapsulated permethrin, which is non-toxic to birds and mammals, to prevent AHBs from colonizing sites where they are not desired. Instead, the bees are "pulled" or attracted to swarm traps using a pheromone, and feral swarms may then be easily destroyed or relocated.

Presenter Bio: At the University of Florida's Everglades Research and Education Center, the barn owl program has been used since 1994 for sustainable rodent control. This program is used for outreach and education to engage the public about the benefits of agriculture. Since 2006, the barn owl program has been threatened by the presence of AHB's.

IMPACTS TO INTEGUMENT FROM LEG BAND-MOUNTED TELEMETRY DEVICES IN WHOOPING CRANES (*GRUS AMERICANA*)

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[3]School of Veterinary Medicine, University of Wisconsin-Madison, Madison, WI, USA

Leg band-mounted radio telemetry devices have been used for field studies of whooping cranes since the 1980s. Newer designs of GPS-enabled satellite (PTT) and cellular (GSM) tags, especially those with rechargeable battery features, have a more limited history of use, with no follow-up investigations of localized effects on the integument from the overall package design. We conducted an observational study of cranes in the reintroduced Eastern Migratory Population through standardized postmortems of suitable carcasses to generate baseline data on pathological effects of leg band-mounted telemetry tags. Our dataset includes gross and histopathological assessment of leg skin from 20 cranes from 2014-2017, including 6 hatch-year (HY) age and 14 cranes ranging in age from 1-15 yrs. (median = 5.5 yrs.) with an approximately equal sex ratio. All cranes carried a leg band-mounted radio tag; 7 cranes carried an additional PTT or GSM tag on the opposite limb. Gross lesions, typically flattened or depigmented areas with or without cutaneous ulceration or scabs, varied in surface dimension from 2mm to >1cm in diameter, and were described in 15 (75%) cranes. Histopathologic lesions were reported in 17 (85%) cases and included hyperkeratosis, epidermal hyperplasia, epidermal ulceration with intralesional bacteria, and dermatitis. Overall, severity of lesions was considered mild in 10 (50%) cranes, and moderate to severe in 7 (35%). In most cranes, lesions associated with leg-mounted telemetry devices were considered unlikely to be associated with loss of function. Distinct risk of bacterial cellulitis in few of the more severely affected cranes, however, was noted. Severe skin lesions developed within weeks of application of telemetry packages in some young cranes. The health and welfare risk from leg-band mounted telemetry devices may be greater than previously believed, and represent a concern when combined with uncertainties over device effects such as increased energy expenditure and reproductive impairment.

Presenter Bio: Barry Hartup is Director of Conservation Medicine at ICF and Chair of the Whooping Crane Health Advisory Team since 2000.

MITIGATING THE EFFECTS OF LIVE TRADE IN ENDANGERED SPECIES: NUTRITIONAL REHABILITATION OF GREY CROWNED CRANES IN RWANDA

***Barry K. Hartup*[1]*, and Olivier Nsengimana*[2]*,*
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[2]Rwanda Wildlife Conservation Association, Kigali, Rwanda

The grey crowned crane is the only species of crane in Rwanda and faces serious threat from domestic live trade. The Rwanda Wildlife Conservation Association has partnered with the Rwandan government since 2014 to undertake public awareness campaigns, formally register cranes held in captivity, and rehabilitate and repatriate a healthy subset of cranes to supplement a remnant population in Akagera National Park (ANP), all to decrease illegal trade of cranes. We conducted a study of the nutritional challenges of cranes coming from illegal captivity and the short-term effects of a balanced, formulated diet used to condition the cranes prior to release. Twelve cranes were randomly selected from 18 individuals that met inclusion criteria. Nutritional analyses from blood samples were conducted before and immediately following provision of Mazuri® Crane Diet for 6 weeks while in a quarantine holding facility. We analyzed serum chemistries (8 analytes), serum triglycerides and non-esterified fatty acids, plasma vitamin A (retinol) and vitamin E (α-tocopherol), and 12 whole blood trace element concentrations. Many cranes were hypoproteinemic or observed with deficiencies in vitamin A and E, selenium or zinc at the beginning of the trial. We observed statistically significant increases in serum total protein, uric acid, cholesterol, triglycerides, plasma vitamin A and E, copper, iron, selenium and zinc by the end of the trial (Wilcoxon signed rank $p < 0.05$). Blood lead declined to baseline levels in 2 cranes with elevated concentrations (> 5 ug/dl) at the beginning of the trial. The results suggest that the current rehabilitation and biosecurity management process is effective in reversing nutritional deficiencies from captivity and improving the condition of cranes prior to release. We expect these effects will improve the success of assimilating the cranes to ANP following their soft release into native habitat.

Presenter Bio: Barry Hartup is Director of Conservation Medicine at ICF, Chair of the Whooping Crane Health Advisory Team, and has experience in the field of wildlife rehabilitation. Olivier Nsengimana is Executive Director of RWCA and a former Gorilla Doctor and USAID-PREDICT team member in Rwanda.

CLINICAL TRIAL AND PHARMACOKINETIC ANALYSIS OF TERBINAFINE NEBULIZATION IN WILD SNAKES WITH SNAKE FUNGAL DISEASE

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Snake fungal disease (SFD) is an emerging wildlife disease caused by the fungus *Ophidiomyces ophiodiicola*. It has been documented in over 30 snake species in North America and Europe and infection causes a wide range of clinical signs, from raised scales and crusts on the head and body to death. We are conducting a clinical trial of nebulization with the antifungal terbinafine in naturally infected, wild-caught snakes to determine the potential of this treatment to produce therapeutic concentrations that result in clinical and molecular resolution of disease. Inclusion criteria included a positive qPCR result and a body weight greater than 150g. Patients were nebulized with a 2mg/mL terbinafine solution for 30 minutes daily for 30 days. Gross skin lesions were documented over the course of treatment, blood was drawn weekly to determine plasma terbinafine concentrations using high-performance liquid chromatography, and qPCR was repeated following treatment. Sixteen snakes of seven different species have been treated with one or more courses of nebulization (n=31) with corresponding qPCR results. All treated snakes demonstrated partial or complete resolution of clinical signs and reduction in the number of fungal copies measured using qPCR. Mean trough plasma terbinafine concentrations in kingsnakes were above the previously reported therapeutic level (15ng/mL) during treatment. These results indicate that terbinafine nebulization is a promising treatment for SFD. Further work remains to determine causes for individual and species variation in response to treatment.

Presenter Bio: Dr. Ellen Haynes is a PhD student studying the epidemiology of Snake Fungal Disease. After receiving her DVM from the Cornell University College of Veterinary Medicine in 2013, she completed small animal and wildlife medicine internships and served as the Director of Animal Care at Wildlife Rescue and Rehabilitation.

WILD MAMMALS AND THEIR PATHOGENS IN LOS ANGELES COUNTY, CALIFORNIA

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University of California, Los Angeles

Urban wildlife can harbor and transmit pathogens with the potential to affect humans and domestic pets, yet little is known about the abundance, population dynamics and pathogen loads of urban mammals in Los Angeles County. To address existing knowledge gaps in urban mammal population health, we are conducting a 2-year pathogen survey of five common mammal species (coyotes, raccoons, skunks, opossums and squirrels) that have the potential to carry zoonoses such as pathogenic *Leptospira* spp. and various intestinal pathogens (e.g. *Giardia, Salmonella, Cryptosporidium,* canine distemper virus) that can be transmitted between humans or domestic pets and urban wildlife populations. Canine distemper virus (CDV) is a pathogen of conservation concern, causing periodic fatal outbreaks in Los Angles wildlife that often lack confirmation by diagnostic testing. We analyzed fecal pathogen DNA by polymerase chain reaction (PCR) in carnivores using a canine IDEXX diarrhea panel (n=27), with positive results for CDV (n=4), *Salmonella* (n=4), *Cryptosporidium* (n=2) and *Giardia* (n=3). Prior exposure to *Leptospira* was assessed via microscopic agglutination testing (MAT), and active infections were assessed using PCR to detect *Leptospira* DNA in urine or kidney. Prior *Leptospira* exposure was detected in coyotes (37%, n=30), Northern raccoons (100%, n=4) and fox squirrels (34%, n=35), and active *Leptospira* infections were detected in coyotes (4%, n=45), Northern raccoons (8%, n=13) and striped skunks (13%, n=16). No fox squirrels (n=61) or Virginia opossums (n=50) had evidence of *Leptospira* infections. This study provides an initial assessment of pathogens of zoonotic and conservation concern in Los Angeles County mammals. Over the course of this 2-year survey, pathogen occurrence will be mapped in relation to indices of urbanization to gain a qualitative understanding of pathogen distribution across this urban landscape, informing local wildlife, veterinary and public health agencies about pathogen occurrence and transmission potential in these urban mammal populations.

MOLECULAR IDENTIFICATION OF POTENTIAL INTERMEDIATE HOSTS OF *AULONOCEPHALUS PENNULA* FROM THE ORDER ORTHOPTERA

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Traditional techniques, such as dissection, are often used when identifying the intermediate hosts of a parasite. Polymerase chain reaction (PCR) is then used to confirm that the larvae are from the parasite of interest. However, dissections are labor intensive and lack sensitivity. For parasites that have low specificity and thus lower prevalence in intermediate hosts, identifying intermediate hosts in this manner can be difficult, and the use of PCR may be a valuable tool that increases larval detection rate. Here, we evaluate the use of PCR as the primary means of identifying the potential intermediate hosts of *Aulonocephalus pennula*, a subulurid that lacks intermediate host specificity and commonly infects the northern bobwhite quail (*Colinus virginianus*), a declining game bird, in the Rolling Plains of Texas. In order to better understand the life cycle of this parasite, various species from the order Orthoptera were collected from a field site in Mitchell County, Texas. Using polymerase chain reaction (PCR), nine potential intermediate hosts were identified from the 35 orthopteran species collected. Later, ten live specimens were collected to identify larvae within the potential intermediate hosts. Larvae were present in three of these and were sent for sequencing. Similarly, the presence of larvae was confirmed from extra tissues of samples in only 20% of samples identified as positive with PCR. This study demonstrates that PCR has increased sensitivity and may be a valuable tool when determining intermediate hosts. While this is the first to document potential intermediate hosts of *A. pennula*, future studies are needed to confirm that these species are capable of transmitting infection to bobwhite. Understanding the life cycle of parasites will be key in determining how infections vary in time and space, especially when climate change is expected to alter the distribution of parasites.

Presenter Bio: I am a Doctoral student in the Department of Environmental Toxicology at Texas Tech University. My research interests include disease ecology, parasitology, wildlife biology, and ecotoxicology.

ADVANCES IN THE TREATMENT AND MANAGEMENT OF *PSOROPTES OVIS* IN BIGHORN SHEEP

*Murray Woodbury[1], **Adam Hering[1]**, Andrew Walker[2], Helen Schwantje[2], Tasha Epp[1], Craig McLean[2], Aaron Reid[2], Sean Odonovan[2], James Pepper[3], Cailyn Glasser[4],*

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Bighorn sheep (*Ovis canadensis)* in northwestern USA and southwestern Canada have shown significant declines after the outbreak of *psoroptes ovis*, a highly pruritic skin mite. This parasite was first confirmed in Canadian bighorn sheep in 2011, and while the range of infestation in Canada is limited, prevalence of infection in affected herds approaches 100%. All affected Canadian herds are in decline, while other nearby unaffected herds are not. A randomized, controlled, treatment trial was performed to test the efficacy of several new treatment approaches for *psoroptes ovis* in bighorn sheep. Twenty (20) naturally infected, free-ranging bighorn sheep were captured and housed in two purpose built 5-acre enclosures. Two different anti-parasitic drugs (eprinomectin and fluralaner) were tested in-vivo using three different routes of administration (injectable, oral, and topical) at several different dosages. Animals were monitored daily and sampled monthly to determine degree of disease resolution through evaluation of clinical signs, microscopic analysis of skin crusting, and antibody titer testing. The eprinomectin showed promising results in pilot studies, however, trial results were discouraging at the dosage used. The topical form of fluralaner was also ineffective at the dosages used, while the oral formulation of fluralaner showed encouraging results at both tested dosages. All orally treated individuals showed significant improvement in clinical signs and some individuals maintained live-mite free status for the 4-month follow-up after treatment despite ongoing infection pressure. Due to a lack of host immunity, the simultaneous treatment of entire herds is ideal in order to accomplish a local eradication of this disease. These findings could provide new management options for the treatment of psoroptic mange in free ranging bighorn sheep through the use of medicated feeds, which would allow for a cost-effective, low-stress option for the management of this disease in heavily affected bighorn sheep herds if necessary.

Presenter Bio: Dr. Adam Hering is a veterinarian and PhD student. He graduated veterinary school from the University of Calgary, spent one year in mixed-animal practice before beginning a PhD at the Western College of Veterinary Medicine. He studies wildlife epidemiology under the supervision of Drs. Murray Woodbury and Tasha Epp.

MASKED RESERVOIRS: SALMONELLA EPIDEMIOLOGY OF THE RACCOON

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Salmonellosis is the top cause for diarrheal disease in the world. Within USA, Georgia ranks first for human salmonellosis cases, a proportion of which are not foodborne but represent environmental serotypes, the source of which is not understood. To understand the potential for animals that are common, abundant and come in direct/indirect contact with households in GA, we undertook studies that involved capturing raccoons to obtain 1 g of feces directly from the rectum. For one study, we additionally swabbed their paws, and to enhance *Salmonella* recovery, both feces and swabs were embedded in 10 ml of dulcitol selenite broth for ~ 48 hrs. before isolation, and utilized standard methodology to isolate *Salmonella* spp. Serotyping was performed at NVSL. Study 1: 56 Raccoons were sampled at 6 sites along an agricultural gradient (from rural farms to natural sites) in two major GA watersheds. The mean prevalence of *Salmonella* was 45% and did not vary between watersheds but was positively correlated with degree of agriculture and with sites where *Salmonella* was also isolated from the water. Study 2: We captured raccoons on coastal GA that a) frequented feral cat feeding stations for food subsidies, and b) lived on natural sites, with no opportunity for contact with people or cats. Raccoons at the natural site had a higher prevalence (100% vs 50%) and had higher agreement between isolation from paws and feces than those from the feral cat feeding stations. In both studies, serotype diversity was very high (>15 serotypes) and serotypes were not associated with a particular habitat, but were in the top 20 of those reported to cause disease in people. Prevalence, serotype diversity and behavioral opportunity indicate raccoons are reservoirs of *Salmonella*, shed at higher than expected rates, even in natural sites, and likely reflect salmonellae in the environment.

Presenter Bio: Sonia M. Hernandez --Associate Professor; obtained DVM from LSU; completed a Small Animal Medicine Internship, a Residency at Cornell University, became a Diplomate in ACZM and obtained a PhD at the Odum School of Ecology; She studies how anthropogenic activities influence health/disease of wildlife.

PHYLODYNAMIC INFERENCE OF AVIAN PARAMYXOVIRUS-1 GLOBAL MIGRATION AND INTER-HOST TRANSMISSION

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Avian paramyxovirus-1 (APMV-1), or Newcastle disease virus, causes economically important disease of varying severity in both domestic and wild birds around the world. Understanding how host and geographic barriers affect viral movement will be crucial to future prevention and control efforts. Employing a Bayesian statistical framework, the evolutionary history of 1,602 APMV-1 complete fusion gene coding sequences of viruses collected from 1970 to 2016 was estimated in order to infer viral transmission between avian host types and viral diffusion between geographic regions, both around the globe and within the United States. Ancestral states were estimated with a non-reversible continuous-time Markov chain model, allowing the putative transition rates between discrete states to be calculated. The evolutionary history and viral migration networks were stratified by the two main APMV-1 lineages, classes I (n=198) and II (n=1,404). In both classes, the bidirectional transitions between domestic chickens and Anseriformes were relatively frequent (1.25 to 3.59 transitions/year) with the highest level of support (Bayes factor [BF] > 100). Moreover, among class II viruses, chickens acted as an important viral source to other host orders with supported transition rates to Anseriformes, Psittaciformes, Columbiformes, and other Galliformes (BF > 100). In the global migration analysis, Europe was estimated as an important node, acting as either a source or sink in 50% (10/20) of the supported class II geographic transitions. While introduction of class I viruses into the US most likely occurred via Alaska, class II viruses have entered the country multiple times independently into different regions (Northeastern, Western and Midwestern US). Though geographic migrations appear to occur less often than host migrations, viral movement plays a larger role in determining viral diversification and population structure. In contrast, host transitions are frequent, but less likely to produce new host specific lineages.

<u>Presenter Bio:</u> Joseph Hicks is a veterinarian and a PhD candidate in epidemiology at the University of Texas School of Public Health at Houston. His research interests center on the evolution, epidemiology and ecology of infectious diseases, with a particular focus on avian viral pathogens.

UNDIAGNOSED PERACUTE SEASONAL MORTALITY AND NEUROLOGIC SYNDROME IN WILD-BORN CAPTIVE WESTERN CHIMPANZEES (*PAN TROGLODYTES VERUS*) IN SIERRA LEONE

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Tacugama Chimpanzee Sanctuary in Sierra Leone is committed to critically endangered Western chimpanzee (*Pan troglodytes verus*) rehabilitation and conservation since 1995, currently housing 75+ chimpanzees in semi free-ranging conditions in the Western Area Peninsula National Park. Diseases, particularly Ebola virus and other infectious diseases such as viral respiratory tract infections or anthrax, have contributed to the decline of wild great apes in Africa. During the last 13 years, 56 semi-free ranging chimpanzees (of 87 mortalities and 190 total individuals) have died mostly from a peracute process with either central nervous system symptoms or no premonitory signs and a morbidity-mortality ratio of 100%. Symptoms include sudden-onset ataxia, vomiting, seizures and lethargy with a peak in the dry season of March/April. Previous diagnostic workup including histopathological and virological studies has failed to identify the cause of this syndrome, although several cases of acute gastric dilatation have been identified. A histopathological review from 25 chimpanzees dying between 2013-2016 has revealed acute shock, pulmonary and pancreatic hemorrhage and proteinaceous edema as the main lesions in most chimpanzees. Several parasitic lesions (e.g., enterobiasis, strongylidiasis, and pulmonary acariasis) have also been found but considered incidental. Next-generation sequencing on tissues from 12 chimpanzees in 2013 has been negative for viruses except for one anellovirus in one case. Currently, the possibility of monofluoroacetate intoxication with the plant *Dichapetalum spp*, present in the enclosures where fatalities have occurred, is being investigated. Molecular analysis for plant DNA in vomit and stool has been inconclusive. Pathogen discovery and toxicological analyses are underway at the University of Wisconsin-Madison. In February 2018, a case occurred for the first time in 2 years, with clinical illness lasting 1 month prior to death. Increasingly comprehensive clinical and pathological data were collected in an effort to solve this disease despite the challenging conditions of Sierra Leone.

Presenter Bio: Ismail Hirji is a graduate of the Ontario Veterinary College, University of Guelph, with a special focus in primate medicine. He was the resident veterinarian for Tacugama Chimpanzee Sanctuary from 2016-2017 and is now a consulting veterinarian for the same institution with a focus on this disease investigation.

ON AND OFF-HOST TICK ABUNDANCE AND INFECTION WITH BORRELIA AND RICKETTSIA SPP. UNDER VARIABLE FIRE MANAGEMENT REGIMES IN EAST TEXAS

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As tick-borne diseases continue to emerge across the United States, a better understanding of the tick and pathogen communities in the southern states and habitat modification measures that could be implemented to reduce transmission risk are increasingly needed. We surveyed questing and on-host ticks in a popular recreation area in east Texas with varied controlled burn histories. Four linear transects were established, two with a history of controlled burns, and two unburned. Drag sampling yielded 218 ticks from two species, *Ixodes scapularis* (*n*=136) and *Amblyomma americanum* (*n*=82). There was a significant difference in questing tick density between burned (22-30 ticks/1000m^2) and unburned (2-4 ticks/1000m^2) transects. Overall, we captured 106 rodents, 8 opossums, and 2 raccoons. Trap success did not differ significantly between burned and unburned transects. We collected 74 ticks, predominantly *Dermacentor variabilis*, from 39 mammals. One unburned transect had significantly more ticks per mammal than any of the other three transects. Of 292 ticks tested via PCR, 146 were positive for *Rickettsia* species, including both the 'Rickettsial endosymbiont of *I. scapularis'* and *Rickettsia amblyommatis*, which is of uncertain pathogenicity to humans. Eight ticks were PCR-positive for relapsing fever group *Borrelia*, including *B. lonestari* in *A. americanum* and *B. miyamotoi* in *I. scapularis*, expanding the known southern distribution of *B. miyamotoi* in the US. No mammal ears or blood samples were positive for *Rickettsia* or *Borrelia* DNA. This study documents differences in tick density in areas with different controlled burn histories, a low prevalence of spotted fever group *Rickettsia* and relapsing fever group *Borrelia* in ticks, and an absence of Lyme-group *Borrelia* in ticks and mammals in an east Texas forested recreation area. These results add important information to the knowledge of tick-borne disease ecology in east Texas which can aid in directing future investigative, modeling, and management efforts.

Presenter Bio: Carolyn Hodo is a veterinary pathologist and postdoctoral research associate in the College of Veterinary Medicine at Texas A&M University, with interests in wildlife pathology, disease ecology, and epidemiology. She studies the transmission ecology of vector-borne diseases with wildlife reservoirs in the southern United States.

COMPARISON OF ALLIGATOR SNAPPING TURTLE (*MACROCHELYS TEMMINCKII*) PLASMA BIOCHEMISTRY PROFILES FROM TWO CLINICAL ANALYZERS

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The alligator snapping turtle (*Macrochelys temminckii*) is a freshwater apex predator threatened throughout its range. Its long lifespan, high trophic level and limited home range, make it a suitable sentinel of ecosystem health. Plasma biochemistry analysis is a principal diagnostic tool used to assess the health of these animals, however, the interpretation of biochemistry profiles can be confounded by the methodologies by which they are produced. This study compared agreement between two biochemistry analyzers for alligator snapping turtle plasma samples. Blood was obtained from the dorsal coccygeal vein of juvenile turtles (n=34), stored in lithium heparin tubes, and centrifuged to separate plasma from whole blood. Plasma samples were stored at 5°C prior to and in between analyses on a standard, laboratory analyzer (Olympus AU640, Beckman Coulter, Brea, CA 92821, USA) and a portable unit suitable for point-of-care use in the field (Vetscan2, Abaxis, Union City, CA 94587, USA). Agreement between the analyzers was investigated using Passing-Bablock regression analysis for aspartate aminotransferase, creatine kinase, glucose, total calcium, phosphorus, total protein, albumin, uric acid, potassium, and sodium. Agreement was outside of acceptance limits and outside of clinical allowable error limits for all analytes as established by the American Society for Veterinary Clinical Pathology. Therefore alligator snapping turtle plasma biochemistry profiles cannot be compared between Vetscan and Olympus analyzers in a clinical setting, although comparison of profiles within analyzer units may still be clinically and scientifically useful. Future studies are warranted to investigate the precision of each analyzer for alligator snapping turtle plasma.

Presenter Bio: Ian Hollinshead obtained his bachelor's degree in biology from The University of Pittsburgh in 2017. He is currently a first-year veterinary student at University of Pennsylvania School of Veterinary Medicine. His focus is on exotic and wildlife medicine.

PRIORITIZATION OF ZOONOTIC DISEASES IN THE UNITED STATES USING A MULTISECTORAL ONE HEALTH APPROACH

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Approximately 60% of human infectious diseases are zoonotic, meaning shared between animals (domestic and wildlife) and people. One Health encompasses a collaborative, multisectoral, and transdisciplinary approach with the goal of achieving optimal health outcomes for people and animals and a safer environment. For the first time, a One Health Zoonotic Disease Prioritization (OHZDP) workshop was conducted in the United States (U.S) in December 2017 to identify zoonotic diseases of greatest national concern that should be jointly addressed by the Centers for Disease Control (CDC), U.S. Department of Agriculture (USDA) and the Department of the Interior (DOI). CDC's OHZDP tool was used for the prioritization of zoonoses. During the workshop, participants selected criteria for prioritization, and developed questions and weights relevant to each criterion. Each disease was then scored resulting in a ranked zoonotic disease list. After the prioritized zoonotic disease list was finalized, participants used components of the One Health Systems Mapping and Analysis Resource Toolkit (OH-SMART™), developed by USDA and the University of Minnesota, to review the procedures and processes for multidisciplinary coordination. Workshop participants included nine voting members representing CDC, USDA and DOI and 27 advisors representing federal and state human, animal, and environmental health sectors. The five criteria selected to prioritize zoonotic diseases were epidemic or pandemic potential, disease severity, economic impact, introduction or increased transmission potential, and national security. Out of fifty-six diseases, eight were prioritized for the U.S.: zoonotic influenzas, salmonellosis, West Nile virus, plague, emerging coronaviruses (e.g. SARS, MERS), rabies, brucellosis, and Lyme disease. Key outcomes included discussion of methods for enhancing One Health coordination among the agencies for surveillance, response, prevention, and control for the prioritized zoonoses. This workshop marked a critical step forward for the U.S. federal agencies involved in strengthening One Health approaches for the prioritized zoonoses.

METAL ACCUMULATION IN TERRESTRIAL MAMMALS

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Metals occur naturally in the environment and are essential for physiological processes in animals, however, an increase in tissue metal concentration above threshold levels can cause adverse effects or become toxic. Determining baseline tissue metal concentrations in terrestrial species can thus increase our understanding of the impact of metal contaminants and anthropogenic activity on wildlife. Unfortunately, baseline metal tissue concentrations in many terrestrial mammals have not been extensively studied. Liver samples from armadillos, bobcats, coyotes, feral cats, grey foxes, opossums, and raccoons were collected from four sites, which experienced relatively similar levels of human disturbance in Georgia and Florida, over four years. Samples were analyzed for multiple metals and concentration differences were analyzed by age (juvenile vs adult), sex, site, species, and year collected. Objectives of this study include 1) assess liver metal concentrations in several common terrestrial mammals in South Georgia and North Florida, and 2) assess whether trophic level and feeding habits influence metal accumulation. This study will be one of the first to examine the accumulation of multiple metals in an assemblage of seven mammal species and will provide the first extensive data set for metal accumulation within these wildlife species.

<u>Presenter Bio:</u> Sarah Hough is currently a graduate student in Biology at Valdosta State University. She is interested in studying toxicology in terrestrial mammal assemblages.

SEASONAL FECAL GLUCOCORTICOID METABOLITES IN BISON LIVING WITH OR WITHOUT WOLVES

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Threat of predation can cause increased adrenal secretion of glucocorticoids, which if sustained, can result in chronic stress that might predispose animals to disease, reduced growth, or poor fertility. This study measured fecal glucocorticoid metabolite (FGM) concentrations September 2011—July 2012 in two Montana bison (*Bison bison*) herds, one herd living with and the other without wolves in their habitat. Physiological relevance of FGM concentrations measured by the corticosterone enzyme immunoassay and confirmation of an acute adrenal response was demonstrated by transient increases ($P<0.05$) in FGM in bison herded through a chute system and following a wolf encounter. FGM concentrations were higher in the herd with wolves than the herd without wolves overall ($P<0.05$), but the monthly differences between the herds were inconsistent (magnitude=0.28-2.87 µg/g; $P<0.03$ *month × herd*). The herd with wolves had higher FGM in April, June, July, September, and November, but the herd without wolves had higher FGM in January, February, and May. Far greater seasonal changes in FGM concentrations ($P<0.001$) were measured across the year in both herds (magnitude=10.15 and 6.88 µg/g, respectively), exceeding any differences between herds potentially attributable to wolf presence. FGM concentrations were highest April—July and were lowest January—February. Evidence of a chronic stress response was not found, and increased disease susceptibility in these bison living with wolves seems unlikely.

MORTALITY OF LITTLE BROWN BATS (*MYOTIS LUCIFUGUS CARISSIMA*) NATURALLY EXPOSED TO MICROCYSTIN-LR

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Cyanobacterial blooms are an increasing problem in natural and man-made aquatic habitats. Cyanotoxins produced during these blooms can results in human and animal intoxications. Previous reports of bat exposure to cyanotoxins are limited, including a mortality event in Alberta, Canada associated with potential exposure to the neurotoxin anatoxin-a and a survey of microcystins in feces from apparently healthy bats in a roost in Michigan USA. In late August 2016, 27 dead and one moribund little brown bat were reported during a visible cyanobacterial bloom affecting Scofield Reservoir, Utah USA. Necropsies were completed by the USGS-National Wildlife Health Center for eight submitted bats. All the bats were in good body condition. The fur of two bats was partially covered with bright green dusty material consistent with dry cyanobacteria, and three bats had abundant green material in the stomach. Microcystin-LR was identified in all water samples collected from the reservoir by quantitative enzyme linked immunosorbent assay (ELISA) or liquid chromatography-tandem mass spectrometry (LC/MS-MS), with concentrations ranging from 14.4 to 60,000 µg/L. Pooled gastrointestinal content from five bats tested by LC/MS-MS presented 5,700 ng/g of microcystin-LR. Based on the exclusion of other causes of death, including rabies lyssavirus infection, bacterial septicemia and trauma, and the detection of high levels of microcystin-LR in the gastrointestinal content of bats and in the water of the reservoir, we considered microcystin-LR intoxication as the most likely cause of this mortality event. To our knowledge, this event provides the first epidemiological and toxicological evidence for bat mortality following exposure to high levels of microcystin-LR. Although more information is needed on the deleterious impact of microcystins on bats, these cyanotoxins may represent a health risk not previously assessed for bats in North America, especially for species that hunt over, or regularly drink from water bodies prone to cyanobacterial blooms.

Presenter Bio: Lee serves as the ungulate health specialist and bison conservation coordinator for the US Fish and Wildlife Service, Natural Resource Program Center's Wildlife Health office. She received a B.A. in Biology from Occidental College in Los Angeles and an M.S. in Biology from Montana State University.

HERPESVIRUS DETECTION AND PREVALENCE IN ALLIGATOR SNAPPING TURTLES (*MACROCHELYS TEMMINCKII*)

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Herpesviruses are significant pathogens of captive and free-ranging chelonians worldwide. In affected individuals, clinical signs of the upper respiratory tract and necrotizing stomatitis are observed to lead to variable rates of morbidity and mortality. Recently, several free-ranging emydid (freshwater) turtle species have been documented with herpesviruses in apparently healthy individuals, with a prevalence from 2-56%. The reintroduction of the alligator snapping turtle (*Macrochelys temminckii*) is currently underway in three states and as part of a health screening, we investigated the presence of herpesvirus in pre-release turtles. Using conventional polymerase chain reaction, we tested oral and cloacal DNA swab samples (n=115) from fully captive alligator snapping turtles pre-released in southern Illinois (n=97) and adult fully captive individuals confiscated from Florida (n=18). Of the 97 juvenile captive turtles, 75 of them were obtained from a breeding program at Tishomingo National Fish Hatchery (TNFH) and 22 additional turtles were obtained from Peoria Zoo in Illinois. No sample was detected with herpesvirus. Possible explanations for the results include lack of exposure, latency in tissues not sampled, and viral quantities below the level of detection of the assay. Conservation efforts of reptiles are increasingly monitoring for pathogens, and herpesviruses appear ubiquitous in certain species, but not in others. Continued surveillance for this and other pathogens is helpful in characterizing the threats from captive reintroduction and will enhance future conservation efforts of this species.

Presenter Bio: My name is Taylor Jones and I am a second year veterinary student at the University of Illinois. I am originally from Sanger, Texas and my goal after graduation is to pursue zoological medicine and conservation.

DETECTION OF A DIVERGENT STRAIN OF LYMPHOPROLIFERATIVE DISEASE VIRUS IN WILD TURKEYS IN ARIZONA

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Lymphoproliferative disease virus (LPDV) is a retrovirus that infects wild and domestic turkeys (*Meleagris gallopavo*). While most infected birds appear to be asymptomatic, lymphoplasmacytic neoplasia expressed as hard, scabby tumors around the head and feet occurs in a small percentage of cases. The first cases of LPDV were recognized in eastern wild turkeys (*M. gallopavo silvestris*) within the United States in 2009 in Arkansas, and subsequent surveillance revealed the virus to be widespread in populations in 24 eastern states. Little surveillance has been conducted in the other subspecies of wild turkeys, three subspecies of which occur in Arizona: Merriam's (*M. gallopavo merriami*), Gould's (*M. gallopavo mexicana*), and Rio Grandes (*M. gallopavo intermedia*). Our objective was to determine whether LPDV is present in Arizona's Merriam's turkey populations. We collected samples of whole blood from 20 live Merriam's turkeys, and whole blood and bone marrow from 28 hunter-harvested turkeys (n=48). Lymphoproliferative disease virus genetic sequences were detected via polymerase chain reaction in 54% (n=26) of samples. Two additional samples were collected from Gould's turkeys; LPDV was not detected in either sample. The 337 base pairs amplicon of the long terminal repeat of 4 of the samples was sequenced and compared to the sequences found in eastern wild turkeys. None of the sequences were identical when compared, ranging from 95.8 to 98.8% identity (4 to 14 b. p. differences) and were 89.9 to 92.9% identity to the prototype strain 12/AR/2009 from the United States. Studies to assess the prevalence across the state and in the other subspecies are planned. Additionally, phylogenetic studies of retroviruses have been used to examine relationships between populations of the host species. A broader analysis of the LPDV strains of the subspecies of North American wild turkeys and the South American ocellated wild turkey (*Meleagris ocellata*) is recommended.

<u>Presenter Bio:</u> As the Veterinarian for the Arizona Game and Fish Department, Anne Justice-Allen directs animal care during wildlife captures, assesses the health of wildlife populations, participates in endangered species reintroduction projects, and researches infectious diseases with projects on sylvatic plague, pigeon paramyxovirus 1 and mycoplasma pneumonia in desert bighorn sheep.

DETECTION OF EHDV-6 IN MULE DEER IN ARIZONA: RANGE EXPANSION OF CLIMATE DEPENDENT VECTOR-BORNE DISEASE

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Epizootic hemorrhagic disease virus is an orbiviral infection of wildlife and domestic animals in North America that is transmitted by biting midges in the genus *Culicoides*. Serologic testing and mortality investigations of wildlife as well as testing of trapped midges previously detected the presence EHDV 1 and 2 as well as strains of bluetongue virus (10, 11, and 17) in Arizona. In 2017, we investigated mortalities of 6 mule deer and a white-tailed deer from northwestern Arizona. Epizootic hemorrhagic disease virus was detected by RT-PCR in tissues from the affected animals. Using serotyping and pcr, the viral RNA detected in the sample was identified as EHDV type 6 based on VP2 gene sequence. This is the first identified occurrence of this serotype in the state, and represents the furthest west detection of the strain. EHDV-6 was first detected in the U.S. in 2006. While it has been detected every year since, there were large scale outbreaks in 2007 in the Ohio River Valley and Mid-Atlantic region and in 2012 in the Missouri River Valley and Upper Midwest region. In 2017, there has been a spread of the serotype into new states including Arizona, Alabama, Connecticut, Pennsylvania, and West Virginia. The expansion of this virus to Arizona is noteworthy for several reasons. *Culicoides sonorensis* has been identified as the vector species for EHDV in the United States however it is not believed to be an efficient vector for EHDV6. In Arizona, EHDV has been detected in another potential vector, *C. mohave*. The occurrence of a more competent vector could affect disease transmission dynamics within the system. The vector of EHDV is sensitive to climate parameters and the highly variable climate of Arizona could also impact incidence. Additional research on regional vectors and the influence of weather on vector ecology is needed.

Presenter Bio: As the Veterinarian for the Arizona Game and Fish Department, Anne Justice-Allen directs animal care during wildlife captures, assesses the health of wildlife populations, participates in endangered species reintroduction projects, and researches infectious diseases with projects on sylvatic plague, pigeon paramyxovirus 1 and mycoplasma pneumonia in desert bighorn sheep.

DISTRIBUTION OF CERVID ADENOVIRUS HEMORRHAGIC DISEASE BY VIRAL GENOTYPE IN THE UNITED STATES

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Cervid adenovirus hemorrhagic disease (AHD) was recognized in 1993 during an outbreak that killed over 1,000 mule deer in California. It is now identified throughout the Western United States, as well as Iowa, Alaska, and Ontario, Canada. The disease affects mule deer (*Odocoileus heminous*), white-tailed deer (*Odocoileus virginianus*), moose (*Alces alces*), elk (*Cervus candensis*), and pronghorn (*Antilocapra americana*). AHD is grossly indistinguishable from bluetongue and epizootic hemorrhagic disease, and causes sporadic mortalities, primarily in young animals in endemic and epidemic cycles. The incidence, distribution, and population effects of AHD are poorly understood. In an ongoing study of survival of neonatal mule deer, death associated with AHD has been as high as 20%. Previous whole genome analysis of cervid adenovirus (CeAdV), the causative agent of AHD, identified three genotypes (A, B, C). The aim of our study is to further describe the epidemiology of AHD by investigating the distribution of CeAdV genotypes by host demographics and geographic region, and to describe *in vitro* viral replication kinetics. Using available diagnostic cases, preliminary findings indicate genotype C appears to be geographically limited to the west coast of the United States, where large-scale mortality events have been observed. Genotype B appears to be limited to mule deer and white tailed deer. Genotype A is over represented in elk and moose, but is not limited by species or geography. We discovered a proposed fourth genotype in one case in an elk during our initial genotyping work; whole genome sequencing is in progress. Initial *in vitro* work between genotype A and the other genotypes indicates differences in cytopathic effect and growth curves. The importance of the genetic variations of CeAdv1 on disease outcome and distribution will provide a basis for the understanding the epidemiology of AHD.

Presenter Bio: Kayla M. Kauffman is a Master's candidate at the University of Wyoming in Veterinary Science and Environment and Natural Resources. She is interested in disease ecology and conservation. Prior to coming to University of Wyoming, she worked as a wildlife technician in the western United States.

HOSTS FACTORS AND ABIOTIC FACTORS UNDERMINING EXPANSION OF *BORRELIA*-INFECTED TICK POPULATIONS IN SOUTHEASTERN STATES

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Lyme disease is caused by the bacterium *Borrelia burgdorferi* (*Bb*), which in the eastern US is vectored by *Ixodes scapularis* (the black-legged tick). Black-legged ticks are found in wooded habitats throughout the eastern United States, however populations infected with *Bb* have been rare in most southeastern states. To explain this pattern, it has previously been suggested that: *i*) tick abundance may be too low in most southern states for *Bb* cycles to easily persist; and *ii*) that immature black-legged ticks in the Southeast may feed primarily on lizards, which are non-reservoir-competent hosts for *Bb*. The past decade has, however, seen emergence of *Bb*-infected tick populations in southwestern Virginia, southeastern Kentucky, and northeastern Tennessee. These emerging disease foci are closely associated with major river systems, which appear to act as corridors for spread of infected ticks. To better understand the characteristics of these foci of infection, we are using GIS techniques to map abiotic and other habitat factors associated with foci. In addition, we are evaluating Stable Isotope Analysis (SIA) of wild-caught blacklegged ticks as a technique for characterizing host selection by ticks at foci. The relative importance of host vs. abiotic factors for emergence of infected tick populations will be discussed. A key goal of this research is to assess the likelihood that *Bb*-infected tick populations will become more widespread in Tennessee and Kentucky in coming years.

PREVALENCE OF RANAVIRUS IN EDIBLE FROGS AND FISH IN ZARIA, KADUNA STATE, NIGERIA

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Ranaviruses are globally emerging pathogens, which, cause systemic infection in fishes, amphibians, and reptiles and have been associated with numerous disease outbreaks in natural and cultured fish and frog populations. Mortality and morbidity due to ranaviruses have been reported in up to 100% of infected animals. The aim of this study was to determine the presence of ranaviruses in fish and edible frogs from dams and ponds in Zaria, Kaduna State, Nigeria. A total of 415 samples comprising 215 frogs (*Rana spp*.) and 200 fishes (*Clarias gariepinus, Labeo senegalensis, Lates niloticus, Marcusenius senegalensis, Oreochromis niloticus, Schilbe mystus, Tilapia zilli*) were collected based on availability. Liver, kidney and spleen from each sample were pooled, homogenised and screened for ranavirus using the antigene capture Enzyme linked Immunosorbent assay (ELISA). An overall prevalence of 47.2% (196/415) was obtained from the study. Frogs had a higher prevalence of 51.2% (110/215) than fish (43% (86/200). There was no statistically significant relationship between prevalence in fish and that of frogs ($P > 0.05$). Among the Fish species, *Marcusenius senegalensis* fish had the highest prevalence of 75% (9/12); this was statistically significant ($P < 0.05$). The prevalence in wild fish (51.3%) compared to farmed fish (18%) was statistically significant ($P < 0.05$). This study establishes the presence of detectable ranavirus antigene in Zaria, Kaduna State, Nigeria. This is the first report on the presence of ranavirus in fishes and edible frogs in Kaduna State Nigeria.

BIO: Grace S.N. Kia (DVM., MSc., PhD., FCVSN), a veterinarian in the Department of Veterinary Public Health and Preventive Medicine, Ahmadu Bello University Zaria. Her research interests are in the epidemiology, prevention and control of viral diseases especially lyssaviruses and the surveillance of neglected and emerging zoonotic pathogens of epidemic potential.

RABIES AND ZOONOTIC DISEASE RISK AWARENESS AMONG BUSH MEAT HUNTERS IN ZARIA KADUNA STATE, NIGERIA

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The activities of **Bushmeat hunters'** has been of increasing importance among both conservationists and public health officials for their threat on biodiversity and increases risk of zoonotic disease transmission from animals to people. This study was conducted to determine the risk awareness of rabies and other viral zoonotic diseases among 163 bushmeat hunters in Sabon Gari Local Government Area- Nigeria. Using a pretested closed-ended well-structured questionnaire their demographic variables, hunting practices and Risk awareness of Rabies and other viral zoonotic diseases were captured. Majority 69 (42.3%) of them were aged 21 - 30 years, 106(65%) were married, 90(55.2%) had at least a form of secondary/high school education, 113(69.3%) were aware of the risk of zoonotic disease and its transmission, while 137(84%) were aware of Rabies as a zoonosis. However, despite the high risk awareness of Rabies and other zoonotic diseases among **bushmeat** hunters in this study, none has been vaccinated nor wears any protective clothing while hunting, transporting, slaughtering or processing of the game. The study also documents dog ownership among all the bush meat hunters. Frequent hunting and the use of guns as the major technique for hunting as in this study area is worrisome in view of the threat it poses to wildlife conservation. Therefore, there is need for awareness among these hunters of the detrimental consequence of their actions on Public health, wild life and the ecosystem in general. Hence, formulation and implementation of regulations to check mate the activities of bush meat hunters is advocated for toward wildlife conservation and minimizing transmission of rabies and other zoonotiv disease among vulnerable communities.

Presenter Bio: Grace S.N. Kia (DVM, MSc., PhD., FCVSN), a veterinarian in the Department of Veterinary Public Health and Preventive Medicine, Ahmadu Bello University Zaria. Her research interests are in the epidemiology, prevention and control of viral diseases especially lyssaviruses and the surveillance of neglected and emerging zoonotic pathogens of epidemic potential.

PREVALENCE OF ZOONOTIC PATHOGENS IN WILD ARMADILLOS IMPORTANT FOR PUBLIC HEALTH

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Since 1909, when the research scientist Carlos Chagas described *Trypanosoma* spp. in armadillos, they have been considered a reservoir for several zoonotic pathogens. Some authors state that armadillos' burrowing behavior and primitive physiology, such as low metabolism, may favor this condition. Accordingly, the Xenarthra Health Initiative developed through the Giant Armadillo Conservation Program, evaluated the prevalence of five zoonotic pathogens (*Toxoplasma gondii, Trypanosoma cruzi, Leishmania* spp*., Mycobacterium leprae* and *Paracoccidioides brasiliensis*) in four wild armadillo species (*Priodontes maximus, Euphractus sexcinctus, Dasypus novemcinctus and Cabassous unicinctus*) in Pantanal wetland and the Cerrado tropical savanna ecoregions of Mato Grosso do Sul state, Brazil. A total of 50 armadillos were studied: 43 from Pantanal (16 *P. maximus*; 17 *E. sexcinctus*; 2 *D. novemcinctus* and 8 *C. unicinctus*) and 7 (5 *E. sexcinctus and 2 D. novemcinctus*) found dead in three different roads of the Cerrado. Blood samples and ear tissue biopsy were collected to perform serodiagnostic and polymerase chain reaction (PCR) analyzes, respectively. Out of the 43 individuals sampled in Pantanal, 13 (30.23%) presented *T. gondii* antibodies; 1 (2.32%) showed antibodies anti-*T. cruzi*; and 4 (9.30%) showed anti-*Leishmania (L.) infantum chagasi* antibodies. PCR analyzes were negative for *M. leprae* and *Leishmania* spp. All 7 (100%) individuals from the Cerrado tested positive for *P. brasiliensis*. The results suggest that armadillos have been exposed to all pathogens studied, except for *M. leprae*. The fact that armadillos spend most of their time inside burrows, with organic matter, in abiotic or biotic conditions and share their burrows with different species, may create an ideal environment for pathogens and vectors. Armadillos are key species in understanding diseases transmission cycles, especially regarding zoonotic pathogens and should be considered a strategic species for health assessment programs, spatial zoonotic distribution or monitoring diseases transmission risk.

Presenter Bio: Danilo Kluyber, D.V.M. MsC. Head veterinarian for the Giant Armadillo Conservation Program (since 2011) and Anteater and Highways Project (since 2017). Research associate of the Naples Zoo at Caribbean Gardens, Florida, U.S. Master of Science in Tropical Diseases and International Health from São Paulo University, Brazil (2016).

HOST AND PATHOGEN DYNAMICS DIFFER WHERE SPILLOVER OCCURS

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For many zoonoses impacting humans, pathogen spillover occurs in conditions that are atypical from enzootic transmission. Comparisons of how populations of reservoir hosts and their zoonotic pathogens differ between enzootic and spillover environments can therefore provide valuable mechanistic insight into factors promoting spillover, yet are rarely investigated. Sin Nombre virus is a zoonotic hantavirus, reservoired by *Peromyscus maniculatus* deer mice that spills over to humans in peridomestic environments, causing hantavirus pulmonary syndrome. Using 19 years of monthly sampling from paired natural/sylvan (where enzootic transmission predominates) and peridomestic (where spillover occurs) environments, we compare reservoir host demographic and SNV dynamics, finding marked differences. Relative to the sylvan environment, peridomestic mice exhibited greater heterogeneity in abundance and growth rate, greater recruitment, lower residency, a more even (on average) and heterogeneous sex ratio, and fewer adults. Within peridomestic environments, SNV prevalence was also greater and more heterogeneous than the sylvan environment. For individual mice where we could track transmission between months, these events occurred later in the year and were not sex biased in peridomestic settings, in contrast to sylvan settings. Combined, our findings demonstrate how host-pathogen ecology can be dramatically different in environments where spillover events occur, and that risk factors for pathogen spillover cannot necessarily be extended from enzootic transmission environments. Combined with human behaviors that promote exposure to SNV, changed host-pathogen ecology appears a key feature of spillover. These findings may shed light on conditions leading to spillover for other zoonotic hantaviruses globally, and other rodent-borne zoonoses impacting humans.

Presenter Bio: Amy Kuenzi is the department head of the Biological Sciences Department at Montana Tech. Her research focuses on the ecology of small mammals, climate, trophic interactions, and Sin Nombre virus in North America.

RANAVIRUS AND AMPHIBIANS: IS THERE A DILUTION EFFECT?

Austin Coleman[1,2], David Scott[1], and ***Stacey L. Lance[1]***
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Biodiversity is being lost at an alarming rate due to anthropogenic activities. Concurrently, outbreaks of emerging infectious diseases affecting wildlife populations are increasing. There has been significant interest in the interaction of these two phenomena and the potential for direct links between biodiversity and infectious disease. The dilution effect hypothesis suggests that more diverse communities constrain pathogen spread through several mechanisms. The dilution effect has been widely debated, but recent meta-analyses suggest it is common and pervasive. Amphibians have been especially subject to emerging infectious disease and biodiversity loss. Pathogens in the genus *Ranavirus* infect ectothermic vertebrates and have contributed to population declines and die-offs. Previous research has suggested a dilution effect for pond-breeding amphibians and a macroparasite. However, the study was conducted in an area with low host diversity. The U.S. DOE Savannah River Site in South Carolina contains 100's of wetlands and over 30 species of pond-breeding amphibians. Previous surveys indicate that ranavirus is widespread across wetlands and species. Our objectives in this study included characterizing the amphibian communities for 20 ephemeral wetlands using standardized capture methods and investigating the drivers of community assembly and the relationship between amphibian communities and ranavirus prevalence and intensity. We captured more than 30,000 individual amphibians representing 23 species. For a subset of individuals captured (2,215) we quantified presence and load of ranavirus via qPCR. Ranavirus prevalence varied significantly across species with the highest seen in *Anaxyrus terrestris* (34%), *Pseudacris nigrita* (32%) and *P. crucifer* (26%). Preliminary analyses suggest time of year, species, temperature, and cumulative species richness all contribute significantly to patterns of prevalence. The relationship between richness and prevalence is nonlinear and the patterns raise interesting questions about the connection between amphibian communities and *ranavirus* dynamics.

Presenter Bio: Stacey Lance is an Associate Research Scientist at the University of Georgia, Savannah River Ecology Laboratory. Her research focuses on the effects of natural and anthropogenic stressors on wildlife disease ecology, population biology, and population genetics with an emphasis on the impacts of contaminants on amphibians.

VAMPIRE BAT MANAGEMENT PROCEDURES IN LATIN AMERICA: WHY DO THEY WORK - OR NOT?

Luis Lecuona
USDA, APHIS, IS, México

The Americas is the only region that has the presence of vampire bats. The three species of hematophagous bats include: the common vampire, *Desmodus rotundus*, the white-winged vampire, *Diaemus youngi* and the hairy-legged vampire, *Diphylla ecaudata*. They are distributed primarily in the tropical areas from México to Chile and Argentina. However, several ecological, climatic, breeding and cattle production factors have an important impact in determination of the presence of vampires, even in areas that are not frequently considered as generally appropriate for their occurrence. Today, *D. rotundus* is the vampire associated with rabies transmission to livestock. Both *Diphylla* and *Diaemus* appear to have much lower densities and their distribution is more limited, feeding preferentially on the blood of birds and other vertebrates, and reports of human attacks are very limited. Rabies virus transmitted by the common vampire to cattle is a permanent problem. Livestock production losses are significant in many areas of Latin America. The Ministries of Agriculture in impacted countries have developed management strategies based in the temporary control and reduction of vampire colonies in affected areas, in accordance with historical collaborative studies of rabies prevention and control developed during the 1970s. Even when each country applies such control activities according with local conditions and needs, essentially all develop similar procedures to mitigate the same problem. During the past 50 years, management and control activities have attempted to reduce the disease impact throughout the region with variable results, according to the results observed and reported in various Latin American settings.

Presenter Bio: Doctor in Veterinary Medicine and Animal Science (UNAM). Specialty in Epidemiology and High Direction of Public Entities Program. He is coordinating the Wildlife Program at the USDA/APHIS/IS-WS Mexico. He was Head of Rabies Department of the Mexican Ministry of Health, Professor of Statistics and Member, Committee for Operative Zoonosis Investigation.

ANTHROPOGENIC CONTAMINANTS IN STRANDED CETACEANS IN THE SOUTHEASTERN UNITED STATES, 2012 – 2017

Catherine F. Lo[1], *Justin R. Perrault*[2], *Branson Ritchie*[3], *Sayed Hassan*[4], *Craig A. Harms*[5], *David Rotstein*[6], *Victoria G. Thayer*[7], *Jill M. Sullivan*[7], *and Annie Page-Karjian*[1]

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[6]Marine Mammal Pathology Services, Olney, MD, USA
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A variety of contaminants are released into coastal marine environments from human activities, including manufacturing, pesticides, and burning of fossil fuels in addition to their uses in plastics, detergents, and antibacterial soaps. These anthropogenic contaminants in the marine environment biodegrade slowly, bioaccumulate in organisms, and can cause reproductive, immune, and developmental effects on wildlife; however, the effects of many of these contaminants have not been extensively studied in cetaceans. The objective of this study was to help expand the knowledge base concerning concentrations and biological effects of anthropogenic contaminants in stranded cetaceans in the southeastern United States sampled during 2012–2017. We analyzed 66 cases of stranded odontocetes. Liver samples were evaluated for 12 inorganic chemicals using inductively coupled plasma-mass spectrometry. Blubber samples were analyzed for 5 known endocrine disrupters using gas chromatography-mass spectrometry. Complete reviews of demographic, pathologic, and toxicologic reports for each individual animal were performed. Using the Mann-Whitney-Wilcoxon test with a Bonferroni correction and $\alpha = 0.05$, significant differences were observed among concentrations of diethyl phthalate ($p=0.000$), nonylphenol ethoxylate ($p=0.005$), Mn ($p=0.002$), Zn ($p=0.00$), and Tl ($p=0.00$) between FL and NC; Mn ($p=0.000$), Pb ($p=0.002$), Tl ($p=0.003$), and Zn ($p=0.00$) between piscivores and cephalopod feeders; and Se ($p= 0.000$) and Hg ($p=0.000$) between adults and juveniles. Relevant histopathologic findings include: multifocal nodular thyroid hyperplasia; bilateral adrenal pheochromocytomas; benign seminoma with tumor necrosis and fibrosis; and pituitary periadenitis, which correlated to relatively higher concentrations of diethyl phthalates, BPA, and triclosan, respectively; and multifocal centrilobular hepatocellular necrosis; biliary hyperplasia; and nodular extramedullary hematopoiesis, which positively correlated to elevated concentrations of Fe and Hg. The results of this study provide information on possible lesions associated with chronic exposure to a subset of contaminants; and highlight meaningful information for investigators of marine ecosystem health.

Presenter Bio: Catherine Lo is a Masters student at Florida Atlantic University-Harbor Branch Oceanographic Institute under the advisory of Dr. Annie Page-Karjian in the Marine Wildlife Veterinary Medicine and Research Program. She received her B.S. from Oregon State University and recently interned at The Marine Mammal Center focusing on disease investigation.

ASSESSING THE REPEATABILITY OF TICK DRAGGING AS A METHOD FOR *IXODES SCAPULARIS* SURVEILLANCE

Katie M. Clow, ***Genevieve A. M. Lumsden,*** *Rachel Finer, Claire M. Jardine*
University of Guelph, ON, CA

Tick dragging is an important tool used by public health for *Ixodes scapularis* surveillance to identify Lyme disease risk areas in Ontario, Canada. Concerns have been raised regarding the repeatability of tick dragging due to fluctuations that occur in the tick population in response to micro- and macroclimatic variations. Our objective was to assess the repeatability of tick dragging over a short timescale by examining three outcome measures: presence/absence of ticks, tick abundance, and likelihood of tick establishment. Likelihood of tick establishment was assessed by integrating data collected on tick life stage, overall abundance, and past surveillance findings and was assessed as non-zero, low, medium or high risk. We conducted tick dragging twice per site within a one month period at a total of 10 sites in eastern and southern Ontario. *Ixodes scapularis* were detected at seven sites. The outcome of presence/absence was consistent at 9 out 10 sites. Abundance was highly variable, changing between each visit at sites where ticks were detected. The measure of likelihood of tick establishment was consistent at 8 of 10 sites. Based on the kappa statistic, there was substantial agreement between measurements for the presence/absence and the likelihood of tick establishment. Our results indicate that both presence/absence and the measure of likelihood of tick establishment provide more consistent outcomes for tick dragging than tick abundance alone; however, applying the dragging data to the likelihood indicator provides additional information about the potential risk associated with *I. scapularis* establishment in the area.

Presenter Bio: Genevieve Lumsden is an MSc student in the department of Pathobiology at the University of Guelph with an interest in wildlife disease ecology. Current research focuses on DNA bloodmeal analysis as a tool for understanding *Borrelia burgdorferi* transmission ecology in *Ixodes scapularis* in the Thousand Islands region, Ontario.

FIRST DETECTION OF LYMPHOPROLIFERATIVE DISEASE VIRUS IN CANADA AND SURVEY FOR OTHER VIRUSES IN ONTARIO WILD TURKEYS (*MELEAGRIS GALLOPAVO*)

Amanda M. MacDonald[1,2], *Claire M. Jardine*[1,2], *Jeff Bowman*[3,4], *Leonardo Susta*[1], *and Nicole M. Nemeth*[1,2]
[1]Department of Pathobiology, University of Guelph, Guelph, ON, Canada
[2]Canadian Wildlife Health Cooperative, Ontario Veterinary College, Guelph, ON, Canada
[3]Environmental & Life Sciences Graduate Program, Trent University, Peterborough, ON, Canada
[4]Wildlife Research & Monitoring Section, Ontario Ministry of Natural Resources and Forestry, Peterborough, ON, Canada

Many potential disease-causing agents pose a threat to the health of wildlife. Wild turkeys (*Meleagris gallopavo*) were extirpated from Ontario in the early 1900's due to unregulated over-hunting. Since their reintroduction in 1984, they have increased in number and geographic range. These populations geographically overlap with domestic turkey farms, an important sector of the provincial agri-food industry. Information on the health and the occurrence of pathogens that may cause disease in this population, however, is lacking. Potential pathogen transmission between wild and domestic turkeys is a concern, as they are susceptible to infection with many of the same pathogens and have direct and indirect contact via the wildlife-livestock interface. Thus, we assessed the prevalence and geographic distribution of geographically relevant viruses in Ontario Wild Turkeys. Oropharyngeal and cloacal swabs were tested for avian influenza viruses (AIV) by real-time reverse-transcriptase (qRT)-PCR (n=207), pooled tissues for lymphoproliferative disease virus (LPDV; n=183) and reticuloendotheliosis virus (REV; n=119) by PCR, and gross skin lesions by real-time RT-PCR for avian poxvirus (n=8). We sequenced a fragment of the gag polyprotein (p31) gene of LPDV on a subset (n=10) of LPDV-positive samples for phylogenetic analysis and tested additional upland gamebird species (n=39) and domestic fowl for LPDV (n=17). We document the first detection of LPDV in Wild Turkeys in Canada, with a prevalence of 65%. Phylogenetic analysis revealed that LPDV sequences from Ontario were genetically similar to other North American strains and did not group into separate clades. Reticuloendotheliosis virus was detected in 5% of LPDV-positive Wild Turkeys. Grossly-evident skin lesions from five Wild Turkeys tested positive for poxvirus and all turkeys tested negative for AIV. This study provides the first evidence of LPDV circulation in Canada, and provides a baseline for comparison with future Wild Turkey pathogen surveillance and monitoring.

<u>Presenter Bio:</u> B.Sc. from the University of New Brunswick, Honors from Saint Mary's University, and M.Sc. from Trent University. At the Ontario Veterinary College, Amanda is finishing her PhD in Pathobiology, under the supervision of Nicole Nemeth and Claire Jardine, performing a survey of potential disease-causing agents in wild turkeys in Ontario.

SURVEY OF POTENTIAL PATHOGENS IN WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN ONTARIO, CANADA

***Amanda MacDonald**[1,2], Claire Jardine[1,2], Leonardo Susta[1], Jeff Bowman[3,4], Evelin Rejman[1], John Barta[1], Nicole Nemeth[1,2]*

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Many potential disease-causing agents pose a threat to the health of wildlife. Wild turkeys (*Meleagris gallopavo*) were extirpated from Ontario in the early 1900's due to unregulated over-hunting. Since their reintroduction in 1984, they have increased in number and geographic range; however, information on the health and the occurrence of pathogens that may cause disease in this population is lacking. To assess the health and pathogen-carrying status of wild turkeys in Ontario we conducted 1) a retrospective analysis of post-mortem findings and diagnoses for 56 wild turkeys over a 20-year period at the Canadian Wildlife Health Cooperative to provide a long-term outlook of detected diseases, and 2) a prospective study investigating pathogens associated with disease outbreaks or decreasing the fitness of 152 wild turkeys in Ontario (e.g., *Mycoplasma* spp., *Eimeria* spp., avian pox virus, and avian influenza viruses). Laboratory tests included culture (*Mycoplasma* spp., *Escherichia coli*, *Salmonella* spp., *Ornithobacterium rhinotracheale*, *Erysipelothrix rhusiopathiae*, *Pasteurella multocida*), fecal floats (*Eimeria* spp.), and PCR (avian poxvirus, avian influenza viruses, lymphoproliferative disease virus, reticuloendotheliosis virus). With respect to the retrospective study, non-infectious diagnostic findings (69.6%) were more common than infectious (28.6%), with emaciation identified most frequently (33.9%) followed by trauma (19.6%). The majority (98.7%) of wild turkeys in the prospective study tested positive for ≥1 Mycoplasma spp. (of 6 identified species). In addition, 76.0% of samples tested positive for *Eimeria* spp., 69.1% were positive for *E. coli*, 66.4% were positive for LPDV with 6 of these having concurrent REV infections, 2 turkeys had avian pox with grossly-evident skin lesions, and all tested negative for avian influenza viruses, *Salmonella*, *O. rhinotracheale*, *E. rhusiopathiae*, and *P. multocida*. This baseline data will aid in future monitoring of disease emergence and will contribute to conservation and management strategies, which help to ensure sustainable populations of wild turkeys in Ontario.

<u>Presenter Bio:</u> B.Sc. from the University of New Brunswick, Honors from Saint Mary's University, and M.Sc. from Trent University. At the Ontario Veterinary College, Amanda is finishing her PhD in Pathobiology, under the supervision of Nicole Nemeth and Claire Jardine, performing a survey of potential disease-causing agents in wild turkeys in Ontario.

ANTIMICROBIAL RESISTANCE IN WILDLIFE SPECIES: THE POTENTIAL FOR SENTINEL SURVEILLANCE IN A ONE HEALTH PERSPECTIVE

Carlos G. das Neves; Anne Margrete Urdahl; ***Knut Madslien****; Silje N. Ramstad; Live L. Nesse; Solveig S. Mo; Jannice Slettemeås; Madelaine Norström; Marianne Sunde*
Norwegian Veterinary Institute, Oslo, Norway

Antimicrobial resistance (AMR) is an emerging problem, and is widely spread in many environments. The use of antibiotics in humans, livestock or agriculture may have a direct impact on wild animals, and these may help the spread of antibiotic resistance genes. We have conducted several studies with different wildlife species in Norway to monitor AMR and understand the potential for wildlife to work as sentinels/bio indicators for AMR. Between 2013-2017 faecal samples were collected from wild species: wild birds (n=357); red foxes (n=387); wild reindeer (n=265); roe deer (n=301); Svalbard reindeer (n=27). Resistant bacteria were identified by culturing on selective media and/or by susceptibility testing of randomly chosen E. coli. Wild birds: E. coli resistant to extended-spectrum cephalosporins were detected in 31 samples (8.7%) and quinolone resistant E. coli in 74 (5.6%). Red foxes: The occurrence of AMR was 9.2%, 6.3% and 14.7% in areas of low, medium and high human population density, respectively. A statistically significant difference in AMR occurrence was observed between medium and high population density areas. Roe deer and wild reindeer: E. coli was isolated from 274 out of 301 (91%) roe deer, and from 230 out of 265 (86.8%) wild reindeer. Resistance to streptomycin was detected in 1.7% of wild reindeer and in 5.1% of roe deer. Svalbard reindeer: Fifteen isolates (55%) were resistant to more than one antimicrobial agent. Resistance regions with high homology to plasmid regions previously described in bacteria from swine in the Netherlands and poultry in China were identified. Results from these studies demonstrate that AMR is present in the environment even in pristine ecosystems such as the Arctic. Longitudinal and spatial broad studies should be prioritized in order to better understand this problem and elucidate the role of wildlife species in the spread of AMR in a one-health perspective.

Presenter Bio: Carlos das Neves is a veterinarian with a PhD in virology in wildlife. He is the Head of Food Safety and Emerging Threats at the Norwegian Veterinary Institute, Associate Professor at the University of Tromsø and a Diplomate in Wildlife Health with the European College of Zoological Medicine. He has been a member of WDA since 2005 and is currently serving as its Vice-President.

CHRONIC WASTING DISEASE IN NORWAY: AN UPDATE ON SURVEILLANCE, RESEARCH AND DISEASE DEVELOPMENT

*Jørn Våge[1], **Knut Madslien[1]**, Turid Vikøren[1], Petter Hopp[1], Hildegunn Viljugrein[1], Carlos G. Das Neves[1], Christer M. Rolandsen[2], Bjørnar Ytrehus[2] and Sylvie L. Benestad[1]*
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Chronic Wasting Disease (CWD) is an invariably fatal neurodegenerative disease of cervids, belonging to the group of transmissible spongiform encephalopathies. The disease is endemic in some areas in North America, with natural infection 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.

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 that live in fragmented sub-populations in remote alpine regions of South Norway. In March 2016, a young adult female wild reindeer was diagnosed with CWD, representing the first detection of CWD in Europe and the first case of natural infection in reindeer worldwide.

Since 2016, through enhanced surveillance, 18 free-ranging reindeers have been diagnosed in Norway along with three cases in moose (*Alces alces*), and one case in red deer (*Cervus elaphus atlanticus*) from a total of 39,496 cervids tested.

Molecular analysis cannot differentiate the CWD-prions detected in reindeer from findings in North America, while prions found in Norwegian moose and red deer have an atypical character. This raises important questions concerning the disease itself (origin, pathogenesis and transmissibility) as well as its future management. CWD research conducted at the Norwegian Veterinary Institute is currently focusing on disease progression and pathogenesis, diagnostics, epidemiology and genetics.

We will present and update on the surveillance and disease status two years post discovery, along with future perspectives and a brief overview of the current research projects.

Presenter Bio: Dr. Knut Madslien is a veterinarian, senior researcher and head of the Health Surveillance Programme for Cervids and Musk ox in Norway, and has been working with wildlife health issues for the last 12 years at the Norwegian Veterinary Institute. Madslien is also OIE National Focal Point on Wildlife in Norway, and the Chair of the WDA Nordic Section

MANAGING MORBIDITY AND MORTALITY THREATS OF SAN CLEMENTE ISLAND FOXES

Jesse M. Maestas*[1]*, *David A. Green*[1]*, Andrew S. Bridges*[1]*, Melissa A. Booker*[2]*, T. Winston Vickers*[1,3]*, Leslie W. Woods*[4]*, David K. Garcelon*[1]

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Like most island endemics, Island foxes (*Urocyon littoralis*) are pivotal to their environments, yet are highly vulnerable to novel predators and disease. Several island fox subspecies declined dramatically and were listed as federally endangered in 2004. Through conservation and threat reduction efforts by the U.S. Navy, the San Clemente Island subspecies was never federally listed. However, as an isolated, discrete island population, it remains susceptible to novel diseases, stochastic events, and anthropogenic threats. Our program objectives were to aid in the detection of potential threats through disease surveillance and population monitoring. To aid in threat detection, we radio collared 60–100 foxes to act as sentinels. Additionally, we opportunistically recovered sick and deceased foxes reported by personnel working on the island. Recovered fox carcasses were shipped to pathologists for necropsy to determine the causes of death and to identify any emergent threats. From 2006–2018, we amassed a total of 518 fox carcasses. All carcasses were given field assessments of cause(s) of death, and 126 were shipped for full necropsy by veterinary pathologists. The leading causes of direct mortality for all carcasses were: vehicular collisions (76.2%), accidental anthropogenic entrapment (5.2%), and accidental exposure to rodenticide (2.3%). Necropsy results also indicated an increasing incidence of interstitial pneumoconiosis (interstitial histiocytic refractile crystalline pneumonia). Pneumoconiosis was detected in 33% of all the submitted carcasses, with incidence of 0% in 2006–2008, increasing to 57–100% in carcasses submitted from 2013–2017. Threat reduction efforts have led to lower accidental entrapment and poisoning in recent years, and although vehicular collisions remains the primary cause of death, it affects less than 10% of the population annually. Pnuemoconiosis has rarely caused direct mortality in foxes, however its prevalence has been increasing and combined with other natural factors may be debilitating to fox health warranting further investigation.

Presenter Bio: Jesse completed his master’s degree in Wildlife Biology at Northern Arizona University. His thesis focused on determining potential rabies transmission dynamics among urban striped skunks. Jesse has been working for the institute for Institute for Wildlife Studies for the past three years, studying island fox population dynamics, disease monitoring, and veterinary care.

SMALL MAMMAL AND ECTOPARASITE POPULATION DYNAMICS AND PLAGUE SURVEILLANCE IN LIGHT OF PLAGUE MANAGEMENT IN THE MIXED GRASS PRAIRIES OF LOWER BRULE, SD

Lauren P. Maestas*, and Hugh Britten*
The University of South Dakota, Vermillion, SD, USA

Sylvatic plague is a prominent primarily flea-borne enzootic disease in North American prairie ecosystems that affects a wide array of species. Understanding the role of small mammals and their ectoparasites in the maintenance of sylvatic plague is pertinent in understanding the ecology of the pathogen and its mode of persistence in nature. Deltamethrin, a granular insecticide, is commonly applied to prairie dog burrows for plague management. The goals of this study were to examine the effects of plague management using deltamethrin on communities of small mammals, their ectoparasite faunas, and on *Yersinia pestis* prevalence. We trapped small mammals from 2014-2016 on the Lower Brule Sioux Reservation, in South Dakota. We collected ectoparasites and population data, and analyzed them for the effects of deltamethrin treatment on 1) small mammal populations, 2) ectoparasite loads per collected animal, and 3) plague prevalence using nested PCR and lateral flow tests. We collected the greatest numbers of small mammals from deltamethrin treated sites. Consequently, we also collected the greatest number of fleas from treated sites. We found significant negative trends in mean flea load per animal between pre-and-post treatment collections, but no significant effects on the mean number of ticks per animal. We found no significant effects of deltamethrin treatment on animal captures pre-and-post treatment within years, but did find significant differences in animal captures by region, and by treatment. We found no serological evidence of the presence of *Y. pestis*, and 1.2% prevalence of *Y. pestis* from fleas based on nested PCR results. Our data suggest that deltamethrin is working to significantly reduce flea load per animal captured, our findings also indicate that small mammals alone are not a likely reservoir for plague.

ESTABLISHING A DIAGNOSTIC TECHNIQUE FOR COELOMOCENTESIS IN THE LONG-SPINED SEA URCHIN (*DIADEMA ANTILLARUM*)

Molly Martony[1], *Deborah Pouder*[2], *Roy Yanong*[2], *Yasunari Kiryu*[3], *Jan Landsberg*[3], *William Sharp*[3], *Ramiro Isaza*[1], *Thomas Waltzek*[4], *Nicole Stacy*[1], *Robson Giglio*[5], *Ruth Francis-Floyd*[1]

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[2]University of Florida, Institute of Food and Agriculture Sciences, Tropical Aquaculture Laboratory, Ruskin, FL, USA
[3]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St Petersburg, FL, USA
[4]University of Florida, Department of Infectious Disease and Pathology, College of Veterinary Medicine, Gainesville, FL, USA
[5]University of Florida, Small Animal Clinical Sciences, Diagnostic Imaging, College of Veterinary Medicine, Gainesville, FL, USA

Coelomic aspiration and bacterial culture have been utilized in echinoderms in both research and clinical settings. Such diagnostic sampling has advanced the knowledge of sea urchin health and has been employed in mass mortality investigations and conservation efforts. At present, detailed procedural descriptions for coelomic fluid sampling in sea urchins are lacking and samples are prone to microorganism contamination. The objectives of this study were to 1) standardize a diagnostic technique for coelomic fluid aspiration in the long-spined sea urchin, *Diadema antillarum*, that maximizes the diagnostic quality of the sample, 2) identify coelomic fluid bacteria isolates, and 3) utilize diagnostic imaging (magnetic resonance imaging, computed tomography, ultrasound) to optimize the coelomocentesis technique. Coelomocentesis, coelomic fluid culture, and bacterial identification were performed on 70 *Diadema antillarum* collected in two groups (March and September 2015) from the Florida Keys using standardized methodology. Positive coelomic bacterial cultures were compared to animal weight, holding time prior to sampling, environmental water temperature, and gross fluid appearance. Bacterial identification was performed using the Biolog GEN III MicroLog system and 16s rDNA sequencing. Positive bacterial cultures were identified in 5% and 44% of animals in the two sampling groups, March and September respectively. *Vibrio* spp. was the predominant genus identified. Positive coelomic fluid bacterial cultures were associated with the animal group that had smaller-sized animals, increased holding times, and elevated environmental water temperatures. Deviation from the typical clear-pink gross coelomic fluid appearance did not reliably predict bacterial contamination and should not be relied upon to rule out contamination. A standardized technique for coelomocentesis was defined that minimizes microorganism contamination from the gastrointestinal tract and the animal's surface. Implementation of this established coelomocentesis methodology may facilitate improved health evaluations of sea urchins and may be useful in research, conservation efforts, and disease investigations.

<u>Presenter Bio:</u> Molly Martony is the current University of Florida Aquatic Animal Health Veterinary Resident. Prior to starting at the university, she completed the SeaWorld California and National Marine Mammal Program aquatic veterinary internship program and was a staff veterinarian at Gulf World Marine Park and Dolphinaris Arizona.

USING SIZE EXCLUSION CHROMATOGRAPHY AS METHOD FOR AVIAN INFLUENZA VIRUS DETECTION IN WETLANDS

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Anseriformes and *Charadriiformes* are the main reservoir for avian influenza virus (AIV) and the predominant bird species found in wetland regions. When reservoir hosts shed virus in their feces, the virus remains active in water and may infect surrounding birds through fecal-oral transmission. The current methods of detection for AIV in water include testing small volumes of surface water and various filtration techniques. As viral particles in natural wetlands vary in density and abundance, a more sensitive and efficient method of detection is needed to test for the presence of AIV within wetland environments. Comprehensive research of AIV in birds exists, but an understanding on the ecology of the virus within these bird's primary environment is poorly understood. In order to understand the viral ecology of AIV in a diagnostically more sensitive fashion, size exclusion chromatography and multiplex PCR were utilized. Specifically, size exclusion chromatography was used to concentrate 100 liters of wetland water into a 50 milliliter retentate. Next, RNA was extracted from the retentate with the QIAcube and RT-qPCR was run to determine if the concentrated samples produced a higher viral yield than the unfiltered surface 'control' water samples. By concentrating 100 liters of water to test for AIV, the sensitivity and ability to detect the virus is increased and provides greater potential to understand the distribution of AIV in the wetland environment.

Presenter Bio: Madeline McCuen is a first year graduate student in the Avian Sciences Graduate Group at University of California Davis. Her primary research focuses on avian influenza virus in water. Madeline conducts her research with the support of Dr. Maurice Pitesky in the UC Davis School of Veterinary Medicine Cooperative Extension.

NEWT RESPONSES TO THE NEXT AMPHIBIAN THREAT: TRANSCRIPTOME ANALYSES OF EASTERN NEWT (*NOTOPHTHALMUS VIRIDESCENS*) SUSCEPTIBILITY TO *BATRACHOCHYTRIUM SALAMANDRIVORANS* (*BSAL*)

***Cait McDonald*[1]**, *Ana Longo*[2], *Karen Lips*[2], *Kelly Zamudio*[1]
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The pathogenic chytrid fungus, *Batrachochytrium salamandrivorans* (*Bsal*), is the most recent emerging threat to salamanders. *Bsal* originated in Asia and has swept through western Europe, but it is not yet present in North America, a global hotspot of salamander biodiversity. While *Bsal* is absent, its sister taxon, *Batrachochytrium dendrobatidis (Bd)*, is widespread in North American salamanders, where prevalence may reach more than 40%. Given this prevalence, *Bsal*-*Bd* co-infection will likely influence future disease emergence; at the individual animal level, we hypothesize that coinfection will amplify disease severity. Our current knowledge of host disease response to *Bsal* is restricted to assessments of clinical signs, histologic lesions, and mortality. Here, we expand this understanding to the level of host gene expression using RNA-sequencing. We compare host transcriptome-wide responses in a highly susceptible species, the Eastern newt (*Notophthalmus viridescens*), to *Bsal*, *Bd*, and *Bsal*-*Bd* co-infection. We correlate this expression to macroscopic signatures of disease and compare differential host response to *Bsal* vs. *Bd* to identify susceptibility and resistance markers in this emerging disease, finding significant variation in host immune response to each pathogen treatment. This study is pertinent not only to our understanding of the *Bsal*-salamander system, but it also has management implications in an era wherein globalization has been identified as a means by which virulent pathogen lineages may gain access to previously naïve host populations. Moreover, our results highlight the importance of informing disease mitigation and conservation programs with functional genomics data.

Presenter Bio: Cait McDonald is a DVM-PhD candidate who studies host-pathogen interactions at multiple timescales, from the course of infection to evolutionary time. She is particularly interested in pathogen-mediated selection, host adaptation, and leveraging this adaptation as a part of conservation genomics-guided disease management strategies.

IMPLICATING *CULICOIDES* SPP. VECTORS IN THE TRANSMISSION OF EPIZOOTIC HEMORRHAGIC DISEASE VIRUS IN FLORIDA

***Bethany L. McGregor*[1]*, Kristin Sloyer*[1]*, Katherine A. Sayler*[2]*, Olivia Goodfriend*[2]*, Carolina Acevedo*[1] *Samantha Wisely*[2]*, Nathan Burkett-Cadena*[1]

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Epizootic hemorrhagic disease virus (EHDV) is an arthropod-borne virus affecting ungulates worldwide, including white-tailed deer (*Odocoileus virginianus)* in the southeastern United States. Biting midges (Diptera: Ceratopogonidae: *Culicoides*), also known as no-see-ums, are the only arthropod vectors known to transmit this pathogen. Of the more than 150 *Culicoides* species in North America, the only confirmed vector of EHDV in the United States is *Culicoides sonorensis*. Although common in the western United States, this species occurs only sporadically in the southeastern US and is considered rare in Florida where EHDV persists annually. The present study aimed to determine which species of *Culicoides* transmit EHDV in Florida through viral RNA detection in wild collected midges. During an active EHDV outbreak in Florida in 2017, *Culicoides* spp. were collected using CDC miniature light traps at several deer farms throughout North Florida. Species were separated into pools of 50 individuals or less and tested for the presence of EHDV RNA by qRT-PCR. Pools that tested positive for virus were further assayed by qRT-PCR with serotype-specific primers for serotype identification. A total of 745 pools from 19 *Culicoides* species were analyzed from September-October 2017 for this study. This resulted in 20 positive pools identified from two species. Serotypes identified in these pools included EHDV-2 and EHDV-6. These data, combined with animal mortality data from deer farms where EHDV-positive midges were collected, blood meal data indicating host use by implicated midge species, and data on midge species aspirated directly from white-tailed deer, support the incrimination of two *Culicoides* species as vectors of EHDV in the state of Florida. This information is critical for developing management plans for vectors to reduce EHDV transmission risk to susceptible game and ranch animals.

<u>Presenter Bio:</u> Bethany McGregor is a PhD candidate at the Florida Medical Entomology Laboratory in Vero Beach, FL. Her dissertation research focuses on the ecology of *Culicoides* biting midges and their role in the transmission of orbiviruses on deer farms in Florida.

GLOBAL PATTERNS OF EMERGING INFECTIOUS DISEASES AFFECTING WILDLIFE

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Emerging infectious diseases (EIDs) are increasingly observed to impact human health, agriculture, and wildlife. Recent large-scale studies have demonstrated that for human EIDs, leading causes include pathogens evolving drug resistance and increased zoonotic disease spillover; for agriculture, monoculture cropping practices and globalization are leading causes. For wildlife, we lack an empirical understanding of the drivers that lead to EIDs in wildlife at a large scale. For this study, we used a literature survey to create a database of more than 700 EID records in wild vertebrates from around the globe over the last 150 years. EID events included records from all five vertebrate classes from 54 countries and infectious diseases included viruses, fungi, bacteria, helminths, protozoans, and ectoparasites. To evaluate factors associated with EID events, we summed events per country and developed an information theoretic approach using general linear mixed models. Candidate models to predict wildlife EID events included each country's gross domestic product as an *apriori* variable to control for bias in wildlife disease surveillance per country. Candidate models then included one or more of the following classes of variables measured per country: pathogen pollution, habitat change, total protected land area, biodiversity loss, and biogeographic climate metrics. Model averaged results demonstrated that invasive species were the strongest predictor of EID events across all vertebrates. When we investigated the dataset by vertebrate group, different subsets of factors emerged as predictors, particularly for mammals and amphibians. Overall, this study suggests that pathogen pollution (pathogen spillover resulting from human-mediated movement of animals outside their native range) is the largest driving factor for EID events affecting wildlife. These results underscore the importance of limiting invasive species and wildlife trade as a way to reduce the impact of infectious disease on animal diversity.

Presenter Bio: Dr. Valerie McKenzie is an Associate Professor in Ecology and Evolutionary Biology at the University of Colorado Boulder. Research in the McKenzie lab centers around wildlife disease and various projects integrate across the fields of microbial ecology, parasitology, community ecology, molecular ecology, and wildlife conservation.

WEB REPORTING AND CITIZEN SCIENCE IN DISEASE DETECTIONS

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Michigan's first cases of bovine tuberculosis, chronic wasting disease, and highly pathogenic avian influenza (H5N2) in free-ranging wildlife were all detected in samples submitted to the Michigan Department of Natural Resources Wildlife Disease Lab (WDL) through citizen science. Citizen science, or public participation in passive surveillance, provides increased observation of wildlife health beyond what wildlife managers can achieve. For the past 15 years, the WDL has used an online observation form to obtain reports of sick and dead wildlife from the public. Originally created as a web-based form to monitor for corvid mortality from West Nile virus, the form was recently replaced with an application and is used to collect any wildlife morbidity and mortality events statewide. The application allows users to select the observation point on a map, provide details of the observation, and upload up to three photographs, audio clips or video clips. Since the observation form's inception, the WDL has received over 35,000 reports from the public involving over 50,000 individual animals. Data generated from the observation form reports are used to create disease risk maps for West Nile virus, estimate mortality during widespread die-offs (e.g. epizootic hemorrhagic disease) and alert the WDL to emerging diseases and localized outbreaks (e.g. type E and type C botulism, verminous hemorrhagic ulcerative enteritis, canine distemper, and mange) in a timely manner.

Presenter Bio: Julie Melotti received her BS and MS in Wildlife Management with a specialization in Conservation Medicine and Disease Ecology at Michigan State University. Julie works at the Michigan Department of Natural Resources, Wildlife Disease Laboratory with most of her work focusing on disease surveillance and necropsies.

MOLECULAR INVESTIGATION OF VECTOR-BORNE PATHOGENS IN FOXES AND ASSOCIATED FLEAS FROM REMOTE AREAS OF ARGENTINEAN PATAGONIA

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With humans and their domestic animals inhabiting almost every corner of the planet, investigating infection with pathogens in carnivores in the absence of dogs is a challenge. Between 2010 and 2015, we captured and sampled 47 chilla (*Lycalopex griseus*) and 2 culpeo (*L. culpaeus*) foxes in two remote and inhospitable areas in Southern Patagonia (Argentina) where dogs are almost absent, namely Bosques Petrificados (n=26) and Monte León (n=23) National Parks. A set of primers were used to analyze fox blood samples preserved in FTA cards (n=49) and flea pools (n=78, from 46 foxes) for the presence of DNA belonging to *Rickettsia*, Anaplasmataceae (*Ehrlichia*/*Anaplasma*), hemotropic *Mycoplasma* (aka hemoplasmas), and *Hepatozoon*. DNA of hemoplasma was detected in four chilla foxes (8.2%, two positives from each area). Interestingly, all the chilla foxes from Bosques Petrificados were positive for *Hepatozoon* sp., whereas all resulted negative in Monte León. *Amblyomma tigrinumn*, the only tick species retrieved from these foxes, might be a competent vector for this parasite. All samples resulted negative for Anaplasmataceae. As for the flea pools, one pool was positive for a *Rickettsia* sp., and the PCR for Anaplasmataceae revealed the presence of endosimbionts in 47 pools (60%). Molecular characterization of the positive cases is pending.

Presenter Bio: Javier Millán holds a PhD in Veterinary Medicine and is a Diplomate of the European College of Zoological Medicine (Wildlife Population Health). He is Full Professor at Universidad Andrés Bello, Santiago, Chile. He is also the director of the doctorate program in Conservation Medicine at the same University.

PATHOLOGY IN NOTOPHTHALMUS VIRIDESCENS COINFECTED WITH *BATRACHOCHYTRIUM DENDROBATIDIS* AND *B. SALAMANDRIVORANS*

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Eastern newts (*Notophthalmus viridescens*) are distributed throughout the eastern United States and are a species susceptible to the recently discovered pathogen *Batrachochytrium salamandrivorans* (*Bsal*) that has caused devastating mortalities in wild newt populations in Europe. We know that wild Eastern Newts often test positive for *B dendrobatidis* (*Bd*), but are uncertain how this might impact their response to *Bsal*, or affect our ability to identify the etiology of a morbidity or mortality event. Adult Eastern newts naturally infected with *Bd* were collected from six populations across four U.S. states and experimentally exposed to *Bsal* at five concentrations (0, 5×10^3, 10^4, 10^5, 10^6) for 24 hours. Their condition was monitored for 15 weeks. At termination of the experiment, full necropsies were performed and qPCR assays were done to quantitate *Bd* and *Bsal*. Discrete ulcerations and skin sloughing were observed; histological evaluation was performed to characterize lesions. Of 117 animals challenged with *Bsal*, 28 were naturally infected with *Bd* at the start of the experiment, but only 20 were co-infected with *Bsal* at the end of the study. Mortality and *Bsal* infection prevalence followed a dose-dependent response; however, it was not possible to differentiate between *Bd* and *Bsal* pathology by routine histological examination. Understanding the impact of co-infection and applying methods for differentiating these pathogens in tissues will help elucidate the role of each pathogen in morbidity and mortality.

Presenter Bio: I have over 20 years of experience in pathology and have been studying amphibian pathology for nearly that entire time, with an emphasis on ranavirus and chytrid fungus for the past 13 years.

A REVIEW OF THE IMPACT THAT CAN OCCUR WITH THE LOSS OF A VIBRANT URBANIZED CANID POPULATION TO SARCOPTIC MANGE: FROM HUMAN HEALTH ISSUES TO MANAGING CASES IN WILDLIFE REHABILITATION

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Sarcoptic mange (*Sarcoptes scabiei*) has probably always been present in the fox (*Vulpes vulpes*) populations on Cape Cod, however the region appears to have been experiencing an epizootic event over the past 4 years. The impact is seen on many levels, with unexpected implications. First, the influx of calls regarding sightings of impacted foxes to governmental and non-governmental agencies from the public can add pressure to respond to what has been considered an individual welfare issue. The foxes impacted appear to be succumbing to the infection, essentially with 100% mortality. This is of concern as regional population-level impacts can be significant as reported during the UK and European outbreaks. The rising incidence of sarcoptes in pet dogs was also noticed by veterinary clinics in the impacted regions, with human cases also being reported. The loss of this mesocarnivore as a major predator of rodents may also be a contributing factor to the rise of rats and mice populations on Cape Cod. Also noted is an increased incidence of secondary rodenticide toxicity in raptorial species. This was already a concern and not uncommon, now it is potentially exacerbated by the rising numbers of rodents being eliminated with the use of rodenticides. As all this is occurring, wildlife rehabilitation centers were and are admitting mange impacted foxes. Till recently, treatment had been by using Ivermectin over several weeks, all the while maintaining these animals in isolation. A new treatment was explored using Bravecto® (Fluralaner) with success. This one dose treatment resulted in the rapid elimination of adult sarcoptes and subsequent recovery of the fox. It opens the door to an effective in-house treatment, which may also lead to field options to manage epizootic mange in wild canids.

Presenter Bio: Lynn Miller, PhD., is a certified wildlife rehabilitator (CWR) and former president of the International Wildlife Rehabilitators' Council (IWRC), with over 35 year's wildlife rehabilitation experience. Her research explored biological markers such as acute phase proteins that could be used in the triage of oiled seabirds.

SEROLOGICAL DIAGNOSIS OF *ELAEOPHORA SCHNEIDERI* INFECTION IN MOOSE (*ALCES ALCES*)

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Elaeophora schneideri is a filarial nematode, which is the causative agent of the disease elaeophorosis in ruminants. This parasite has been reported in multiple domestic and wild ruminant species in North America, including moose (*Alces alces*). Elaeophorosis is a known cause of morbidity and mortality in moose from various western states and provinces. Between 2006 and 2015, the Minnesota moose population decreased by 60%, and it is possible that the emergence of *Elaeophora* is a factor in this recent decline. Currently available methods for diagnosing *Elaeophora* infection status require examination of adult nematodes or arterial lesions in deceased moose. The lack of a serological diagnostic test has made the prevalence, clinical significance, and eco-epidemiology of this parasite difficult to assess. Previous research has indicated several proteins extracted from adult *Elaeophora* nematodes are reactive to seropositive moose serum and nonreactive to seronegative serum. Our research is a continuation of the investigation of antigenic potential of *Elaeophora* proteins to develop an Enzyme-Linked Immunosorbent Assay to detect anti-*Elaeophora* antibodies in sera collected from moose and other cervids. Whole genome sequencing, coupled with liquid chromatography-mass spectrometry and a B-cell epitope predictor, proved effective in isolating five unique antigen candidates from *Elaeophora*. The ELISA will be developed by testing antigenic peptides using known positive and negative control samples until consistent results are produced. This will be followed by testing of banked cervid serum. The resultant data will be very useful in elucidating the population and host dynamics and geographical distribution of the parasite as well as the population impacts the parasite may have on wild and domestic ungulates.

AN EPIZOOTIC OF MYCOTIC SHELL DISEASE ASSOCIATED WITH *NANNIZZIOPSIACEAE* FUNGAL INFECTION IN JUVENILE WOOD TURTLES (*GLYPTEMYS INSCULPTA*) IN A CONSERVATION HEAD-STARTING PROGRAM

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The Toronto Zoo participates in the conservation of endangered wood turtles (*Glyptemys insculpta*). Eggs from non-viable wild nests are collected, incubated, and juveniles raised in a protected zoo environment (head-started) for one to two years before release back to the wild. In May 2017, 40/85 turtles hatched in 2016 developed multifocal, white, flaky lesions of the shell. In order to investigate the hypothesis that lesions were due to fungal infection, full-thickness shell biopsies were collected from four turtles. Histopathology revealed marked parakeratotic hyperkeratosis with numerous fungal hyphae limited to the outer keratinized layer of the scutes, with no dermal inflammation. Although fungal cultures were negative, PCRs using both generic fungal primers and those specific for *Nannizziopsiaceae* were positive. Sequencing of a 634-bp fragment was 80-90% homologous with *Nannizziopsiaceae* sequences obtained from other aquatic turtle species, suggesting that the wood turtle pathogen may be a novel species. Shell lesion scores and body weights for the entire wood turtle cohort were tracked during the course of the outbreak, and animals remained otherwise normal during this time period. Suboptimal water quality and high stocking densities were possible precipitating factors. All lesions stopped progressing by January 2018, and some resolved, following topical chlorhexidine/clotrimazole, nebulized terbinafine, and husbandry improvements. Shell scrapes from similar lesions were collected from three wild wood turtles originating from the same habitat as the head-started turtles, and fungal isolates were identical to those obtained from the captive animals. The long-term implications for this conservation program remains unclear at this stage.

<u>Presenter Bio:</u> Ellie Milnes graduated from the University of Cambridge, UK in 2010. After working for several years as a large animal veterinarian in New Zealand, Ellie is currently a resident in zoological medicine and pathology at the Toronto Zoo, Canada.

MIGRATORY BIRDS, TICK-BORNE DISEASE, AND DEER IN A CHANGING CLIMATE: INVESTIGATING THE EMERGENCE OF BABESIA ODOCOILEI IN ONTARIO, CANADA

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Global climate change supports the range expansion of disease vectors, potentially exposing wildlife to novel tick-borne pathogens. *Babesia odocoilei*, a protozoan hemoparasite of white-tailed deer (*Odocoileus virginianus*) transmitted by *Ixodes scapularis* ticks, is an increasingly recognized cause of disease in cervids in North America. Following an outbreak in reindeer (*Rangifer tarandus tarandus*) and wapiti (*Cervus canadensis*) at the Toronto Zoo in Ontario, Canada, we utilized a prospective post-mortem survey to investigate the prevalence of *B. odocoilei* in wild, farmed, and zoo cervids in Ontario (*n*=270; 2016-2018) by PCR and DNA sequencing of spleen samples. We detected *B. odocoilei* in two farmed red deer, the first record for this species, as well as in a zoo wapiti and three wild white-tailed deer. In addition, a study was designed to investigate the hypothesis that birds can disperse *Babesia*-infected ticks along migratory flyways. Birds (*n* = 1,102) were captured during spring migration: prevalence of *I. scapularis* infestation was 3.2% in 2016 and 6.7% in 2017. A total of 1.2% of bird-borne ticks were positive for *B. odocoilei*. Questing *I. scapularis* ticks were sampled by blanket dragging (*n* = 200), and 1.5% were positive for *B. odocoilei.* Results show that *B. odocoilei* is capable of infecting a wider range of cervid hosts than previously suspected, confirmed the presence of *B. odocoilei*-positive questing ticks in Canada, and identified *Babesia*-infected ticks on northward-migrating birds. Thus, tick dispersal by migratory birds could contribute to the spread of *B. odocoilei* throughout Canada, potentially threatening vulnerable native caribou populations.

Presenter Bio: Ellie Milnes graduated from the University of Cambridge, UK in 2010. After working for several years as a large animal veterinarian in New Zealand, Ellie is currently a resident in zoological medicine and pathology at the Toronto Zoo, Canada.

EXAMINING THE RELATIONSHIP BETWEEN THE LIFE HISTORY OF CHIROPTERA SPECIES IN CENTRAL-EAST AFRICA AND CORONAVIRUS SHEDDING

***Diego Montecino-Latorre*[1]**, *Kirsten Gilardi*[1], *Tracey Goldstein*[1], *David Wolking*[1], *Elizabeth Van Wormer*[2], *Rudovick Kazwala*[3], *Benard Ssebide*[4], *Julius Nziza*[4], *Zikankuba Sijali*[5], *Michael Cranfield*[4] *and Jonna A. K. Mazet*[1]
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Bats serve important roles in ecosystems and are also reservoirs for several zoonotic viruses. Currently, it is thought that bats may be the natural and ancestral reservoirs of some coronaviruses (CoV), and data suggest that the CoVs related to Severe Acute and Middle East Respiratory Syndromes (SARS and MERS) outbreaks may be associated with certain bat families. However the question of the ecology of bats as related to their reservoir role and timing of viral shedding has not been examined extensively. We tested the hypothesis that the detection of CoV RNA from bats in East Africa is associated with seasonal life history events that occur in each species, such as mating and birth pulses. We sampled and tested for CoV RNA from 900 bats in Tanzania, Uganda, and Rwanda representing more than dozen species. We assigned one of four life reproductive periods (mating, post mating, birth and rearing, and post rearing) to each individual based on our records of pregnancy, previous studies, and latitude of capture. We also considered other behavioral traits of the species, such as roosting size, preferred roost type and contact within roost. Using Bayesian inference, we obtained the posterior probability distribution for the odds of CoV RNA detection in different reproductive periods (with 'birth and rearing' as reference), while controlling for other biological characteristics. Our results suggest that CoV RNA detection varies across bat species and the life history of these animals is associated with CoV shedding in feces. Our intent is for our findings to be used to support our understanding of viral shedding in bats across species, in order to reduce CoV spillover risk, while protecting bats and their ecological value.

<u>Presenter Bio:</u> Diego Montecino-Latorre holds a graduate degree in Bachelor of Veterinary Medicine and a master's degree in Preventive Veterinary Medicine, and is a PhD candidate in Epidemiology at the University of California, Davis. His research focuses on management, consequences and dynamics of wildlife diseases, and the impacts of free-ranging dogs in Chile.

PESTE DES PETITS RUMINANTS: USING A ONE HEALTH APPROACH TO PROTECT PASTORALIST LIVELIHOODS

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Peste des petits ruminants (PPR) is a highly infectious viral disease of small ruminants, with a primary emphasis on domestic sheep and goats. Worldwide, there are 76 countries, which have current infections or are at-risk for PPR, affecting an estimated 1.7 billion sheep and goats, resulting in annual losses between $1.45-2.10 billion (USD) to approximately 330 million of the world's poorest. This Feed the Future Innovation Lab for Livestock Systems (UF/IFAS) project, in conjunction with partners Tufts University, Mercy Corps, and Makerere University, serves to assess innovative approaches to control PPR through the creation of self-sustaining vaccination delivery models and to scale vaccination in select regions of Kenya and Uganda. A "One Health" approach utilizing mixed methods of qualitative data collection and analysis, community based participatory research, participatory epidemiology (PE), and disease modeling is being used to leverage qualitative data for optimum vaccine uptake in order to reach the necessary vaccination level to attain herd immunity. Peste des petits ruminants is a severe drain on pastoralist livelihoods in the region, which dramatically impacts human health and nutritional outcomes within the human population.

Presenter Bio: Emi Moore is a doctoral student at the University of Florida getting her PhD in Public Health (One Health) with a certificate in African Studies. Her research focuses on safeguarding animal source food consumption to better human health and nutrition by protecting livelihoods of pastoralists in Uganda through livestock vaccination.

AVIAN MALARIA PREVALENCE AND TRANSMISSION IN CATTLE EGRET (*BUBULCUS IBIS*)

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Avian Haemosporidia are widely distributed blood parasites that are transmitted by arthropod vectors and their avian hosts. Cattle egret (*Bubulcus ibis*) are a rapidly expanding avian species, yet little is known about the potential for this host to transport pathogens. The objective of this project is to determine cattle egrets' role in the transmission of Avian Haemosporidia parasites: *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*. Live cattle egret are trapped and sampled for blood. Euthanized cattle egret are collected from USDA Bird Air Strike Hazard (BASH) control efforts and sampled for spleen. PCR and gel electrophoresis are used to determine prevalence of *Plasmodium*, *Haemoproteus*, and *Leucocytozoon* and positive samples are sequenced for genetic analyses. As of March 2, 2018, 495 cattle egret have been sampled and screened from 16 locations around the southeast United States. Of the 495 cattle egret, 24.6% screened positive for *Haemoproteus* or *Plasmodium* and 37.2% screened positive for *Leucocytozoon*. Of the 495 samples, 133 have been sequenced for Avian Haemosporidia parasites: 29.3% are positive for *Plasmodium*, 0% are positive for *Haemoproteus*, 17.3% are positive for *Leucocytozoon*, and 4.5% are co-infected with *Plasmodium and Leucocytozoon*. Cattle egret sequencing for Haemosporidia parasites is ongoing. Phylogeny of sequenced Avian Haemosporidia parasites shows *Leucocytozoon* grouped as one large clade with a small divergent clade whereas *Plasmodium* is grouped into five clades. A weighted matrix map shows *Leucocytozoon* to be geographically widespread and equally connected between sampling sites. *Plasmodium* is also widespread, however the weighted matrix map indicates stronger connection between certain sampling sites, suggesting longer range movements may play a large role in the movement of Avian Haemosporidia across the landscape. Avian Haemosporidia may be a good model for investigating arbovirus emergence. This project will provide a better understanding of disease transmission in cattle egret.

Presenter Bio: Shannon is a second year Master's student at the University of Florida. After graduating with a Bachelor's degree in Wildlife Ecology and Conservation, Shannon worked for a year as a research technician before beginning her Master's. She is especially interested in avian species and their role in the ecosystem.

THIAMINE DEFICIENCY IN THE BALTIC SEA ENVIRONMENT – AN ECOLOGICAL CATASTROPHE

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The Baltic Sea faces an environmental disturbance of considerable magnitude. During the last 20 years, there have been dramatic population declines in common ducks, such as common eider (*Somateria mollissima*), long-tailed duck (*Clangula hyemalis*), and velvet scoter (*Melanitta fusca),* gulls, such as herring gull (*Larus argentatus*), common gull (*L. canus*), and black-headed gull (*Chroicocephalus ridibundus*), and waders, such as turnstone (*Arenaria interpres)* and redshank (*Tringa totanus*). Many fish populations have also declined during this time. Thiamine (vitamin B_1) deficiency has been observed in spawning Atlantic salmon (*Salmo salar*) in the Baltic Sea since 1974, when it was noted that the offspring of certain females showed neurological symptoms and died at the swim-up stage. This mortality has occurred episodically in both time and space and the proportion of females with dying offspring has varied between 0 and 100 %. More recently, thiamine deficiency has been demonstrated also in European eel (*Anguilla anguilla*) and blue mussel (*Mytilus* sp.). Thiamine is synthesized mainly by the plants, but also by certain fungi and bacteria, whereas all animals must obtain thiamine from their food. Thiamine deficiency causes many disorders, including reduced sensory functions, memory and learning disorders, altered behavior, anorexia, reduced growth, fatigue, ataxia, convulsions, paralysis, immunosuppression, and impaired reproduction. We have shown that thiamine deficiency in water birds causes excess mortality, reduced number of eggs, and mass mortality of pulli shortly after birth. Our results so far, point towards insufficient amounts of thiamine in the food of the animals. Because all thiamine is originally provided by the producers at the bottom of the food web, we suspect that this step could be impaired. The recent population declines of many bird and fish species in the Baltic Sea are so large that they may be regarded as an ecological catastrophe.

GUT MICROBIAL DIVERSITY DECREASES WITH URBANIZATION AND MEDIATES A ZOONOTIC PATHOGEN IN A WADING BIRD

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The gut microbiome influences many aspects of host health, including metabolism and susceptibility to pathogen colonization. These relationships are thought to be largely mediated by microbiome composition and diversity, both of which are influenced by host diet, age, and environment. Studies of humans and livestock have demonstrated the importance of these relationships, but the drivers and health consequences of microbiome differences in wildlife have received less attention. American white ibises (*Eudocimus albus*) experience substantial shifts in diet when residing in increasingly urbanized habitats in south Florida, particularly, increased consumption of human-provisioned food items, (e.g. bread and other processed foods rich in carbohydrates). We assessed the effects of habitat use, bread consumption, and age on microbiome composition and diversity, and tested whether ibises with less diverse microbial communities were more likely to be shedding *Salmonella enterica*. We sampled 82 free-living ibis from 16 sites along an urbanization gradient in south Florida, USA. We aged ibis using plumage and measured assimilation of bread using stable isotope analyses of red blood cells. We isolated *Salmonella* spp. from fresh fecal samples and characterized the gut microbiome from frozen feces using 16S rRNA Illumina sequencing. Ibises captured at more urbanized sites had a lower proportion of Firmicutes but higher proportions of Bacteroidetes, Proteobacteria, and TM7, and this shift was primarily associated with higher consumption of bread. The average Shannon diversity of genera detected in ibis gut microbiomes was significantly negatively associated with urbanization and bread consumption, positively associated with age, and lower diversity was associated with higher *Salmonella* prevalence. Our results suggest that shifts in both habitat use and diet for birds in urban areas significantly alter gut microbial community composition and diversity in ways that may influence health and pathogen susceptibility as species adapt to urban habitats.

<u>Presenter Bio:</u> Maureen H. Murray studied urban white ibis health as a Postdoctoral Research Associate at the University of Georgia and is now the Wildlife Disease Ecologist at the Lincoln Park Zoo. Her research focuses on how urbanization affects wildlife health to promote wildlife conservation and mitigate conflict with people.

SMALL MAMMAL DIVERSITY AND PREVALENCE OF *BORRELIA BURGFORDERI* ACROSS AN URBAN TO EXURBAN GRADIENT

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Local biodiversity can influence pathogen prevalence due to changes in the relative abundance of competent and dead-end hosts. A negative relationship between wildlife biodiversity and pathogen prevalence, known as the dilution effect, has been supported in some contexts but little is known about the effects of urbanization on these factors. We examined the relative abundance of small mammal hosts and prevalence of *Borrelia burgforderi*, the causative agent of Lyme disease, across an urban to exurban gradient in Chicago where rates of Lyme disease are increasing. In summer 2017 we trapped and sampled small mammals at 10 grassland patches surround by urban land use (4 sites), urban-suburban transition areas (3 sites), or exurban forest preserves (3 sites). We recorded small mammal species to estimate the relative abundance of hosts and collected any attached ticks and conducted tick drags at each site. We collected 54 ticks, 36 of which were *Ixodes scapularis*, the primary vector for *B. burgforderi*. All but one *I. scapularis* were nymphs and seven were positive for *B. burgforderi* (prevalence = 19%), which were present at three of 10 sites and in the urban, suburban, and exurban zones. Although we detected *I. scapularis* ticks more often on meadow voles (*Microtus pennsylvanicus*) relative to deer mice (*Peromyscus maniculatus*), deer mice had a higher prevalence of *Borrelia*-positive ticks (deer mice: 2/6 or 30% positive; meadow voles: 5/29 or 17%). Of over 400 trapped small mammals, the relative abundance of deer mice increased over the urban gradient (48%, 39%, and 13% of small mammals in urban, transition, and exurban sites respectively) while meadow voles were most abundant at exurban sites (42%, 37%, and 69%). Our results suggest that the risk of Lyme disease is still present in highly urban areas and especially where competent hosts are abundant.

Presenter Bio: Maureen H. Murray is the Wildlife Disease Ecologist at the Lincoln Park Zoo. Her research focuses on how urbanization affects wildlife health to promote wildlife conservation and mitigate conflict with people.

WHAT MHC CAN TELL US ABOUT PATHOGENS: IMMUNOGENETIC VARIATION IN THE WILD FELID GUIGNA ACROSS LANDSCAPES WITH DIFFERENTIAL ANTHROPOGENIC DISTURBANCE IN CHILE

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The guigna (*Leopardus guigna*) is a threatened small wild felid endemic to Chile and Argentina, and a good model species due to its close association with native rainforests. Threats to guignas include habitat loss and fragmentation, direct persecution as retaliation for poultry predation and recently discovered pathogens transmitted by domestic cats. Investigating functional diversity at the major histocompatibility complex (MHC), genes responsible for vertebrate immune response, is key to understanding the evolutionary and adaptive potential of populations in the face of emerging disease threats. Variation at MHC loci is partly maintained by balancing selection driven by pathogenic selective pressures. We characterized and compared genetic diversity at MHC class I and II in guignas from landscapes with differential anthropogenic disturbance and also assessed pathogen prevalence (by PCR) in guignas and domestic cats. We sampled guignas across their whole distribution range in Chile (32-46 º S). MHC class II had higher genetic diversity compared to MHC class I in guignas. For MHC class II, guigna populations from extreme southern Chile had significantly lower genetic diversity than the rest of the studied areas, associated with a historic genetic bottleneck that occurred during the Last Glacial Maximum when ice sheets completely covered this area. We found evidence of positive selection acting over MHC class I and class II genes in guignas. Our results show a direct significant correlation between MHC class II genetic diversity and proximity to houses, and also with fragmented landscapes (agricultural matrix with domestic animals). Higher pathogen prevalences in guignas were also significantly associated to these two environmental variables. Guigna populations inhabiting landscapes with higher human and (non-vaccinated) domestic cat and dog densities probably have higher pathogen exposure. Both pathogen-driven selective pressures and neutral genetic processes could influence MHC evolution and its diversity, finally influencing fitness, long-term survival and extinction risk.

<u>Presenter Bio:</u> Dr. Constanza Napolitano (DVM) is an associate researcher in the Institute of Ecology and Biodiversity at University of Chile. Her current research investigates cross-species pathogen transmission from domestic cats to threatened wild felid populations and genetic diversity of immune genes as adaptive potential in the face of current disease threats.

POWASSAN VIRUS IN TICKS AND WILDLIFE IN ONTARIO, CANADA, AND GROUNDHOGS AS POTENTIAL RESERVOIR HOSTS

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Wildlife are an integral component of many vector-borne pathogen transmission cycles, the dynamics of which are affected by anthropogenic factors such as climate change and landscape usage. Powassan virus (POWV) is thought to be maintained between wild mammals (e.g., groundhogs) and ticks (e.g., *Ixodes* spp.) and can cause fatal encephalitis in humans. Recently, case reports of human POWV infection in the northeastern US have increased concurrently with evidence of circulation in Ontario. However, many aspects of POWV eco-epidemiology, including transmission dynamics, remain unknown. Thus, a survey of Ontario wildlife was conducted to: 1) investigate the magnitude of tick infestations in peridomestic wild mammals; 2) test wildlife and ticks for POWV RNA; and 3) assess POWV seroprevalence. We also evaluated groundhogs as virus-amplifying hosts by experimental infection. Tissues and ticks from wildlife (live-trapped or donated carcasses) were tested by reverse transcriptase-PCR in 2015-16 and ticks from diagnostic cases in 2011-13; blood was collected when possible. Ticks (n=1,619; median: 2 ticks/animal; range: 1-36 ticks) of six species were removed from 283 individuals of 11 species, most commonly raccoons. One of 98 tick pools was POWV-positive and consisted of *I. cookei* from a Canada goose. Sequence analysis delineated deer tick virus (DTV) lineage with 94% homology to an *I. scapularis* tick in Wisconsin and human brain in New York. All tissues (n=724 animals) were negative for POWV RNA. Antibodies to POWV were detected by virus neutralization test in 0.8% (2/265) of samples, including a groundhog and striped skunk. Experimentally-inoculated groundhogs (2/8 with prototype POWV and 1/8 with DTV) had low, transient viremia titers ($\leq 10^{2.8}$ plaque forming units/ml serum) on 3-4 days post-inoculation and no clinical signs or significant pathology. Results reveal evidence of POWV in wildlife and ticks in Ontario and emphasize the need for additional data to better delineate virus-amplifying wildlife hosts.

Presenter Bio: Nicole Nemeth is a wildlife pathologist and researcher at the Southeastern Cooperative Wildlife Disease Study at the University of Georgia. Her research interests include vector-borne disease ecology, diseases of free-ranging birds, and diseases at the wildlife-livestock interface.

ENVIRONMENTAL SURVIVAL OF SARCOPTES SCABIEI FROM SKIN SAMPLES OF AMERICAN BLACK BEARS (*URSUS AMERICANUS*)

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For two decades, the incidence of sarcoptic mange in American black bears (*Ursus americanus*) in Pennsylvania, USA has increased. The causative agent, *Sarcoptes scabiei,* can be directly or indirectly transmitted, so data on persistence in the environment is important for guiding management decisions (i.e., transmission within dens, trap sites, areas where feeding occurs, or around bear carcasses). The objective of this study was to determine the survival of *S. scabiei* at different temperatures. When a bear was euthanized due to severe mange, full-section skin samples (meant to represent carcasses of bears with mange) and skin scrapes (meant to represent dens, traps, or other fomites) were collected and shipped on ice packs overnight to UGA. Samples were placed in petri dishes at 0, 4, 18, or 30°C, and the percentage of mites alive, by life stage, was recorded at 4, 12, and 24 hours, and each day thereafter until all mites were dead for at least two time points. Mites survived the shortest amount of time at 0°C (≤ 4 hours) and the longest at 4°C (up to 14 days at which point experiment was ended). No mites survived beyond 8 days at 18°C or 3 days at 30°C. For all temperatures, mites from skin sections survived longer than those from skin scrapes. At all temperatures except 30°C, adult mites survived longer than nymphs and larvae. These data indicate that at lower temperatures, *S. scabiei* can survive for multiple days to weeks, especially if on or near host skin. The environment should be considered in any management effort to mitigate the risk of *S. scabiei* transmission. Although survival in the environment might facilitate indirect transmission of mites between bears via the environment, the survival data suggests mites would not survive over the spring, summer, and fall to transmit between denning seasons.

Presenter Bio: Kevin is a diagnostician and graduate student at the Southeastern Cooperative Wildlife Disease Study at the University of Georgia. In addition to his roles in wildlife morbidity and mortality investigations, he is working on a PhD that studies the causes and potential solutions of mange in black bears.

THE USE OF SEROLOGY AS A TOOL TO INVESTIGATE SARCOPTIC MANGE IN AMERICAN BLACK BEARS (*URSUS AMERICANUS*)

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The number of American black bears (*Ursus americanus)* with sarcoptic mange has increased over the last two decades in Pennsylvania, USA. The cause for the increased number of cases is unknown but may be related to high densities of bears, climate change, the recent emergence of a novel mite variant, or an unknown risk factor making bears increasingly susceptible to overt disease. To understand the causes of mange in black bears, it is important first to determine if all bears that are exposed to the mites develop clinical disease, or does clinical disease only occur in a proportion of exposed bears. To investigate these scenarios, a commercially available enzyme-linked immunosorbent assay (ELISA) used to diagnose sarcoptic mange in dogs, was validated for black bears (maximum combined sensitivity and specificity of 91.1 and 91.2%, respectively; AUC=95.7%). Samples from sero-negative cubs from sero-negative sows without mange were used as negative controls and samples from bears with clinical confirmed sarcoptic mange were used as positive controls. After the test was validated for use in bears to detect antibodies to *S. scabiei*, serum was collected from clinically normal (i.e., no mange) hunter-harvested bears from two regions in Pennsylvania, USA in November of 2017. These regions were designated as “endemic mange” and “non-endemic mange” areas based on historical records of clinical mange at the county level. There was a statistically significant difference in the number of sero-positive bears in the high-mange (11/172; 6.4%) compared to the low-mange (0/189; 0) counties. In addition to supporting the validity of the test as a whole, this data suggests that bears are likely exposed to mites more frequently in mange-endemic areas. Additional studies would address the mechanisms of sero-conversion in bears as well as attempt to understand antibody persistence to more reliably identify naïve vs. exposed individuals and populations.

Presenter Bio: Kevin is a diagnostician and graduate student at the Southeastern Cooperative Wildlife Disease Study at the University of Georgia. In addition to his roles in wildlife morbidity and mortality investigations, he is working on a PhD that studies the causes and potential solutions of mange in black bears.

HAS VIRUS ISOLATION OUTGROWN ITS USEFULNESS?

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Virus isolation has for decades been regarded as the “gold standard” for diagnosing viral diseases but has been increasingly replaced by nucleic acid detection methods in both the human and animal clinical setting. Molecular methods are more sensitive and provide answers more quickly than virus isolation and technological improvements have made these methodologies even more appealing to clinicians. Virus isolation is a slow process relying on the replication and expansion of virus in cell culture; however virus isolation is arguably the best way in a research setting to identify new emerging viruses in spite of its many shortcomings. Marine mammals are charismatic animals garnering considerable media attention when they strand or become sick. Determining the cause(s) becomes a priority for government agencies responsible for their well-being, especially when endangered species are involved and diagnostic virology testing (both nucleic acid detection and virus isolation) is a component of those investigations. In the Arctic, marine mammals are harvested by indigenous peoples for their subsistence use and they are acutely interested in the health of the animals from a food safety perspective. Again, diagnostic virology has become an integral part of the health assessments carried out on these animals. Results of investigations from both stranded and Arctic marine mammals will be presented indicating that virus isolation coupled with high-throughput next-generation sequencing and subsequent development of specific polymerase chain reaction (PCR) methodologies has been a key component in the identification of new viruses of importance to marine mammals.

Presenter Bio: Mr. Nielsen has worked as a virologist for the Department of Fisheries and Oceans Canada for over forty years. He has isolated a number of new emerging marine mammal and fish viruses during that time as well as participating in the investigation of marine mammal die offs world-wide.

FIRST DETECTION OF ANTIMICROBIAL RESISTANCE GENES BY QPCR IN FREE-LIVING GALAPAGOS GIANT TORTOISES

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Antimicrobial resistance presents an ever-increasing global public health threat, with mechanisms of major epidemiological impact encoded by plasmid-mediated antimicrobial resistance genes (ARGs). Free-living wildlife play a fundamental role as sentinels, reservoirs, and potential spreaders of ARGs whilst human-induced ecological degradation has progressed rapidly in Galapagos due to recent land transformations. Our main objective was to identify and quantify for the first time in Galapagos, the presence of ARGs in free-living tortoises (*Chelonoidis porteri*) across a gradient of human-modified landscapes on Santa Cruz Island. Feces from the cloaca were collected from 30 tortoises in three different locations where tortoises freely roam as part of their seasonal migration (protected, rural, and urban zones). The analysis of ARGs was performed by quantitative PCR (qPCR) directly from fecal samples. Samples were analyzed by a panel of up to 18 different ARGs. 11 of 18 tested ARGs were present in at least one sample. Clustering the ARGs by antimicrobial families, 100% were positive to one or more gene encoding resistances to tetracycline, 46.4% for aminoglycosides, 32.1% for beta-lactams, 28.6% for quinolones, 17.8% for macrolides, 7.1% for sulfonamides and 0% for phenicols. Regarding multi-resistance, three tortoises (32.1%) were multi-resistant (beta-lactams/quinolones/tetracyclines). Results of ARG quantification showed that the highest level was a sample with 0.29% of bacteria harboring the *tet*(Q) gene, but the rest of values for all the ARGs were below 0.01%; a level far lower than results obtained in wildlife species living in countries with large human populations. No significant difference was found between the three distinct scenarios. As we are facing a low exposure scenario in a pseudo-pristine ecosystem, more research is mandatory to better understand how resistance patterns spread throughout the archipelago, and how we may implement management methods using a One Health approach for the well-being of Galapagos' human and non-human inhabitants.

Presenter Bio: Ainoa Nieto Claudin is a wildlife veterinarian enrolled in a PhD program with Complutense University of Madrid and Saint Louis Institute for Conservation Medicine. The current study is part of her PhD dissertation thesis "Assessing the health of endangered free-living Galapagos Tortoise species across a gradient of human-modified landscapes".

INACTIVATED *MYCOBACTERIUM BOVIS* IN MOLOKAI-ORIGIN FERAL PIGS EXPERIMENTALLY INFECTED WITH VIRULENT *M. BOVIS*

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The wild pig population on Molokai, Hawaii, USA is a possible reservoir for bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, and has been implicated in decades past as the source of disease for domestic cattle. An effective vaccine against bTB would be useful for managing *M. bovis* in the Molokai wild pig population. Application of a heat-inactivated *M. bovis* vaccine to bovine tuberculosis-affected wild boar populations in Spain appears to help reduce disease prevalence. We therefore designed an experiment to test this vaccine in feral pigs of Molokai genetics. Fifteen 3-4 month old pigs were orally treated with approximately 10^6 – 10^7 colony forming units (cfu) inactivated *M. bovis* (vaccinates; n=8; 0.2 ml) or phosphate buffered saline (controls; n=7; 0.2 ml). Each dose was administered in a 0.5 ml tube embedded in a fruit candy/cracked corn mix. Boosters were given seven weeks post-prime in the same manner and dose. Nineteen weeks post-prime, pigs were orally challenged with 1×10^6 cfu virulent *M. bovis.* Three months post-challenge, pigs were euthanized and necropsied, at which time 25 different tissues in head, thorax, and abdomen were collected and examined. Each tissue was assigned a lesion score. Data were analyzed using both general linear model (GLM) and non-parametric Wilcoxon Signed Rank test (WSR). Four of eight vaccinates and four of seven controls had visible gross lesions. Average lesion score of vaccinates versus controls were 0.09 and 0.18 respectively (50.8% reduction; p=0.1955, GLM). While there were no abdominal lesions, nor significant differences in the head region, thoracic scores were significantly lower in the vaccinated pigs (0.31 vs. 0.01; p=0.0053; GLM and p=0.09; WSR at $p \leq 0.1$ for small sample sizes). Culture and histopathology are pending. These results are indicative that some degree of infection containment can occur with this vaccine in Molokai feral pigs.

Presenter Bio: Pauline Nol is currently a veterinary epidemiologist with USDA Veterinary Services and has spent the past 15 years exploring tools for diseases at the wildlife-livestock interface. Dr. Nol received her BS and DVM at the University of Florida, MS at the University of Wisconsin-Madison, and PhD at Colorado State University.

MESHING REHABILITATION, EDUCATION, AND RESEARCH: THE JEKYLL ISLAND DIAMONDBACK TERRAPIN (*MALACLEMYS TERRAPIN)* MODEL

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The Georgia Sea Turtle Center (GSTC) is a conservation organization that focuses its efforts on native chelonians and integrates rehabilitation, education and research. Thousands of reproductively mature female diamondback terrapins (*Malaclemys terrapin)* are injured and killed by motor vehicles on causeways going to developed barrier islands throughout their range during the nesting season. On the Jekyll Island Causeway (JIC) alone an average of 174 and a range of 91 to 300 terrapins have been hit annually and a total of 1910 have been hit between 2007 and 2017. A "Diamondback Terrapin Conservation Initiative" started in 2006 with the GSTC staff rescuing them off the road after being hit, rehabilitating them, recovering their eggs for incubation and eventual release of any that were successfully rehabilitated or hatched. In 2009, a partnership was established with the University of Georgia. This program has evolved into a multifaceted conservation program and is serving as a model for other similar initiatives. Research has focused on investigating the extent of the problem on the JIC and demonstrating that per capita terrapin mortality from vehicle strikes and nest predation rates are both sufficient to cause population declines along the JIC. Hot and warm spots for terrapin nesting and crossing have been established. Additionally, a large percentage of terrapins come up to nest during a 3-hour window surrounding high tide. A male-biased population has been demonstrated through regular monitoring of creeks surrounding the causeway. These results have been used to design our management strategies including solar powered flashing light signs that turn on during the 3-hour surrounding high tide window and nest mounds with protective boxes placed in the hot spots along the JIC.

Presenter Bio: Terry M. Norton earned his Doctor of Veterinary Medicine at Tufts University in 1986 and completed a residency in Zoo and Wildlife Medicine at the University of Florida in 1989. He became a Diplomate in the American College of Zoological Medicine in 1992. He has provided veterinary care for White Oak Conservation Center, Riverbanks Zoo, North Carolina State Zoo and the Wildlife Conservation Society's St. Catherines Island Wildlife Survival Center. Currently, he provides veterinary care for the Georgia Sea Turtle Center and St. Catherines Island Foundation programs. He is the Director and Founder of the Georgia Sea Turtle Center on Jekyll Island. He has published numerous articles for referred journals, book chapters, and most recently was a Co-editor for the book entitled Sea Turtle Health and Rehabilitation.

DEVELOPMENT OF VACCINE TO PROTECT KOALAS AGAINST KOALA RETROVIRUS

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Koala retrovirus (KoRV) infects the majority of Australia's koalas (*Phascolarctos cinereus*) and has been linked to several life-threatening diseases such as lymphoma and leukemia as well as *Chlamydia,* and thus poses a threat to the continued survival of this species. While quarantine and antiretroviral drug treatment are possible control measures, they are impractical, leaving vaccination as the only realistic option. In this study, we examined the effect of a novel recombinant envelope protein based anti-KoRV vaccine in two groups of South Australian koalas: KoRV infected or KoRV free. We report a successful vaccination response in the koalas with no vaccine associated side effects. The vaccine induced a significant humoral immune response as well as the production of neutralizing antibodies in both groups of koalas. We also identified B-cell epitopes that were differentially recognized in KoRV infected or KoRV free koalas following vaccination. Importantly, we also showed that vaccination had a therapeutic effect on koalas infected with KoRV by reducing their circulating viral load. Together, this study highlights the possibility of successfully developing a vaccine against KoRV infection in koalas.

INTERANNUAL SITE FIDELITY OF WILD AND FARMED WHITE-TAILED DEER IN FLORIDA: IMPLICATIONS FOR DISEASE INTERVENTION

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Epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) are two vector-borne orbiviruses that cause large annual financial losses in farmed and wild white-tailed deer (*Odocoileus virginianus*) herds across North America. In order to identify proper disease intervention strategies (e.g. integrated pest management, vaccination, and feeder or food plot placement), it is important to understand the movement behaviors and home range fidelity of animals from year to year. High fidelity between years would indicated areas of best intervention. This study was initiated to address a paucity of information related to both farmed and wild inter-annual site fidelity in the southeastern US. Our study sites included a 450 acre high-fenced game preserve and adjacent state-managed public lands in Gadsden County, Florida. During the EHDV and BTV transmission risk period (May 1st-October 31st), we monitored animals with GPS collars programmed to collect hourly locations. In 2016 and 2017 we monitored 4 wild deer (2 male and 2 female) and in 2015 and 2016 we monitored 4 farmed deer (3 male and 1 female). We used the “ctmm” package in Program R to estimate, and compare, autocorrelated kernel density estimates of core (50% of locations) and activity spaces (95% of locations) during the disease transmission period for subsequent years. Our results indicated that there was a high level of inter-annual home range fidelity for most, but not all, wild and farmed animals monitored during the study. Some wild deer had complete shifts in home range, as did one farmed deer. Additionally, we identified important behavioral similarities between wild and farmed animals in Florida. This may indicate that disease intervention strategies identified through research of wild herds may be applicable to private herds, and vice versa. Currently, there has been little research investigating movement behaviors on private game farms and it may be applicable to utilize conclusions drawn from wild studies to address immediate disease management concerns on game farms. The results of our study will help inform disease management and intervention strategies that require a foundation in understanding deer movement and home range fidelity.

LIFELONG IMMUNITY AFTER CANINE DISTEMPER SURVIVAL? SEROLOGY OF RACCOONS REVEALS POOR MULTI-YEAR ANTIBODY STABILITY

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Canine distemper virus (CDV) is a significant cause of mortality in many wildlife species, particularly for many carnivores including gray foxes (*Urocyon cinereoargenteus)*, coyotes (*Canis latrans*) and raccoons (*Procyon lotor*). Activities such as habitat modification and supplemental feeding may increase transmission risk among animals at different interfaces (domestic, feral, and wild). Also, transmission is likely variable across different host demographics and landscapes. Therefore, a better understanding of the epidemiology of CDV in a species that is widespread, abundant, and often associated with human-altered environments is paramount. Serum samples from 37 free-ranging raccoons (25 adult, 4 juveniles, and 8 yearlings) captured multiple times between 2007 and 2010 within an agricultural ecosystem in Indiana were tested for CDV antibodies using a serum neutralization assay. In at least one sample year during this period, 15 (41%) had titers ≥100, 29 (78%) had titers ≥64 and 31 (84%) had titers ≥32. Some individuals had CDV titers that remained stable but others had titers that fluctuated. Antibody titer distributions were either increasing, stable, normal, decreasing or binomial in 27%, 13%, 27%, 11% and 22% of individuals, respectively. Mean CDV antibody levels were higher in adults than juveniles, and higher in juveniles than yearlings, but no significant difference was noted between females (n=24, 76.4) and males (n=13, 84.5). Because our data show that titers can fluctuate greatly within individuals as a function of age and between years, it emphasizes the need to re-evaluate assumptions that individuals that survive CDV possess lifelong immunity due to exposure or protection from subsequent infection. In addition, individuals with titers ≥100 are usually considered protected, yet our data show individuals with low titers survive over multiple years with some having an increase in titer, thus cell-mediated immunity may help protect these raccoons from disease despite having low neutralizing antibody titers.

Presenter Bio: Sebastian is a PhD student in the Integrative Conservation program and graduate research assistant at the University of Georgia.

FURTHER INVESTIGATION INTO THE PATHOPHYSIOLOGY OF CHELONID HERPESVIRUS 5 AND ITS POTENTIAL RELATIONSHIP TO RENAL FIBROSIS IN JUVENILE GREEN TURTLES (*CHELONIA MYDAS*)

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Fibropapillomatosis (FP) is an infectious disease characterized by cutaneous and internal tumors that can be devastating and sometime fatal for afflicted marine turtles. Strong experimental and observational data indicate that chelonid herpesvirus 5 (ChHV5) plays an etiologic role in FP pathogenesis. Molecular evidence of ChHV5 infection has been previously detected in kidney tissues as well as urine samples, possibly representing a source of virus production and transmission and suggesting the possibility that ChHV5 may be horizontally transmitted via renal-urinary excretion. This study aims to determine whether there is an association between renal medullary fibrosis, a commonly observed lesion in juvenile green turtles (*Chelonia mydas*), and the presence of ChHV5 DNA. Kidney sections samples from 65 juvenile green turtles stranded or salvaged in Florida were analyzed for ChHV5 DNA using a probe-based quantitative PCR (qPCR) assay targeting ChHV5 DNA and confirmatory sequencing. Kidneys sampled for qPCR were also examined histologically to evaluate for the presence or absence, and degree of renal fibrosis. Viral prevalence data were analyzed and compared for kidney samples from turtles with and without renal fibrosis, and with and without FP tumors. Overall, 36/65 (55.4%) of the kidney samples tested positive for ChHV5 DNA, including from 9 turtles with and 56 without FP. The study is ongoing and final data will be presented. In addition to evaluating the relationship between histopathological study of archival kidney samples done in conjunction with molecular testing allows us to examine several other important elements, such as frequency of occurrence in different life stages.

Presenter Bio: Annie Page-Karjian, DVM, PhD, is an Assistant Research Professor and Clinical Veterinarian in the Comparative Medicine Department at Florida Atlantic University. Brian Stacy, DVM, PhD, DACVP, is Veterinary Medical Officer for NOAA Fisheries, Office of Protected Resources.

VETERINARIANS AND BIOLOGISTS: MAKING THE DREAM WORK THROUGH TEAMWORK

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Wildlife species have intrinsic value and are owned by the "public trust", and wildlife health is fundamentally connected to human and domestic animal health and well-being. Thus, it is a social responsibility to promote the health of both local and global ecosystems that sustain healthy wildlife. Veterinarians and biologists both play important roles in maintaining and promoting the health of wildlife populations. In Florida, monitoring coastal wildlife health has a crucial function in creating and implementing effective management plans for local wildlife populations. Collaborative relationships between veterinarians and biologists at Florida Atlantic University and Loggerhead Marinelife Center take an interdisciplinary, holistic, "One Health" approach to understanding the health effects of mismanaged and imperiled ecosystems. Working together, we strive to find and implement solutions to critical health challenges facing marine wildlife species today, from infectious disease outbreaks to environmental contaminants, with the common goal of attaining optimal health for wildlife. Our combined efforts and overlapping areas of expertise allow us to synergistically accomplish more to help improve wildlife health regionally and internationally than we would achieve by working alone.

Presenter Bio: Annie Page-Karjian, DVM, PhD, is an Assistant Research Professor and Clinical Veterinarian in the Comparative Medicine Department at Florida Atlantic University, where she leads the Marine Wildlife Veterinary Medicine & Research Program.

SEROPREVALENCE TO MYCOBCATERIUM TUBERCULOSIS COMPLEX IN WILD BOAR IN CAMPANIA REGION

Serena Montagnaro[1], *Antonio Parisi*[1], ***Ugo Pagnini***[1], *Vincenzo Veneziano*[1], *Ferrara Gianmarco*[1], *Daniela Rocco*[1], *Nicola D'Alessio*[2], *Alessandro Fioretti*[1], *Giuseppe Iovane*[1]
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Bovine tuberculosis bTB is an infectious disease caused by Mycobacterium bovis and related members of the mycobaterium tuberculosis complex (MTBC), undegoing to specific eradication plans worldwide. In Italy the eradication process has led to the eradication of bTB in several regions, however, it is still present in livestock in Campania region. In the last decade, a growing attention has been paid to the role that wild animals can have in the epidemiology of tuberculosis and particularly to Eurasian wild boar. Thus, in the present study we carried out a cross-sectional survey in wild boars in Campania region to assess the sero-prevalence against Mycobacterium bovis or cross-reacting members of the MTBC and to provide information on associated risk factors using an enzyme linked immunosorbent assays developed using MPB83-antigen.

Fifty-six out of 513 (10,92%; 95% CI: 19,47-2,36%) sampled animals presented antibodies against M. bovis in MPB83-ELISA. Statistical analysis indicated that the sero-positivity to M. bovis was not associated with age, sex or location of sampling. We also evaluated the correlation between the seropositivity in wild boar and the presence of tuberculosis outbreaks in livestock. The mean distance from a TB outbreak for the seropositive subjects ranged from 0 to 20 km (mean 7.38 km). Our results showed that exposure of wild boar to MTC is consistent with TB outbreaks in cattle, in fact, the mean distance between a seropositive wild boar and the nearest cattle outbreak was 7,38 km which is compatible with the daily movement capacities of a wild boar (1 - 16 km).

In conclusion, the sero-prevalence observed in the present study indicates a wide exposure to MTBC in wild boar in Campania region, which may have important implications not only for conservation but also for animal and public health.

Presenter Bio: Professor Ugo Pagnini was born in Napoli on March 20, 1970 and graduated in 1995 in Veterinary Medicine at the University of apoli Federico II. Since 2006, Pagnini has served as Associate Professor of Infectious Diseases at the University of Napoli Federico II. Major area of research includes infectious diseases of domestic and wild animals.

AN INTERVENTION TRIAL OF TWO TARGETED VACCINATION STRATEGIES AGAINST TUBERCULOSIS IN WILD MEERKATS

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In wild animal populations, targeting vaccination at specific high-risk individuals is an attractive proposition, as it requires fewer vaccine doses than traditional strategies. Whilst this has previously been suggested as an efficient strategy, empirical evidence for its application is lacking. In this study, tuberculosis (TB) in meerkats (*Suricata suricatta*) was used as a model system for an individually targeted vaccination program based upon identifiable traits. Dominant meerkats have previously been implicated as superspreaders of TB due to rates of aggressive behaviours, whilst subordinates are likely to be susceptible due to levels of grooming activity.
Our objective was to determine if trait-based vaccination reduces TB infection rate within a population of wild meerkats. We conducted a two-year intervention study in a free-living population of meerkats in South Africa's Kalahari Desert. Nine social groups of meerkats were randomly allocated to either High Contact (HC), High Susceptibility (HS), or Control study arms. Vaccination, using BCG, was administered at the study outset to dominant individuals in the HC groups, and in HS groups to pups shortly after birth. Three diagnostic tests were used on all individuals across the three study arms throughout the trial. Survival analysis was used to investigate protocol effects on individual animals' lifespans, and the risk of unvaccinated animals being infected was compared using odds ratios. Being a member of a dominant-vaccination group (HC) had a protective effect on individuals' survival times (Hazard Ratio=0.5, 95% Confidence Interval: 0.29-0.88, p=0.02). Odds of testing positive for TB increased by more than five times in control groups (odds ratio=5.40, 0.94-30.98, p=0.058), with no increases in either type of treatment group. In conclusion, trait-based vaccination reduces infection rates and therefore may offer an alternative to traditional mass vaccination policies. The reduced numbers of animals to be treated make this an advantageous option for policy makers.

Presenter Bio: Following five years in clinical practice, Stuart studied for master's degrees in veterinary epidemiology, and conservation medicine before undertaking his PhD in wildlife disease control. This work focused on the Kalahari meerkats as a model population. Stuart is now a lecturer in wild animal health at London's Royal Veterinary College.

PLASTIC-DERIVED CONTAMINANTS IN LEATHERBACK SEA TURTLES: IMPLICATIONS FOR HEALTH AND HATCHLING QUALITY

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Contaminants in the marine environment are known to have a number of reproductive, immune, and developmental effects on wildlife; however, relatively little is known about the effects of contaminants on sea turtles. Even fewer reports are available regarding the effects of chemicals derived from plastics, detergents, pesticides, and antibiotics in leatherback sea turtles (*Dermochelys coriacea*), which are produced from various anthropogenic sources. During the 2017 nesting season, we collected blood from nesting leatherback turtles on Juno and Jupiter Beach, Florida. Plasma was separated from the red blood cells and was analyzed for atrazine, bisphenol A, diethylphthalates, nonylphenol ethoxylates, and triclosan. Additionally, a number of blood health analytes were examined including white blood cell counts, protein electrophoresis, hormones, and indicators of antioxidant capacity. Hatchlings from each of the sample nests were collected at nest emergence for measurements of mass, morphometrics, and body condition index. Unhatched, undeveloped eggs from the sampled nesting females were also collected during routine nest inventories to analyze for the contaminants of interest. All measured contaminants were above limits of quantitation for plasma and egg except for triclosan and the majority of atrazine samples. Although blood health analytes were within expected ranges for healthy nesting female leatherbacks, the most intriguing findings were (1) a positive correlation between nonylphenol ethoxylates and eosinophils, (2) correlations suggestive of altered energy metabolism, electrolyte balance, and immune function, and (3) a negative correlation between diethylphthalates and hatchling body condition index. These results suggest that plastic-derived contaminant exposure has the potential to alter blood health analytes and hatchling quality in leatherback turtles.

Presenter Bio: Justin Perrault, PhD, is the Director of Research at Loggerhead Marinelife Center where he oversees the Research Institute. He has 13 years of experience examining marine organismal toxicology and health.

IMPACTS OF ENVIRONMENTAL CONDITIONS ON PRAIRIE DOG FLEAS: IMPLICATIONS FOR SYLVATIC PLAGUE

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Sylvatic plague, caused by the bacterium *Yersinia pestis*, is endemic in ground squirrels and prairie dogs of the western United States. Plague epizootics are devastating to prairie dog communities, often leading to 100% mortality. Prairie dog fleas (*Oropsylla* species) are responsible for the majority of transmission events that drive plague epizootics; however, little is known about flea life history. Survival and development of other flea species is impacted by environmental factors such as temperature and relative humidity; these factors should also be important for prairie dog fleas. Because prairie dog fleas spend most of their time in burrows, burrow microclimates are probably the most important factor in flea development. Our goal was to determine the impacts of weather conditions on prairie dog burrow microclimates and the impact of burrow microclimate on flea abundance. We measured flea abundance by swabbing 300 prairie dog burrows at each of 6 sites across a wide latitudinal gradient while simultaneously measuring burrow and ambient temperature and relative humidity. Sites were sampled in both early (May-June) and late (August) summer in 2016 and 2017. We found that burrow microclimate was strongly correlated with ambient temperature. Flea abundance was also positively correlated with burrow temperature. Although this relationship was seen in both 2016 and 2017, overall flea abundance also varied between years. Patterns of flea abundance also varied regionally, declining from early to late sampling at southern sites and increasing at northern sites. Information gathered during this research will be used to predict the impacts of climate change on plague dynamics and to inform plague management.

Presenter Bio: Julia Poje is a Master's student in the Department of Forest and Wildlife Ecology at the University of Wisconsin – Madison. Her research is focused on how environmental conditions impact flea populations on prairie dog colonies.

THE MAINTENANCE AND MIGRATION OF INFLUENZA A AND PARAMYXOVIRUSES WITH THEIR SHOREBIRD HOSTS

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During May every year, Delaware Bay (DB), USA represents a critical stopover site for shorebirds to replenish energy reserves during long distance migratory flights from austral wintering to Arctic breeding grounds. Influenza A viruses (IAV) and avian paramyxoviruses (APMV) have been consistently recovered from shorebirds and gulls at this location for more than three decades, with most isolates originating from Ruddy Turnstones (RUTU; *Arenaria interpres*). However, IAV and APMV isolations from shorebirds sampled outside of DB and at other times of year have been infrequent/rarely documented; as such, this stopover site has been termed a "hotspot" for IAV. Despite long-term longitudinal surveillance and research, sources of IAV introduction to DB remain largely unknown. Expansion of surveillance efforts to overwintering and staging sites in the southeastern United States is informing our understanding of one mechanism by which IAV are introduced to DB. From RUTU and shorebird feces sampled in the southeast (Florida, Georgia, South Carolina; December – May, 2011-2018), more than 50 IAV and greater than 30 APMV have been isolated thus far; the same IAV HA/NA combinations and APMV serotypes have often been recovered at DB in the same year. Additionally, highly similar IAV genomic segments have been identified at both locations, allowing us to start to piece together how IAV genomes migrate with their shorebird hosts. These findings shed light on the use of areas outside of DB where shorebirds may be infected with IAV and APMV and subsequently transport these viruses to the "hotspot." Continued surveillance at underexplored migratory staging and/or stopover sites in the southeastern United States will advance our understanding of the ecology and epidemiology of IAV and APMV in shorebird hosts both within and outside of DB.

FADE-OUT OF AN ENDEMIC PATHOGEN IN A WILDLIFE HOST: DID ENVIRONMENTAL STRESS CAUSE *LEPTOSPIRA* TO DISAPPEAR FROM THE CALIFORNIA SEA LION (*ZALOPHUS CALIFORNIANUS*) POPULATION?

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Leptospira interrogans serovar Pomona was first detected in California sea lions (CSL: *Zalophus californianus*) during an outbreak in 1970. The Marine Mammal Center (TMMC) data indicate that since at least 1984, yearly seasonal outbreaks have occurred, with large outbreaks occurring every 3-5 years. Genetic, serologic and other data indicate that CSL maintained unbroken *Leptospira* transmission between outbreaks, probably via chronic shedders, suggesting that this pathogen is endemic. In 2010, we began tracking *Leptospira* exposure (anti-*Leptospira* antibodies via microscopic agglutination test – MAT; n>1200) and incidence (leptospire DNA in urine via real-time qPCR; n>1700) in wild-caught CSL throughout their range to complement similar exposure (n>2000) and incidence (n>700) data from stranded CSL at TMMC, and to better understand CSL-*Leptospira* dynamics. Intriguingly, after the last major outbreak in 2011 until mid-2017, yearly antibody seroprevalence in both the stranded and free-ranging populations declined, approaching zero. Also within this period (mid-2013 to mid-2017), antibody titer magnitude in seropositive CSL was low and declining and animals born during this period were seronegative. This unprecedented lull in CSL-*Leptospira* activity suggests that *Leptospira* transmission among CSL essentially ceased, indicating pathogen fade-out from this population. In addition, only one case of leptospirosis was detected in CSL at TMMC between mid-2013 and mid-2017, and this case was the only animal shedding of 1242 stranded and wild-caught CSL tested, providing further evidence of fade-out. We suspect that this single case was a failed re-emergence event that occurred just prior (October 2016) to pathogen re-emergence in mid-2017 when >50 CSL stranded with leptospirosis. We hypothesize that fade-out was driven by recent oceanographic anomalies through the combined action of two mechanisms: (1) reduced susceptible buildup due to reduced pup production and increased pup mortality; and (2) changes in age and sex specific movement patterns which altered population mixing and hence transmission dynamics.

Presenter Bio: I am a veterinarian and disease ecologist with >20 years studying disease dynamics of zoonotic and multi-host pathogens in wildlife. For the last 8 years I have been investigating *Leptospira* dynamics in California sea lions throughout their range, and in Channel Island foxes and spotted skunks on Santa Rosa Island.

COMBINING LANDSCAPE GENOMICS AND BLOODMEAL ANALYSIS TO DISENTANGLE DRIVERS OF PARALYSIS TICK DISPERSAL

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As urbanization is increasing, the conservation of many wildlife species requires finding creative ways for wildlife and people to co-exist in the same landscape. In Queensland, Australia, tick paralysis (caused by *Ixodes holocyclus*) is an economically important issue. Yet some aspects of this species' ecology are unclear, such as host identities and the role of host communities in determining variation in paralysis tick distributions and abundances over the urban-rural interface. Here, we present a conceptual model of tick dispersal and distribution across an urban-rural gradient and a framework for empirically testing this model. In a multidisciplinary approach, our model incorporates: (1) tick occurrence data gathered from field sampling; (2) host species identification gathered from deep sequencing of tick bloodmeal analysis; and (3) population genetic structure quantified using a RADSeq (restriction site-associated DNA sequencing) protocol[2]. Results will provide new insights into the scale over which tick genetic dispersal occurs, identify barriers to tick movements across urban-rural gradients, and resolve whether bandicoots, previously described as a principal host of the paralysis tick[1], play a disproportionately important role in maintaining tick populations. Using landscape genomics techniques, our approach will also generate high resolution maps of tick distributions that can be used to forecast outbreak clusters of tick paralysis in pets. Finally, this project will provide novel genetic tools to improve our knowledge of wildlife host use and to describe the genetic structure of ticks, supporting future tick research projects.

COMMENSAL BACTERIAL SHARING IS NOT PREDICTED BY HOST SOCIAL INTERACTIONS: IMPLICATIONS FOR DISEASE TRANSMISSION NETWORKS

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The spread of infectious diseases within a population is often dependent on the degree of contact between individuals, and so disease transmission is influenced by social structure[1]. Accordingly, social network analysis has been postulated as an approach to estimate potential for pathogen transmission among individuals. However, obtaining empirical pathogen transmission data is difficult, especially in wildlife populations. Sharing of bacterial genotypes has been proposed as a proxy for host contact networks based on the assumption that individuals in close contact will share commensal bacteria[2]. We tested this hypothesis by asking if a commensal bacterial network (based on sharing of bacterial genotypes) could predict the structure of the host's social network. We focused on a well-studied population of eastern grey kangaroos from Sundown National Park in Australia (Queensland/New South Wales border). Using natural markings, each individual was identified. Associations between kangaroos were recorded in the field and used to construct social networks across two years. To construct commensal bacterial networks, we collected faecal samples from kangaroos, isolated a common commensal bacteria (*Escherichia coli*) and genotyped isolates using BOX-PCR. Two individuals were considered connected in the commensal network if they shared an *E. coli* genotype. From a population level, we found that the overall structure of social and commensal bacterial networks were not related, contrary to previous studies. From an individual level, measures of social and commensal network structure varied between years but were generally dissimilar. Commensal network structure was sensitive to model parameters controlling whether *E. coli* subtypes were deemed identical. These findings suggest that commensal and social networks are not always similar, and inference of disease transmission from social network structure may be complex and inaccurate.

DEVELOPING SUSTAINABLE WILDLIFE HEALTH SURVEILLANCE IN CAMBODIA AND LAOS

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In many developing countries in Southeast Asia, such as Cambodia and Laos, infectious diseases are a high burden on animal and public health, and risks of zoonotic disease emergence or re-emergence are great. With public and animal health systems already overburdened, wildlife health surveillance is rarely prioritized. However, it is essential to the early detection and response to emerging health threats and to the understanding of the dynamics of endemic diseases, and an integral part of international health monitoring standards. We piloted the development of sustainable wildlife health surveillance mechanisms in Cambodia and Laos following a One Health approach, based on existing field and laboratory resources and drawing from the public health, animal health and natural resource management sectors. In Cambodia, the pilot surveillance network expanded to 18 protected areas and three rescue centers, through trainings of forest rangers and NGO partners who routinely sent wildlife morbidity reports or mortality cases detected in natural areas and/or occurring at rescue centers. In Laos, the pilot network included two national protected areas and helped establish cross-sectoral agreements in five provinces to conduct wildlife health surveillance in coordination with wildlife trade law enforcement activities. In both countries, the pilot networks allowed routine sampling of sick, dead or traded wildlife, as well as the investigation of larger mortality events and outbreaks, demonstrating their effectiveness at detecting and responding to health threats. A formal performance evaluation of these networks is on-going to use as baseline to monitor future improvement. These pilot networks are also the basis for policy development in each country, toward national-level multi-ministerial Standard Operating Procedures for wildlife health surveillance. Linking a broad range of government and non-government partners, particularly in the conservation and health sectors, allowed the rapid establishment of effective surveillance mechanisms while taking important steps toward the co-development of cross-sectorial policy tools.

Presenter Bio: Mathieu Pruvot is an epidemiologist at the Wildlife Conservation Society, Wildlife Health Program. His research focuses on land-use change, wildlife trade and wildlife –livestock interfaces. Over the past 4 years, he was based in Cambodia from where he led zoonotic disease surveillance and research in Cambodia and Laos.

VECTOR-HOST INTERACTIONS UNDERLYING HEMORRHAGIC DISEASE TRANSMISSION: WHAT CAN NETWORK ANALYSIS UNCOVER?

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Bluetongue virus (BTV) and Epizootic hemorrhagic disease virus (EHDV) cause hemorrhagic disease in many ruminant species worldwide, both wild and farmed, with important ecologic, economic and social impacts. Various *Culicoides* species transmit these viruses between infected and uninfected ruminants. As the vector-host interaction is necessary for arbovirus maintenance in this system, a network analysis framework could highlight actors and processes masked by the complex nature of the disease system. Here we show how blood feeding behavior, through the structure and composition of *Culicoides*-vertebrate interactions, sets the transmission scenario for EHDV and BTV with implications for management activities for protecting ruminants. We built *Culicoides*-vertebrate network projections and calculated network, node and edge measurements from a blood engorged *Culicoides* dataset of a deer ranch in northwest Florida. The network dataset comprised 1,684 blood feeding interactions from 14 *Culicoides* species and 25 vertebrate species, where only 20% of the possible interactions were realized. The structure showed an isolated specialist compartment and another generalist blood feeding compartment with a high level of nestedeness. *Culicoides stellifer, C. biguttatus* and *C. venustus* fed on 68%, 40% and 36% of the available vertebrates, respectively, although 86% of the interactions came from *C. stellifer*. A noticeably over-connected ruminant compartment and a moderately sparse bird-mammal community emerged in the vertebrate projection. The high level of generalization in host use on exotic, domestic and wild ruminants sets up a permissive scenario for EHDV and BTV transmission. Therefore, preventive and control activities might best be focused on the entire ruminant community and not only the clinically susceptible species. In the future this network intervention approach needs to be validated and improved by taking into consideration the temporal and spatial changes in the host use by midges.

Presenter Bio: During my veterinary bachelor and PhD, I had worked in topic related to the birds of prey ecology and conservation medicine and ecology of arbovirus in Argentina. Currently, I am fully focused in the complex phenomena of blood feeding interactions, the dynamics and control vector-borne diseases studying through network's tools.

CANINE DISTEMPER IN BIG CATS - STATUS IN CENTRAL INDIA

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Canine distemper is posing a threat to big cats all over the world. There have been mass mortalities along with the individual case reports in wild as well as captive big cats. The state of Madhya Pradesh in central India consists of 10 National parks and 25 wildlife sanctuaries. The study was undertaken on the samples received from state forest department for regular health screening and disease investigations. Samples were collected during veterinary interventions like health monitoring, immobilization or necropsy of big cats. These samples were tested for antibodies to canine distemper virus (CDV) as well as for molecular diagnosis of pathogens in suspected cases. The study revealed serological and genomic evidences of CDV in wild carnivores including tigers and leopards. As the CDV has immunosuppressive effect allowing other secondary infections to develop, it proved fatal in some cases of captive big cats. Additionally, in free-ranging big cats, canine distemper was observed as occasional finding during necropsy, which also raised a concern as to be the mediator of unnatural death. Epidemiology of canine distemper is complex and mostly domestic dogs in the peripheral villages of protected areas have been reported to be the source of infection in wild carnivores. However, status of canine distemper in other wild carnivores like jackals, foxes and hyaena is largely unknown and to establish the same, sporadic samples from these carnivores were also tested for CDV. Through the data obtained, a baseline was formed to facilitate the advanced research on genomic variations of CDV in various species of wild carnivores.

MORTALITY INVESTIGATION OF EASTERN BOX TURTLES (*TERRAPENE CAROLINA CAROLINA*) IN CENTRAL ILLINOIS FROM 2016 - 2018

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Disease events in Eastern box turtles (*Terrapene carolina carolina*) threaten conservation efforts across the species range. Mortality events are often under-diagnosed, and when observed, fail to identify health factors prior to the die-off. At Kickapoo State Park in central Illinois, ranaviruses have caused observed mortality events in amphibians and chelonians in 2014 and 2015. Following these outbreaks, twenty-two Eastern box turtles were affixed with VHF radiotransmitters and iButtons to obtain repeated location and temperature data from Spring 2016 – Spring 2018. Bi-monthly, we collected blood and oral/cloacal swabs to investigate health parameters (hematology) and multiple pathogen presence. Additional turtles were recruited to fill empty slots for a total sample size of 36. Deaths occurred in 2016 (N=5) and in 2017 (N=15). Most occurred in February 2017 (N=7), likely due to a rapid temperature drop during an unseasonably warm winter. Thirteen turtles were necropsied and revealed multifactorial causes of death, including emaciation (N=5), egg-bound (N=2), sepsis (N=2), ulcerative dermatitis (N=1), coelemitis (N=1), meningoencephalitis (N=1), and stomatitis (N=1). Some individuals (N=7) were too decayed for necropsy. No consistent pathogen was identified as a singular cause for the high mortality at this site, including negative ranavirus status in all animals. Cox proportional hazard models identified significant predictors of survival. Decreased survival time was associated with highest lymphocyte counts, presence of any clinical signs, lowest temperature experienced, and number of days below freezing experienced as measured by iButton. These factors should be considered for population health and survivorship models, especially in sensitive systems. Monitoring these deaths gave insight to an unusually high mortality event, but no single causal factor could be identified. The deaths may be random, or the animals at this particular site may have increased risk of death from all causes. Still, the investigation provided information to better inform future research projects.

Presenter Bio: Jeremy is a combined DVM/PhD student in the Wildlife Epidemiology Laboratory of Dr. Matthew Allender. He has completed his first year of the DVM, and in the third year of the PhD. His research focuses on natural and experimental exposure and response of chelonians to ranavirus.

THE FEASIBILITY OF CONTROLLING RABIES IN VAMPIRE BATS (*DESMODUS ROTUNDUS*) THROUGH TOPICAL APPLICATION OF VACCINE.

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Rabies transmitted by vampire bats (*Desmodus rotundus*) in Central and South America is a significant threat to humans and also a tremendous economic burden due to widespread cattle mortality and prophylaxis. Current efforts to minimize this threat focus on vaccination of livestock and culling of vampire bats through the use of anticoagulants spread 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%). Ongoing work includes vaccine efficacy and rabies challenge studies in vampire bats. If successful, topical application of vaccine could be an effective method of vaccinating large numbers of vampire bats, providing another tool for managing rabies.

Presenter Bio: Tonie E. Rocke, Ph.D., is employed as a research scientist at the USGS National Wildlife Health Center. Her current research is focused on the ecology and management of diseases in wild mammals (e.g. plague, monkeypox, rabies and white-nose syndrome) with the overreaching goal of conservation of threatened and endangered species.

COMPLETE GENOME SEQUENCING OF TWO NOVEL PAPILLOMAVIRUS TYPES IN BOTTLENOSE DOLPHINS (*TURSIOPS TRUNCATUS*)

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A next generation sequencing approach was used to characterize viruses in the feces of 12 free-ranging bottlenose dolphins (BDs). Nucleic acid was extracted from the fecal samples, libraries constructed and sequenced on an Illumina MiSeq, reads assembled in CLC Genomics Workbench, and the resulting contigs subjected to BLAST searches. One contig was identical to a papillomavirus (PV) sequence encoding the partial L1 gene recovered from a papillomatous penile lesion in a male killer whale that stranded in the UK. Primers based on the L1 contig sequence were used to generate the full genome sequence by nested inverse PCR and Sanger sequencing. Inspection of the BD papillomavirus (BDPV) genome revealed it represents a new type of *Dyopipapillomavirus 1* (DyopiPV1), a species previously sequenced from a penile papilloma in a harbor porpoise. A second contig was recovered containing the full genome of a new type of *Omikronpapillomavirus 1* (OmikronPV1), a species previously sequenced from cetacean papillomas. Both BDPV genomes displayed typical PV genome organization, including four early genes, two late genes and a long control region. Genetic analyses supported these two BDPV as novel types of DyopiPV1 (TtPV8) and OmikronPV1 (TtPV9). Separate specific endpoint PCR assays targeting the L1 genes were used to determine the prevalence of the novel PV types in fecal samples of the BDs. An adult female BD displaying a genital papilloma was positive by PCR for DyopiPV1 (TtPV8). Three adult male BDs, one of which displayed a genital papilloma, were positive by PCR for OmikronPV1 (TtPV9). The identical PV sequence found in a BD and a killer whale suggests certain cetacean papillomaviruses are capable of infecting multiple delphinid species. These findings may have management implications for facilities with mixed cetacean populations. Further investigation into the prevalence and associated health impacts of PVs on free-ranging BDs are warranted.

Presenter Bio: Thaís Rodrigues (DVM, MS and PhD candidate) is a veterinary researcher with experience working with infectious diseases of wildlife, including Amazonian aquatic mammals. She is currently a postdoctoral associate in the Wildlife and Aquatic Veterinary Disease Laboratory, University of Florida, studying emerging aquatic pathogens affecting Florida marine mammals.

PATHOLOGICAL SURVEY OF PULMONARY DISEASE IN FREE-RANGING BRAZILIAN RIVER DOLPHINS

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The Amazon River dolphin (*Inia geoffrensis*) and tucuxi (*Sotalia fluviatilis*) are data deficient species. Threats to the long-term health of these species include incidental mortality in fishing gear, habitat loss and environmental pollution. Pneumonia and other respiratory diseases are recognized as important causes of death in cetaceans, but almost nothing is known about the impact of respiratory diseases in *I. geoffrensis* and *S. fluviatilis*. Thus, we conducted a retrospective study analyzing gross and microscopic pulmonary lesions in *I. geoffrensis* and *S. fluviatilis* carcasses collected in the Mid-Solimões River region, Brazil, from 1995 to 2016. Approximately 85% of the examined animals presented with lung disease characterized as verminous pneumonia (25%), bacterial pneumonia (25%), and others (32.7%), including the first case of meconium aspiration syndrome reported in *S. fluviatilis* (1.9%). All verminous pneumonia cases in which it was possible to identify the nematode were caused by *Halocercus brasiliensis* including the first report in *I. geoffrensis*. Although bacteriology was not performed, Gram-positive cocci were observed within lung tissues in cases of suppurative bronchopneumonia and/or pleuropneumonia. The zoonotic bacteria *Streptococcus iniae*, originally characterized from *I. geoffrensis*, was considered the most likely etiology. Injuries likely acquired as the result of fishing activities were observed in 46.1% of carcasses. Additionally, some of these anthropogenic induced injuries were correlated with lung disease. Further research is needed to better evaluate the impact of lung disease in these riverine species and to generate badly needed baseline data to inform future medical and conservation efforts.

Presenter Bio: Thaís Rodrigues (DVM, MS and PhD candidate) is a veterinary researcher with experience working with infectious diseases of wildlife, including Amazonian aquatic mammals. She is currently a postdoctoral associate in the Wildlife and Aquatic Veterinary Disease Laboratory, University of Florida, studying emerging aquatic pathogens affecting Florida marine mammals.

PANSUSCEPTIBLE *E. COLI* ISOLATES OBTAINED FROM FECES OF FREE-RANGING BAIRD'S TAPIRS (*TAPIRUS BAIRDII*), SUGGESTS A LOW ANTHROPOGENIC ACTIVITY, IN THE HIGHLANDS OF THE CORDILLERA DE TALAMANCA, COSTA RICA

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Antibiotic resistance is an emerging global problem that encompasses human and animal health, also with agriculture, aquaculture and pharmaceutical industry. A main issue is an abusive and indiscriminant usage of antibiotics, in which dissemination of resistant bacteria throughout the environment, humans and animals occurs. Wild animals, in rare occasions, are expose to antibiotics, therefore antibiotic resistance levels in these animals are expected to be low. Nevertheless, as the interactions between humans, domestic and wild animals are increasing, there is a growing risk that intestinal microbiota from wild animals may acquire resistant bacteria or genes due to close contact with other animals and/or humans. This study's main objective is to analyze the antibiotic resistance profile of *Escherichia coli* isolates obtained from feces of free-ranging Baird's tapirs (*Tapirus bairdii*) in the highlands of the Cordillera de Talamanca. *Escherichia coli* isolates were recovered using the selective and differential media MacConkey. The biochemical identification and antibiotic resistant profiles were performed using the computerized system Vitek 2 Compact (Biomeriux), where nine classes of antibiotics where tested. Resistance levels detected in *E. coli* isolates obtained from feces of free-ranging *T. bairdii* were very low. Ninety-eight percent where characterized by pan-susceptibility, and 2% where resistant to only nalidixic acid. One of the isolates obtained from a captive tapir presented a multirresistant phenotype, with resistance to cefalotine, cefotaxime, cefepime, ampicillin and ampicillin/sulbactam. Additionally, an ESBL was identified in the same isolate. This study demonstrates a very low antibiotic resistance of *E. coli* from free-ranging Baird's tapirs, and this supposes a low selective pressure against this commensal bacteria. In contrast with the isolate obtained from the captive tapir. This could be because captive tapirs are in closer contact with humans and other animals, antibiotic usage, polluted water sources, food manipulated by humans, among others, leading its intestinal microbiota to gain resistant genes. Finally, the results suggest that the commensal microbiota of free-ranging Baird's tapirs (*T. bairdii*) of the Cordillera de Talamanca, remain secluded from antibiotic selective pressure, probably because of a low anthropogenic activity throughout landscape variables, in the habitat where they inhabit.

INVESTIGATING THE ROLE OF DROMEDARY CAMELS AND THEIR TICKS IN Q FEVER EPIDEMIOLOGY IN LAIKIPIA COUNTY, KENYA

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Query (Q) Fever is a zoonotic disease of conservation, public health and economic importance, caused by the bacterial pathogen *Coxiella burnetii*, which may infect both livestock and wildlife. Camels are a hardy livestock species that are increasingly important in semi-arid landscapes where they may compete for forages with sympatric wildlife species. Laikipia County, Kenya is a known area of dense and diverse wildlife. This shared habitat provides the opportunity for disease transmission, with implications on regional biodiversity. While *Coxiella burnetii* seroprevalance reports in camels in Laikipia range from 18-46%, the source of infection remains unexplored. In this study, we investigate the role of ticks in Q Fever epidemiology. We collected blood from 253 camels from three herds in Laikipia and collected 4,835 ticks from those camels. We ran ELISAs on the camel serum to test for seroconversion to *C. burnetii* and PCR tested the ticks for the presence of *C. burnetii* to evaluate whether there is an association between camel exposure to the bacterium and camels carrying ticks that test positive for *C. burnetii*. An improved understanding of livestock-wildlife interaction and the role of ticks in Q Fever epidemiology will contribute valuable information pertaining to the spread of infection. In addition, we conducted a survey with camel ranchers to assess tick awareness, camel husbandry practices, land use, and herd health history. While each herd reported using various topical acaricides at least once monthly, every camel had at least one tick with up to 69 ticks on one individual. This discrepancy suggests either lack of adherence to the acaricide usage protocol or resistance in the ticks. Two herds reported significant camel-wildlife interface, including deliberately approaching wildlife on camelback for tourism safaris. Statistical analyses will be completed by the end of April 2018.

Presenter Bio: Theresa Rooney is a third-year student in the DVM/MPH program at Tufts CSVM, and a candidate for the International Veterinary Medicine Post-Graduate Certificate. Through the Saint Louis Zoo Institute for Conservation Medicine, Theresa completed this capstone project for her MPH degree; combining her interests in wildlife-livestock interface and international development.

DETECTION AND CHARACTERIZATION OF MYCOBACTERIAL INFECTIONS OCCURRING IN *PHACOCHOERUS AFRICANUS* (GMELIN, 1788) (COMMON WARTHOG)

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Mycobacterium bovis is the infectious agent causing bovine tuberculosis (bTB). bTB is frequently reported in the family Suidae, which include species such as domestic pigs, wild boar and warthogs. No diagnostic tools are currently available for identifying bTB in warthogs. This is the first attempt at describing the pathological or epidemiological consequences of this disease in warthogs from South Africa.We set out to develop and evaluate assays based on the adaptive immune response. Therefore, we had to determine if warthogs develop a measurable humoral and/or cell mediated immune response, after *M. bovis*-infection. Furthermore, we genetically characterized various *M. bovis* strains isolated from warthogs. This allowed recording the prevalence and describing the epidemiology of bTB in warthogs from bTB endemic regions of South Africa. To assess the humoral response, serological assays were used, which detect the presence of antibodies. Assays that were evaluated included an indirect PPD ELISA, TB ELISA-VK®, DPP® VetTB and Bovid Assay. Assessing the cell-mediate immune response, the QuantiFERON® system was assayed with a sandwich ELISA, measuring cytokine (i.e. IP-10) release, and a gene expression assay was developed from this system. The humoral assays had sensitivity (Se) of 88-95% and specificity (Sp) of 84-91% whereas the IP-10 assay had a Se of 68% and Sp of 84%. Successful development of the gene expression assay indicated that *CXCL 9, 10* and *11* are useful markers for disease in warthogs. Whole genome sequences of *M. bovis* isolates from warthogs, is genetically like isolates from other species in the area, although warthog isolates formed a separate clade. Therefore, warthogs develop a measurable adaptive immune response against *M. bovis*-infection and the *M. bovis* isolates, from warthogs, resemble that of the region. The study contributed to increasing our understanding of the epidemiology of bTB in African wildlife.

Presenter Bio: Eduard Roos completed his BSC in Zoology and was introduced to disease ecology in the lab of Prof Armanda Bastos. His BSc Hons. Zoology investigated the phylogenetic relationship of haemoparasites in lizards and he stared his PhD of as an MSc investigating bTB in warthogs.

VIRAL SHEDDING OF CLADE 2.3.4.4 H5NX HIGHLY PATHOGENIC AVIAN INFLEUZNA VIRUSES IN PERIDOMESTIC WILDLIFE

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During 2014-2015, clade 2.3.4.4 H5 highly pathogenic (HP) avian influenza viruses caused one of the largest agricultural emergencies in U.S. history. To evaluate the potential roles that peridomestic wildlife might play in the epidemiology of these viruses at the farm and between farm levels, we experimentally infected five common synanthropic wildlife species (European starlings [*Sturnus vulgaris*], house sparrows [*Passer domesticus*], rock doves [*Columba livia*], American robins [*Turdus migratorius*], and cottontail rabbits [*Sylvilagus* sp.]) with a HP H5N8 virus, as well as two HP H5N2 reassortant viruses isolated from a captive gyrfalcon (*Falco rusticolus*), a wild Northern pintail (*Anas acuta*), and from a domestic turkey (*Meleagris gallopavo*), respectively. Of the five species tested, house sparrows, American robins, and cottontail rabbits were shown to shed the HP viruses and cottontail rabbits and American robins shed the highest viral loads. Overall, these studies suggest that select peridomestic wildlife species, both birds and mammals, may pose a risk to the transmission and/or trafficking of some of these HP viruses.

EMERGENT BACTERIAL INFECTION THREATENING ENDANGERED CHRISTMAS ISLAND REPTILES

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Christmas Island, Indian Ocean, is a unique part of Australia with a high level of endemism among its flora and fauna. Due to natural vulnerabilities of small island species and the introduction of invasive predators, many of the island's species are in peril. Four of five endemic lizard species on the island are extinct in the wild or persist in very low numbers. The critically endangered Lister's gecko (*Lepidodactylus listeri*) and blue-tailed skink (*Cryptoblepharus egeriae*) are conservation dependent, remaining only within breeding colonies on Christmas Island (CI), and Taronga Zoo. This presentation describes the emergence and characterization of a novel bacterial pathogen found to be causing multi-systemic infections initially in captive endangered species and ultimately in free-ranging invasive geckos on CI.

Unusual lesions were first observed in Lister's geckos in October 2014. Affected animals had excessive sub-spectacular fluid, cranial subcutaneous nodules, gingival swelling, emaciation, reduced mobility and they invariably died. Histological examination of affected geckos revealed vast pools of PAS and Gram positive organisms surrounded by a thick extracellular matrix within the soft tissues of the head and internal organs. The most severely affected animals had pools of organism replacing 30-60% of vital organs, associated with minimal host inflammatory response.

Since the first identification of this unusual organism, similar infections have been noted in two invasive gecko species on CI, *Hemidactylus frenatus* and *Gehyra mutilata*, as well as a blue-tailed skink *Cryptoblepharus egeriae*.

Attempts to grow the bacterium in culture have been unrewarding. Whole genome sequencing of the organism places the bacterium as a novel *Enterococcus* species.

Disease was contained and eventually eliminated from the colony of reptiles through extended quarantine. The organism described has the potential to pose a significant threat to Christmas Island lizards and to the biodiversity of Australian herpetofauna should the organism reach the mainland.

Presenter Bio: Dr. Karrie Rose enjoys a multi-faceted role in wildlife health research, education, and disease investigation as manager of the Australian Registry of Wildlife Health, a conservation research program of Taronga Conservation Society Australia.

FRANCISCELLA TULARENSIS HOLARCTICA DISCOVERED IN NATIVE AUSTRALIAN WILDLIFE

***Karrie Rose*[1,2,3]**, *John-Sebastian Eden*[3,4], *Mang Shi*[3,4], *Jimmy Ng*[5], *Qinning Wang*[5], *John Bingham*[6], *Jemma Bergfeld*[6], *Vitali Sintchenko*[3,5], *Edward Holmes*[3]

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A metagenomic approach has been undertaken during a broad study to identify pathogens associated with neglected diseases of Australian wildlife identified over the past 20 years. One of the neglected diseases included acute mass mortality of ringtail possums (*Pseudocheirus peregrinus*) with enteritis and hepatitis.

To identify potential infectious agents, RNA was extracted from affected liver tissue. Host ribosomal RNA was deleted and libraries were prepared prior to an unbiased, high-throughput RNA sequencing approach. Data from pair-end sequence reads (100 nucleotide length) were assembled de novo using Trinity and screened for viral, bacterial and fungal pathogens through comparisons with existing databases. Through this approach we identified two cases of tularemia in ringtail possums (*Pseudocheirus peregrinus*), and these findings were confirmed following the isolation of *F. tularensis* ssp. *holarctica* biovar *japonica* from diseased liver tissue from one animal. Re-mapping the RNA sequence data against the complete genome of the F. *tularensis ssp. holarctica* reference strain T01 produced an assembly of 80,516 reads with 46.9% genomoe coverage with pairwise identity of 99.8%.

Affected ringtail possums emanated from acute mass mortality events reported one year apart from the same forested suburb of Sydney, Australia. Both possums had gross lesions of gastritis or enteritis and a consistent pattern of splenic necrosis, hepatocellular necrosis, pulmonary congestion with perivascular haemorrhage and fibrinoid vasculopathy. Immunohistochemistry confirmed the presence of *F. tularensis ssp holarctica* within the lesions.

The investigation confirms the existence of this zoonotic pathogen in southern hemisphere wildlife. Additional research is required to better understand the ecology of *F. tularensis ssp. holarctica* sufficiently to inform public health risk assessments, risk communication and biodiversity conservation.

Presenter Bio: Dr. Karrie Rose enjoys a multi-faceted role in wildlife health research, education, and disease investigation as manager of the Australian Registry of Wildlife Health, a conservation research program of Taronga Conservation Society Australia.

IDENTIFICATION OF PATHOGENIC *ESCHERICHIA ALBERTII* IN AUSTRALIAN WILD AND CAPTIVE BIRDS

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Escherichia albertii is a recently described organism that has been linked to diarrhea in humans, as well as epornithic mortality events in wild finches in Scotland and Alaska. To date, asymptomatic *E. albertii* infection has been described in a range of Australian avian species, as well as a single human bacteremic case. We report on the first identification of *E. albertii* associated disease in Australian passerine and psittacine birds, and the challenges in achieving accurate diagnosis. Fifteen cases over a period of 14 months were seen collectively by Taronga Zoo and the Australian Registry of Wildlife Health, in which 11 mortalities occurred. Standard necropsies were performed on deceased animals, as well as bacteriology and whole genome sequencing. Affected captive bird species included little lorikeets (*Glossopsitta pusilla*), a superb parrot (*Polytelis swainsonii*), a turquoise parrot (*Neophema pulchella*), a red tailed black cockatoo (*Calyptorhynchus banksii*), galahs (*Eolophus roseicapilla*) and an Australian raven (*Corvus coronoides*). Two wild bird species consisted of a rainbow lorikeet (*Trichoglossus moluccanus*) and an Australian magpie (*Cracticus tibicen*). Gross and histopathologic examination identified poor body condition and gastrointestinal disease with inconsistent hepatitis. Lack of identification and misidentification of the cultured non-lactose fermenting gram-negative bacilli occurred in all cases using commercial biochemical panels and the national reference laboratory. Whole genome sequencing provided the definitive diagnosis of *E. albertii*. These cases illustrate the presence of a pathogen of veterinary significance, with public health ramifications, whose importance is likely underappreciated due to the challenges associated with its identification in a commercial laboratory setting. Given that the majority of cases identified were from a public zoo, we recognize the potential for zoonotic transmission and advocate continued expedited disease investigation and public health measures. We also encourage the development of tests that will effectively identify *E. albertii* within public health laboratories.

Presenter Bio: Dr. Crouch is a veterinarian currently undertaking a Cornell University and Wildlife Conservation Society Combined Residency in Zoo and Wildlife Pathology. Her primary interests lie in Australian wildlife and the interface of emerging wildlife disease and human health.

TRACKING AN EXTINCTION-LEVEL DISEASE OUTBREAK IN REAL-TIME: THE BELLINGER RIVER SNAPPING TURTLE (*MYUCHELYS GEORGESI*)

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A previously health population of Australian freshwater turtle, the Bellinger River Snapping Turtle (*Myuchelys georgesii*), was rendered functionally extinct in the wild over a five week period. Although geographically limited to a 60 km stretch of the Bellinger River in Northern NSW, the population was considered to be locally abundant with a population estimated to range between 1500 and 4000 individuals prior to the event. The species has cultural significance as a locally iconic species, and is considered by members of the community to reflect the state of river ecosystem health. Beginning in February 2015, a disease outbreak resulted in the death of nearly every adult, and the majority of juvenile turtles. The species has since been listed as critically endangered and is dependent on the conservation management of a small population of animals taken from the wild ahead of the disease front.

The pattern of the disease outbreak, the highly consistent pattern of lesions in animals examined, and the lack of detectable toxins led to an early conclusion that the outbreak was likely to be caused by an infectious agent. Common pathogens of reptiles and aquatic species were ruled out through collaboration with six universities and two agriculture laboratories. A novel virus was subsequently isolated within the tissues of affected animals and there is a body of evidence sufficient to incriminate this as the primary etiological agent for the mortality event.

The outbreak investigation and response was multi-organizational and multi-disciplinary. This unusual mortality event presented a number of challenges with regard to resourcing, community engagement, biosecurity, risk assessment and containment measures by a range of stakeholders. The management and challenges of this disease investigation and response, as well as future considerations will be discussed.

Presenter Bio: Dr. Karrie Rose enjoys a multi-faceted role in wildlife health research, education, and disease investigation as manager of the Australian Registry of Wildlife Health, a conservation research program of Taronga Conservation Society Australia.

A MIXTURE OF BUTORPHANOL, AZAPERONE, AND MEDETOMIDINE FOR IMMOBILIZATION OF AMERICAN BEAVERS (*CASTOR CANADENSIS*)

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A total of 58 American beavers (*Castor canadensis*) were immobilized with butorphanol, azaperone, and medetomidine (BAM) for the purpose of health assessments, sex determination, and placement of VHF tail transmitters in a subset of animals. Isoflurane gas anesthesia was available to aid with induction when needed, and all animals received supplementary oxygen. Thirty-one beavers immobilized with a mean (standard deviation, SD) dose of 0.65 (0.15) mg/kg butorphanol, 0.22 (0.05) mg/kg azaperone, and 0.26 (0.06) mg/kg medetomidine did not require supplemental isoflurane during induction and the mean induction time was 8 min (range: 3-21 min). This dose was equivalent to 0.024 (0.005) mL of BAM per kg. A total of 29 beavers that were immobilized with a mean (SD) of 0.51 (0.07) mg/kg butorphanol, 0.17 (0.02) mg/kg azaperone, and 0.2 (0.03) mg/kg medetomidine needed supplementary isoflurane at 5% and 5 L/min for <1 minute to induce full anesthesia. In none of the beavers, did BAM alone provide sufficient depth of anesthesia to drill a hole in the tail for transmitter placement, and supplementary isoflurane was administered to reach a sufficient level of analgesia for the procedure. The beavers were reversed with 5 mg atipamezole per mg medetomidine and 1 mg naltrexone per mg butorphanol. No adverse effects or mortalities were observed. Butorphanol-azaperone-medetomidine can be considered safe for use in American beavers for minor procedures.

SHAPE ANALYSIS: A NEW FRONTIER IN WILDLIFE DISEASE ECOLOGY

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Geometric morphometrics uses shape analysis to compare physical traits across species, populations, and ecological niches. Historically, its application has been restricted to the fields of evolutionary and organismal biology. However, this tool could also be of great utility to disease ecologists by mapping the pathologic changes to normal host anatomy during infection. Particularly for diseases in which clinical signs manifest externally, geometric morphometrics provides a tool for quantitatively measuring lesions on a continuous scale. Such is the case with finch mycoplasmosis, an infectious disease of North American songbirds that can cause severe inflammation of the soft tissues surrounding the eye. The current convention is to score this pathology on a four-point scale (0-3) of increasing severity. Yet, use of a discrete scale may fail to capture the true range of disease phenotypes we observe in naturally-infected and experimentally-inoculated individuals. Moreover, there is currently no way to reliably compare scores across studies. Here, I use multidimensional shape analysis to track eye pathology using images of experimentally infected, captive house finches. Results correlated well with observer-assigned eye scores, validating the use of shape analysis in this system. Future studies will incorporate trajectory analysis to explore if variations in eye shape can distinguish critical stages in the disease cycle (i.e. early infection versus recovery). Notably, finch mycoplasmosis is just one of a myriad of wildlife diseases that cause external pathology, for which shape analysis might help predict disease outcomes, transmission potentials, and humane endpoints. This study marks the first time geometric morphometrics has been applied to the field of disease ecology and highlights a valuable new tool for wildlife diagnostics and health management.

<u>Presenter Bio:</u> Rachel Ruden is a doctoral student at Iowa State University and a 2016 graduate of the University of Pennsylvania School of Veterinary Medicine. She works in the Adelman Lab studying wildlife ecology and avian disease cycles. Captive experiments and field surveys explore mycoplasmal infection in house finches and backyard poultry.

UNDERSTANDING HEMORRHAGIC DISEASE: ARE MATERNAL ANTIBODIES AGAINST EHDV IMPORTANT FOR FAWNS?

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Hemorrhagic disease (HD) is caused by epizootic hemorrhagic disease (EHD) virus (EHDV) and/or bluetongue virus, and can cause large-scale mortality in white-tailed deer (*Odocoileus virginianus*). However, the apparent impact on deer populations throughout their range varies. These variable patterns of infection and disease are most apparent when comparing southern and northern populations. Numerous host, virus, vector, and environmental factors explain these patterns. Among potential host factors involved, previous studies in white-tailed deer demonstrated that innate resistance and previous exposure to EHDV are important factors. Additionally, although maternal antibodies against EHDV are known to persist in fawns for 3-4 months, the importance of these antibodies has not been investigated. Our objective was to determine the role of maternal antibodies in the protection of fawns against EHDV-2 infection and disease. Fawns (n=10) were removed from does at 2-3 days old and hand-raised. Fawns were divided into two groups, EHDV-2 antibody positive (n=6) and EHDV-2 antibody negative (n=4) and were inoculated at four to eight weeks of age. Animals were monitored daily for clinical signs and blood was collected for virology, serology, and hematology on 0, 3, 5, 7, 10 and 14 days post inoculation (dpi). Antibody negative fawns all developed viremia, had mild clinical signs, and seronconverted. For antibody positive fawns, two developed a transient and low-titer viremia and four had no detectable viremia and no increase in antibody titer by 14 dpi. These data demonstrate the importance of maternally derived antibodies in protecting fawns from EHDV infection and disease.

Presenter Bio: Mark Ruder is an Assistant Research Scientist at the Southeastern Cooperative Wildlife Disease Study at the University of Georgia.

VARIATION IN EHDV-2 INFECTION RATES IN *CULICOIDES SONORENSIS* AFTER FEEDING ON INFECTED WHITE-TAILED DEER OVER THE COURSE OF VIREMIA

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Epizootic hemorrhagic disease virus (EHDV) is transmitted by *Culicoides* biting midges (Diptera: Ceratopogonidae) to numerous wild and domestic ruminants and is a significant pathogen of white-tailed deer (WTD; *Odocoileus virginianus*). In North America, the only confirmed vector of EHDV is *C. sonorensis*, although other *Culicoides* species are suspected vectors. Previous experimental infections have demonstrated WTD-to-*Culicoides* transmission of EHDV, but the impact of fluctuations in deer viremia on *Culicoides* infection rates has not been characterized. It is well-known that peak viremia occurs between 5 and 8 day post infection (dpi) and that WTD may remain viremic for as long as 60 days. Our objective was to determine how EHDV-2 infection rates in *C. sonorensis* vary over the course of viremia in experimentally infected WTD. Five hand-raised WTD were inoculated with 10^6 median tissue culture infective doses ($TCID_{50}$) by intradermal and subcutaneous injection. On 3, 5, 7, 10, 12, 14, 18, and 24 dpi, deer were sedated for blood collection, examination, and blood feeding by colonized *C. sonorensis*. Ten days post feeding, virus isolation and titration was performed on individual *C. sonorensis* to determine midge infection rates over the course of viremia in each deer. All five deer had a detectable viremia 3-14 dpi (mean peak titer: 10^4 $TCID_{50}$/ml, 5 dpi). We found that increases in deer EHDV blood titer significantly increased both the likelihood that midges would successfully acquire EHDV and the proportion of midges that became competent vectors ($\geq 10^{2.7}$ $TCID_{50}$/midge). Unexpectedly, we identified low numbers of infected midges after feeding on deer 5 on 18 and 24 dpi, after the deer had a detectable viremia by virus isolation. The ability of ruminants with low-titer viremia to serve as a source of EHDV for feeding *Culicoides* is an interesting finding and should be explored further to better understand the potential significance.

Presenter Bio: Mark Ruder is an Assistant Research Scientist at the Southeastern Cooperative Wildlife Disease Study at the University of Georgia.

VAMPIRE BAT (*DESMODUS ROTUNDUS*) DISTRIBUTION, IMPACT AND MANAGEMENT: TIME FOR A RE-ASSESSMENT

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Unlike their mythical European literary and cinematic humanoid counterparts, vampire bats are real and abundant, albeit only found in the American tropics and sub-tropics below ~2400 meters. Such bats and their relatives were once much more widespread, even within North America and the Caribbean. Post-Pleistocene, several taxa went extinct. Introduction of European livestock during the 1500s provided an ample resource for subsequent population growth. Today, various climate models suggest opportunities for range expansion over the next several decades, especially as vampires lack cold tolerance. Given an exclusive diet consisting of blood, rabies virus transmission during feeding is a major public health and agricultural concern, as is the impact upon livestock production from blood loss, fly-strike and damaged hides for leather. In turn, vampires have a concert of anatomical, physiological and behavioral adaptations honed for this very distinctive sanguivorous life style, including: a low level stealthy flight to minimize disturbance during approach; acoustics devoted to detection of breathing sounds of sleeping prey; locomotor agility to avoid injury from the movements of larger mammals; infrared thermo-receptive identification of peripheral vessels; specialized scalpel-like incisors for an efficient, nearly pain-less bite; copious saliva with anti-coagulant properties; a grooved tongue to assist in lapping blood; an effective immune system for recognition of blood-borne pathogens; a highly absorptive GI tract for protein concentration and renal dynamics for rapid water excretion after a voluminous liquid meal; unique micro-biome for digestive aid of a hematophagous diet; superior cerebral capacity for recall of spatial locations of successful hunts; and regurgitated blood for social feeding of related roost-mates. In addition, vampires are gregarious and form colonies of ~20-100 individuals or larger, within caves, hollow trees, mines, tunnels, wells and abandoned buildings. They are highly responsive to environmental disturbance from human activities related to logging, mining, hydropower, etc. towards invasion of new areas and foreign prey. Control methods were developed during the late 1970s, in part to reduce more coarse-grained practices with severe detrimental effects upon multiple beneficial taxa. Vampire-specific population reduction typically employs anticoagulants spread upon the fur of captured bats, which are then released back to their roosts for exploitation of social grooming to target multiple individuals. As might be imagined, such techniques are labor-intensive and limited in scope. Regardless of any potential increase in overall future distribution of vampire bats, including to the USA, a more holistic One Health approach to modern wildlife management is long overdue for practical application to this unique bat species. Clearly, there is no ideal 'one-size-fits-all' approach for all affected ecosystems from rural grasslands, offshore islands, arid deserts, urban habitats or ever-shrinking Neotropical forests within Amazonia. Such strategies should entail improved public education and training, promotion of bat conservation, enhanced laboratory-based surveillance, application of economic models for goodness of fit to varying circumstances, differential farming and environmental practices, vaccination of livestock and humans at risk of infection and novel research applications for better community management of local vampire bat populations. Besides historical introspection by FAO, OIE and WHO, the international research community at large, within academia, government, industry and NGOs, is invited for renewed engagement on this fascinating but neglected wildlife disease issue towards new policies.

<u>Presenter Bio:</u> Dr. Charles E. Rupprecht obtained his veterinary degree from the University of Pennsylvania during 1985 and his Ph.D. in Biological Sciences from the University of Wisconsin. He currently serves as an Expert Technical Advisor on Rabies for the World Health Organization and is an independent biomedical consultant and CEO at LYSSA LLC.

DESCRIPTION OF GASTROINTESTINAL AND CARDIORESPIRATORY ENDOPARASITES IN GUIGNAS (*LEOPARDUS GUIGNA*) FROM CHILE

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The guigna (*Leopardus guigna*) is the smallest wild cat in the American continent. It has a restricted geographic distribution only in central-southern Chile and Argentina. It is one of the most endangered wild felids in Latin America, classified as Vulnerable by the IUCN Red List. Main threats for guignas are habitat fragmentation, diseases, illegal killing and road kills. In the current fragmented landscapes, domestic animals and wildlife increase their contact probabilities. In this context, it is possible to investigate the contact between guignas and domestic carnivores through the pathogens and parasites they could share. Previous studies on endoparasites of guignas were based on *coprological analysis*, direct techniques in a low number of animals and only targeting gastrointestinal parasites. The objective of this study was to describe the gastrointestinal and cardiorespiratory endoparasites of guignas in Chile. Between 2015 and 2017, dead guignas were collected from road-kills or after deceased or euthanized in wildlife rescue centers. Gastrointestinal tract, heart and lungs were analyzed through direct analysis with *stereo microscope and artificial digestion.* 24 guignas were analyzed, 20 (83%) animals were positive to gastrointestinal parasites and 7 (29%) were positive to cardiorespiratory parasites. The most prevalent Nematode species found were *Toxocara cati* (37.5%), *Toxascaris leonina* (37.5%) and *Uncinaria* sp. (54%). Cestodes were found in 13 (54.2%) guignas, identified as *Taenia* sp. (54%) or belonging to *Pseudophyllidea order (46.1%).* Cardiorespiratory parasites identification is still in progress. The endoparasites found in this study are the same species previously described in guignas and other wild and domestic felids. The molecular identification of the helminths will be performed in the near future to understand the transmission of parasites between domestic carnivores and wildlife. Our results will be valuable to inform conservation decisions for guignas and other wild carnivores.

Presenter Bio: Irene Sacristán Yagüe is a PhD student of the Conservation Medicine Program at Andrés Bello University of Chile. She is currently investigating the effects of anthropization in guignas, focusing specially in the interspecific transmission of pathogens between domestic species and wildlife.

SPATIAL OVERLAP BETWEEN FREE-ROAMING DOMESTIC CATS AND THREATENED GUIGNAS NEAR CONSERVATION AREAS IN CHILE: IMPLICATIONS FOR DISEASE TRANSMISSION

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Free-roaming domestic cats can affect wildlife in different ways, including disease transmission. This study was conducted in the coastal range of Los Ríos region, in southern Chile, near sensitive areas for conservation in the Valdivian rainforest ecoregion. We evaluated the possibility of pathogen transmission by assessing spatial and temporal overlap between free-roaming domestic cats and threatened guignas (*Leopardus guigna*). We monitored 49 owned, free-roaming domestic cats with GPS tracking devices to assess their movements into guigna habitat and blood samples were also obtained to detect feline leukemia virus (FeLV) and feline immunodeficiency virus (FIV) infection (by PCR). We found evidence of spatial overlap between both species, that may facilitate contact and possibilities for direct and indirect pathogen transmission. Domestic cats in this study had variable home range areas, ranging from 0.9 to 45.5 hectares. The maximum distance recorded from the household was 2 kilometers, whereas the maximum distance into guigna habitat was of 1.3 kilometers. Seasonality, house density and cat density were the identified factors associated with the spatial use of free-roaming cats. We found 10.8% and 4.3% FeLV and FIV prevalence in domestic cats, respectively. We applied questionnaires to 66 households in the study area. The domestic cat population in the area was abundant (3 cats/household), with low birth control (13.1%) and deficient health management, most of them lacking both vaccines and antiparasitic treatments (85.7%). Most of the cats had a local origin (89.2%), with low immigration, supporting the implementation of successful birth control and vaccination campaigns. To reduce the risk of pathogen spillover from domestic cats to wildlife, we recommend promoting responsible ownership of domestic cats and environmental education, as well as improving access to pet birth control and health care services in remote areas, and reducing the presence of free-roaming domestic cats near conservation priority areas.

Presenter Bio: Irene Sacristán Yagüe is a PhD student of the Conservation Medicine Program at Andrés Bello University of Chile. She is currently investigating the effects of anthropization in guignas, focusing specially in the interspecific transmission of pathogens between domestic species and wildlife.

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UNDERSTANDING THE EPIDEMIOLOGY OF HEMOTROPIC MYCOPLASMA IN THE WILD FELID GUIGNA IN CHILE

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The guigna (*Leopardus guigna*) is a wild felid species endemic to Chile and Argentina, considered Vulnerable by the IUCN. Hemotropic mycoplasmas (i.e., hemoplasmas) infect mammalian erythrocytes. In Chile, natural hemoplasma infections have been reported in domestic dogs and cats, and in wild Darwin's foxes (*Lycalopex fulvipes*). Our goals were to evaluate the presence and risk factors for hemoplasma infection in guignas and its prevalence in domestic cats inhabiting guigna distribution range. Blood and spleen samples of 96 wild guignas from nine regions (the whole species distribution in Chile) and 234 rural domestic cats from five of these regions, were analyzed by conventional and real-time PCR targeting the 16S RNA gene. Biological and spatial variables were tested in order to determinate the infection prevalence.
Hemoplasma prevalence in guignas and domestic cats did not differ (19.7% and 15.3%, respectively). No differences in guigna prevalence were observed in regards to sex, age or region. Two *Mycoplasma* species were identified: *Candidatus* M. haemominutum (CMhm: 57.89% of guignas; 63.8% of cats), with nine different haplotypes; and *M. haemofelis* (15.7% of guignas; 30.55% of cats), with one haplotype. A unique sequence was obtained from two guignas and one cat, presenting 100% nucleotide identity with a sequence obtained from a Darwin´s fox. Guignas and domestic cats shared two out of nine CMhm haplotypes, and another one was present solely in guignas. A spatial analysis showed that a higher vegetation cover was related to higher *hemoplasma* prevalence in guignas. Since higher vegetation cover is assumed to be inversely related with the probability of contact with cats, this suggests that intra-specific transmission might be important in guignas. This is the largest and most comprehensive study of hemoplasmas in wild guignas and its domestic counterpart.

Presenter Bio: Irene Sacristán Yagüe is a PhD student of the Conservation Medicine Program at Andrés Bello University of Chile. She is currently investigating the effects of anthropization in guignas, focusing specially in the interspecific transmission of pathogens between domestic species and wildlife.

A CAN OF WORMS: ONE HEALTH STUDIES ON THE EPIDEMIOLOGY AND TRANSMISSION OF THE RACCOON ROUNDWORM (*BAYLISASCARIS PROCYONIS*) AMONG HUMAN, DOMESTIC, AND WILDLIFE HOSTS

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A One Health approach to disease investigation is especially well suited to parasites of wildlife, many of which have complex life cycles and whose transmission is influenced by many host and environmental factors. *Baylisascaris procyonis* (raccoon roundworm) is a ubiquitous parasite of raccoons, a highly adapted urban species. Infection with larval stages of *B. procyonis* can have fatal consequences in >150 species of birds and mammals, including humans, making this pathogen a major threat to both public and wildlife health. Our goal was to investigate aspects of *B. procyonis* epidemiology and transmission among humans, domestic, and wildlife, including the risk of occupational exposure among wildlife rehabilitators, evaluating infection dynamics and variability in survival among wild rodent hosts, and investigating the role of domestic dogs as *B. procyonis* definitive hosts. Among wildlife rehabilitators, 7% (24/327) had antibodies to *Baylisascaris* suggesting prior subclinical infection. Significant risk factors included region, *B. procyonis* prevalence in raccoons, and consistency of hand hygiene after contact with raccoons/their feces. A questionnaire on knowledge, attitudes and practices revealed that correct knowledge and attitudes depend on factors such as educational background and experience. Use of personal protective equipment and infection control by raccoon rehabilitators depended on similar factors. Studies on tolerance and survival among *Peromyscus* spp. (deer mice) demonstrated species-level differences in infection dynamics which may influence parasite transmission and maintenance. Finally, studies on *B. procyonis* in dogs revealed aspects of epidemiology and infection biology. From a national reference laboratory database, *Baylisascaris* eggs were detected in 0.005% (504/9,487,672) of dogs. Experimental infections in dogs and raccoons revealed lower host competence in the domestic host versus the natural raccoon host. Only 2/12 dogs became infected compared to 12/12 raccoons, with longer prepatent periods and lower egg outputs among dogs. Collectively, these studies answer important questions on a high-consequence zoonosis.

<u>Presenter Bio:</u> Sarah Sapp recently graduated with her PhD in infectious diseases from the University Of Georgia College Of Veterinary Medicine. Currently, she is a postdoctoral fellow with the Parasitic Diseases Branch at the Centers for Disease Control and Prevention. Her research interests include diagnosis and epidemiology of emerging zoonotic helminth species.

AN OUTBREAK OF PARVOVIRUS IN MUSCOVY DUCKS (*CARINA MOSCHATA)* AT A WILDLIFE REHABILITATION CENTER

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Waterfowl parvoviruses have been described in several countries, including China, France, Germany, Hungary, and Israel. Muscovy duck parvovirus (MDPV) affects ducklings under 6 weeks of age, resulting in an extremely high rate of morbidity and mortality. Reports of MDPV in the United States are rare and have only occurred in commercial duck operations in both California and Pennsylvania around 1997. In May 2017, the South Florida Wildlife Center in Fort Lauderdale, Florida started to observe high morbidity and mortality in young Muscovy duck orphans admitted from a large urban feral population, on admission and at various times post-admission. Clinical signs included ataxia, weakness, dyspnea, and sudden death. Post-mortem samples were submitted to several laboratories; initial testing ruled out avian influenza and duck viral enteritis. Histologically, non-specific lesions were found, including enteritis, lung and kidney congestion, and hepatitis. In August 2017 a diagnosis of MDPV was made by PCR and confirmed through genetic sequencing (>98% similarity to several MDPV strains). Following this diagnosis, the wildlife center depopulated all young ducklings and rehomed a small number of adults. All indoor and outdoor habitats were thoroughly disinfected with bleach (1:30 dilution) or sodium chlorite. A 5-day in-cage quarantine protocol was implemented for all Muscovy ducklings; however, when staff continued to encounter mortalities, the intake quarantine was extended to 10 days. Deaths are still occurring at the wildlife center, and testing of additional samples is pending for further confirmation and characterization of this parvovirus. The viral outbreak has presented numerous challenges to the wildlife center, requiring staff to re-evaluate housing, disinfection protocols, and tracking of mortalities. In addition, the occurrence of MDPV in a feral Muscovy duck population raises the concern of this virus becoming an emerging disease across the Florida urban landscape, where large populations of this non-native waterfowl thrive alongside native waterfowl.

<u>Presenter Bio:</u> Renata Schneider, DVM, is a graduate of the University of Montreal, Canada. In 2002, she completed an internship at the Broward Avian and Exotic Animal Hospital in Fort Lauderdale, Florida. In 2003, she began work at the SFWC and was promoted to Director of Wildlife Rehabilitation in 2012.

COMPARATIVE ANALYSIS OF SEROLOGICAL CROSS-REACTIVITY USING CONVALESCENT SERA FROM FILOVIRUS-EXPERIMENTALLY INFECTED, CAPTIVE-BORN EGYPTIAN ROUSETTE BATS

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The family *Filovirdae* includes three genera: *Ebolavirus*, *Marburgvirus* and *Cuevavirus*. The genus *Ebolavirus* includes five species comprised of one virus each (Ebola, Bundibugyo, Tai Forest, Sudan and Reston viruses), while the genus *Marburgvirus* includes one species comprised of two viruses (Marburg and Ravn viruses). With the exception of Reston virus, the ebolaviruses and marburgviruses can cause large hemorrhagic fever outbreaks in Africa. The Egyptian rousette bat (*Rousettus aegyptiacus*) has been identified as a natural reservoir host for the marburgviruses and cumulative evidence suggests that bats are also reservoirs for the ebolaviruses. The search for the natural reservoir hosts of the ebolaviruses has involved testing wild-caught bats for evidence of past infection. Collectively, serological reactivity of bat sera with various ebolavirus-specific antigens have been detected in >300 bats representing at least 17 species throughout sub-Saharan Africa and Asia. However, interpretation of this mounting serological data has been difficult due to the use of various recombinant viral antigens, different methods for establishing cut-off values for seropositivity, and the absence of positive and negative control sera for assay validation and quality control. In this study, we generated filovirus-specific antisera by inoculating 124 captive-born Egyptian rousette bats with one of seven filoviruses. Two months later, the bats were boosted with homologous virus and 2-3 weeks thereafter antisera was collected. To examine the extent of serological cross-reactivity between the seven filoviruses, we tested the IgG antibody reactivity of the antisera against the filoviruses using non-recombinant, infectious virus-based antigens prepared from each of the filoviruses by ELISA. No cross-reactivity was observed between marburgvirus antisera and ebolavirus antigen, nor ebolavirus antisera and marburgvirus antigen. However, strong cross-reactivity was observed between Marburg virus antisera and Ravn virus antigen and vice-versa; while, varying levels of cross-reactivity were observed between antisera generated from the five ebolavirus groups and the ebolavirus antigens. This data will be critical for interpreting the results of serological studies aimed at identifying the natural reservoir hosts of the five known ebolaviruses.

Presenter Bio: Amy Schuh, PhD, MPH works with the Virus-Host Ecology Team within the Viral Special Pathogens Branch at the Centers for Disease Control and Prevention. The team uses captive-born *Rousettus aegyptiacus* bats to study the mechanisms of filovirus maintenance and spillover to humans.

CAUSES OF MORTALITY IN NEW YORK STATE WHITE-TAILED DEER AND PREDICTIVE UTILITY FOR CLINICIANS

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White-tailed deer are the number one game animal in the country and are an important species in ecosystems. Deer health is important for maintaining their status as an economic and recreational resource. Records of 734 dead white tailed deer (*Odocoileus virginianus*) that died in New York State between January 2011 and November 2017 were analyzed in this retrospective study. The objective was to determine major and minor sources of mortality in the population and determine demographic and seasonal trends associated with these mortalities. Abnormal deer were recruited prioritized for examination as part of CWD surveillance; no positive CWD cases were detected. We determined thirteen major causes of death, such as bacterial infection (n=110), trauma (n=85), and nutritional (n=32) issues. Bacterial deaths were the most common in all sex and age groups and acted as the baseline for modeling efforts. Using a multinomial logistic regression, we quantified likelihood of death with age, sex, and time of year. The model found an increased risk of death from hunting (p=0.0003) and nutritional issues (p=0.0004) with time of year, as well as juvenile animals having an increased risk of death from fungal (p=0.00) and nutritional (p=0.01) causes. Our study will assist clinicians and wildlife biologists in determining likely causes of death in subsections of sick or abnormal free-ranging white-tailed deer.

WANTED DEAD OR ALIVE: MOOSE HEALTH IN NEW YORK STATE

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Moose in the Adirondacks region of northern New York State represent the southern extent of the eastern moose (*Alces alces*) subpopulation. Currently, there is a multi-institution study examining population metrics. One component is to assess factors that may affect survival of New York moose. We collected samples from live moose (n=26; 3 males, 23 females) and necropsied moose mortalities (n=138) over the course of 18 years. Survival rate of live moose was high, despite exposure to *Parelaphostrongylus tenuis* (78% prevalence). Moose in New York appear to have fewer ectoparasites (e.g., winter tick, *Dermacentor albipictus*) than reported in other eastern states. However, we found *Neospora caninum* (52% prevalence) was common in this population. Pregnancy (16 of 22) and calving rates (15 of 20) were high. An average of 7.3 mortalities were examined annually with more males (51%) than females (38%); the number of juvenile (≤2.5-years-old) mortalities was twice that of adults. More than half the animals we examined had died or were euthanized after being struck by a vehicle. Mortalities directly from *P. tenuis* (8%) or *F. magna* (2%) were not common, but we found these parasites frequently at necropsy (12% and 23%, respectively) even if they were not the primary cause of death. Additionally, we identified echinococcus cysts in 10% of examined animals. Although parasitic infections are common in this population, they do not appear to be affecting reproduction. However, higher mortalities rates in juveniles may be limiting population growth.

WEST NILE VIRUS SEROCONVERSION IN LOGGERHEAD SHRIKE AFTER VACCINATION WITH A KILLED VIRUS VACCINE WITH APPLICATION FOR DEVELOPMENT OF A VACCINATION PROTOCOL

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The Loggerhead Shrike is a migratory songbird that has undergone massive population declines in Ontario since the 1950s. As part of a broad strategy of recovery, a captive breeding population was established in the late 1990s, and release of captive-bred hatchlings into native habitat began in 2001. This species appears to be exquisitely sensitive to West Nile virus (WNV) infection, with prior outbreaks at Ontario breeding facilities suggesting a 100% mortality rate. A vaccination program using a killed equine WNV vaccine is currently in place for retained fledglings and adult breeding birds, but a knowledge gap exists regarding the response of fledglings to single versus serial vaccinations, the long-term support provided by vaccination and the seroprevalance of WNV neutralizing antibodies in unvaccinated wild-caught adult shrike. This study aims to investigate the humoral response to vaccination in hatch-year birds given single versus serial booster vaccinations, by assessing WNV-neutralizing antibodies via the plaque reduction neutralization test. Given the critical importance of each individual in this small population and the potentially devastating impacts of WNV on the species, developing an effective vaccination strategy for captive-bred young is a very important tool in the recovery of this species. In addition, demonstration of a sustained virus neutralizing titre in fledglings given only a single vaccination will inform vaccination protocols for wild-caught individuals who cannot be reliably recaptured for a booster vaccination. To be initiated in April 2018, this research aims to help conserve wild Loggerhead Shrike populations while also improving the health and welfare of their captive zoo counterparts, thereby strongly reflecting the role of veterinary challenges in field conservation. We will present preliminary data gathered through collaboration between veterinarians, biologists, and zookeepers.

Presenter Bio: Kerry graduated from the Ontario Veterinary College in 2017, and currently practices in Ontario as part of the veterinary team for the African Lion Safari. Prior to pursuing veterinary medicine, Kerry earned an M.Sc. studying forest ecosystem dynamics from the University of Guelph and worked as a contract conservation biologist.

ENUMERATING AND DIFFERENTIATING SPORE TYPES OF *BATRACHOCHYTRIUM SALAMANDRIVORANS* BY FLOW CYTOMETRY

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Batrachochytrium salamandrivorans (Bsal) has caused declines of wild fire salamanders (*Salamandra salamandra*) in Europe and is pathogenic to species in several salamander families. Predicting risk of *Bsal* to native salamander species requires comprehensive understanding of pathogen epidemiology, including pathogen persistence and environmental concentrations. Unlike *B. dendrobatidis* (*Bd*), *Bsal* has two zoospore types: a motile, flagellated zoospore and a non-motile, highly adhesive encysted zoospore, which differ in their environmental persistence and likelihood of overland transport by animals. Our goal was to optimize flow cytometry to differentiate between viable and dead zoospores as well as encysted and flagellated types. Flow cytometry could provide a rapid and robust approach to estimating live zoospore concentrations in the environment. Understanding the shedding rate of viable zoospores for each lifeform type is fundamental to modeling *Bsal* epidemiology and predicting likelihood of emergence and geographic spread. We tested variability in *Bsal* enumeration using hemocytometry, then optimized a flow cytometry protocol to enumerate *Bsal* spores and determine spore viability. Flow cytometry counts were more precise compared to hemocytometry counts performed by technicians of various skill levels. Hemocytometry counts made by an experienced observer were similar to those made by flow cytometry means respectively. Propidium iodide (PI) selectively stained nonviable spores and revealed that viability of *Bsal* spores in vitro ranged from 85-97%. Evaluation of Calcoflour White (CFW) stained cells using fluorescent microscopy revealed CFW selectively stains encysted spores making it an ideal candidate for differentiating *Bsal* spore types.

Presenter Bio: Ciara N. Sheets is an undergraduate student in Wildlife and Fisheries Science at the University of Tennessee, Knoxville. She is interested in amphibian disease ecology and determining the impact pathogens have on amphibian populations.

A PROBABLE SEWAGE-RELATED OUTBREAK OF SALMONELLOSIS IN A BLACK SKIMMER (*RHYNCHOPS NIGER*) COLONY IN FLORIDA

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The North American black skimmer (*Rynchops niger niger*) is a primarily coastal seabird whose eastern breeding range spans from Massachusetts south to Florida and the Gulf of Mexico. In Florida, this species is classified as "state threatened," chiefly from habitat loss associated with coastal development. Highly sensitive to disturbance, most FL skimmer colonies, especially those at recreational beaches, are closely monitored and managed. In August 2016, field researchers noted an unprecedented number of fledgling mortalities at the St. Petersburg Beach colony. Over approximately four weeks, 46 fledglings died, representing nearly 50% of the colony's offspring. Cooperative efforts between field personnel and the Florida Fish and Wildlife Conservation Commission led to the collection and necropsy of nine birds. Gross examination, histology, and microbiological assays revealed that the mortality event was due to salmonellosis. Serotyping at the National Veterinary Services Laboratories identified *S. enterica* serotype Typhimurium. The first skimmer mortality was observed 5 days following a sanitary sewage overflow (SSO) that released around 302,400 gallons of untreated sewage into the bay where the skimmers foraged. From August 8 to September 9, extreme weather events (i.e. tropical storms and hurricanes) resulted in the release of >100 million gallons of sewage from multiple wastewater reclamation facilities in the region. Although we cannot definitively conclude that SSOs caused the salmonellosis outbreak, the circumstantial evidence is highly suggestive. The events surrounding the SSOs received constant media attention, and criminal and civil lawsuits were filed. This outbreak illustrates how stochastic events can severely impact local wildlife populations. Climate change scientists have predicted an increase in frequency and severity of extreme weather events. Thus, wildlife management plans should include measures to address metapopulation losses associated with stochastic events, especially those compounded by human population growth.

<u>Presenter Bio:</u> Dr. Shender is a wildlife veterinarian at the Florida Fish & Wildlife Conservation Commission, where her primary role is to coordinate response to avian mortality events, provide wildlife veterinary technical assistance, and conduct disease surveillance and research. She mentors student externs and consults on a variety of wildlife health subjects.

ABUNDANCE AND POPULATION GENETICS OF AN EXPANDING POPULATION OF BLACK BEARS (*URSUS AMERICANUS*) IN CALIFORNIA'S CENTRAL COAST RANGE

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California's black bear (*Ursus americanus*) population has increased over the past 30 years resulting in geographic range expansion throughout the state. One area of interest is the Central Coast Range of California, San Luis Obispo and Monterey counties, which were historically inhabited by grizzly bears (*Ursus arctos*) that likely competitively excluded black bears from the region. Since the extirpation of grizzly bears in the 1900s, black bears from the southern Sierra Nevada Mountain Range colonized this region. We used non-invasive genetic capture-mark-recapture to estimate baseline population abundance, examine population structure, and describe genetic variability of black bears in a 1,140 km^2 area in San Luis Obispo County and a 1,360 km^2 area in Monterey County. Over an eight week sampling period in 2013 in San Luis Obispo County we identified 63 unique individual black bears. The total population estimates for San Luis Obispo County generated by two models were nearly identical, 101 (95% CI: 84-134) for Capwire and, 100 (95% CI: 78-143) for MARK. We identified only four unique individual black bears during a 10 week sampling period in Monterey County in 2014, despite a greater sampling area and longer sampling season. We were unable to model abundance for Monterey County due to the low number of individuals identified. Based on genetic population structure analysis, the 67 individuals from San Luis Obispo and Monterey counties belong to a single panmictic population. This study represents the first effort to estimate abundance, examine population structure, and describe genetic variability of black bears in San Luis Obispo and Monterey counties. Results will help inform conservation and management decisions in the future by providing baseline population estimates and genetic structure.

Presenter Bio: Jamie Sherman is a PhD and DVM candidate from the UC Davis School of Veterinary Medicine. Her research focuses on diseases, genetics and effective management of black bear populations. Jamie plans to combine her passion for research and veterinary knowledge to advance wildlife population health and welfare into the future.

ASSESSMENT OF THE SERUM PREGNANCY-SPECIFIC PROTEIN B TEST TO DETERMINE PREGNANCY IN FREE-RANGING ELK (*CERVUS ELAPHUS*)

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Since the re-introduction of 177 elk (*Cervus elaphus*) into Pennsylvania from 1913-1926, the population has grown to a minimum count exceeding 1,000 animals. Historically, pregnancy rates in the free-ranging elk herd in Pennsylvania have been monitored through examination of uteri collected in the field by hunters and delivered to a mandatory check-station. In addition to being burdensome for the hunters, sample sizes each year are significantly reduced as a result of sampling error. A serum pregnancy test would improve these post-mortem efforts and provide a comparable test that could be used on live animals. BioPRYN®$_{\text{wild}}$ is a commercially-available Enzyme-Linked Immunosorbent Assay (ELISA) for the detection of Pregnancy-Specific Protein B (PSPB), a protein produced by the placenta of the fetus. This assay has been used to accurately detect pregnancy in multiple domestic ruminant species after 40 days post-breeding. From 2013-2017, paired serum samples and uteri were collected from 245 free-ranging elk during the annual 5-day hunting season in November. Uteri were examined to determine pregnancy status and the age of the embryo based on published data. ELISA testing was performed by BioTracking, Inc. (Moscow, ID). Sensitivity and specificity of the ELISA were determined using uterine examination results as the gold standard. Sensitivity and specificity were calculated both with ELISA high-rechecks considered as pregnant and open, and were reported herein as a range. Of the 245-examined uteri, 96 were pregnant and 149 were open. Embryos ranged in age from $\leq$ 14 to 55 days (n=74). The BioPRYN®$_{\text{wild}}$ ELISA test had a sensitivity of 93-95% and specificity of 91-93%. The positive and negative predicted values were 87-90% and 95-96% respectively. These results suggest that the PSPB ELISA is an accurate test for pregnancy in elk, and could serve as a useful tool for monitoring pregnancy rates in the free-ranging herd in Pennsylvania.

Presenter Bio: Julia Silva Seixas was born in Rio de Janeiro, Brazil and studied biology and bioethics at the Pennsylvania State University as an undergraduate. She graduated with honors in May 2018. She intends to work as a researcher after getting a Ph.D. in wildlife conservation and a degree in veterinary medicine.

DEFINING AND MEASURING WILDLIFE HEALTH ACCORDING TO THE EXPERTS

Diana Sinclair[1], *Craig Stephen*[2,3], *Jane Parmley*[1,3], *Andria Jones-Bitton*[1], *Claire Jardine*[1,3]
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Wildlife populations face a multitude of challenges in today's environment. Understanding which wild animal populations are healthy, and thus able to withstand these challenges, and which are vulnerable is essential for wildlife conservation. However, defining and measuring wildlife health is challenging, particularly because the wildlife health field includes a wide range of professionals with different educational backgrounds who use different professional terminology and concepts. The purpose of our study was to provide greater understanding of expert stakeholder perspectives on the meaning of health for wildlife. To ascertain the opinions of experts in terms of what wildlife health is and how it is measured, we held focus group meetings with eight homogenous stakeholder groups: veterinarians (n=2 groups), biologists and ecologists (n=2 groups), wildlife rehabilitators (n=2 groups), hunters (n=1 group) and trappers (n=1 group). A qualitative phenomenologic approach was used to analyze the data using a constructivist paradigm and thematic analysis. Results showed that there was no single, shared definition of health for wildlife, not even within a specific stakeholder group. There were similarities identified in the methods used to evaluate health and the language used to describe health both within and even between groups. Ultimately, whether an individual animal or a population is deemed "healthy" depends on the context and scale used by the evaluator, which depends on that person's goals and values.

Even though the wildlife health field is made up of a diverse group of professionals, commonalities found within this analysis, such as the importance of the ability to cope and adapt, suggest that a shared health definition is feasible. The wildlife health field would benefit from further discussions and development of a standardized and clear definition of health as this would make communicating findings across professional divisions easier and increase our ability to inform and improve wildlife management.

Presenter Bio: Diana Sinclair is a PhD Candidate at the University of Guelph. She completed her DVM through the Ontario Veterinary College in 2008 and a Masters of veterinary studies (conservation medicine) through Murdoch University in 2012. She is currently one of the staff veterinarians at the Toronto Wildlife Center.

ECOLOGICAL NICHE MODELING OF FOUR CULICOIDES SPECIES OF VETERINARY SIGNIFICANCE IN FLORIDA USING GENETIC ALGORITHM FOR RULESET PREDICTION (GARP)

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Epizootic Hemorrhagic Disease (EHD) is a viral arthropod-borne affliction affecting wild and domestic ruminants, predominantly white-tailed deer, as well as sheep and cows to a lesser extent. Animal morbidity and mortality due to EHD threatens ecosystems and poses economic hardships to deer and cattle farmers. EHD virus (EHDV) is transmitted to vertebrate animal hosts by biting midges in the genus *Culicoides*. *Culicoides sonorensis* is the only confirmed vector of EHDV throughout the United States, but is considered rare in Florida and not sufficiently abundant to support EHDV transmission. The present study used an ecological niche modeling approach, known as the Genetic Algorithm for Rule Set Prediction (GARP), to model the potential geographical distributions of four *Culicoides* species suspected of transmitting EHDV in Florida, including *Culicoides insignis, Culicoides stellifer, Culicoides debilipalpis* and *Culicoides venustus*. Models were developed in the DesktopGARP program, using species occurrence data from field sampling at >3,000 sites from 2008-2016, along with 23 environmental variables from Worldclim and Trypanosomiasis and Land use in Africa (TALA) describing precipitation, temperature, and vegetation indices. For three *Culicoides* species (*C. insignis, C. stellifer* and *C. debilipalpis*) 96-98% of the presence points were correctly predicted across the majority of the Florida landscape (63.77% - 72.53%). For *Culicoides venustus*, models correctly predicted 98.00% of presence points, but across a small portion of the Florida landscape (27.42%). Models for three of the four species were then validated with separate datasets of *Culicoides* spp. presence collected by independent mosquito control districts around the state of Florida (2017 data). Because vector borne disease pathogens cannot exist in the environment without the vector, these model outputs can be used to estimate the potential risk of disease across Florida, which by extension predicts regions where the pathogen poses higher risk to the host animals.

Presenter Bio: Kristin Sloyer is a graduate research assistant at the Florida Medical Entomology Laboratory, a Research and Education Center and part of the Institute of Food and Agricultural Sciences at the University of Florida. Kristin's research interests focus on the spatial and vector ecology of arthropods of medical and veterinary significance.

INFLUENZA A VIRUS EXPOSURE AND DIVERSITY IN AFRICAN MAMMALS IS DRIVEN BY DIET BUT NOT SOCIALITY OR PHYLOGENY

Sanatana E. Soilemetzidou[1], *Erwin. de Bruin*[2], *Franz Mathias*[1], *Ortwin H.K. Aschenborn*[3], *Peter Seeber*[1], *Marion Koopmans*[2], *Alex D. Greenwood*[1,4*], *Gábor Á. Czirják*[1*]

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Influenza A viruses (IAV) represents repeatedly emerging pathogens with a near worldwide distribution. While the natural hosts for IAV are generally considered to be among different avian species, several mammalian species can be productively infected. Sub-Saharan Africa is home to a taxonomically diverse avian and mammalian fauna for which little information exists on influenza dynamics. In many cases, human and domestic animal populations border or overlap with wild mammal which could promote potential pathogen spill-over and spill-back among populations. Moreover this region is the over-wintering site for many Eurasian migratory bird species, including several reservoirs for IAV, allowing a cross-continental transmission between different hosts. The objective of this study was to investigate the influenza exposure in free-ranging, sympatric mammalian species in Namibia and understand the potential ecological factors influencing the rate of exposure and the viral diversity. Using a protein microarray on 111 serum samples from 16 different African mammals, we determined the seroprevalence and hemagglutinin diversity and tested whether diet, sociality and phylogeny are related to variation in these parameters. Our results indicate that wild mammals are exposed to a surprisingly diverse influenza subtypes. Herbivores presented low prevalence of H4, H5 and H11, while carnivores showed a higher prevalence and diversity of HA protein reaction, for H1, H3, H5, H7, H8, H9, H11, H14 and H16. Phylogeny and sociality had no statistical association, while diet significantly explained both the prevalence and hemagglutinin diversity ($p < 0.001$ for seroprevalence and $p= 0.009$ for hemagglutinin diversity). This effect was mainly driven by high seroprevalence and diversity in carnivores which regularly feed on birds such as the black-backed jackals (*Canis mesomelas*), caracals (*Caracal caracal*) and honey badgers *(Mellivora capensis*). These findings suggest that wild mammals could represent an overlooked influenza reservoir and they could play a role in the influenza transmission.

Presenter Bio: Sanatana-Eirini Soilemetzidou is a veterinarian and doctoral candidate in the Department of Wildlife Diseases of the Leibniz Institute of Zoo and Wildlife Research. Her research interests are wildlife diseases and conservation medicine. Her current research focus is on influenza diversity and disease transmission in wildlife of Central Asia and Africa.

SAVING ENDANGERED KILLER WHALES: A CAPTIVE AND FREE-RANGING COLLABORATION

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Conservation of free-ranging killer whales (*Orcinus orca*) relies on understanding individual and population health threats. Examining and extrapolating diseases from display animals directly to free-ranging populations as is often done with smaller cetaceans, birds and terrestrial species is not necessarily feasible for killer whales. Similarly, while the use of alternative sympatric or parapatric cetacean species may provide insights into ecosystem health, these species may not be as effective for understanding the natural history or diseases specific to killer whales. However, captive orca and data from them can be effectively used to develop models and techniques to better inform efforts with free ranging populations. Study design, data collection and evaluation are collaborative efforts with the final goal being enhanced monitoring of free–ranging populations to facilitate conservation measures. Non-invasive techniques include collecting data and samples from post-mortem examinations, validation of fecal endocrine studies, microbial analysis of exhaled breath samples, development of microbiome libraries, capturing overhead photographic images to simulate those collected from free-ranging whales utilizing drones, and collecting data and samples such as blood and milk, in association with routine monitoring. These data have advanced studies of population morbidity and mortality, evaluation of changing animal morphometrics, caloric consumption, endocrine profiles during pregnancy, changing nutritional states and toxin transfer from adult females to their off-spring. When beach cast animals are available, natural mortality events are thoroughly investigated and findings documented. In cases of ongoing, low grade sublethal impacts or catastrophic events, such as oil spills, blast injuries, micro-plastics, contaminants and other insults, health assessment and comparison of findings through retrospective analysis of captive whale data or prospective investigations with live display animals can provide invaluable baseline information into the health care and management of wild stocks. Non-invasive studies directly inform population monitoring techniques on free-ranging animals in a variety of impactful ways.

Presenter Bio: Judy St. Leger is a veterinary pathologist and the Vice President for Research and Science at SeaWorld. She integrates conservation science and actions into the world of display animals. She wants to be a farmer someday when she can find the time.

EPIDEMIOLOGICAL INVESTIGATION OF AN OUTBREAK OF EPIZOOTIC HEMORRHAGIC DISEASE IN KENTUCKY

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An outbreak of epizootic hemorrhagic disease (EHD) virus serotype 2 (EHDV-2) was responsible for significant mortality of white-tailed deer in Kentucky in the summer and fall of 2017. From July 19 to October 21, a total of 1812 reports were received, representing 4581 cases of sick (20%) or dead (80%) deer. The geographic distribution of the outbreak zone in Kentucky was defined by the Appalachian plateau region where over 90% of cases were reported. Epizootic hemorrhagic disease virus, serotype 2 was isolated from 38 of 43 deer sampled statewide; 24.9% (1141) of reported deer were male, 62.5% (2865) were female, and 5.5% (254) were fawns. Of the 1832 reports received, most (1051, 57.4%) described deer that were found at or near water. The remaining 13.9% (254), 12.8% (234), 11.3% (208), and 4.6% (85) were from woods, fields, roads and yards, respectively. Serological testing during the fall of 2017, demonstrated high prevalence of EHD antibodies in deer harvested at wildlife management areas within the outbreak zone, ranging from 50-83%. Based on radio-telemetry data from 59 collared does within the outbreak zone, a crude mortality rate of 42.5% was calculated. Bone marrow from seven of 12 carcasses (58.3%) tested positive for EHDV via RT-PCR, with a calculated EHD-specific mortality rate of 24.7%. Given the advanced state of decomposition at the time of testing, it is estimated the EHD specific mortality rate could be higher and approach the crude mortality rate, with significant population level impact across parts of the Appalachian region.

Presenter Bio: Iga graduated from the Ontario Veterinary College in 2007 and obtained her DVSc in zoological medicine and pathology in 2012. For the past three years, she has been the wildlife veterinarian for the Kentucky Department of Fish and Wildlife Resources, and recently accepted a position with the Government of Saskatchewan.

CAN HARM REDUCTION BE ADAPTED AS A STRATEGY FOR WILDLIFE HEALTH ACTION IN THE FACE OF UNCERTAINTY AND CONFLICT?

***Craig Stephen*[1]**, *Christa Gallagher*[2]
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[2]Ross University School of Veterinary Medicine, St. Kitts and Nevis

Unprecedented threats to wildlife health and sustainability are inspiring conversations on the need to change how we work to protect and promote healthy wildlife. Scientific uncertainty and social conflict over the importance of healthy wildlife often delay actions to reduce harms. This presentation explores harm reduction as a new model for action. Harm reduction is a set of perspectives and practices that support policies and programs to reduce the negative health, social and ecological consequences of hazards to individuals, communities, and ecosystems from persistent and complicated problems, such as pathogens or pollutants, without requiring elimination of the hazard. Its origins lie in well-established public health actions aimed at protecting entire communities, rather than only addressing effects on individuals. It recognizes that harms from persistent hazards cannot solely be addressed by targeting one part of the network but instead requires a broader societal response. It recognizes that the harms associated with persistent hazards are spread across individuals, communities, and systems. This presentation uses 2 cases studies (BC salmon aquaculture and human-monkey conflicts in St. Kitts) to explore how harm reduction might be applied to help promote action to protect wildlife health. We used scoping literature reviews and key informant interviews to assess the potential value of harm reduction. In both cases; (i) the approach was seen as a means to reduce conflict by reorienting to collaborative governance and promoting a shared understanding of issues; (ii) it was no one's responsibility to integrate and coordinate the social and ecological dimensions of harms to identify opportunities for collaborative governance or action; (iii) diverging values, scientific uncertainty, and multiple ideologies prevented a simple path forward. Based on outputs from this project, harm reduction processes and principles were incorporated into a multi-stakeholder government advisory panel's recommendations as a mechanism to motivate action associated with wild-farmed fish conflicts.

Presenter Bio: C. Stephen is the director of the Canadian Wildlife Health Cooperative and Professor in Population Health. C. Gallagher is an Assistant Professor of Public Health and Epidemiology.

REVIEW OF DISEASE RISKS IN WILD GREATER ONE-HORNED RHINOCEROSES (*RHINOCEROS UNICORNIS*)

***Virginia Stout**, Deborah McCauley, Gretchen Kaufman*
Veterinary Initiative for Endangered Wildlife

The greater one-horned rhinoceros has been listed as CITES Appendix 1 since 1975 and lives in fragmented populations in Nepal and India. Several case reports and one review have been published about diseases in the captive greater one-horned rhinoceros (*Rhinoceros unicornis*) but there have been no comprehensive literature reviews published and only one case report from the wild. Due to the status of greater one-horned rhinoceroses it is imperative to increase disease surveillance and investigation of the remaining wild populations. A literature review has been conducted to identify diseases of interests for these populations. Little information is available for the greater one-horned rhinoceros therefore the review was expanded to include all species of rhinoceros and then evaluated by likelihood of each disease in the geographical area. Gastrointestinal problems, cardiac problems, respiratory problems (including tuberculosis), foot disease, neoplasia (including leiomyomas), intravascular hemolysis (including leptospirosis), neosporosis, and tick-borne diseases were published as the major causes of morbidity and mortality. This review will be used to direct further field studies of health in wild greater one-horned rhinoceros populations and prioritize diseases for surveillance to prevent further loss of this species.

Presenter Bio: Dr. Virginia Stout is a veterinarian who has experience in wildlife capture, field surgery, research, and disease surveillance. She has worked in many different environments including sites across the USA and Canada as well as Nepal. She currently contracts with VIEW, and the US Fish and Wildlife Service, Wildlife Health Office. She graduated from Auburn University Veterinary School and has a Masters of Conservation Medicine from Tufts University. She is the Bozeman representative for VIEW.

VACCINATING VAMPIRE BATS AGAINST RABIES: CRAZY LIKE A FOX?

Daniel G. Streicker[1,2], *Rachel Abbott*[3], *Kevin Bakker*[1], *Julio Benavides*[1], *Laura Bergner*[1], *Jorge Osorio*[4], *Tonie Rocke*[3] *and Carlos Tello*[5]

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Across Latin America, vampire bats have been culled for over 30 years with hopes of reducing attacks on humans and livestock and preventing rabies. Whether culls reduce rabies transmission has been questioned on epidemiological and theoretical grounds, but few empirical studies have quantified the effects of culling on the burden of human or domestic animal rabies. Our analysis of an intensive, multi-year bat cull in southern Peru showed that culls drastically reduced vampire bat populations, providing short-term relief to bat-livestock conflicts. However, culls had negligible effects on the burden of livestock rabies and failed to prevent viral invasions into or out of culled areas. The inability of culls to eradicate rabies implies a perpetually-incurred cost with limited benefits for rabies prevention, motivating interest in alternatives for rabies management. As vaccines have been the cornerstone of rabies management in carnivores, topically-spread oral vaccines might provide a useful supplementary strategy to manage bat rabies. By conducting field experiments with inert biomarkers, we demonstrated that vaccine coverage could be attained at levels that epidemiological models suggest would be sufficient to prevent viral invasions. Major regulatory issues aside, the main challenge for vaccine-mediated elimination of vampire bat rabies is scalable delivery. Engineering non-pathogenic, naturally-occurring, vampire bat-specific viruses as self-perpetuating rabies vaccines is an exciting prospect for enhanced delivery that might bring the vaccination success stories of North American raccoons and Western European foxes to Latin American bats.

Presenter Bio: Daniel Streicker is a Wellcome Trust and Royal Society Sir Henry Dale Research Fellow at the University of Glasgow in Scotland. His research over the last 12 years has used longitudinal field studies, phylogenetics and mathematical modeling to understand the drivers of rabies transmission within bats and to other species.

DEVELOPMENT OF *EDWARDSIELLA PISCICIDA* VACCINE VECTOR STRAINS WITH REGULATED DELAYED ATTENUATION FOR FISH PATHOGENS

***Banikalyan Swain**, Roy Curtiss III*
University of Florida, Department of Infectious Diseases & Immunology, College of Veterinary Medicine, Gainesville, FL, USA

Aquaculture is the fastest growing part of agriculture worldwide. It plays a great role in food security, livelihood and is a source of income and social development. However, infectious diseases of bacterial, viral and parasitic have caused most significant destructive impact to aquaculture production and result economic losses in the global aquaculture industry. *Edwardsiella piscicida* causes edwardsiellosis is more common fish disease outbreaks in a variety of freshwater and marine fish species. Vaccination would be the most effective method to prevent infectious diseases and their associated economic losses. In this study, we have successfully designed and constructed a recombinant attenuated *Edwardsiella* vaccine (RAEV) vector system with regulated delayed attenuation *in vivo* attributes that synthesizes *Ichthyophthirius multifiliis* (Ich) protective antigens to enable vaccination of fish susceptible to white spot disease and edwardsiellosis. We designed strains that display features of wild-type virulent strains of *Edwardsiella piscicida* at the time of immunization to enable strains to effectively colonize lymphoid tissues and then to exhibit a regulated delayed attenuation in vivo to preclude inducing disease symptoms. To achieve regulated delayed attenuation in vivo that based on the substitution of a tightly regulated araC PBAD cassette for the promoters of the fur and crp genes such that expression of these genes is dependent on arabinose provided during growth. Thus, following colonization of lymphoid tissues, the Fur and Crp proteins cease to be synthesized due to the absence of arabinose such that attenuation is gradually manifest in vivo to preclude induction of diseases symptoms. These strains will exhibit a desirable balance between safety and immunogenicity. Our RAEV vaccine will protect teleost fish against multiple bacterial and parasitic infectious diseases.

THE SEA TURTLE MICROBIOME: A CASE STUDY ON THE IMPORTANCE OF MARINE MICROBIOME SCIENCE FOR ECOSYSTEM HEALTH

Aubrey M. Tauer
Cūra Earth, Minneapolis, MN, USA

The Human Microbiome Project taught us a lot about how important the microbiome is to mammals, and we are still learning how the microbiome can influence health or be influenced by outside forces (such as diet, toxins, infections). Comparatively little is known about the microbiome of reptiles or marine animals. As the waters that sea turtles live in become increasingly polluted and with climate change the pH, temperature, and even amount of salt in the ocean will change. Climate change and its effects could change the microbiome in sea turtles, or their diet, and therefore affect their basic physiology. Recent work has found that knowledge of the microbiome of endangered species can be critical for conservation efforts. Research in rehabilitated green turtles (*Chelonia mydas*) on opposite parts of the world has shown a drastic change in the gut bacterial communities during hospitalization, confirming that changes in diet and environment can have a significant impact on sea turtles. Baseline wild microbiome studies have only been published for *Caretta caretta* (Loggerhead Turtle) and green turtles, leaving 5 more sea turtle species currently understudied. Conservation challenges for all sea turtle species include a number of issues, one of which is pathogen infection of eggs. This is also a public health issue, as sea turtle eggs and meat are still consumed in a number of regions, with documented transmission of zoonotic diseases to humans. Learning more about the microbiome of all sea turtle species at different stages of development could help with conservation and public health strategies, such as pretreating eggs in hatcheries with probiotics. A multi-year research study into the skin and cloacal microbiome of wild Eastern Pacific hawksbills (*Eretmochelys imbricate*), green turtles, and Olive Ridleys (*Lepidochelys olivacea*) is underway in Nicaragua.

<u>Presenter Bio:</u> Aubrey Tauer received her DVM and MPH at the University of Minnesota, and worked in private practice and zoo and wildlife epidemiology before founding Cūra Earth in 2011. Dr. Tauer conducts research and capacity building on issues at the intersection of conservation and public health primarily in Latin America.

PATHOLOGY OF NEONATAL HAWKSBILL SEA TURTLES (*ERETMOCHELYS IMBRICATA*) IN ST. KITTS

Michelle M. Dennis[1], ***Alissa Tepedino***[1,2], *Kimberly Stewart*[1,2]

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[2]St. Kitts Sea Turtle Monitoring Network, Basseterre, St. Kitts, West Indies

Great efforts are made to sustain production of critically endangered hawksbill sea turtle (*Eretmochelys imbricata*) hatchlings, since few will survive until adulthood. Conservation programs which monitor hawksbill nests often hand-rear hatchlings that do not make it to sea until fit for release, yet there is a paucity of literature addressing diseases, which may impede rehabilitation. The objective of this study was to describe the pathology affecting neonatal hawksbill turtles of St. Kitts that died at the nesting site or while in pre-release care. Data was compiled retrospectively from necropsy reports of mortalities occurring from 2015-early 2017. From then forward, all deceased hawksbills identified by the St. Kitts Sea Turtle Monitoring Network were enrolled in this study. From 2015 to present, 33 turtles from 22 nests have been subject to a complete postmortem examination with histology and lesions were compared in turtles less than or equal to 1 week old to turtles greater than 1 week old. Common lesions identified in turtles ≤1 week old included thromboses (n = 5, 28%), pulmonary congestion and edema (n = 5, 26%), nephrosis (n = 4, 29%), bacterial pneumonia (n = 3, 16%), fungal dermatitis (n = 3, 25%), bacterial dermatitis (n = 2, 17%), bacterial omphalitis (n = 2, 20%), and skeletal malformations (n = 2, 12%). A greater assortment of lesions affected turtles >1 week old, but gastrointestinal lesions (n = 4, 50%) and coelomic effusion (n=4, 29%) were common among this group. Gonads were histologically female in 14 of 15 turtles assessed, raising concern for high nest incubation temperatures. At the conclusion of this study, the findings can be used to better focus prophylaxis and treatment efforts in rehabilitated neonatal and juvenile hawksbill turtles.

PREVALENCE OF TICK INFESTATION AND THE PHYSICAL AND LIFE HISTORY TRAITS OF MIGRATING BIRDS IN SOUTHERN ONTARIO, CANADA

Grace Thornton[1], *Ellie Milnes*[1,2] *and Nicole Nemeth*[1]
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Ticks that feed on migratory birds can be transported over vast geographic distances, potentially permitting spread and establishment of novel tick species and tick-borne diseases in northern latitudes. We sought to analyze relationships between physical (e.g., nutritional condition) and life history characteristics (e.g., foraging guild) of birds and the prevalence of tick infestation. Migratory birds were captured and inspected for ticks during spring migration in 2016 and 2017 at the Long Point Bird Observatory in southern Ontario, Canada. Bird species, body fat score, and age class (e.g., hatch year) were recorded. Any observed ticks were removed and identified by taxonomic key to species and life stage. Data were analyzed by negative binomial regressions to assess whether tick infestation was higher on avian migrant species that spend more time on the ground (i.e., ground foragers), are in poor nutritional condition, and are younger and thus less efficient foragers. 7.2% of birds (n=1,109) representing 32% of species sampled (n=77) carried at least one tick (range 1-48; mean=2.6). The most common tick species observed on these birds was *Ixodes scapularis* (n=165), followed by *Haemaphysalis leporispalustris* (n=38), *I. dentatus* (n=6), *Amblyomma americanum* (n=2), and *I. marx*i (n=1), with 144 nymphs and 68 larvae. The prevalence of tick-infested birds differed annually from 3.7% (n=596) in 2016 to 11.3% (n=513) in 2017. The most common bird species were the Magnolia warbler (n=127) and Blue jay (n=102); age distribution included adults (n=1,000) and hatch-year birds (n=7; 102 had unknown age). A significant relationship was found between the prevalence and intensity of tick infestation and foraging guild. Since tick infestations on birds upon northward migration is not uncommon, monitoring of these birds and the ticks they carry is important in assessing for the risk of spread of tick-borne diseases into Canada and other northern latitudes.

Presenter Bio: Grace Thornton completed a BSc. with a major in Wildlife Biology and Conservation at the University of Guelph and will be pursuing a Bachelor of Veterinary Medicine in 2018.

DYNAMICS OF AND FACTORS AFFECTING THE OCCURRENCE OF RABIES IN HUMANS AND ANIMALS IN SOUTH AMERICA

Meske Mauro, Lina Awada, Lina Mur, Kiyokazu Murai, Scott Epperson, ***Paolo Tizzani***
OIE – World Organisation for Animal Health, Paris, FRANCE

The dynamic of rabies in South America is complex and includes two main cycles: a terrestrial cycle involving domestic animals and an aerial cycle with the vampire bat (*Desmodus rotundus*) playing the main epidemiological role. The impact of the two cycles on public health is significantly different, with most of the human cases related to the aerial cycle. The objective of this work was to describe the dynamic of the disease in South America and to analyze the factors affecting its occurrence within the framework of the OIE strategy for the elimination of dog – mediated rabies. Rabies cases in humans and animals reported to the World Organisation for Animal Health (OIE) and the Pan American Health Organization (PAHO) by the national authorities from 2009 to 2015 were analyzed. The global number of rabies cases declined significantly over time (rho = -0.5; $p<0.05$), with a marked reduction for wildlife (rho = -0.6; $p<0.05$) and humans (rho = -0.7; $p<0.05$). Rabies cases were reported in 67% of the 239 administrative divisions in the region, with two main clusters of animal cases in Colombia and Brazil, and one main cluster of human cases in Peru. The majority of human cases (90/129) were due to contact with wildlife, vampire bats being the main source of infection (87/90). Of the factors impacting the occurrence of rabies cases, a significant association ($p<0.05$) with deforestation was observed. Although rabies continues to cause significant losses in South America, its occurrence has significantly declined during the last years. Different clusters of infection were identified depending on the population affected, the vampire bats being the main source of infection for humans. This information will help to elaborate targeted control and preventive programs for reducing the exposure to rabies in the region.

DEVELOPMENT OF A RAPID CANINE DISTEMPER VIRUS TEST USING PORTABLE, SMART-PHONE DRIVEN, MOLECULAR DIAGNOSTIC TECHNOLOGY

***Ania Tomaszewicz Brown**, Denise McAloose, Paul P. Calle, and Tracie A. Seimon*
Wildlife Conservation Society, Zoological Health Program, Bronx, NY, USA

Canine distemper virus (CDV) is a major conservation threat in captive and wild carnivores. Infection can result in rapid progression of clinical symptoms including respiratory disease and fatal encephalitis. Important challenges in monitoring wildlife for CDV include the inability to test samples in remote or under resourced locations and production of rapid results that allow immediate, appropriate interventions for many, including endangered, species. Investigation of diseases like CDV has historically required a significant investment of resources in the form of dedicated equipment, utilities infrastructure, and skilled personnel, making understanding disease ecology in these locations problematic. However, innovative new technologies are revolutionizing the field of molecular diagnostics. Expensive, resource-heavy platforms are being miniaturized and becoming more cost effective, allowing these tools to be placed in the hands and within the financial reach of many, and enabling diagnostics to travel farther and field teams to perform immediate, on-site sample processing and testing. We present the development of a new rapid CDV test that utilizes a five-minute extraction protocol, smart-phone driven, hand-held qPCR machine, temperature-stable qPCR reagents, and a small solar battery for off-grid capabilities. Systematic, comparative CDV testing between these new extraction and qPCR technologies and our standard, commercially available, bench-top protocols and equipment produced comparable virus detection sensitivity and efficiency. These tools provide a novel way to bring complicated molecular diagnostic tests directly to remote field locations, saving time and resources while eliminating the difficulties of international shipment for sample testing. These advancements will greatly improve our ability to diagnose infectious diseases in wildlife in the field and protect wildlife in wild places.

Presenter Bio: Ania Tomaszewicz Brown (MA) is the WCS Pathology Technician and Research Assistant. Since joining the WCS in 2014, Ania has worked with a wide range of species and taxa and performs comprehensive diagnostic testing for pathogens in our zoo-based animal collections and field based conservation projects.

ANALYSIS OF PLASMA PROTEINS OF GREEN TURTLES (*CHELONIA MYDAS*) WITH FIBROPAPILLOMATOSIS BY CAPILLARY PROTEIN ELECTROPHORESIS

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[2]Loggerhead Marinelife Center, Juno Beach, FL, USA

Fibropapillomatosis (FP), a debilitating neoplastic disease in sea turtles, can result in plasma protein alterations. Typically, these proteins are analyzed using agarose gel electrophoretic methods, which are well-established for use in reptiles. In the current study, capillary electrophoresis was used to examine plasma samples from juvenile green sea turtles (*Chelonia mydas*) with varying tumor burden: Balazs tumor score (TS) 0 (N=21), TS 1 (N= 12), TS 2 (N= 10), and TS 3 (N=2). Data obtained from agarose gel electrophoresis was compared to capillary electrophoresis using Passing-Bablok regressions. The following fractions showed a good significant correlation between the two methods: albumin, alpha-1-globulins, beta-globulins, and gamma-globulins (r_s=0.37 to 0.52, $P \leq 0.010$). Prealbumin and alpha-2-globulin fractions showed a poor non-significant correlation (r_s=0.02 to 0.14, P>0.360). The prealbumin fraction was visually the most striking as 2–3 bands could be observed via capillary electrophoresis versus one band for gel electrophoresis. Given the higher resolution of the capillary method, 9 fractions could be consistently defined, compared to 6 with gel electrophoresis. Comparisons between clinically normal animals and those with FP were conducted using a generalized linear model nesting straight carapace length within the TS. Given the small sample size, TS 2+3 turtles were combined for statistical analyses. There were no significant differences between these groups when analyzing the absolute values in g/dL. By percentage, fraction 3, a prealbumin migrating fraction, was significantly decreased in TS 2+3 turtles (P=0.015). In addition, fraction 9, a gamma migrating fraction, showed a significant increase in TS 0 v. TS 1 and TS 0 v. TS 2+3 turtles with approximately 6–7% more protein in this fraction in the FP-afflicted turtles ($P \leq 0.001$). Notably, tumor-bearing turtles showed substantial electrophoretic differences versus normal turtles. These data support continued examination of capillary electrophoresis as a research tool in green turtle FP.

Presenter Bio: Madison Toonder is a high school student at Stanford University Online High School. My research interests lie in veterinary science and conservation. I have conducted research on oysters, sea turtles, alligators, and pangolins in association with numerous universities. I also received the Environmental Excellence Award from SeaWorld in 2016.

DOES PRECIPITATION AFFECT HELMINTH COMMUNITY STRUCTURE IN A POPULAR GAMEBIRD SPECIES?

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The northern bobwhite (*Colinus virginianus*) has been experiencing a long-term decline throughout Texas, and it is unclear what role parasitism plays, if any. Bobwhite populations in Texas physiographic regions display variations in abundance among years—a boom-and-bust cycle—and are believed to be regulated by fluctuations in precipitation and temperature. However, it is unclear how parasite population dynamics are affected by changes in annual precipitation. Our objective was to examine species richness, prevalence, and mean intensity for bobwhite helminths over a 5-year period (2012–2017) to determine if helminth community structure changes with annual precipitation. Bobwhite carcasses were obtained from south Texas via hunter donation during the Texas quail hunting seasons of 2012–2013, 2013–2014, 2014–2015, 2015–2016, and 2016–2017. Each bird was examined for helminths. Species richness, prevalence, and mean intensity were calculated for each hunting season. Annual precipitation and Palmer Modified Drought Indices were acquired from the National Centers for Environmental Information interactive GIS map portal. Four potentially pathogenic helminths (*Aulonocephalus pennula*, *Oxyspirura petrowi*, *Tetrameres pattersoni*, and *Oncicola canis*) were found in all five years, regardless of annual precipitation. Eleven additional helminths rarely occurred; five of which did not occur during years with severe drought (2012–2013 and 2013–2014). The highest species richness (10) occurred during 2015 when south Texas experienced above average rainfall. Nematodes occurred in all years; however, although rare, cestodes occurred more frequently in years with normal or above average rainfall. Variation in precipitation appears to correlate with changes in helminth community structure within northern bobwhites in south Texas. It remains unclear if cestode prevalence is driven by rainfall. Future research needs to be conducted to determine pathogenicity effects of these helminths on bobwhites; meanwhile, ranch managers and quail hunters should expect to find helminths inside bobwhites, even in drought conditions.

SPECIFIC MOLECULAR DETECTION OF PIROPLASMS AND CHARACTERIZATION OF A BETA-TUBULIN GENE FOR A NOVEL *BABESIA* SPECIES IN SIKA DEER (*CERVUS NIPPON YESOENSIS*)

Mohamed Moustafa[1], Elzahraa Elbaz[1], Kyunglee Lee[2], Michito Shimozuru[1], Mariko Sashika[1], ***Toshio Tsubota**[1]*

[1]Hokkaido University, Hokkaido, Sapporo, Japan

[2]Cetacean Research Institute, National Institute of Fisheries Science, Ulsan, Republic of Korea

Piroplasms are protozoal parasites carried by ticks and very common to cause diseases in animals and humans. The diseases caused by *Babesia* species are manifested by fever, anemia and hemoglobinuria. Recently, an undescribed *Babesia* sp. and *Theileria capreoli* were detected, for the first time, in sika deer blood samples that were collected from Hokkaido, however, there is no information available on the epidemiology of these two protozoa in Japan. In this study, a touch down polymerase chain reaction and RLB hybridization were used to perform an epidemiological survey of the undescribed *Babesia* sp. and *T. capreoli* infections in 82 sika deer blood samples, which were collected from Hokkaido, Japan. This was followed by partial sequencing and phylogenetic analysis of the 18S rRNA and beta-tubulin genes to characterize the detected piroplasm species. A total of 43 (52.4%) and 3 (3.7%) of the sika deer blood samples were positive for *T. capreoli* and *Babesia* sp. (Bab-SD) species-specific probes, respectively. The obtained 18S rRNA gene partial sequences were divided into *T. capreoli* and the undescribed *Babesia* species (Bab-SD). The beta-tubulin gene partial sequences for the detected *Babesia* species were completely separated from the previously published sequences of *Babesia* species in the GenBank. The phylogenetic analysis showed that the sequences of the novel *Babesia* sp. are more related to *B. caballi, B. bigemina* and *B. ovata* than the other *Babesia* spp. sequences for 18S rRNA and beta-tubulin genes.

Here, the species-specific probes for both *T. capreoli* and *Babesia* sp. (Bab-SD) showed high specificity in the detection of these piroplasm species and the results were confirmed by cloning and sequencing. This study showed the first characterization of the novel *Babesia* sp. (Bab-SD) based on the partial sequencing of beta-tubulin gene from sika deer in Japan. Further studies are required to understand the ecology of the newly detected tick-borne pathogens in Hokkaido, Japan.

BAT VALUES VERSUS VAMPIRE COSTS—FINDING A BALANCE

Merlin D. Tuttle
Merlin Tuttle’s Bat Conservation, Austin, TX, USA

Of the more than 1,300 species of bats, only 3 are vampires. All are restricted to the New World, from Mexico to Argentina. Overall, the benefits from insectivorous, nectivorous and frugivorous bats of Latin American vastly outweigh the harm done by the common vampire. Unfortunately, only the harm Is easily seen, while the benefits go unnoticed. Furthermore, most vampire control is carried out by uneducated frontiersmen, who believe all bats to be vampires. Unfortunately, large colonies of insectivorous bats, worth millions of dollars to human economies, are often the most conspicuous and the first to be destroyed, when whole colonies are burned in their roosts. Killing the *wrong* bats only multiplies the problems and sometimes even killing the *right* ones appears to cause more harm than good. Nevertheless, vampires cannot be ignored. Considering the relative biodiversity and values of Latin America’s bats, rational and practical improvements are needed in dealing with vampire issues. There are no simple solutions, but grossly exaggerated media stories, most recently painting all bats as potentially dangerous, will only exacerbate current difficulties throughout the region.

Presenter Bio: Merlin Tuttle obtained his Ph.D. with honors at the University of Kansas, published extensively on bat population ecology and behavior, wrote two books, is the father of modern bat conservation, and currently directs Merlin Tuttle’s Bat Conservation. He has broad experience with Latin American bats.

CHANGING NEST SUBSTRATES INFLUENCES NEST PARASITES (*PROTOCALLIPHORA PARORUM)* AND PRODUCTIVITY OF CORDILLERAN FLYCATCHERS *(EMPIDONAX OCCIDENTALIS):* A COMPARISON OF NATURAL WITH ARTIFICIAL NEST SITES

***Charles Van Riper III*[1,2]**, *Andrew Boyce*[2] , *and Harold Greeney*[2]
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[2]School of Natural Resources and the Environment, University of Arizona, Tucson AZ, USA

Cordilleran Flycatchers are cavity-nesting birds that are nest-site limited in the southwestern US (Martin 2008). For nest-site limited birds, providing artificial nest boxes can enhance productivity (Duckworth 2016). In an attempt to enhance Cordilleran Flycatcher productivity, we developed nesting platforms and in 2008 provided them in a 1 X 2 X 6 experimental array. During this 10-year study (2008-2018) in southwest Colorado, throughout the first six years of platform usage flycatcher productivity increased by 46%. However, in year seven (2015) one nest was found parasitized by *Protocalloiphora parorum* maggots and all nestlings died. *Protocalloiphora parorum* is currently known to only parasitize cavity-nesting species and the nest maggots are not known to kill their hosts (Beckworth 2015). In year eight (2016) of our study over half of flycatcher nests on platforms were parasitized by these maggots, and bird productivity decreased to 15.4 %. In year nine (2017) 14 of 15 nesting platforms contained maggots and productivity was decrease by 88%. None of the natural “control” Cordilleran Flycatcher nests that we monitored were parasitized by *Protocalloiphora paror* during this 10-year period. We hypothesize that a novel situation developed with the introduction of nesting platforms, and a parasitic fly took advantage of this new nesting situation. Since the flycatchers are not parasitized in natural nesting situations, there has been little history of parasite-host coevolution. Therefore, the Cordilleran Flycatcher young are highly susceptible to the maggots of this newly introduced parasite, and all young are killed in every nest that is parasitized. This information provides another example of the consequences of parasites and diseases introduced into new regions, and will be important for managers who utilize artificial nesting platforms to enhance productivity of rare bird species in an attempt to conserve Neotropical migratory bird species of the Americas.

NEW TOOLS FOR DOCUMENTING MIGRATION ROUTES OF PASSERINE BIRDS IN THE AMERICAS: PROVIDING A BETTER UNDERSTANDING OF POTENTIAL ZOONOTIC DISEASE SPREADING PATTERNS

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Because of their small size, the movement patterns of most passerine (song) birds are poorly understood, as are their contributions to the potential spread of avian zoonotic diseases. A number of new research tools have been developed that will assist wildlife disease workers to better understand the timing and location of bird migration patterns in North America. In western NA, lowland riparian areas and upper mountain zones are known to be important migration corridors and stopover sites, and are thus the primary locations for potential zoonotic disease movement in song birds. However, species distributions and habitat associations of *en route* migratory birds across upland habitats are poorly understood, particularly in arid mountain regions. The Madrean Archipelago of southeast Arizona and northern Mexico provides vital "stepping stones" of relatively rare upland vegetation communities between the Central and South America wintering grounds and breeding areas in the United States, and Canada. We will discuss: 1) Geolocators and their use to examine the timing and movement patterns of migratory passerine birds, 2) the new tool “Geoscape” and how this can more clearly identify the origins of passerine birds carrying wildlife diseases, and (3) discuss potential zoonotic disease spread by migratory passerine birds. This information is important for a better understanding of the epidemiology of disease movement, and for wildlife disease workers working to conserve Neotropical migratory bird species of the Americas.

A NOVEL TREATMENT OPTION FOR SARCOPTIC MANGE IN AMERICAN BLACK BEARS (*URSUS AMERICANUS*)

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Sarcoptic mange has been a recent topic of concern for American black bears (*Ursus americanus*) in the mid-Atlantic United States. This parasitic disease has the potential to cause significant morbidity and even mortality in affected individuals, necessitating treatment or humane euthanasia. To date, the most common treatment for mange in wildlife is the administration of ivermectin often in two doses administered approximately two weeks apart. Though effective, this treatment option requires the animal to remain in a treatment facility or be recaptured in the field in order to be re-dosed. In the summer of 2017, the staff at the Wildlife Center of Virginia successfully treated an adult black bear affected by sarcoptic mange with a single oral dose of fluralaner (Bravecto®), an ectoparasitic preventative drug used in companion animals. After drug consumption was confirmed, the patient was monitored daily for signs of hair regrowth and improvement in skin condition and was periodically anesthetized for skin scrapes, all of which were negative for live mites. Approximately three months after fluralaner administration, the patient had made a full recovery and was released back into the wild with identification ear tags and a GPS radiocollar for future tracking efforts. This case report has major implications for the treatment options for sarcoptic mange in black bears, as it is the first to document the administration of this drug to this species. If fluralaner continues to prove to be safe and effective against sarcoptic mange, its use in the field could substitute the current treatment protocol using ivermectin. This novel treatment option may eliminate the need to capture or euthanize affected individuals in the wild.

VARIATION IN VOLATILE PROFILES BY SEX AND VIRUS INFECTION STATUS IN WHITE-TAILED DEER COULD INFLUENCE CULICOIDES BITING MIDGE FEEDING PREFERENCES

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White-tailed deer present in the wild and on farms throughout the United States are at risk of contracting the deadly virus epizootic hemorrhagic disease virus (EHDV). Culicoides spp. biting midges are the vector for this pathogen. As with other host– vector systems, biting midges (the vector) are likely to be attracted to deer (the host) due to the presence of certain compounds released from the deer's body. The objective of this study was to determine if the volatile chemical profile of EHDV infected and uninfected deer varied by infection status. To determine this, body swabs were collected from farmed deer (n=18), which were classified as EHDV infected or uninfected by detection of EHDV RNA in peripheral whole blood by real-time reverse transcriptase PCR. A total of 11 males and 7 females were tested. The samples were analyzed using a gas chromatograph (GC) to obtain the volatile profile for each animal. Multivariate statistics were then used to analyze the volatile profiles to show the clustering of animals by presence and absence of GC peaks. Animals clustered tightly by sex and females clustered by infection status. GC peaks associated with infection status have been determined and will be further elucidated by GC coupled with mass spectrometry. If volatile profile significantly differs by infection status, then it is possible that midges may be more or less attracted to EHDV infected animals, which could impact transmission dynamics. This on-going experiment has implications for EHDV management in farmed animals by providing further evidence for the need to quarantine infected animals to reduce virus transmission.

CORAL CAPTURE AND ANESTHESIA OF ASIATIC WILD ASS IN IRAN AND KAZAKHSTAN

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The Asiatic wild ass (*Equus hemionus*) is listed as an Endangered Species on the IUCN Red List and scientific evidence suggests their range has declined by 70% since the 19th century while abundance has declined by 50% in the past 20 years. In the wild, the species still occurs in Mongolia, China, Kazakhstan, Turkmenistan, Iran and India. Mongolia's population comprises 80% of the global population, with an estimated population of 35,000-40,000 individuals. Capture, sampling and satellite radio collaring of this species is a mainstay in conservation activities. The wild ass is generally extremely skittish—most probably due to poaching activities—and in some areas, flees human presence at several kilometers' distance. Several distinct techniques have been successfully employed in the past by these authors to capture 150+ individuals of this species in Mongolia. However, due to geomorphological constraints, capture events in Iran and Kazakhstan required a novel approach employing capture corals. In Bahram-e-Goor protected area in Iran, two small capture corals with remotely triggered doors were built and baited with water and fodder. Following several weeks of pre-baiting, 15 individuals were successfully captured. In the Altyn Emel national park in Kazakhstan, a large multi-segmented capture coral was built and wild ass were driven into the coral using 4x4 vehicles. Two drives resulted in the capture of 50 + individuals. At both sites individuals were selected from the coral and remotely darted with a combination of 4.4mg etorphine (Captivon, Wildlife Pharmaceuticals, Whiteriver, South Africa) 10-mg Detomidine–HCl (Domosedan, Orion Corp. Farmos) and 10-mg Butorphanol (Torbugesic, Fort Dodge Animal Health) and individually walked out into a processing enclosure. Following sampling and collaring the animals were either released (Iran) or treated with long-acting neuroleptics and loaded into crates for translocation to a release site (Kazakhstan).

INTO THE WILD – FRAMING WILDLIFE VETERINARY MEDICINE TO BETTER ADDRESS PRESSING GLOBAL CONSERVATION CHALLENGES

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Understanding wildlife health, containing and mitigating disease threats while considering human well-being, conserving biodiversity and the provision of ecosystem services, constitutes an international imperative. Since the first zoo veterinarian was employed 1831 in London, the world's population has grown from 1 billion to over 7.5 billion people. Today, practically all species live in dynamic multi-use landscapes in which anthropogenic activities are the main driver of change. While scientific communities consistently strive forwards in ever narrowing, clearly delineated and possibly protectionist specialty fields, similarly reflected in our respective organizations, in actuality there is but one 'wildlife'. This holds true irrespective of animals' housing conditions and context. Today, all wildlife survives along a gradient of increasing human encroachment and disturbance. Consensus exists that wildlife health, like human health, must be viewed beyond parasites and pathogens, incorporating social evolutionary and environmental factors while considering individual attributes and behaviors. In order for veterinarians to fully participate and even lead in the field of wildlife health in the future, they must necessarily embrace a holistic approach to health and be fully aware of and understand the pressing present-day conservation challenges. Wildlife health incorporates the capacity to cope with change and results from complex dynamic interactions of biologic, environmental, and socio-economic factors. Clearly, a modern and all-inclusive approach to wildlife medicine must integrate input across previously distinct disciplines such as physiology, ecology, animal behavior, conservation biology, economics, social sciences and many more. Particularly worrying has been the obstinate persistence of the traditional veterinary medicine and ecology silos. Integrating fitness, life-history traits and trade-offs when evaluating wildlife health in the face of chronic stress from anthropogenic pressures appears indispensable. Overcoming the traditional disciplinary boundaries while integrating novel approaches in describing and evaluating health in an ever-changing environment constitutes the major challenge for wildlife veterinarians in the future.

NEXT-GENERATION SEQUENCING AND CHARACTERIZATION OF NEWCASTLE DISEASE VIRUSES FROM DOMESTIC AND WILD BIRD SPECIES IN NIGERIA

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Newcastle Disease Virus (NDV) has a wide avian host range and large genetic variability, and virulent strains cause Newcastle Disease (ND), a leading worldwide concern for poultry health. NDV transmission at the agriculture-wildlife interface likely occurs between wild birds and poultry at feeding and water stations. The ecological effects of virulent viruses transmitted to wild birds from domestic poultry are of major concern. Although NDV has been long studied in Nigeria, phylogenetic analyses of NDV genotypes have only recently become available. Next-generation sequencing was conducted to provide complete genome sequence and characterization of NDV from both poultry and non-poultry birds in Nigeria. From this analysis, we found similarities across NDV isolated from domestic and wild birds. Of particular interest, two velogenic viruses (class II, genotype XIVb) were isolated from a healthy free-range domesticated duck and a migratory raptor that was originally banded in Finland but captured in Nigeria. Another three velogenic viruses (class II, genotype XVII) were isolated from a domesticated duck, a Malachite Kingfisher, and a White-backed Vulture. Furthermore, two virulent viruses (class II, genotype II) similar to the mesogenic Komarov vaccine virus that is used in Nigeria were isolated from a domestic chicken and a Black Kite, suggesting previous spillover and evolution of this virus. The similarities of genotypes in multiple species suggest that transmission of NDV to and from poultry and non-poultry birds is common. This is especially significant when considering the viruses were isolated from species of conservation concern under the International Union for Conservation of Nature. Although apparently healthy individuals were sampled, ND may have great effects on and is likely underrepresented in wild bird populations, e.g., undetected infected individuals or mortalities or migratory movements out of the study area; thus, emphasizing the significance of further surveillance and epidemiology of NDV in wild bird species.

CHYTRIDIOMYCOSIS CAUSES MICROBIAL COMMUNITY SHIFTS IN EASTERN HELLBENDER SALAMANDERS (*CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS*)

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Global amphibian biodiversity is threatened by the pathogenic fungus *Batrachochytrium dendrobatidis* (Bd) and associated clinical disease chytridiomycosis. Eastern hellbender salamanders (*Cryptobranchus alleganiensis alleganiensis*) are widely viewed as Bd-tolerant but Bd-naïve animals experience mortality due to chytridiomycosis after release to watersheds containing the pathogen. The cutaneous microbiome of amphibians is known to play a protective role in host response to chytridiomycosis and has been suggested to function as innate immunity. The microbiome of Bd-susceptible hosts is vulnerable to community shifts due to chytridiomycosis, but the impact of Bd on the microbiome of tolerant species is poorly understood. To characterize the effect of Bd on the microbial community of a tolerant host, we used next generation 16S rRNA gene sequencing to identify bacterial species present in swab samples collected from 38 eastern hellbenders during an experimental Bd infection spanning 187 days. All animals received treatment with killed Bd, then 32 animals were infected with competent Bd and six animals were sham infected. Clinical chytridiomycosis was observed in all infected and no sham infected animals with no mortality. Bacterial community changes throughout treatment and infection were quantified using alpha- and beta diversity metrics for each animal pre-exposure, post-killed Bd exposure, early chytridiomycosis and late chytridiomycosis. Experimental day was the most important predictor of microbiome structure, with all communities exhibiting increased species richness and phylogenetic diversity following initial sampling. Exposure to competent Bd affected the microbiome, most notably causing an increase in phylogenetic diversity. Our results demonstrate that Bd changes the microbiome of infected eastern hellbenders and support the hypothesis that the microbiome plays a role in host defense. Further investigation including transcriptomic analysis may elucidate the impact and function of the microbiome in Bd infection of eastern hellbenders and improve our understanding of successful host immune response to a pathogen of global importance.

CUTTING-EDGE APPROACHES FOR VIRAL PATHOGEN SURVEILLANCE IN NORTH AMERICAN VERNAL POOLS

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Ranaviral disease outbreaks have negatively impacted economically, ecologically, and culturally valuable populations of amphibians around the world. Current ranavirus surveillance methods fall short in their ability to non-invasively detect pathogen pressures on wild populations. Environmental DNA (eDNA) is the collection and identification of free DNA and has recently emerged as a powerful tool for detection of diverse host species and pathogens. To evaluate the efficacy of eDNA as a ranavirus surveillance tool, we adapted eDNA methods for detection of ranavirus in amphibian breeding pools. We sampled four vernal pools of known ranavirus history in Tully, NY, USA biweekly from May to October 2016 and compared non-invasive eDNA methods with classic lethal surveillance of larval amphibians using qPCR to quantify ranavirus abundance in each case. The vernal pool sites were located within one km^2 and included three pools with recent history of ranavirus-associated annual die-offs and large populations of ranavirus-susceptible target species, wood frog (*Lithobates sylvaticus*) and green frog (*Lithobates clamitans*). Environmental ranavirus was undetectable during expected peak ranavirus activity during June-July and increased to peak abundance in September-October in all four pools, revealing environmental ranavirus activity beyond the expected disease seasonality. Surprisingly, susceptible hosts showed almost no infections, indicating that ranavirus eDNA dynamics can be decoupled from dominant host populations. No alternative known ranavirus host species were identified in the vernal pools to explain the observed pathogen dynamics. Several regional environmental variables statistically associate with observed ranavirus eDNA trends, but no candidate direct mechanism such as resuspension of a ranavirus eDNA reservoir was identified. Thus, eDNA has proved to be a highly sensitive pathogen surveillance tool able to identify pathogen DNA in the environment in the absence of active infections in the dominant host population but further work is needed to relate ranavirus eDNA abundance to relative infectivity.

EXPERIMENTAL DENSITY REDUCTION TO DECREASE PREVALENCE OF CHRONIC WASTING DISEASE IN ELK

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Until recently, long-term persistence at low prevalence (<1%) was thought to be characteristic of chronic wasting disease (CWD) in elk (*Cervus elaphus nelsoni*). Low reported prevalence tended to alleviate concern about population effects and therefore minimized interest in CWD in elk. However, recent studies in Rocky Mountain National Park (Colorado) elk have revealed the potential for population level effects due to decreased survival. Further, at Wind Cave National Park (South Dakota) where the disease was first recognized in 2002, CWD was a leading cause (3.4% annually) of adult mortality (13.2%) within 5 years of detection. Within 10 years, adult mortality from CWD reached 9.4-12.5% and total mortality reached 18.7%. In context with other vital rates (adult pregnancy = 76.8%; juvenile survival < 0.5), mortality from CWD was unsustainable. Faced with increasing CWD prevalence and existing elk numbers that exceeded park objectives, the NPS reduced elk numbers at Wind Cave National Park by 50% during 2017. A detected CWD prevalence of 13.7% (90% HDI = [0.102, 0.174]) was similar to prevalence at Rocky Mountain National Park where elk survival has decreased in the last decade. Sustainability of the Wind Cave elk population will depend on a density dependent decrease in CWD transmission and/or compensatory increase in pregnancy and recruitment. To evaluate whether this hypothesized response will occur, we will hold the population at half the density observed in 2016 for at least 5 years and monitor CWD prevalence and vital rates to evaluate the effects of decreasing population density on disease prevalence, recruitment, and survival. Longterm research conducted at landscape scale, and ideally replicated across geographic locations, is crucial to developing effective management strategies to address CWD.

DIVERSITY AND ABUNDANCE OF ECTOPARASITES OF BREEDING SEABIRDS ON MIDDLETON ISLAND, ALASKA AND POTENTIAL GROWTH IMPACTS ON NESTING BLACK-LEGGED KITTIWAKE CHICKS

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Nesting bird colonies on Middleton Island, Alaska have undergone population fluctuations including a decline of breeding Black-legged Kittiwakes (Rissa tridactyla) since the 1980s. These population fluctuations are likely due to a variety of factors, but ectoparasites could be a contributing factor as studies on other bird species indicate fitness may be reduced with high tick intensities. From June-August 2014 and 2015, we sampled Black-legged Kittiwakes (n=611), Pelagic Cormorants (Phalocrocorax pelagicus) (n=154), Tufted Puffins (Fratercula cirrhata) (n=85), and Rhinoceros Auklets (Cerorhinca monocerata) (n=125) to: 1) determine the prevalence and diversity of ixodid ectoparasites 2) conduct a molecular survey for haemoparasites and 3) test if treatment of kittiwake nest sites with a mild insecticide reduces parasite loads and/or results in increased growth of nestlings in treated nests compared to those in control nests. Our data indicate that there were high burdens of Ixodes uriae on kittiwakes (mean 6, range 0-40, prevalence 63% and 10% in chicks and adults, respectively) and cormorants (mean 5, range 0-20, prevalence 73% and 19%), whereas lower tick burdens and prevalence were found on puffins (mean 1, range 0-3, prevalence 10% and 0%) and auklets (mean 1, range 0-2, prevalence 12% and 0%). Ixodes signatus was only detected on cormorants and in low numbers (mean 1, range 0-29). Kittiwake chicks sampled in 2015 (n=101) had higher tick burdens and lower weight and fledging success compared to 2014 (n=151). Kittiwake chicks from treated nest sites (n=139) had significantly lower average tick body burdens across years and higher average body weights across discrete time periods compared with kittiwake chicks from untreated sites (n=113). Furthermore, preliminary analyses indicate that treatment had a positive effect on fledge success (p=0.006 by logistic regression) and growth rate over a forty day period prior to fledging (p=0.004 by repeated measures ANOVA). No tick-borne pathogens (Borrelia) or other vector-borne parasites (Haemoproteus, Plasmodium, Babesia) were detected by PCR in the 747 sampled birds. These data suggest that while vector-borne pathogens are not transmitted at this site, ixodid ectoparasites may be common among seabirds on Middleton Island and could have negative effects on productivity.

CHARACTERIZING THE EPIDEMIOLOGY OF MULTIPLE PATHOGENS IN THE BLANDING'S TURTLE (*EMYDOIDEA BLANDINGII*)

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Pathogens such as herpesviruses, *Mycoplasma* spp., and frog virus 3-like ranavirus have been identified in many species of chelonians and are considered major contributors to morbidity and mortality in captive and free-ranging populations. However, their prevalence has scarcely been studied in Blanding's turtles (*Emydoidea blandingii*). To assess presence of these pathogens, 214 Blanding's turtles were sampled in Lake County, Illinois in 2017. DNA from cloacal-oral swabs was assayed for four ranaviruses, three *Mycoplasma* sp. two *Salmonella* sp., Emydoidea herpesvirus 1, tortoise intranuclear coccidiosis, and *Anaplasma phagocytophilum* using a multiplex quantitative polymerase chain reaction (PCR). Additionally, a subset (n=60) of samples was assayed for novel mycoplasmas using conventional PCR. *Emydoidea* herpesvirus 1 was detected in 17 individuals, most (n=16) occurred in May. Individuals were rarely positive for *Salmonella typhimurium* (n=2), both in July. A novel *Mycoplasma* sp. sharing high homology to other emydid mycoplasmas was detected in a single turtle. Pathogens were only detected in adult turtles with possible causes including increased lifetime exposure to pathogens and more inter-individual interactions compared to juveniles. No significant differences were seen in pathogen detection between different sexes or capture locations. The efficacy of using pathogens to assess population health as a response to land management practices is discussed. Continued monitoring of this population and habitat will be useful in determining which factors may contribute to pathogen occurrence in Blanding's turtles.

UPDATE ON ADENOVIRUS HEMORRHAGIC DISEASE IN DEER IN CALIFORNIA

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Case records from the California Animal Health and Food Safety Laboratory and the California Department of Fish and Wildlife were reviewed from 1990-2014 for all deer accessions submitted to CAHFS in order to determine the prevalence of adenovirus hemorrhagic disease (AHD) in California. We also examined histopathology, spatial and temporal distribution, age, and mule deer subspecies in deer that died from AHD. Of 483 deer submitted to CAHFS for diagnostic testing from 1990 to 2014, 17.2% were diagnosed with AHD. Of 83 deer with systemic infection, all had pulmonary edema and 26.5% had hemorrhage in the intestinal tract. 24% of deer with systemic infection also had ulcerative/necrotizing lesions in the upper alimentary tract. 45 of 483 deer had lesions confined to the upper alimentary tract and were suspected adenoviral infections. Columbian black-tailed deer (*Odocoileus hemionus columbianus*), particularly fawns/juveniles, were most frequently affected. Additionally, seroprevalence of AHD and prevalence of the virus (*Odocoileus* adenovirus -1; OdAdV-1) infecting retropharyngeal lymph nodes and tonsils were examined to determine if asymptomatic/latent infection occurs in deer bridging the time between outbreaks. Seroprevalence was low with only 30/471 serum samples testing positive for antibodies to OdAdV-1 by the virus neutralization test, all in counties and years in which mortalities due to AHD were diagnosed. Deer adenovirus was detected by RT-qPCR in only 4/1038 retropharyngeal lymph node/tonsil pools of hunter-killed deer. Interspecies infections were performed to determine if virus is maintained in other species between infections. Experimental infection studies in calves, lambs and squirrels indicate these species do not become infected and do not shed virus. Preliminary studies were performed in mice collected from counties during AHD herd mortality events in deer. OdAdV-1 was not detected by RT-qPCR in mice. Studies indicate rare deer carry the virus in tonsil/nodes and seroprevalence is low.

IMPACT OF OCEAN HEALTH ON MARINE ANIMAL AND PLANT COMMUNITIES

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Marine animals and plants face numerous threats including overexploitation, invasive species, environmental degradation and climate change. Whilst these problems are bad for marine organisms per se, unhealthy marine ecosystems can have ramifications above and beyond declines of species. This is because healthy marine ecosystems provide services to coastal human populations that promote social stability and preservation of terrestrial species, particularly in coastal watersheds. Given that most people live near the coasts, we have a vested interest in maintaining healthy ecosystems and gaining a better understanding of just how to assess the health their associated biota. Fortunately, it is not all bad news, and there are tools being developed to address or at least mitigate some of these problems that are exacerbating coastal degradation.

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MANAGING AN INVASIVE ANEMONE THREATENING CORAL REEFS AT PALMYRA ATOLL NATIONAL WILDLIFE REFUGE, LINE ISLANDS, CENTRAL PACIFIC

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Coral reefs are some of the most diverse ecosystems in the world but are under threat from land based pollution, overfishing, disease, and global climate change. When sufficiently stressed, coral reefs can undergo phase shifts where the ecosystem abruptly transitions from coral dominated to a monoculture of invasive organisms, typically macroalgae, thereby leading to loss of biodiversity. In 2007, a phase shift from corals to corallimorpharians (a type of anemone) was documented at Palmyra Atoll, Line Islands, covering a ca. 1 km^2 area centered around a shipwreck. In 2011, surveys revealed expansion of the CM smothering corals over a 3 km^2 area potentially placing coral ecosystems in the atoll at risk. This prompted the U.S. Fish and Wildlife Service, the lead management agency, to remove the shipwreck in 2013. Subsequent surveys in 2016 showed reversal of spread of CM around the ship impact site. We explain patterns of spread of the CM in terms of life history and local currents and show with a pilot study that pulverized bleach may be an effective tool to eradicate CM on a local scale. If applied strategically, particularly in heavily infested (>66% cover) areas, active intervention such as this could be an effective management tool to reduce CM impact on localized areas and decrease colonization rate of remaining reefs. This is the first documentation of the response of an invasive cnidarian to shipwreck removal. While this was a singular event in Palmyra, the spatial and temporal patterns of this invasion, as well as the eradications lessons described herein, are useful for anticipating and controlling similar situations elsewhere.

BIO: Thierry Work has a BS (entomology) from Texas A&M University, and an MS (entomology), DVM, and MPVM from University of California, Davis (UCD). He heads the USGS National Wildlife Health Center Honolulu Field Station and works on wildlife health issues in terrestrial and marine systems.

PATHOLOGICAL FEATURES OF NEMATODE INFECTION IN THE LUNG, MENINGES AND SKULL IN TSUSHIMA LEOPARD CATS

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Tsushima leopard cat (*Prionailurus bengalensis euptilurus*) is the subspecies of a Bengali wildcat habiting in Tsushima Island, Nagasaki, Japan. We performed the forensic pathological study of Tsushima Leopard cats provided by the Tsushima Wildlife Conservation Center. From 2014 until date, approximately 30 cases of Tsushima leopard cats have been submitted to Gifu University for forensic necropsies. At necropsy, various organs and tissues were collected and fixed, and HE sections were made for histopathology. Most of these 30 deaths were accidental, caused by traffic. Grossly the lungs often showed rough surfaces or slight multifocal consolidations. Histologically, there were various degrees of nematode infections in 19 of the 30 cases examined. The characteristic indications of this nematode disease were occasional to frequent occurrences of nematode larvae in the bronchioles and alveoli, and interstitial pneumonia caused by thickening of alveolar wall with infiltration of macrophages and epithelial cell hyperplasia. In severely affected cases, alveoli and the alveolar wall had marked thickenings with moderate granulomatous inflammation. Various degrees of smooth muscle hyperplasia in the wall of the bronchioles and small arteries, moderate fibromuscular hyperplasia, and peri-bronchial submucosal gland hyperplasia were detected. Moreover, nematodes occurred frequently in the skull and meninges with or without pulmonary nematode larvae. Morphological identification from impression smears of lung tissue specimens showed the existence of first stage larvae that belonged to the genus Gurltia. Molecular characterization of the detected larval stages in the lung, and adult nematodes in the skull and meninges, based on PCR, sequencing of 18S rRNA, and ITS-2 genes, suggested the presence of a species phylogenetically close to *Gurltia paralysan*. These parasitic infections including nematode larvae in the lungs and adult nematodes in the skull and meninges may cause various degrees of respiratory failures as well behavioral defects.

RESOURCE SELECTION DIFFERENCES BETWEEN SOUTHWESTERN MONTANA MALE AND FEMALE ELK (*CERVUS CANADENSIS*) DURING THE ANTHRAX RISK PERIOD

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Anthrax, caused by the spore-forming, environmentally maintained bacterium *Bacillus anthracis*, is a zoonosis afflicting both animals and humans globally. In the United States, disease outbreaks occur in wildlife and livestock species. Vaccination is used as the primary means of anthrax control in livestock, however, it is untenable in wildlife. Current anthrax control in wildlife includes surveillance and decontamination of carcasses. Therefore, identifying the geographical distribution of *B. anthracis* and understanding how risk areas are used by wildlife species is essential for disease management. Morris et al. (2016) previously studied male elk (*Cervus canadensis*) resource selection during the anthrax risk period and observed significant overlap between areas male elk prefer and *B. anthracis* potential. Female and male elk could be under different resource selection pressures in summer, which could lead to different anthrax exposure. Here, we captured a female elk herd in the same study areas as the male elk in Morris et al. (2016). We first followed Morris et al. (2016) and adopted the best resource selection function model (*i.e.* the mixed effects generalized linear model with elevation, slope, forest, distance to tertiary road and secondary road as covariates) for bull elk to adapt for female elk. However, the model showed poor predictive accuracy, which indicated different resource uses between bull and cow elk. We then modified the resource selection function models by adding two additional predictors, the seasonal difference of NDVI and distances to stream. We overlaid preferred habitats of cow and bull elk to identify the difference in resource uses in summer, and also overlaid preferred habitats of cow and bull elk with the distribution of *B. anthracis* to identify differences in potential anthrax exposure. Our study could improve disease management for anthrax in southwestern Montana and have important public health and economic implications.

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