70th Annual International Conference

Wildlife Disease Association

Holistic Solutions For Wildlife Health

July 23-29, 2022

Madison, Wisconsin, USA

70th Annual International Conference Wildlife Disease Association

July 23-29, 2022

Madison, WI

Planning Committee

Jonathan Sleeman, *USGS, National Wildlife Health Center*
Periegrinei Wolf*, Wildlife Disease Assocation*
Tami Ryan*, Wisconsin Department of Natural Resources*
Lindsey Long*, Wisconsin Department of Natural Resources*
Tony Goldberg*, University of Wisconsin School of Veterinary Medicine*
Kurt Sladky*, University of Wisconsin School of Veterinary Medicine*
Barry Hartup*, International Crane Foundation*
Anne Justice Allen*, American Association of Wildlife Veterinarians*
Shelli Dubay*, University of Wisconsin-Stevens Point*
Haley Lin*, 4th Year Student, University of Wisconsin School of Veterinary Medicine*
Keegan Lim*, University of Wisconsin, School of Veterinary Medicine*
Rebecca Schroeder, *USGS, National Wildlife Health Center*

Scientific Program Committee

Casey Barton Behravesh
Moses Chimbari
Sonja Christensen
Thomas DeLiberto
Colin Gillin
Tiggy Grillo
Maria-Richetta Hopkins
Jusun Hwang
Becki Lawson
Gladys Kalema Zikusoka
Mark Gregory Ruder
Craig Stephen
Eri Togami
Wendy Turner
LeAnn White

Student Workshop Committee

Dan Small
Craig Pittman
Irene Wright
Scott Wright
Shelli Dubay
Dr. Lorelei Lynee Clarke
Dr. Anne Justice Allen
Dr. Peri Wolff
Dr. Kurt Sladky
Barb Bodenstein
Dr. Anne Ballmann
Dr. Betsy Elsmo
Keegan Lim
Dr. Jennifer Ballard
Dr. Lindsey Long
Haley Lin

Table of Contents

Sponsors……....iv

Mission Statement & Charter of Values……viii

Sustainability……..ix

Conference Schedule……..……xi

Oral & Poster Presentation List.....xx

Oral Presentations……..……1

Poster Presentations……...97

Author Index……222

Continuing Education Form……239

Platinum Sponsors

USGS
science for a changing world

World Organisation for Animal Health
Founded as OIE

U.S. FISH & WILDLIFE SERVICE
NATIONAL WILDLIFE REFUGE SYSTEM

USDA

Silver Sponsors

School of Veterinary Medicine
UNIVERSITY OF WISCONSIN–MADISON

JACOBSON & SCHMITT ADVISORS

American Association of Wildlife Veterinarians

INTERNATIONAL WILDLIFE VETERINARY SERVICES, INC.

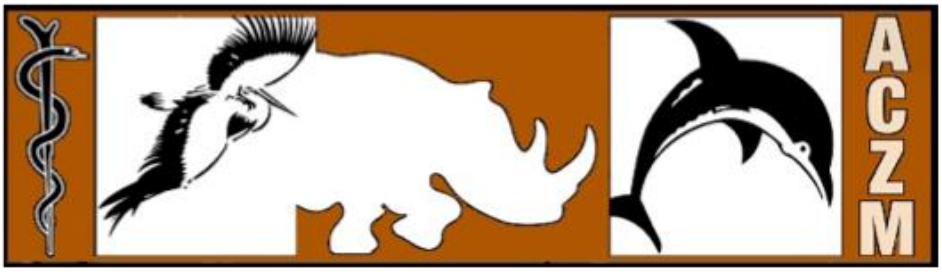
WISCONSIN DEPT. OF NATURAL RESOURCES

MORRIS ANIMAL FOUNDATION

Bronze Sponsors

EcoHealth Alliance

WCS



In Kind Sponsors

MISSION STATEMENT

The mission of the Wildlife Disease Association is to promote healthy wildlife and ecosystems, biodiversity conservation, and environmentally sustainable solutions to One Health challenges.

CHARTER OF VALUES

The Wildlife Disease Association holds these values in common:

- That the conservation of biological diversity is of benefit and essential to human societies now and in the future;
- That the health of wild animals, humans and domestic animals are interconnected and interdependent within a shared environment (‘One Health’);
- That wildlife health is a global challenge transcending cultural and political boundaries and demanding international integration and cooperation of the scientific community, stakeholders and society;
- That knowledge of wildlife health is best achieved through rigorous science, recognition of other accumulated forms of knowledge (e.g. traditional, experiential, professional), and open and respectful debate;
- That our Association is most effective by being multidisciplinary, diverse, inclusive, fair and equitable;
- That communicating the science of our members and values of our Association through advocacy and outreach is integral to achieving our mission;
- That the future of our community and accomplishment of our mission depends on the fostering of student and early career learning and professional development;
- That our Association should conduct its business according to principles of environmental sustainability.

SUSTAINABILITY

We ask that all attendees of the 70th Annual International Conference of WDA help us uphold principles of environmental sustainability outlined in **WDA's Charter of Values**. The conference planning committee is reviewing each day's activities to help achieve a "Green Event" status, similar to the program at the **University of Wisconsin-Madison Office of Sustainability**.

Everyone registered for the conference should bring their own re-useable mug for refreshments – better yet, bring your mug from the Lake Tahoe meeting! This will serve as your coffee/beer/wine/water drinking vessel all week. Any individual water bottles will be sourced from Dasani who make their Plant Bottle® bottles from recyclable PET plastic, partially sourced from plants. These bottles are also fully recyclable. Catering and service vendors for the picnic are local small businesses, to help reduce their travel costs and keep WDA's economic impact in the community. Beer and wine were sourced from respected, award-winning Wisconsin producers.

We have also purchased some WDA branded materials including stainless steel coffee mugs and men's and women's styled t-shirts and jackets. The shirts are made from 100% recycled cotton and 100% recycled polyester, in a 60/40 blend. Jackets are made of 50% recycled polyester and 40% polyester French Terry blend. These items will be for sale at registration.

Almost all the event information will be available in electronic format for ease of use and to minimize printed materials. Name tags have been printed on recycled paper, the plastic badge holders and lanyards are made of recycled materials and there will be collection bins available at the end of the conference so they can be used for another event.

Recycling and composting options will be front and center in all venues; please use them whenever possible.

Live in the Midwest? Consider taking a bus to Madison instead of flying. Madison is a great walking and biking city. The Concourse Hotel maintains a shuttle that can be used to get downtown from the Madison airport; no need to rent a car. Madison has an excellent **bike share program**; there is a station around the corner from the conference hotel and several throughout the university campus. We also encourage use of public transportation and ridesharing whenever possible in the Madison area.

Similar to what was done after Cuenca (financially supporting a local post-wild fire reforestation project), the Wisconsin local host committee would like to support a local conservation project with a goal of achieving a carbon offset or local community environmental justice objective. The project that the committee has chosen is a long-term forest preservation project near Baraboo, also home of the International Crane Foundation, and is described as follows:

For over 50 years The Nature Conservancy has been working with many conservation partners and private landowners to help protect and restore a large block of forest across the Baraboo Hills totaling over 14,000 acres (in addition to the ~10,000 acres of state lands at DLSP and the ~10,000 acres of the former Badger Army Ammunition Lands). From an aerial view, the Baraboo Hills are one of the most extensively forested areas in the region, supporting over 26 distinct natural communities, and providing critically important block of nesting and stopover habitat for many forest interior neotropical migratory songbirds.

TNC's current land stewardship efforts are focused on restoring, promoting, and perpetuating the biodiversity harbored in the oak ecosystems of the Baraboo Hills through actively thinning and restoring overcrowded oak woodlands, planting old fields to expand the forest block, and re-introducing prescribed fire that has played an essential role in helping maintain healthy oak ecosystems for thousands of years. A gift in support of this work could be utilized to help defray the cost of restoration contract expenses (such as tree thinning, brush removal, and select treatment of invasive plants) or to cover cost of purchasing tree seedlings and supplies and staff coordination for tree planting projects.

Once the conference finances have been tallied, this project, and a request for WDA's potential financial support will be brought before Council.

The WDA takes our charter value, *that we should conduct our business according to principles of environmental sustainability*, seriously. If you have thoughts about what we can do better in the future, then please don't hesitate to reach out to Executive Manager, Peri Wolff.

CONFERENCE SCHEDULE

Day 1	Sunday, July 24th	
8:00 AM - 5:00 PM	**Registration**	**2nd Floor Atrium**
8:30 AM - 5:00 PM	American College of Zoological Medicine Introductory Workshop	Assembly & Caucus
8:30 AM - 10:00 AM	Student Workshop – Writing for Scientific Publications	University Room
10:15 AM - 12:00 PM	WDA Editorial Board Meeting	Parlor Room 629
11:00 AM - 1:00 PM	Student Workshop – Communicating Science	University Room
12:00 PM - 1:00 PM	**Joint Lunch – Editorial Board & Council**	**Capitol Ballroom B**
1:15 PM - 4:30 PM	Council Meeting	Parlor Room 629
5:30 PM - 7:30 PM	**Icebreaker Picnic**	**UW Campus**

Day 2	Monday, July 25th	
7:15 AM - 8:00 AM	Yoga	Parlor Room 629
7:30 AM - 2:00 PM	**Registration**	**2nd Floor Atrium**
7:30 AM **- 8:30 AM**	**Breakfast**	**Capitol Ballroom A**
8:30 AM - 9:10 AM	**Welcome and Opening Session**	**Madison/Wisconsin Ballroom**
8:30 AM	Opening Remarks from the Conference Host	Jonathan Sleeman *National Wildlife Health Center*
8:35 AM	Land Acknowledgement & Welcome from WDA President	Andrew Peters *Wildlife Disease Association*
8:40 AM	Welcome from Secretary of the Wisconsin Department of Natural Resources (DNR)	Preston Cole
8:50 AM	Opening Remarks from the Association of Fish and Wildlife Agencies	Colin Gillin *Oregon Department of Fish and Wildlife*
8:55 AM	Welcome from the Conference Student Hosts	Haley Lin & Keegan Lim
9:00 AM	Opening Remarks from the Director General of the World Animal Health Organization	Monique Eliot
9:10 AM – 10:00 AM	**Keynote Address**	**Madison/Wisconsin Ballroom**
9:10 AM	Holistic Solutions for Wildlife Health: What Does it Mean and What can We Do?	Brett Elkin *GNWT Environment & National Resources*
10:00 AM – 10:30 AM	**Morning Break**	**Capitol Ballroom A**
10:30 AM	**Wildlife Disease Association Carlton M. Herman Founder's Fund, Cutting-Edge Speaker**	**Intro: Tonie Roeke**

10:35 AM	The Many Hosts of SARS-CoV-2	Vivek Kapur
11:15 AM	**American Association of Wildlife Veterinarians, Al Franzmann Speaker and Award**	**Intro: Anne Justice-Allen**
11:20 AM	Wildlife Vaccination as a Disease Management Tool: Current State of the Art and Prospects for the Future	Tonie Rocke
12:00 PM	**Lunch & Mini Business Meeting**	**Capitol Ballroom A**
1:00 PM - 9:00 PM	**International Crane Foundation Tour and Dinner**	**International Crane Foundation**

Day 3	**Tuesday, July 26th**	
7:00 AM – 8:30 AM	AAWV Business Meeting	University Room CD
7:15 AM - 8:00 AM	Yoga	Parlor Room 629
7:30 AM - 8:30 AM	**Breakfast**	**Capitol Ballroom A**
7:30 AM - 1:00 PM	**Registration**	**2nd Floor Atrium**
8:30 AM – 9:05 AM	**Graduate Student Research Recognition Award Winner and Keynote Speaker**	**Madison/Wisconsin Ballroom**
8:30 AM	Emerging California Serogroup Viruses in Northern Canada Wildlife	Kayla Buhler *University of Saskatchewan*
9:15 AM – 10:00 AM	**Student Presentations**	**Madison/Wisconsin Ballroom**
9:15 AM	Viral Surveillance in Sanctuary Chimpanzees (Pan troglodytes) Across Africa	Emily Dunay *University of Wisconsin-Madison, School of Veterinary Medicine*
9:30 AM	"Healthy Children, Healthy Chimps": Reducing Reverse Zoonotic Respiratory Virus Transmission from Humans to Chimpanzees in Kibale National Park, Uganda	Taylor Weary *University of Wisconsin-Madison, School of Veterinary Medicine*
9:45 AM	Human Herpesvirus and Mycobacterium Tuberculosis Complex in Confiscated and Rescued Neotropical Primates in Peru	Fernando Javier Vilchez Delgado *Tufts University*
10:00 AM - 10:45 AM	**Morning Break & Poster Session Poster Numbers 97-133**	**Buffet in Ballroom A & Posters in Ballroom B**
10:45 AM - 12:00 PM	**Student Presentations Continued**	**Madison/Wisconsin Ballroom**
10:45 AM	Diagnostic Assays to Detect Entomopathogenic Serratia spp. In the Critically Endangered Lord Howe Island Stick Insect (Dryococelus australis)	Nicholas Doidge *University of Melbourne*
11:00 AM	Black-legged Ticks (Ixodes scapularis) Harbor and Excrete Chronic Wasting Disease Prions from Infected Blood Meals	Heather N'te Inzalaco *University of Wisconsin-Madison*
11:15 AM	Laparoscopic Oviductal Artificial Insemination with Frozen Semen for Conservation Management of Endangered Ocelots in Southern Texas	Ashley Reeves *University of Tennessee*
11:30 AM	Cataloging Retinal Lesions in Asiatic Black Bears (Ursus thibetanus)	Kylie McDaniel *Tufts University*
11:45 AM	Immobilization of Helicopter-Captured Elk (Cervus canadensis) with Butorphanol-Azaperone-Medetomidine Versus Nalbuphine-Medetomidine-Azaperone	Kathleen Williams *University of Kentucky*

12:00 PM - 1:30 PM	**Lunch & Business Meeting**	**Capitol Ballroom A**
1:30 PM - 3:00 PM	**Student Presentations Continued**	**Madison/Wisconsin Ballroom**
1:30 PM	Multi-Strain Domestic Spillover of Mycoplasma Ovipneumoniae and Severe Epizootic Pneumonia Affecting Bighorn Sheep (Ovis Canadensis) in Badlands National Park, South Dakota	Treana Mayer *Colorado State University*
1:45 PM	Synanthropic Mesomammals and the Peridomestic Transmission Cycle of Trypanosoma cruzi in Florida	Carson Torhorst *University of Florida*
2:00 PM	Don't poop here! Detection and genetic characterization of Toxoplasma gondii in feral cat feces near Southern sea otter (Enhydra lutris nereis) habitat	Sophie Zhu *University of California, Davis*
2:15 PM	Are Urban Rookeries Ecological Sources or Sinks? Trade-offs to Urban Nesting in a Wetland Bird	Julia Silva Seixas *University of Georgia*
2:30 PM	Effect of Food Addition and Helminth Removal on Spatial Overlap Networks in Wild Bank Voles (Myodes Glareolus)	Janine Mistrick *University of Minnesota*
2:45 PM	Hijacking Bat Keratinocytes: Mechanistic Insights into the Early Stages of White Nose Syndrome	Marcos Isidoro-Ayza *University of Wisconsin-Madison*
3:00 PM - 3:45 PM	**Afternoon Break & Poster Session** **Poster Number 97-133**	**Buffet in Ballroom A & Posters in Ballroom B**
3:45 PM - 5:00 PM	**Student Presentations Continued**	**Madison/Wisconsin Ballroom**
3:45 PM	Highly Pathogenic Avian Influenza: Clinical Presentation, Pathology, and Shedding Profiles in a Variety of Southeastern Birds	Chloe Goodwin *Southeastern Cooperative Wildlife Disease Study*
4:00 PM	Comparison of Natural and Experimental West Nile Virus Infections in Free-Ranging Ruffed Grouse (Bonasa Umbellus)	Melanie Kunkel *Southeastern Cooperative Wildlife Disease Study, University of Georgia*
4:15 PM	House Sparrows and Culex quinquefasciatus Mosquitos are Capable of Transmitting Usutu Virus	Sarah Kuchinsky *Virginia-Maryland College of Veterinary Medicine*
4:30 PM	Nowhere to Fly: Ubiquitous Avian Malaria Transmission on O'ahu	John Neddermeyer *Northern Arizona University*
4:45 PM	Avian Haemosporidian Infection and Cloacal Bacterial Diversity in Maine Waterfowl	Olivia Choi University of Maine
5:30 PM - 6:30 PM	**Student-Mentor Mixer**	**Assembly Room**
6:30 PM - 10:00 PM	**Reception, Auction, Blues Band and Drinks**	**Madison/Wisconsin Ballroom**

Day 4	**Wednesday, July 27th**	
7:00 AM – 8:00 AM	Wildlife Veterinary Section Business Meeting	University Room
7:15 AM - 8:00 AM	Yoga	Parlor Room 629
7:30 AM - 8:30 AM	**Breakfast**	**Capitol Ballroom A**
7:30 AM - 1:00 PM	**Registration**	**2nd Floor Atrium**

8:30 AM - 10:00 AM	**Panel Session I: Can we Create Change in Wildlife Health?** Moderator: LeAnn White Panelists: Thijs Kuiken, Purnamita Dasgupta & Hans Keune	**Madison/Wisconsin Ballroom**
10:00 AM - 10:30 AM	**Morning Break & Poster Session** **Poster Numbers 134-220**	**Buffet in Ballroom A & Posters in Ballroom B**
Concurrent Sessions		
Session A **10:30 AM - 12:00 PM**	**Wildlife and Environmental Zoonoses** *Moderator: Ria Ghai*	**Assembly Room**
10:30 AM	The Genome of Rocky Mountain Elk Offers Insights into their Immunologic Responses to Bucella Abortus	Steven Olsen *Agricultural Research Service, United States Department of Agriculture*
10:45 AM	Uncovering the Role of Northern Elephant seals (Mirounga angustirostris) in Maintaining Leptospira in the Marine Ecosystem	Katie Prager *University of California, Los Angeles*
11:00 AM	Non-Invasive Saliva Collection for Evaluation of Peri-Urban Primate Exposure to Arboviruses of Public Health and Conservation Concern	Tierra Smiley Evans *University of California, Davis*
11:15 AM	Urban Host-Parasite Dynamics of Two Small Mammals	Kimberly Fake *Lincoln Park Zoo, Urban Wildlife Institute*
11:30 AM	The Wild Life of Ticks: Using Passive Surveillance to Determine the Distribution and Host Range of Ticks and the Exotic Haemaphysalis Longicornis, 2010-2021	Michael Yabsley *University of Georgia*
11:45 AM	Assessing the Effects of Saxitoxin Ingestion by Common Murres	Matthew Smith *Alaska Science Center, United States Geological Survey*
Session B **10:30 AM - 12:00 PM**	**Emerging and Legacy Contaminants and One Health** *Moderator: Thierry Work*	**Senate Room**
10:30 AM	Impact of Lead Ammunition on Bald Eagle Dynamics in the Northeast United States	Krysten Schuler *Cornell Wildlife Health Lab*
10:45 AM	Assessing Neonicotinoids Exposure in Free-Ranging White-Tailed Deer in Minnesota	Michelle Carstensen *Minnesota Department of Natural Resources*
11:00 AM	Causes of Death and Disease Prevalence in Bottlenose Dolphins (*Tursiops truncatus*) Stranding in Alabama Between 2015 and 2020, Following the Deepwater Horizon Oil Spill	Jennifer Bloodgood *Dauphin Island Sea Lab*
11:15 AM	Investigating Levels of Per-and Polyfluoroalkyl Substances (PFAS) in Minnesota White-Tailed Deer	Kelsie LaSharr *Minnesota Department of Natural Resources*
11:30 AM	One Health for All: Advancing Wildlife, Human, and Ecosystem Health in Cities by Integrating an Environmental Justice Lens	Jacqueline Buckley *Lincoln Park Zoo*
11:45 AM	Wildlife Health as Part of a Transformative Change to Operationalize One Health Governance in a Post-Pandemic World	Carlos Das Neves *Norwegian Veterinary Institute*
Session C **10:30 AM - 12:00 PM**	**Systems Thinking and Approaches to One Health and Wildlife Health** *Moderator: LeAnn White*	**University Room**
10:30 AM	Commodity-Based Trade of Beef: A Holistic Solution for the Future of KAZA's People and Wildlife	Steven A. Osofsky *Cornell University College of Veterinary Medicine*
10:45 AM	Wildlife Health in Environmental Impact Assessments: Are We Missing a Key Metric?	Oscar Alejandro Aleuy *University of Notre Dame*

11:00 AM	Systems Thinking applied to Wildlife Health: Building a One Health Framework to Facilitate Adaptive Change within a State Wildlife Agency and Beyond	Sherri Russell *Missouri Department of Conservation*
11:15 AM	A Large-Scale Empirical Study of Hibernating Bat Energetics and Modeled Implications on White-Nose Syndrome Susceptibility	Sarah Olson *Wildlife Conservation Society*
11:30 AM	One Health and Wildlife Conservation: Insights from Wood Bison and Beyond	Craig Stephen *McEachran Institute*
11:45 AM	Landscape of Participatory Surveillance Systems in Wildlife Health	Carrie McNeil *One Health Specialist*
12:00 PM - 1:00 PM	**Boxed Lunch**	**Capitol Ballroom A**
12:00 PM - 1:30 PM	Lunchtime Session: What's Happening with Wildlife *Moderator: Tiggy Grillo, World Organization for Animal Health*	University Room
12:00 PM - 1:30 PM	Lunchtime Session: Ending Pandemics Moderator: Carrie McNeil, *One Health Specialist*	Conference Room III
12:00 PM - 1:30 PM	Association of Fish and Wildlife Agencies Meeting	Conference Room V
12:00 PM - 1:30 PM	Lunchtime Session: Student Roundtable – Development of a North American Student Section *Moderator: Marianthis Ioannidis, Utrecht University*	Senate A&B
1:00 PM	**Free Afternoon/Dinner on Own**	
4:00 PM - 8:00 PM	Appreciation Event Sponsored by Jacobson & Schmitt Advisors	The Edgewater Hotel Sky Bar
7:00 PM	Concerts on the Square	Capitol Lawn

Day 5	**Thursday, July 28th**	
7:00 AM-7:45 AM	WDA Committee Chair Meeting	Conference Room V
7:15 AM - 8:00 AM	Yoga	Parlor Room 629
7:30 AM – 8:30 AM	**Breakfast**	**Capitol Ballroom A**
7:30 AM – 7:00 PM	**Registration**	**2nd Floor Atrium**
8:30 AM - 10:00 AM	**Panel Session II: The Power of Collaborations for One Health Outcomes** Moderator: Carlos Goncalo des Neves Panelists: Casey Barton Behravesh, Catherine Machalaba & Danielle Buttke	**Madison/Wisconsin Ballroom**
10:00 AM - 10:45 AM	**Morning Break & Poster Session** **Posters 134-220**	**Buffets in Ballroom A & Posters in Ballroom B**
Concurrent Sessions		
Session A **10:45 AM - 12:00 PM**	**Association of Fish and Wildlife Agencies Special Session on Wildlife Disease Management/Monitoring/Evaluation** *Moderator: Colin Gillin*	**Assembly Room**

10:45 AM	Invasive Corallimorpharians at Palmyra Atoll National Wildlife Refuge are No Match for Lye and Heat	Thierry Work *United States Geological Survey*
11:00 AM	Epidemiology of Pathogens in Endangered Peninsular Bighorn Sheep (Ovis canadensis nelsoni)	Jessica N. Sanchez *San Diego Zoo Wildlife Alliance*
11:15 AM	Cause of Death, Pathology, and Chronic Wasting Disease Status of White-Tailed Deer Mortalities in Wisconsin	Marie Gilbertson *University of Wisconsin-Madison*
11:30 AM	Behavioral Scrapes as a Route of Transmission and Potential Environmental Sentinel for Chronic Wasting Disease	Miranda Huang *Mississippi State University*
11:45 AM	Relatedness of White-Tailed Deer from Culling Efforts Within a Disease Management Zone in Minnesota	Alberto Fameli *Pennsylvania Cooperative Research Unit*
Session B **10:45 AM - 12:00 PM**	**Disease Outbreaks and Investigations** *Moderator: Barry Hartup*	**Senate Room**
10:45 AM	Monitoring and Surveillance of Unprecedented Wildlife Mortality Due to Highly Pathogenic Avian Influenza Virus Infections 2020-2022	Paul James Duff *Animal and Plant Health Agency*
11:00 AM	Highly Pathogenic Avian Influenza is Maintained by Conspecific Scavenging in Black Vultures (Coragyps atratus) in Florida	Mark Cunningham
11:15 AM	Feline Leukomyelopathy in Florida Panthers and Bobcats	Hollis Ann Stewart
11:30 AM	Retroviral Infections Affect Survival and Reproduction of Female Wild Turkeys	Stephanie Shea *University of Maine*
11:45 AM	A Sarcoptic Mange Outbreak Devastates Wild Camelid Populations in a Protected Area in Argentina	Marcella Uhart *University of California, Davis*
Session C **10:45 AM - 12:00 PM**	**American Association of Wildlife Veterinarians Special Session on Innovations in Diagnostics and Surveillance** *Moderator: Daniel Grove*	**University Room**
10:45 AM	Spatiotemporal Bayesian Model of Pseudogymnoascus destructans Spread	Juan Francisco *University of Wisconsin-Madison*
11:00 AM	The Importance of Case Definitions in Wildlife Health	E.Jane Parmley *University of Guelph*
11:15 AM	A Field-Deployable Diagnostic Assay for the Visual Detection of Chronic Wasting Disease Prions	Peter Christenson *University of Minnesota*
11:30 AM	Histopathology and Genomic Analysis Suggest White-Nose Syndrome / Pseudogymnoascus Destructans Evolved from and Maintains Invasion Strategies of Plant Fungal Pathogens	Carol Meteyer *NWCH*
11:45 AM	WildHealthNet: A One Health Approach to Sustainable Wildlife Health Surveillance	Mathieu Pruvot *Wildlife Conservation Society*
12:00 PM - 1:30 PM	**Lunch & Business Meeting**	**Capitol Ballroom A**
1:30 PM - 3:00 PM	**Panel Session III: The Future of Training Wildlife Health Professionals** Moderator: Kirsten Gilardi Panelists: Mark Ruder, Kelly Straka & Chris Walzer	**Madison/Wisconsin Ballroom**
3:00 PM - 3:45 PM	**Afternoon Break & Poster Session** **Posters 134-220**	**Buffet in Ballroom A & Posters in Ballroom B**
Concurrent Sessions		
Session A **3:45 PM - 5:00 PM**	**Association of Fish and Wildlife Agencies Special Session on Wildlife Disease Management/Monitoring/Evaluation Continued** *Moderator: Sonja Christiansen*	**Assembly Room**

3:45 PM	Widespread Detection of Batrochochytrium dendrobaditis on Urodele and Anuran Species is Driven by Temperature and Fine-Scale Taxonomy in the United States	Daniel Grear *United States Geological Survey, National Wildlife Health Center*
4:00 PM	Using Mosquito Surveillance to Inform Risk of West Nile Virus Exposure to Ruffed Grouse Populations in Pennsylvania	Kristin Bondo *Pennsylvania Cooperative Research Unit*
4:15 PM	Demographic Risk Factor Variation in an Initial Outbreak of Chronic Wasting Disease in West Virginia	Brian Dugovich *United States Geological Survey*
4:30 PM	Associations of White-Tailed Deer with and without Chronic Wasting Disease	W. David Walter *Pennsylvania Cooperative Research Unit*
4:45 PM	Predicted Probability of Chronic Wasting Disease Infection Among Cervids in Kansas using a Generalized Additive Model	Zoe Koestel *University of Missouri*
Session B **3:45 PM - 5:00 PM**	**Disease Outbreaks and Investigations Continued** Moderator: Shelli Dubay	**Senate Room**
3:45 PM	Sharp Decline in Bald Eagle (Haliaeetus leucocephalus) Nesting Success Associated with Highly Pathogenic Avian Influenza Outbreak	Mark Ruder *Southeastern Cooperative Wildlife Disease Study, University of Georgia*
4:00 PM	Metagenomic Sequencing to Identify the Etiologic Agent Responsible for Pneumonia-Related Mortality in Wisconsin White-Tailed Deer	Melanie Prentice *University of Maine*
4:15 PM	2021 Songbird Mortality: Part 1 and 2– Outbreak, Response, and Diagnostic Findings	Sabrina Greening *University of Pennsylvania*
4:30 PM	A 20+ Year Retrospective of Amphibian and Reptile Disease Events in the United States	Megan Winzeler *United States Geological Survey, National Wildlife Health Center*
4:45 PM	A Mortality Event of Double-Crested Cormorants (Phalacrocorax auritus) in Florida Caused by a Novel Eimeria Species	Lisa Shender *National Park Service*
Session C **3:45 PM - 5:00 PM**	**American Association of Wildlife Veterinarians Special Session on Innovations in Diagnostics and Surveillance Continued** *Moderator: John Bryan*	**University Room**
3:45 PM	Hoiho & Malaria: A Real-Time Avian Malaria Warning System to Aid Yellow-Eyed Penguin Conservation Efforts in New Zealand	Chris Niebuhr *Landcare Research-New Zealand*
4:00 PM	Geographic Risk Assessment of Batrachochytrium salamandrivorans Invasion in Costa Rica	Henry Adams *Lincoln Park Zoo*
4:15 PM	Maps, Math, and Models: Data-Driven Decisions to Inform Chronic Wasting Disease Surveillance	Corey Mitchell *Desert Centered Ecology, LLC*
4:30 PM	Data Collection and Management Tools for Wildlife Health Surveillance	Diego Montecino-Latorre *Wildlife Conservation Society*
4:45 PM	What's All the Noise about WHISPers? An overview of Initial Successes and Future Improvements for the USGS NWHC Wildlife Health Sharing Partnership – Event Reporting System.	Katherine Richgels *United States Geological Survey, National Wildlife Health Center*
5:00 PM - 6:00 PM	**WDA Annual Business Meeting**	**Senate Room**
6:00 PM - 7:30 PM	**Cocktail Hour**	**Madison/Wisconsin Ballroom**
7:30 PM - 11:00 PM	**Closing Banquet, Awards Ceremony & Dancing**	**Madison/Wisconsin Ballroom**

Day 6	Friday, July 29th	
8:00 AM - 1:00 PM	**Registration**	**2nd Floor Atrium**
8:00 AM - 9:00 AM	**Breakfast**	**Capitol Ballroom A**
	Concurrent Sessions	
Session A **9:00 AM - 10:30 AM**	**Association of Fish and Wildlife Agencies Special Session on Wildlife Disease Management/Monitoring/Evaluation Continued** *Moderator: Anne Justice-Allen*	**Assembly Room**
9:00 AM	Two Years of Hemorrhagic Disease in North Dakota	Charlie Bahnson *North Dakota Game and Fish*
9:15 AM	Climate Influenced Disease Expansion of Hemorrhagic Disease	Sonja Christensen *Michigan State University*
9:30 AM	Using Surveillance to Inform Wildlife Disease Management: Mandatory Chronic Wasting Disease (CWD) Sampling in Missouri as a Case Study	Jasmine Batten *Missouri Department of Conservation*
9:45 AM	Environmental Transmission of Treponeme-Associated Hoof Disease in Captive Elk	Margaret Wild *Washington State University*
10:00 AM	Toward Feasible Control of Sarcoptic Mange in Wombats	Scott Carver *University of Tasmania*
10:15 AM	Epizootic of Quail Bronchitis Virus in Captive Northern Bobwhite Quail (Colinus virginianus) and Masked Bobwhite (C. virginianus ridgwayi) Reveals Apparent Species Difference in Susceptibility	Anne Justice-Allen *Arizona Game and Fish Department, Terrestrial Wildlife Branch*
Session B **9:00 AM - 10:30 AM**	**Lessons Learned from COVID-19 Pandemics and the role of Wildlife Scientists in the Response** *Moderator: Ariel Leon*	**Senate Room**
9:00 AM	SARS-CoV-2 Surveillance of White-Tailed Deer in the United States	Jeffery Chandler *National Wildlife Research Center*
9:15 AM	Experimental Infection of Wild Canids with SARS-CoV-2	Stephanie Porter *United States Department of Agriculture*
9:30 AM	Mobilizing Multiple Sectors, Disciplines and Communities at Varying Levels for Pandemic Primary Prevention: The International Alliance against Health Risks in Wildlife Trade	Hannah Emde *Deutsche Gesellschaft Für Internationale Zusammenarbeit (giz) GmbH*
9:45 AM	Using a One Health Approach to Structure Federal Coordination on SARS-CoV-2 Transmission in Wildlife	Ria Ghai *Centers for Disease Control and Prevention*
10:00 AM	Structural Biology of Zoonotic Diseases: GM/CA@APS, and PREVENT Proposal	Michael Becker
10:15 AM	Experimental infection of Mexican free-tailed bats (Tadarida brasiliensis) with SARS-CoV-2	Jeffery Hall *United States Geological Survey, National Wildlife Health Center*
Session C **9:00 AM - 10:30 AM**	**Human Dimensions and Wildlife Health** *Moderator: Craig Stephen*	**University Room**
9:00 AM	Using Population Genetics to Trace the Origins of Ophidiomyces ophidiicola, the Causative Agent of Snake Fungal Disease, in North America	Jeff Lorch *United States Geological Survey, National Wildlife Health Center*
9:15 AM	Wildlife Disease Surveillance - Just the Tip of the Iceberg	Anne Ballmann *United States Geological Survey, National Wildlife Health Center*
9:30 AM	Knowledge Basis for the Management of Chronic Wasting Disease in Norway and current status: Will we manage to eradicate the disease?	Bjørnar Ytrehus *Norwegian Scientific Committee for Food and Environment (VKM)*

		& Swedish University of Agricultural Sciences (SLU)
9:45 AM	Supplementary Salt Licks as Transmission Hot-Spots Between Wild and Domestic Ruminants	Kjersti Selstad Utaaker *Nord University*
10:00 AM	Chronic Wasting Disease Show and Tell: Gauging Hunters Willingness to Adopt	Sonja Christensen *Michigan State University*
10:15 AM	Broader Participation in Wildlife Health Research Endeavours: Why Do We Need It, Who Do We Need and What Could It Look Like?	Andrew Peters *Wildlife Disease Association*
10:30 AM – 11:00 AM	**Morning Break & Poster Session Posters 134-220**	**Buffet in Ballroom A & Posters in Ballroom B**
11:00 AM - 12:00 PM	**Panel Session Re-Cap and Wrap Up**	**Madison/Wisconsin Ballroom**
12:00 PM - 12:30 PM	**Closing Remarks**	**Madison/Wisconsin Ballroom**

ORAL PRESENTATIONS & POSTER LIST

1 Holistic Solutions for Wildlife Health: What does it Mean, and What can we do?
Brett Elkin

2 The Many Hosts of SARS-CoV-2
Vivek Kapur

3 Wildlife Vaccination as a Disease Management Tool: Current State of the Art and Prospects for the Future
Rocke Tonie

4 Emerging California Serogroup Viruses in Northern Canadian Wildlife
Kayla Buhler, Xavier Fernandez, Lisa-Marie Leclerc, Geraldine G. Gouin

5 Viral Surveillance in Sanctuary Chimpanzees (Pan troglodytes) Across Africa
Emily Dunay, Leah Owens, Christopher Dunn, Joshua Rukundo, Rebeca Atencia, Megan Cole, Averill Cantwell, Melissa Emery Thompson, Alexandra Rosati, Tony Goldberg

6 "Healthy Children, Healthy Chimps": Reducing Reverse Zoonotic Respiratory Virus Transmission from Humans to Chimpanzees in Kibale National Park, Uganda
Taylor Weary, Tressa Pappas, Jim Gern, Tony Goldberg

7 Human Herpesvirus and Mycobacterium Tuberculosis Complex in Confiscated and Rescued Neotropical Primates in Peru
Fernando Javier Vilchez Delgado, A. Patricia Mendoza, Raul Bello, Paola Santa, Xiomara Zavala Peña, Michael Talledo Albujar, Marieke H. Rosenbaum

8 Diagnostic Assays to Detect Entomopathogenic Serratia spp. in the Critically Endangered Lord Howe Island Stick Insect (Dryococelus australis)
Nicholas Doidge, Ms. Joanne Allen, Professor Glenn Browning, Mr. Rhys Bushell, Dr. Michael Lynch, Dr. Marc Marenda

9 Black-legged Ticks (Ixodes scapularis) Harbor and Excrete Chronic Wasting Disease Prions from Infected Blood Meals
Heather N'te Inzalaco, Dr. Stuart S. Lichtenberg, Francisca Bravo-Risi, Dr. Rodrigo Morales, Dr. Dan P. Walsh, Dr. Dan J. Storm, Dr. Wendy C. Turner, Dr. Joel A. Pedersen

10 Laparoscopic Oviductal Artificial Insemination with Frozen Semen for Conservation Management of Endangered Ocelots in Southern Texas
Ashley Reeves, Dr. William F. Swanson, Dr. Tyler Campbell, Dr. Clayton D. Hilton, Dr. Hilary M. Swarts, Dr. Thomas deMaar, Dr. Debra L. Miller

11 Cataloging Retinal Lesions in Asiatic Black Bears (u. thibetanus)
Kylie McDaniel, Dr. Felicia Nutter, Dr. Rachel Sanki, Dr. Stephanie Pumphrey

12 Immobilization of Helicopter-Captured Elk (Cervus canadensis) with Butorphanol-Azaperone-Medetomidine versus Nalbuphine-Medetomidine-Azaperone
Kathleen E. Williams, Nathan D. Hooven, John T. Hast, Dr. Christine L. Casey, R. Daniel Crank, Matthew T. Springer, John J. Cox

13 Multi-Strain Domestic Spillover of Mycoplasma ovipneumoniae and Severe Epizootic Pneumonia Affecting Bighorn Sheep (Ovis canadensis) in Badlands National Park, South Dakota
Treana Mayer, Terry Spraker, Paul Roghair, Chad Lehman, Trent Haffley, Eddie Childers, Nathan Galloway, Laurie Baeten

14 Synanthropic Mesomammals and the Peridomestic Transmission Cycle of Trypanosoma Cruzi in Florida
Carson Torhorst, Zoe White, Michael P. Milleson, Dr. Normal L. Beatty, Dr. Samantha M. Wisely

15 Don't Poop Here! Detection and Genetic Characterization of Toxoplasma gondii in Feral Cat Feces near Southern Sea Otter (Enhydra lutris nereis) Habitat
Sophie Zhu, Dr. Elizabeth VanWormer, Dr. Lauren Camp, Anika Patel, Dr. Karen Shapiro

16 Are Urban Rookeries Ecological Sources or Sinks? Trade-offs to Urban Nesting in a Wetland Bird
Julia Silva Seixas, Sonia Hernandez, Lindsey Garner, Elizabeth Kurimo-Beechuk, Katherine Christie, William Norfolk, Melanie Kunkel, Alisia Weyna, Michael Yabsley, Lisa Shender, Robert Cooper, Nicole Nemeth, Erin Lipp, Peter Frederick

17 Effect of Food Addition and Helminth Removal on Spatial Overlap Networks in Wild Bank Voles (Myodes glareolus)
Janine Mistrick, Shannon M. Kitchen, Jasmine S.M. Veitch, Samuel Clague, Dr. Clayton E. Cressler, Dr. Richard J. Hall, Dr. Sarah A. Budischak, Dr. Kristian M. Forbes, Dr. Meggan E. Craft

18 Hijacking Bat Keratinocytes: Mechanistic Insights into the Early Stages of WNS
Marcos Isidoro-Ayza, Bruce Klein

19 Highly Pathogenic Avian Influenza: Clinical Presentation, Pathology, and Shedding Profiles in a Variety of Southeastern Birds
Chloe Goodwin, Dr. Rebecca Poulson, Dr. Caitlin Burrell, Dr. Melanie Kunkel, Dr. Rebecca Radisic, Dr. Alisia Weyna, Dr. Mark Ruder, Dr. David Stallknecht, Dr. Mark Cunningham, Dr. Rebecca Hardman, Dr. Nicole Nemeth

20 Comparison of Natural and Experimental West Nile Virus Infections in Free-Ranging Ruffed Grouse (Bonasa umbellus)
Melanie R. Kunkel, Justin D. Brown, Lisa Williams, Kevin D. Niedringhaus, Heather Fenton, Mark G. Ruder, Nicole M. Nemeth

21 House Sparrows and Culex quinquefasciatus Mosquitos are Capable of Transmitting Usutu Virus
Sarah Kuchinsky, Jeffrey Marano, Seth Hawks, Emma Loessberg, James Weger-Lucarelli, Nisha Duggal

22 Nowhere to Fly: Ubiquitous Avian Malaria Transmission on O'ahu
John H. Neddermeyer, Katy L. Parise, A. Marm Kilpatrick, Jeffrey T. Foster

23 Avian Haemosporidian Infection and Cloacal Bacterial Diversity in Maine Waterfowl
Olivia Choi, Ann Bryant, Kelsey Sullivan, Dr. Pauline Kamath

24 Can We Create Transformative Change in Wildlife Health?
Thijs Kuiken, Purnamita Dasgupta, Hans Keune

25 The Genome of Rocky Mountain Elk Offers Insights into Their Immunologic Responses to Bucella Abortus
Steven Olsen, Rick Massonbrink, David Alt, Darrell Bayles, Paola Boggiatto, Jennifer Wilson-Welder, Andrew Severin

26 Uncovering the Role of Northern Elephant Seals (Mirounga angustirostris) in Maintaining Leptospira in the Marine Ecosystem
Katie Prager, Daniel Costa, Daniel Crocker, Ana Carolina Ribeiro Gomez, Riley Mummah, Sarah Helman, Benny Borremans, James Lloyd-Smith

27 Non-Invasive Saliva Collection for Evaluation of Peri-Urban Primate Exposure to Arboviruses of Public Health and Conservation Concern
Tierra Smiley Evans, Ohnmar Aung, Olivia Cords, Lark Coffey, Talia Wong, Min Thein Maw, JoAnn Yee, Kodumudi Venkateswaran, Neeraja Venkateswaran, Peter Nham, Koen Van Rompay, Marc Valituto, Susan Murray, Christine Johnson

28 Urban Host-parasite Dynamics of Two Small Mammals
Kimberly Fake, Matthew Mulligan, Mason Fidino, Michael Yabsley, Rachel Santymire, Seth Magle

29 The Wild Life of Ticks: Using Passive Surveillance to Determine the Distribution and Host Range of Ticks and the Exotic Haemaphysalis longicornis, 2010-2021
Michael Yabsley, Alec Thompson, Seth White, Emily Doub, Prisha Sharma, Kenna Frierson, David Shaw, Stacey Vigil, Mark Ruder

30 Assessing the Effects of Saxitoxin Ingestion by Common Murres
Matthew Smith, Caroline Van Hemert, Robert Dusek, Tuula Hollmen, Kristen Pelo, Aidan Lee, Jenna Schlenner, Dave Kulis, Donald M. Anderson, Sherwood Hall

31 Impact of Lead Ammunition on Bald Eagle Dynamics in the Northeast United States
Krysten Schuler, Brenda Hanley, André Dhondt, Kevin Hynes, Maria Forzan, Elizabeth Bunting, Mark Pokras

32 Assessing Neonicotinoids Exposure in Free-Ranging White-Tailed Deer in Minnesota
Michelle Carstensen, Patrick Hagen, Eric Michel, John Buchweitz, Justin Zyskowski, Jon Lundgren

33 Causes of Death and Disease Prevalence in Bottlenose Dolphins (*Tursiops truncatus*) stranding in Alabama Between 2015 and 2020, Following the Deepwater Horizon Oil Spill
Jennifer Bloodgood, Alissa Deming, Kathleen Colegrove, Mackenzie Russell, Cristina Díaz Clark, Ruth Carmichael

34 Investigating Levels of Per- and Polyfluoroalkyl Substances (PFAS) in Minnesota White-Tailed Deer
Kelsie LaSharr, Dr. Michelle Carstensen, Dr. Barbara Keller, Dr. Eric Michel, James Kelly, Sophie Greene

35 One Health for All: Advancing Wildlife, Human, and Ecosystem Health in Cities by Integrating an Environmental Justice Lens
Ms. Jacqueline Buckley, Dr. Maureen Murray, Dr. Kaylee Byers, Ms. Kimberley Fake, Ms. Elizabeth Lehrer, Dr. Seth Magle, Dr. Christopher Stone, Dr. Holly Tuten, Dr. Christopher Schell

36 Wildlife Health as Part of a Transformative Chang to Operationalize One Health Governance in a Post-Pandemic World
Dr. Carlos G. das Neves, Dr. Knut Madslien

37 Commodity-Based Trade of Beef: A Holistic Solution for the Future of KAZA's People and Wildlife
Steven A. Osofsky, Shirley J. Atkinson, Dr. Mary-Louise Penrith, Nidhi Ramsden, Dr. Gavin R. Thomson

38 Wildlife Health in Environmental Impact Assessments: Are We Missing a Key Metric?
O. Alejandro Aleuy, Susan J. Kutz, Mark L. Mallory, Jennifer F. Provencher

39 Systems Thinking Applied to Wildlife Health: Building a One Health Framework to Facilitate Adaptive Change Within a State Wildlife Agency and Beyond
Sherri Russell, Lorisa Smith, Sara Parker Pauley, Jason Sumners, Kathi Moore, Jasmine Batten, Maria Anderson

40 A Large-Scale Empirical Study of Hibernating Bat Energetics and Modeled Implications on White-Nose Syndrome Susceptibility
Sarah H. Olson, Dan Crowley, Brett Dickson, Yvonne A. Dzal, Nathan Fuller, Catherine Haase, David T. S. Hayman, Reed Hranac, Emily M. Johnson, Emma L. Kunkel, Cori L. Lausen, Meredith L. McClure, Liam P. McGuire, Raina K. Plowright, Kirk Silas, Craig K. R. Willis

41 One Health and Wildlife Conservation: Insights from Wood Bison and Beyond
Craig Stephen, Jennifer Provencher, Alana Wilcox, Sarah Sine

42 Landscape of Participatory Surveillance Systems in Wildlife Health
Carrie McNeil, Sarah Verlander, Nomita Divi, Mark Smolinski

43 What's Happening with Wildlife at the World Organisation for Animal Health?
Tiggy Grillo

44 Participatory Surveillance System Data Parameters Workshop
Carrie McNeil

45 Association of Fish and Wildlife Agencies Meeting
Sonja Christiansen

46 Student Roundtable – Development of a North American Student Section
Marianthis Ioannidis

47 The Power of Collaborations for One Health Outcomes
Casey Barton Behravesh, Catherine Machalaba, Danielle Buttke

48 Invasive Corallimorpharians at Palmyra Atoll National Wildlife Refuge are No Match for Lye and Heat
Thierry Work, Renee Breeden, Bob Rameyer, Vernon Born, Tim Clark, Jeremy Raynal, Chris Gillies, Julia Rose, Alex Wegmann, Stefan Kropidlowski

49 Epidemiology of Pathogens in Endangered Peninsular Bighorn Sheep (Ovis canadensis nelsoni)
Jessica N. Sanchez, Dr. Brandon A. Munk, Janene Colby, Steve G. Torres, Dr. Ben J. Gonzales, James R. DeForge, Aimee J. Byard, Lora Konde, Nicholas J. Shirkey, Dr. Pranav S. Pandit, Randy A. Botta, Dr. Annette Roug, Dr. Michael H. Ziccardi, Dr. Christine K. Johnson

50 Cause of Death, Pathology, and Chronic Wasting Disease Status of White-Tailed Deer Mortalities in Wisconsin
Marie Gilbertson, Ellen Brandell, Marie Pinkerton, Nicolette Meaux, Matthew Hunsaker, Dana Jarosinksi, Wesley Ellarson, Daniel Walsh, Daniel Storm, Wendy Turner

51 Behavioral Scrapes as a Route of Transmission and Potential Environmental Sentinel for CWD
Miranda Huang, Steve Demarais, Bronson K. Strickland, Anna Grace Welch, Alejandro Banda, Scoty Hearst, Allan Houston, Kim Pepin, Kurt C. VerCauteren

52 Relatedness of White-Tailed Deer from Culling Efforts Within a Disease Management Zone in Minnesota
Alberto Fameli, Jessie Edson, Christopher Jennelle, W. David Walter

53 Monitoring and Surveillance of Unprecedented Wildlife Mortality Due to HPAIV Infections 2020-2022.
Mr. Paul Duff, Dr. Craig Ross, Dr. Bart Donato, Dr. Rowena Hansen

54 Highly Pathogenic Avian Influenza is Maintained by Conspecific Scavenging in Black Vultures (Coragyps atratus) in Florida
Mark Cunningham, Rebecca Hardman, Bryan Kluever, Nicole Nemeth, Rebecca Poulson, Lijuan Zhou, Trevor Zachariah, Kyle Donnelly, Michael Milleson, Veronica Guzman-Vargas, Mark Ruder, Y. Reddy Bommineni, Dave Stalknecht

55 Feline Leukomyelopathy in Florida Panthers and Bobcats
Hollis Stewart, Mark Cunningham, Dave Onorato, Nicole Nemeth

56 Retroviral Infections Affect Survival and Reproduction of Female Wild Turkeys
Stephanie Shea, Matthew Gonnerman, Erik Blomberg, Kelsey Sullivan, Pauline Kamath

57 A Sarcoptic Mange Outbreak Devastates Wild Camelid Populations in a Protected Area in Argentina
Marcela Uhart, Hebe Ferreyra, Jaime Rudd, Janet Foley, Ralph E. T. Vanstreels, Ana M. Martin, Emiliano Donadio

58 Spatiotemporal Bayesian Model of Pseudogymnoascus destructans Spread
Juan Francisco Mandujano Reyes, Anne Ballmann, Robin Russell, Daniel Walsh, Jun Zhu

59 The Importance of Case Definitions in Wildlife Health
E. Jane Parmley, Kimberli Miller, Julia Lankton, Marnie Zimmer, Tonia von Hugo, Megan Jones, Anne Ballmann, Jennifer Buckner, C. LeAnn White, Patrick Zimmer, Jonathan Sleeman

60 A Field-Deployable Diagnostic Assay for the Visual Detection of Chronic Wasting Disease Prions
Peter Christenson, Manci Li, Gage Rowden, Marc Schwabenlander, Tiffany Wolf, Sang-Hyun Oh, Peter Larsen

61 Histopathology and Genomic Analysis Suggest White-Nose Syndrome / Pseudogymnoascus destructans Evolved from and Maintains Invasion Strategies of Plant Fungal Pathogens
Carol U. Meteyer, Julien Y. Dutheil, M. Kevin Keel, Justin G. Boyles, Eva H. Stukenbrock

62 WildHealthNet: A One Health Approach to Sustainable Wildlife Health Surveillance
Mathieu Pruvot, Dr. Sarah H. Olson, Khongsy Khammavong, Phonesavanh Milavong, Alice Porco, Dr. Sothyra Tum, Sokha Chea, Sours Sreyem, Emily Denstedt, Dr. Watthana Theppayna, Souchinda Phouangsouvanh, Dr. Sithong Phiphakhavong, Dr. Phouvong Phommachanh, Dr. Alice Latinne, Dr. Phan Thanh Long, Nga Nguyen, Thanh Vo, Ngoc Pham, Dr. Diego Montecino, Dr. Amanda Fine

63 The Future of Training in Wildlife Health Professionals
Mark Ruder, Kelly Straka, Cris Walzer

64 Widespread Detection of Batrochochytrium dendrobaditis on Urodele and Anuran Species is Driven by Temperature and Fine-Scale Taxonomy in the United States
Daniel Grear, Michael J. Adams, Adam Baklin, William J. Barichivich, Adrianne B. Brand, Daniel L. Calhoun, Robert N. Fisher, Brad M. Glorioso, Evan H. Campbell Grant, Brian J. Halstead, Blake R. Hosack, Patrick Kleeman, Jeffrey Lorch, Brome McCreary, Erin Muths, Cristopher Pearl, Mark F. Roth, Walt Sandinski, Brent Sigafus, J. Hardin Waddle, Susan C. Walls, Megan E. Winzeler

65 Using Mosquito Surveillance to Inform Risk of West Nile Virus Exposure to Ruffed Grouse Populations in Pennsylvania
Kristin Bondo, Lisa Williams, W. David Walter

66 Demographic Risk Factor Variation in an Initial Outbreak of Chronic Wasting Disease in West Virginia
Brian Dugovich, Ethan Barton, James Crum, David Stallknecht, Mark Ruder

67 Associations of White-Tailed Deer with and Without Chronic Wasting Disease
W. David Walter, Dr. Christopher Rosenberry, Dr. Alberto Fameli, Jessie Edson

68 Predicted Probability of Chronic Wasting Disease Infection Among cervids in Kansas Using a Generalized Additive Model
Zoe Koestel, Myungsoo Yoo, Levi Jaster, Shane Hesting, Isabella B. Richardson, Christopher K. Wikle, Ram K. Raghavan

69 Sharp Decline in Bald Eagle (Haliaeetus leucocephalus) Nesting Success Associated with Highly Pathogenic Avian Influenza Outbreak
Mark Ruder, Bob Sargent, Rebecca Poulson, David Stallknecht, Mark Cunningham, Samantha Gibbs, Nicole Nemeth

70 Metagenomic Sequencing to Identify the Etiologic Agent Responsible for Pneumonia-Related Mortality in Wisconsin White-Tailed Deer
Dr. Melanie B. Prentice, Dr. Marie Gilbertson, Dr. Daniel Storm, Dr. Wendy C. Turner, Dr. Daniel Walsh, Dr. Marie E. Pinkerton, Dr. Pauline L. Kamath

71 The 2021 Songbird Mortality Event – A Summary of Findings and Discussion of Ongoing Investigations
Sabrina S. Greening, Bryan Richards, Nicole Nemeth, Nicole Lewis, David Needle, Joseph Sevigny, Michael Oglesbee, Seth Faith, Julie Ellis

72 A 20+ year Retrospective of Amphibian and Reptile Disease Events in the United States
Megan Winzeler, Daniel Grear, Magdalena Twarowski, Stephanie Steinfeldt, David Green

73 A Mortality Event of Double-Crested Cormorants (Phalacrocorax auritus) in Florida Caused by a Novel Eimeria Species
Lisa Shender, Constance Roderick, Kailyn McKibben, Susan Knowles, Melanie Kunkel, Nicole Nemeth, Veronica Guzman-Vargas, Heather Walden, Rebecca Cole

74 Hoiho & Malaria: A Real-Time Avian Malaria Warning System to Aid Yellow-Eyed Penguin Conservation Efforts in New Zealand
Chris Niebuhr, Simon Howard

75 Geographic Risk Assessment of Batrachochytrium salamandrivorans Invasion in Costa Rica
Henry C. Adams, Katherine E. Markham, Dr. Marguerite Madden, Dr. Matthew J. Gray, Dr. Sonia M. Hernandez

76 Maps, Math, and Models: Data-Driven Decisions to Inform Chronic Wasting Disease Surveillance
Corey Mitchell, Brenda Hanley, Nicholas Hollingshead, Rachel Abbott, Cara Them, Md Sohel Ahmed, Krysten Schuler

77 Data Collection and Management Tools for Wildlife Health Surveillance
Diego Montecino-Latorre, Alice Porco, Alice Latinne, Emily Denstedt, Kevin Brown, Bevan Federko, Kongsy Khammavong, Jonathan Palmer, Chris Walzer, Sarah H. Olson, Mathieu Pruvot

78 What's All the Noise about WHISPers? An Overview of Initial Successes and Future Improvements for the USGS NWHC Wildlife Health Sharing Partnership – Event Reporting System
Katherine Richgels, Bryan Richards, Jonathan Sleeman, C. LeAnn White

79 Two Years of Hemorrhagic Disease in North Dakota
Charlie Bahnson, William Jensen, Bruce Stillings, Brent Weston, David Stallknecht, Mark Ruder

80 Climate Influenced Disease Expansion of Hemorrhagic Disease
Sonja Christensen, Brett Skelly, Mark Ruder, James Crum, David Stallknecht

81 Using Surveillance to Inform Wildlife Disease Management: Mandatory Chronic Wasting Disease (CWD) Sampling in Missouri as a Case Study
Jasmine Batten, Dr. Sherri Russell

82 Environmental Transmission of Treponeme-Associated Hoof Disease in Captive Elk
Margaret Wild, Zachary Robinson, Devendra Shah, Kyle Taylor

83 Toward Feasible Control of Sarcoptic Mange in Wombats
Scott Carver

84 Epizootic of Quail Bronchitis Virus in Captive Northern Bobwhite Quail (Colinus virginianus) and Masked Bobwhite (C. virginianus ridgwayi) Reveals Apparent Species Difference in Susceptibility
Anne Justice-Allen, Bill Radke, Hannah Pierce

85 SARS-CoV-2 Surveillance of White-Tailed Deer in the United States
Jeffrey Chandler, Susan Shriner, Kristina Lantz, Richard Chipman, Kelsey Dawson, Jourdan Ringenberg, Robert Pleszewski, Christopher Quintanal, Jeremy Ellis, Dennis Kohler, Mary Killian, Timothy Linder, Rachel Tell, Mia Torchetti, Suelee Robbe-Austerman, Thomas DeLiberto, Julianna Lenoch

86 Experimental Infection of Wild Canids with SARS-CoV-2
Stephanie Porter, Airn Hartwig, Helle Bielefeldt-Ohmann, Angela Bosco-Lauth, J. Jeffrey Root

87 Mobilizing Multiple Sectors, Disciplines and Communities at Varying Levels for Pandemic Primary Prevention: The International Alliance Against Health Risks in Wildlife Trade
Hannah Emde, Kathrin Norda, Johannes Keil, Ulrike Buehler, Constanze Riedle, PhD Kim Gruetzmacher

88 Using a One Health Approach to Structure Federal Coordination on SARS-CoV-2 Transmission in Wildlife
Ria Ghai, Ann Carpenter, Danielle Buttke, Tom Deliberto, Laurie Gage, Samantha Gibbs, Patrice Klein, Steven Rekant, Teri Rowles, Lisa Shender, Sara Taetzsch, Jonathan Towner, Kate Varela, Michelle Verant, Casey Barton Behravesh, Jonathan Sleeman

89 Structural Biology of Zoonotic Diseases: GM/CA@APS, and a PREVENT Proposal
Michael Becker, Stephen Corcoran, Dale Ferguson, Mark Hilgart, David Kissick, Oleg Makarov, Craig Ogata, Sergey Stepanov, Nagarajan Venugopalan, Qingping Xu, Shenglan Xu, Kristin Ahrens, Robert Fischetti, Janet Smith

90 Experimental infection of Mexican free-tailed bats (Tadarida brasiliensis) with SARS-CoV-2.
Jeffrey Hall, Udeni Balasuriya, Mariano Carossino, Elizabeth Falendyz, Erik Hofmeister, Hon Ip, Susan Knowles, Ariel Leon, Carly Malavé, Sean Nashold, Tonie Rocke

91 Using Population Genetics to Trace the Origins of Ophidiomyces ophidiicola, the Causative Agent of Snake Fungal Disease, in North America
Jeff Lorch, Jason Ladner, Jonathan Palmer, Cassandra Ettinger, Jason Stajich, Terence Farrell, Brad Glorioso, Becki Lawson, Steven Price, Anne Stengle, Daniel Grear

92 Wildlife Disease Surveillance - Just the Tip of the Iceberg
Anne Ballmann, Daniel Walsh, Robin Russell, John Grider, Kyle George, Jeffery Lorch, David Blehert, Katherine Richgels

93 Knowledge Basis for the Management of CWD in Norway and Current Status: Will We Manage to Eradicate the Disease?
Bjørnar Ytrehus, Dr. Michael A. Tranulis, Dr. Maria G. Asmyhr, Dr. Danica Grahek-Ogden, Dr. Merethe Aasmo-Finne

94 Supplementary Salt Licks as Transmission Hot-Spots Between Wild and Domestic Ruminants
Kjersti Selstad Utaaker, Bjørnar Ytrehus, Marie L. Davey, Olav Strand, Per Anders Robertsen, Geir Rune Rauset, Frode Fossøy

95 CWD Show and Tell: Gauging Hunters' Willingness to Adopt Management Practices
Sonja Christensen, Krysten Schuler, Danielle Ufer, Nick Pinizzotto, David Ortega

96 Broader Participation in Wildlife Health Research Endeavours: Why Do We Need It, Who Do We Need and What Could It Look Like?
Andew Peters, Dr. Lisa Adams, Dr. Scott Carver

P97 Investigating the Relationship Between Mercury, Urbanization, and Salmonella spp. in the American White Ibis (Eudocimus albus)
Matthew Tatz, Dr. Sonia Hernandez, Dr. Stacey Lance

P98 Lead (Pb) and its Health Effects in Scandinavian Brown Bears (Ursus arctos)
Hydeskov HB, Arnemo JM, Fuchs B, Rodushkin I, Boesen AH, Evans AL, Miller AL, Græsli AR, Thiel A, Lloyd Mills C, Gentle LK, Zedrosser A, Kindberg J, Uzal A

P99 Stakeholder Attitudes and Perspectives on Wildlife Disease Surveillance as a Component of a One Health Approach in Thailand
Serena George, Moniek Smink, Nareerat Sangkachai, Anuwat Wiratsudakul, Walasinee Sakcamduang, Sarin Suwanpakdee, Jonathan Sleeman

P100 Analysis of the situation of Wild Animals for Pets in Brazil
Victória Lage, Rafael Lage, Gabriel Lage, Ricardo Borovoski, PHD Elisângela Sobreira

P101 Application of the Heuristic-Systematic Model to Risk Perceptions about Wildlife Disease
Kyle Smith, Dr. Adam Landon, Dr. David Fulton

P102 Effects of Filter Paper Strip Storage Duration and Method on Anti-West Nile Virus Antibody Detection in Northern Bobwhite (Colinus virginianus) and Wild Turkeys (Meleagris gallopavo)
Melanie R. Kunkel, Roy D. Berghaus, Daniel G. Mead, Kayla G. Adcock, James A. Martin, Mark G. Ruder, Nicole M. Nemeth

P103 Spatial Methods for Describing Wildlife Health in Ontario
Daniel Bayley, Shoshanah Jacobs, Claire Jardine, Emmanuelle Arnaud, E Jane Parmley

P104 Methods Used to Identify Novel Antigens for Serological Diagnosis of Parelaphostrongylus tenuis Infections in Cervid Hosts
Jessie Richards, Stephen Kania, Katherine Kurth, Brad Miller, Lisa Muller, Richard Gerhold

P105 Comprehensive, Fine-Scale Spatial Models Predict the Presence and Abundance of Blacklegged Ticks in Ohio
Allison Williams, PhD Risa Pesapane, PhD Bill Peterman

P106 Viral Copy Number Detected by a Novel Diplex Probe-Hybridization Quantitative PCR For Miroungine Gammaherpesvirus 3 Significantly Correlates with Lymphoma in Northern Elephant Seals (Mirounga Angustirostris)
Molly Horgan, Dr. Margaret Martinez, Linda Archer, Dr. Pádraig Duignan, Dr. James Wellehan

P107 Investigating Viruses Associated with Freshwater Mussel Mass Mortality Events
Jordan Richard, Eric Leis, Christopher Dunn, Cleyo Harris, Rose Agbalog, Lewis Campbell, Susan Knowles, Diane Waller, Joel Putnam, Tony Goldberg

P108 Evaluating the Effectiveness of Using Water Filtration Methods to Detect the Chytrid Fungus, Batrachochytrium dendrobatidis
Leah Joyce, Dr. Dan Grear, Dr. Angie Luis, Dr. Winsor Lowe

P109 Assessing Sampling Technique for Mycoplasma Bovis in American Bison (Bison bison)
Katherine Schwartz, Erin Schwalbe, Maggie Johnson, Tesia Lin, Danielle Buttke, Tom Bragg, Kerry Sondgeroth, Jennifer Malmberg

P110 Integrative Conservation of the Baird's Tapir as a Flagship Species to Protect a Fragmented Landscape in Northwestern, Costa Rica
Jorge Rojas, Dr. Sonia M. Hernandez, Dr. Richard Chandler, Dr. Jeffrey Hepinstall-Cymerman, Dr. Theodore Gragson, Dr. Christopher Jordan

P111 A Preliminary Evaluation for Subclinical Renal Disease using Serum Creatinine in California Sea Lions, Zalophus californianus, exposed to Domoic Acid
Dr. Ami Krasner, Dr. Padraig Duignan, Dr. Cara Field, Dr. Spencer Fire, Dr. Kelli Hunsucker, Dr. Maggie Martinez, Dr. Glenn Miller

P112 Risky Business: Deer Behavior and Chronic Wasting Disease
Samantha Courtney, Dr. Dwayne Etter, Dr. Sonja Christensen, Dr. David Williams

P113 Surveillance of Parasites and Canine Distemper Virus in Free-Ranging Canada Lynx (Lynx canadensis) and Fishers (Pekania pennanti) from Maine, USA
Michael Yabsley, Natalie Heyward, Corinna Hazelrig, Shevenell Webb, Jennifer Vashon, Kayla Garrett, David Needle, Christopher Cleveland

P114 Surveillance and Assessment of Skin Keratin Abundance Associated with Batrachochytrium dendrobatidis Prevalence in Red-Spotted Newts (Notophthalmus viridescens viridescens) and Mole Salamanders (Ambystoma talpoideum)
Michael Yabsley, Corinna Hazelrig, Kayla Garrett, Corrie Navis, John Maerz, Nicole Nemeth

P115 Parasitic Infections an Energetic Burden for River Otter (Lontra canadensis) and Mink (Neogale vison) in Western Canada.
Kyle Shanebeck, Dr. Stephanie Green, Dr. Clement Lagrue

P116 Co-infection of Anaplasma Bacteria and Winter Ticks Decreases Moose Calf Survival in Maine
Alaina Woods, Lee Kantar, James Elliott, Sandra De Urioste-Stone, Pauline Kamath

P117 Use of Implants for Terbinafine Administration to Prevent Chytridiomycosis in Greater Sirens (Siren lacertina)
Anastasia Towe, Dr. Rebecca Hardman, Dr. Wesley Sheley, Joseph DeMarchi, E. Davis Carter, Debra Miller

P118 Fatal Gastric Amoebiasis in a Linnaeus's Two-Toed Sloth (Choloepus didactylus)
Jeongha Lee, Anibal Armien, Daniel Paulsen

P119 Novel Avibacterium Species Associated with Sinusitis and Conjunctivitis in a Merriam's Wild Turkey (Meleagris Gallopavo Merriam) Flock in Colorado, USA
Jayne Ellis, Christopher MacGlover, Kerry Sondgeroth, Derek Brown, Joshua Daniels, Karen Fox

P120 Risk of Bacteremia Associated with Probiotic Treatment of Batrachochytrium salamandrivorans
Anastasia Towe, Dr. Debra Miller, Dr. Wesley Sheley, Dr. Sree Rajeev, E. Davis Carter, Joseph DeMarchi, Dr. Matthew Gray

P121 Widespread Hepatozoon sp. Infection in Southeastern Coyotes
Eliza Baker, Dr. Richard Gerhold, Dr. Debra Miller, Alex Jensen

P122 Finding Normal in a Warming World: Baseline PCV and TS Data and its Relation to Incubation Temperature in Leatherback Sea Turtle Hatchlings and Post Hatchlings
Samantha Kuschke, Debra Miller, Jeanette Wyneken

P123 Landscape Feature Determinants of Parelaphostrongylus Tenuis Transmission in Northeastern Minnesota
Tyler Garwood, Dr. Seth Moore, Dr. Nicholas Fountain-Jones, Dr. Peter Larsen, Dr. Tiffany Wolf

P124 A Multiplexed Magnetic-Capture Tool for Monitoring Polar Bear Health and Wildlife Disease Surveillance
Christina Tschritter, Marsha Branigan, Peter V. C. de Groot, Markus Dyck, Zhengxin Sun, Kayla Buhler, Dr. Emily Jenkins, Dr. Stephen C. Lougheed

P125 Challenges to IUCN Guideline Implementation in the Rehabilitation and Release of Trafficked Primates in Peru
Siena Mitman, Marieke Rosenbaum, Raul Bello, Cambrey Knapp, Felicia Nutter, Patricia Mendoza

P126 Mange and Microbes: Microbial Changes Associated with Sarcoptic Mange in Bare-Nosed Wombats (Vombatus ursinus)
Christina Næsborg-Nielsen, Dr. Raphael Eisenhofer, Dr. Tamieka A. Fraser, Vicky Wilkinson, Dr. Christopher Burridge, Dr. Scott Carver

P127 Persistence of Low Pathogenic Avian Influenza Viruses in Artificial Streams Mimicking Natural Conditions of Waterfowl Habitats
Albert Perlas Puente, Dr. Kateri Bertran, Dr. Xavier Abad, Dr. Carles M. Borrego, Dr. Miquel Nofrarías, Rosa Valle, Dr. Antonio Ramis, Dr. Martí Cortey, Dr. Vicenç Acuña, Dr. Natàlia Majó

P128 Investigating SARS-CoV-2 Infection and Exposure in Norway Rats (Rattus norvegicus) from Ontario, Canada
Sarah Robinson, Jonathon Kotwa, Simon Jeeves, Chelsea Himsworth, David Pearl, J. Scott Weese, L. Robbin Lindsay, Antonia Dibernardo, Bradley Pickering, Melissa Goolia, Hsien-Yao Chee, Juliette Blais-Savoie, Emily Chien, Winfield Yim, Lily Yip, Samira Mubareka, Claire Jardine

P129 No Abstract Assigned

P130 Pathogen Surveillance and Discovery in Vampire Bats (Desmodus rotundus) Distributed Across Ecologically Distinct Regions of Guyana, South America
Lexi Frank, Marissa Milstein, Evan Kipp, Roxanne Larsen, Laramie Lindsey, Elisha Marawanaru, Christopher Shaffer, Phillip Suse, Tiffany Wolf, Peter Larsen

P131 The Impacts of Resource Provisioning on the Frequency and Diversity of Antimicrobial Resistance Genes Carried by the White Stork (Ciconia ciconia) in Madrid, Spain
Raquel Francisco, Dr. Sonia Hernandez, Dr. Jose Aguirre, PhD Canidate Alejandro Lopez-Garcia, Dr. Irene Sacristan, Dr. Fernando Esperon

P132 Streamlining Mitochondrial Genome Assembly and Bloodmeal Identification in Hematophagous Insects Using Nanopore Adaptive Sampling
Evan Kipp, Laramie Lindsey, Cristina Blanco, Julia Baker, Marissa Milstein, Christopher Faulk, Jonathan Oliver, Peter Larsen

P133 Proximal Land-use Drives Salmonella Population Dynamics in Surface Water
Jared Smith

P134 Legacy and Contaminants of Emerging Concern (CECs) in Tree Swallows Nesting in Three Drainages of the Milwaukee Estuary, WI
Christine Custer, Thomas Custer, Paul Dummer, Natalie Karouna-Renier, Chi-yen Tseng, Cole Matson

P135 Bald Eagles as Indicators of Emerging Contaminants and Ecosystem Health
Sean Strom

P136 A Comparative Burden of Lead in Virginia Opossums in Illinois
Alysha McDaniel, *Will Sander*

P137 Osteofluorosis in a Free Ranging California Sea Lion
Margaret Martinez, *Michelle Rivard, Jaclyn Isbell, Chelsea Sykes, Robert Poppenga, Padraig Duignan*

P138 Disorders of Sexual Development in Free Ranging California Sea Lions
Margaret Martinez, *Barbie Halaska, Robert Foster, Padraig Duignan*

P139 Mercury (Hg) Concentrations of Adult and Nestling Red-Shouldered Hawks (Buteo lineatus) in Central and Northeastern Wisconsin
Matthew Hanneman, *PhD Cady Sartini, PhD Shelli Dubay, PhD Marie Perkins, PhD Jason Riddle, Eugene Jacobs, John Jacobs*

P140 Developing a Large Volume Filtration Method to Recover Infectious Avian Influenza Virus from the Aquatic Environment
Laura Hubbard, *Carrie Givens, Erin Stelzer, Dana Kolpin, Rebecca Poulson*

P141 Profiling Research on PFAS in Wildlife: A Systematic Map and bibliometric Analysis
Catharina Vendl, *Dr Matthew D. Taylor, Dr. Jennifer Bräunig, Mr. Matthew J. Gibson, Professor Daniel Hesselson, Professor G. Gregory Neely, Dr. Malgorzata Lagisz, Professor Shinichi Nakagawa*

P142 Thermal Processing Reduces PFAS Concentrations in Blue Food – Asystematic Review and Meta-Analysis
Catharina Vendl, *Mr. Patrice Pottier, Dr. Matthew D. Taylor, Dr. Jennifer Bräunig, Mr. Matthew J. Gibson, Professor Daniel Hesselson, Professor G. Gregory Neely*

P143 Biological Collections as a Resource in Wildlife Contaminant Research
Marie Perkins

P144 How Will the End of Bear Bile Farming in Vietnam Influence Consumer Choice?
Dr. Elizabeth Davis, *Dr. Diogo Verissimo, Mr. Brian Crudge, Mr. Son Sam, Mr. Dung Cao, Mr. Po Ho, Ms. Nhung Dang, Mr. Hien Nguyen, Professor Trung Cao, Dr. Jenny Glikman*

P145 Impacts of the COVID-19 Pandemic on Wildlife Rehabilitation in the United States
Ellen Haynes, *Lindsey Guerra, Dr. Kyle Woosnam, Dr. Michael Yabsley*

P146 Wilderness City: Health Surveillance in Urban Red Foxes Reveals Implications for Public Health in Whitehorse, Yukon, Canada
Cassandra Andrew, *N. Jane Harms, Maud Henaff, Kristenn Magnusson, Jodie Pongracz, Emily Jenkins, Cody Malone, Temitope Kolapo*

P147 Causes of Wildlife Morbidity and Mortality Identified Using Wildlife Rehabilitation and Post-Mortem Data in Canada
Claire Jardine, *Meagan King, Jolene Giacinti, Sara Dubois, Stéphane Lair, Jane Parmley*

P148 Asymptomatic Carriers of Beak and Feather Disease Virus: Lessons Learnt from Infection in a Wild Parrot Population
Berta Blanch-Lázaro, *Dr Anthony Chamings, Dr Raoul F.H. Ribot, Dr Mathew L. Berg, Professor Soren Alexandersen, Professor Andrew T.D. Bennett*

P149 Quantitative Measurements of Chronic Wasting Disease Prions Recovered from Swab Samples and Environmentally Relevant Surfaces
Qi Yuan, Gage Rowden, Peter Larsen, Shannon Bartelt-Hunt, Jason Bartz

P150 Assessment of Standardization for Data Analysis for RT-QuIC-based detection of Chronic Wasting Disease
Gage Rowden, *Dr. Catalina Picasso-Risso, Manci Li, Marc Schwabenlander, Dr. Tiffany Wolf, Dr. Peter Larsen*

P151 Detection of an Enzootic Mycoplasma ovipneumoniae Strain in Alaska, USA, Wildlife
Kimberlee Beckmen, *Camilla Lieske, Robert Gerlach, Marla Francis, Kimberly R. Andrews, E. Frances Cassirer*

P152 Detection of Chronic Wasting Disease (CWD) Prion in Blood by Real-Time Quaking-Induced Conversion (RT-QuIC)
Estela Kobashigawa, *Shuping Zhang, Michael Zhang, Sherri Russell, Jasmine Batten*

P153 Implementing a Veterinary Forensics Approach to Investigate Chronic Wasting Disease at a Deer Carcass Disposal Site
Marc Schwabenlander, *Gage Rowden, Suzanne Stone, Rachel Shoemaker, Laramie L. Lindsey, Jonathan D. Oliver, Linda Glaser, Michelle Carstensen, Jason C. Bartz, W. David Walter, Roxanne J. Larsen, Tiffany M. Wolf, Peter A. Larsen*

P154 CWD Sentinels: Detecting Environmental Prion Protein (ePrP) Via Surfaces for the Early Discovery of Chronic Wasting Disease
Marc Schwabenlander, *Gage Rowden, Qi Yuan, Erik Hildebrand, Patrick Hagen, Shannon L. Bartelt-Hunt, Jason C. Bartz, Tiffany M. Wolf, Peter A. Larsen*

P155 Sentinels of Emerging Infectious Diseases in South American Wildlife: The Role of Zoos and Rescue Centers in Identifying Health Threats to Pudu (Pudu puda) in Chile
Ezequiel Hidalgo-hermoso, *Javier Cabello, Francisco Ruiz Fons, Sebastián Muñoz, Galaxia Cortes, Frank Vera, Carolina Valencia, Sebastián Celis, Dario Moreira, Paulina Sepúlveda, Jose Pizarro Lucero, Victor Neira, Adriana Santodomingo, Sofia Robbiano, Rocio*

Vicencio, Juan Verasay, Nour Abuhadba Medrano, Carolina Ortiz, Ronni Atencio, Belén Bustamante, Ignacio Kemec, Rocio Lagos, Galia Ramirez, Pedro Abalos, Barbara Parra, Antonio Garnham, Ananda Muller, Fernando Esperon

P156 No Abstract Assigned

P157 Proposing a New Approach for CSFV Detection Using Environmental Samples and Swabs Wiped on the Skin
Kei Nabeshima, Mayumi Yokoyama, Shun Takagi, Taro Sugimoto, Takeo Kuriyama, Manabu Onuma

P158 No Abstract Assigned

P159 Detection of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) Utilizing Reverse transcriptase Real-Time Polymerase Chain Reaction (RT-rtPCR) on Alternative Sample Types
Katie Luukkonen, Jessica Jennings-Gaines, Kara Robbins, Nadine Vogt, Adam Vogt, William Edwards, Dr. Samantha Allen

P160 Nested and RT-PCR Assays for Detection of Elaeophora schneideri from Infected Host Tissues in Wyoming, USA
Kara Robbins, Samantha Allen

P161 Agreement of Point-of-Care Blood Uric Acid Meter and Benchtop Chemistry Analyzer in Eastern Box Turtles (Terrapene Carolina Carolina)
Carly Clark, Matthew C. Allender, Laura Adamovicz, Julie Sheldon, Kaitlin Moorhead, Kelcie Fredrickson

P162 Application of Precision Medicine to Detect Age-Related Changes in the Immunome of Black Rhinoceros (Diceros bicornis)
AA Aguirre, Molly Corder, Weidong Zhou, Timothy P. Cleland, Parker Penningtom, Jennifer Nagashima, Emanuel Petricoin, Budhan Pukazhenthi

P163 Isolation, Characterization, and Antimicrobial Susceptibility of Bacteria Isolated from Sea Lion Pups (Zalophus californianus) in Northwestern Mexico
AA Aguirre, Alan A Zavala-Norzagaray, Uriel A Angulo-Zamudio, Cesar Paul Ley-Quiñonez, Hector Flores-Villaseñor, Nidia León-Sicairos, Jorge Velázquez-Román, Fernando R Elorriaga-Verplancken, Kevin Zavala-Félix, Catherine E Hart, Adrian Canizalez-Román

P164 Drivers of Contact Rates in Wintering Elk and Methods for Assessing Disease Risk.
William Janousek, Tabitha Graves

P165 An Update on Utilizing Test and Cull to clear M. ovi from a Bighorn Sheep Herd in Nevada
Dr. Nate LaHue, Mike Cox, Matt Jeffress, Ed Partee, Chris Morris

P166 Evaluation of RT-QuIC Detection for CWD Prion Seeding Activity in Soil
Stephanie Katircioglu, Dr. Stuart Lichtenberg, Heather Inzalaco, Dr. Allen Herbst, Dr. Paul Cross, Dr. Brant Schumaker, Dr. Daniel Walsh

P167 Hellbender Mortality Post Captive-to-Wild Translocation Involves Bd, but it's Complicated
Rebecca Hardman, Sherri Reinsch, Wesley Sheley, Marley Machara, Heather Schwartz, Sandy Skeba, Dale McGinnity, Debra Miller, William Sutton

P168 Barcoding Approaches to Characterizing the Parasites and Pathogens of Endangered Hawaiian Land Snails
Bonnie Derne, Dr. David Sischo, Dr. Norine Yeung, Dr. Kenneth Hayes

P169 Parasite Genotyping Yields Insights into Post-Translocation Transmission in an Endangered Lizard
Bonnie Derne, Dr. Stephanie Godfrey, Dr. Mark Hutchinson, Professor Philip Weinstein, Professor Michael Gardner

P170 Protocols for Human Exposure to Opioids and Concentrated Medetomidine Used in Field Applications
Jenny Powers, James McCue, Geoff Stroh, William Lance

P171 No Poster Assigned

P172 Beachcast Seabird Investigation Reveals Bycatch in the Purse Seine Fishery
Bjørnar Ytrehus, Dr. Signe Christensen-Dalsgaard, Magdalena Langset, Jørgen Ree Wiig, Dr. Kim Magnus Bærum

P173 Evaluation of a Vaccine for Chronic Wasting Disease Based on Measurements of Serologic Responses in Captive Rocky Mountain Elk (Cervus canadensis nelsoni)
Peach Van Wick, Andrew Fang, Samantha Allen, Holger Wille

P174 Protecting Endangered Riparian Brush Rabbits from RHDV2 in California
Megan Moriarty, Deana Clifford, Jaime Rudd, Daniel Applebee, Fumika Takahashi, Eric Hopson, Kim Forrest, Colleen Kinzley, Darren Minier, Alex Herman, Andrea Mikolon, Tristan Edgarian, Patrick Kelly, Beate Crossley, Ashley Hill

P175 Management and Ecological Effects of High Pathogenicity Avian Influenza on Southern African Seabirds
David Roberts, Laura Roberts, Azwianewi Makhado, Pierre De Villiers

P176 Survey of Haemosporidian Parasites from Lesser Prairie Chickens (Tympanuchus pallidicinctus) from Texas and Kansas
E. Morgan Tolliver, Nubia Salinas, Nicolas Triana, Dr Kristin Bondo, Blake Grisham, D. S. Sullins, Whitney Kistler

P177 Terrestrial Gastropod Species-Specific Responses to Forest Management: Implications for Parelaphostrongylus tenuis Transmission to Moose
William Severud, Matt Petz Giguere, Tyler Walters, Tyler Garwood, Kim Teager, Katherine Marchetto, L. Gustavo R. Oliveira-Santos, Seth A. Moore, Tiffany M. Wolf

P178 Retrospective Study of Tumors in Wild and Captive Virginia Opossums (Didelphis Virginiana)
Dr. Elizabeth Howerth, Dr. Rita McManamon, Dr. Nicole Gottdenker, Dr. Brittany McHale

P179 Pilot Study Investigating Shiras Moose Mortalities in Jackson and Sublette County, Wyoming
Virginia Stout, Benjamin Wise, Alyson Courtemanch, Hank Edwards, Dr. Jacqueline Kurz, Troy Koser, Dr. Deborah McCauley

P180 Detection and Identification of Coronaviruses in North American Bats from Environmental Guano
Tyler Mclaughlin, Kathryn Griffin, Hon Ip, Anne Ballmann

P181 Comparison of Attachment Methods for Passive Integrated Transponder (PIT) tags in Big Brown Bats (*Eptesicus fuscus*) and Little Brown Bats (*Myotis lucifugus*) used in White Nose Syndrome Research
Elizabeth Falendysz, Connor Whalen, Harrison Lamb, Dr. Ariel Leon, Dana Calhoun, Dr. Tonie Rocke

P182 Suppurative Polyarthritis in Wild-Caught Big Brown Bats (*Eptesicus fuscus*) at Two Institutions in Wisconsin, Caused by a Novel *Mycoplasma* Species
Elizabeth Falendysz, Dr. Mary Thurber, Dr. Valerie Shearn-Bochsler, Dr. Jeffrey Lorch, Dr. Jenna Motz

P183 Evaluation of the Efficacy of Carbon Dioxide for Euthanasia of Big Brown Bats (*Eptesicus fuscus*) as Compared to Isoflurane
Elizabeth Falendysz, Dr. Michelle Verant, Dr. Emma Brown, Carly Malave, Dr. Ariel Leon, Dana Calhoun, Harrison Lamb, Dr. Devin Tunseth, Rachel Lambert, Dr. Tonie Rocke

P184 Avian Influenza A Virus Transmission to Quail from a Flocking Passerine
Jeff Root, Jeremy Ellis, Susan Shriner

P185 Current Antimicrobial and Probiotic Use in Wildlife Rehabilitation Facilities in the United States
Irene Bueno, Elizabeth A. Miller, Rachel Amato, Julia B. Ponder

P186 Strain Types for Chronic Wasting Disease and a Plea for a National Tissue Repository
Chia-Hua Lue, W. David Walter

P187 Staphylococcal Arthritis and Osteomyelitis with Sandspur-Associated Injury in Immature Black Skimmers (Rynchops niger) in Southwest Florida
Dr. Nicole Nemeth, Michelle van Deventer, Brittney Piersma, Veronica Guzman-Vargas, Dr. Heather Barron, Dr. Alexandro Troiano, Dr. Alisia Weyna, Dr. Melanie Kunkel, Dr. Andrew Allison, Dr. Lisa Shender, Dr. Rebecca Hardman, Dr. Susan Sanchez

P188 Batrachochytrium salamandrivorans Lesions in Larval Northern Two-Lined Salamanders (Eurycea bislineata)
Debra Miller, E. Davis Carter, Wesley Sheley, Anastasia Towe, Matthew Gray

P189 Evaluation Tolazoline or Vatinoxan for Alleviating Adverse Effect of Butorphanol-azaperone-medetomidine Immobilization in Rocky Mountain Elk
Annette Roug, Pauline Nol, Khursheed Mama

P190 Amphibian Infection Tolerance and Resistance in the Context of Chytridiomycosis
Laura Grogan, Matthew Mangan, Hamish McCallum

P191 Host Genomic Variation and Beak and Feather Disease Virus Infection in Crimson Rosellas (Platycercus elegans)
Candice Lachenicht, Dr. Flavia Garcia-Termignoni, Miss Berta Blanch-Lázaro, Dr. Raoul Ribot, Dr. Mathew Berg, Professor Soren Alexandersen, Professor Scott Edwards, Professor Andrew Bennett

P192 Treponeme-Associated Hoof Disease in Free-Ranging Wild Elk in Southwestern Washington USA: Correlation of Bacterial Community and Visual Disease Progression
Jenny Wilson-Welder, David Alt, Darrel Bayles, Kristin Mansfield, Sushan Han

P193 Canine Distemper Virus Ecology: Insights from a Longitudinal Serological Study in Wild Raccoons (Procyon lotor)
Jolene Giacinti, David Pearl, Davor Ojkic, Kristin Bondo, Claire Jardine

P194 No Abstract Assigned

P195 Hepatitis and Hepatic Necrosis Associated with Chlamydiales sp. in the Endangered Santa Cruz Long-Toed Salamander (Ambystoma macrodactylum croceum)
Valerie Shearn-Bochsler, Jeffrey Lorch

P196 Comparative Response of Smallmouth Bass (Micropterus dolomieu) and Largemouth Bass (Micropterus salmoides) to a Short-Term Poly I:C challenge
Jessica Leet, Dr. John Hansen, Dr. Catherine Richter, Dr. Donald Tillitt, Dr. Justin Greer, Dr. Luke Iwanowicz

P197 No Abstract Assigned

P198 Host Immune Responses to Enzootic and Invasive Pathogen Lineages Vary in Magnitude, Timing, and Efficacy
Coby Mcdonald, C. Guilherme Becker, Carolina Lambertini, Felipe Toledo, Célio Haddad, Kelly Zamudio

P199 Nasopulmonary Mites (Acari: Halarachnidae) as Potential Vectors of Bacterial Pathogens, including Streptococcus phocae, in Marine Mammals
Risa Pesapane, Andrea Chaves, Janet Foley, Nadia Javeed, Samantha Barnum, Katherine Greenwald, Erin Dodd, Christine Fontaine, Padraig Duignan, Michael Murray, Melissa Miller

P200 One Health Community-Based Wildlife Mortality Surveillance for Ebola
Sarah H. Olson, Alain U. Ondzie, Marc-Joël Akongo, Trent Bushmaker, Kenneth N. Cameron, Morgane Cournarie, Dania M. Figueroa, Robert J. Fischer, Cynthia Goma-Nkoua, Serge D. Kaba, William B. Karesh, Eeva Kuisma, M. Jeremiah Matson, Jean-Vivien Mombouli, Vincent J. Munster, Patricia E. Reed, Stephanie N. Seifert, Chris Walzer

P201 Developing a Wildlife Health Information System: Insights and Opportunities
Sabrina S. Greening, Katie Haman, Lowell Ballard, Stephanie Herman, Chris Lutz, Julie Ellis

P202 Avian Vibriosis: A Rising Barometer for One Health
Andrea Ayala, Miles Goldenberg, Salvador Almagro-Moreno, C. Brandon Ogbunugafor

P203 Fish Eating Birds Can Spread Bacterial Diseases Between Catfish Ponds
Fred Cunningham, Lorelei Ford, Larry Hanson

P204 Epistylid Infestation Resulting in Morbidity in Two Species of Mud Turtles (Kinosternon spp.) in the American Southwest
Audrey Owens, Jennifer Smith, Rebecca Cole, Jeffrey Lorch, Anne Justice-allen, Daniel Grear

P205 Erysipelothrix rhusiopathiae: An Increasingly Significant Pathogen for Critically Endangered Cook Inlet Beluga Whales
Natalie Rouse, DVM, DACVP Kathy Burek-Huntington

P206 Causes of Morbidity and Mortality in Free-Ranging Sea Turtles Found on St. Kitts and Nevis (2015-2022)
Heather Fenton, Angela Picknell, Michelle Dennis, Maria-Jose Navarrete, Pompei Bolfa, Kimberly Stewart

P207 Diet-Induced Thiamine Deficiency in Canada Geese (Branta canadensis) Recovered from Low-Head Dam Site in Iowa
Rachel Ruden, Dr. Jenni Boonjakuakul, Dr. Yuko Sato

P208 White-Tailed Deer Lung Cells are Susceptible to Japanese Encephalitis Virus
Leela Noronha, Emily Hedden, Jeana Owens, Dana Mitzel

P209 Evidence of Tick-borne Virus Circulation in Virginia via Serosurveillance in Wildlife Species
Gillian Eastwood, Dr. Alexandra Cumbie, Peter Schiff, Ahmed Garba, Rebecca Trimble, Dr Jen Riley

P210 Parasites of the Invasive North American Raccoons (Procyon lotor) in Central Spain
Michael Yabsley, Carlos García, Jose Aguirre, Silvia Villaverde, Eva Banda, Sonia Hernandez

P211 Echinococcus Species Infections Among Wild Canids in Pennsylvania, USA
Christopher Cleveland, Kayla Garrett, Dr. Justin Brown, Ryan Grunert, Jonathan Hunter, Dr. Mark Ruder, Kyle Van Why, Dr. Michael Yabsley

P212 Francisella Tularensis Exposure in Arctic Wildlife: A Need for Renewed Surveillance in Alaska?
Matthew Smith, Caroline Van Hemert, Todd C. Atwood, David R. Sinnett, Jerry W. Hupp, Brandt W. Meixell, David D. Gustine, Layne G. Adams, Andrew M. Ramey

P213 Plague-Positive Mouse Fleas on Prairie Dog Colonies: Flea Blood Meal Identification by Amplicon Deep Sequencing
Gebbiena Bron, Leah A. Owens, Chris D. Dunn, Professor Tony L. Goldberg, Dr. Tonie E. Rocke

P214 Investigating Host Ecology of Lyme Disease Causative Agent Borrelia burgdorferi in Ohio
Ningzhu Bai, Dr. Andreas Chavez, Dr. Risa Pesapane

P215 SARS-CoV-2 in White Tail Deer in Pennsylvania
Roderick Gagne, Andrew Marques, Scott Sherrill-Mix, John Everett, Hriju Adikhari, Shantan Reddy, Julie Ellis, Haley Zeliff, Sabrina S. Greening, Carolyn Cannuscio, Katherine Strelau, Ron Collman, Brendan J. Kelly, Kyle Rodino, Frederic D. Bushman, Eman Anis

P216 Genetic Detection of Sin Nombre Virus in Rodent Assemblages of East New Mexico, A Region with No Known Human Infection
Jaecy Banther-McConnell, Thanchira Suriyamongkol, Robert Nofchissey, Samuel Goodfellow, Steven Bradfute, Ivana Mali

P217 Complex Virus Diversity Among Wild-Caught Rodents in Sierra Leone – Insights into Virus Ecology at High-Risk Interfaces
Bruno Ghersi, James Bangura, Matej Vucak, Emmanuel Amara, Marilyn Kanu, Victor Lungay, Edwin Lavalie, Willie Robert, Jenna Nichols, David Wolking, Corina Monagin, UC Davis PREEMPT consortium, Andrew Davison, Brian Bird

P218 Salmonella Environmental Persistence Informs Management Relevant to Avian and Public Health
Kimberly Perez, Sonia Hernandez, Olivia Seiverts, William Norfolk, Raquel Francisco, Susan Sanchez, Erin Lipp

P219 Cryptococcus Gatii Infections in Oregon Roosevelt Elk (Cervus Canadadensis Rooseveltl).
Julia Burco, Deborah Chong, Emilio DeBess

P220 Development and Implementation of a Strategic Bio-Risk Management Plan in the Context of Viral Zoonoses
Tristan Burgess, Dr. Katie Prager, Dr. Bruno Gerci, Dr. Jonathan Gass, Dr. Felicia Nutter, Ms. Colleen Cronin, Dr. David Brett-Major, Dr. Deborah Kochevar

ORAL PRESENTATIONS

Oral Presentation #1

Holistic Solutions for Wildlife Health: What does it Mean, and What can we do?

Brett Elkin[1]
[1]Government of the Northwest Territories Department of Environment and Natural Resources

Wildlife management and conservation initiatives in countries around the world play an important role in our collective efforts to support wildlife, environmental and planetary health. Wildlife health is broadly defined as the resilience of individuals and their capacity to cope with stressors, leading to long-term sustainability of populations and species. Today, there are a wide range of biological, social and environmental factors that significantly impact wildlife health, sustainability and biodiversity at a global scale, including climate and environmental change. These factors and their cumulative impact on wildlife populations can also impact people through food safety and security, environmental health, and alteration of important social and culture connections with wildlife and the environment. The COVID-19 pandemic highlighted some of the societal challenges we face in addressing these big issues, but also highlighted the ability to work together to take action to protect and promote health. It also highlighted the importance of societal values and expectations when we address these complex issues. This presentation will build on impressive advances in our understanding and management of wildlife diseases in recent decades, and explore ways that this knowledge and expertise can be most effectively applied in an overall holistic approach to influence and support wildlife and ecosystem health. It will highlight the importance of strategic and targeted research to provide information to support local, regional and global wildlife management and conservation efforts, and how to most effectively use this information to inform and influence public opinion and decisions makers to support change.

Oral Presentation #2

The Many Hosts of SARS-CoV-2

Vivek Kapur

SARS-CoV-2 is a generalist pathogen. Since its early description in humans, secondary host jumps of SARS-CoV-2 to an expanding array of domesticated and free-living animal hosts have been reported, as has occasional spill back to humans from animals including mink, hamsters and white-tailed deer. This presentation will summarize our current understanding of the many hosts of SARS-CoV-2, describe recent findings of extensive infection of white-tailed deer, and explore the opportunities for establishment of sylvatic transmission chains and potential consequences for human, domestic animal, and wildlife health.

Oral Presentation #3

Wildlife Vaccination as a Disease Management Tool: Current State of the Art and Prospects for the Future

Rocke Tonie[1]
[1]U.S. Geological Survey National Wildlife Health Center

Vaccination is increasingly being considered as a tool to manage diseases of concern in wildlife, primarily to control pathogens that also infect humans and domestic animals (e.g. rabies in terrestrial carnivores), but also when disease management is considered crucial to the survival and conservation of threatened and endangered species (e.g. plague in black-footed ferrets). Building on the success of oral rabies vaccination campaigns in carnivores that began in the 1980's and continue today, a number of wildlife vaccines have been developed and tested in field settings for a wide variety of pathogens and wild animal species. Not surprisingly, each case has unique challenges, with different objectives, disease dynamics, delivery methods, scales of application, and criteria for success. The U.S. Geological Survey National Wildlife Health Center, in collaboration with partners at the University of Wisconsin, Madison, has developed several vaccines using raccoon poxvirus as a platform for mucosal delivery of bacterial, fungal, or viral antigens. The first, sylvatic plague vaccine (SPV), was tested for use in prairie dogs, primarily to manage this flea-borne bacterial disease for conservation purposes, as it is a significant hazard for several threatened and endangered species. Field testing has demonstrated consumption of SPV laden baits increases rates of prairie dog survival and stabilizes populations, but large-scale distribution of baits (up to thousands of acres) would be required to generate significant herd immunity. We also developed and are in the process of testing two vaccines for use in bats that could be delivered via topical application in a viscous medium that the animals ingest upon grooming. One is designed to mitigate the effects of white nose syndrome (WNS), a fungal disease that has caused significant population declines in several species of bats. In initial field trials, bats hand-vaccinated against WNS by oral administration had lower fungal loads, and higher survival was noted in some cohorts compared to controls. The second targets rabies transmitted via vampire bats, a disease that afflicts cattle and other domestic animals, as well as humans, in Latin America. Although field testing has not yet started, laboratory trials have demonstrated that vaccination blocks shedding of rabies virus from rabid bats, effectively hindering transmission to bats and other species. The most important considerations, challenges, and future prospects of using vaccination to manage disease in wildlife will be discussed using these three case studies and others as examples.

Oral Presentation #4

Emerging California Serogroup Viruses in Northern Canadian Wildlife

Kayla Buhler[1], Antonia Dibernardo[2], Nicholas Pilfold[3], John Blake[4], N. Jane Harms[5], Heather Fenton[6], Suzanne Carriere[7], Allicia Kelly[7], Helen Schwantje[8], Xavier Fernandez Aguilar[9], Lisa-Marie Leclerc[10], Geraldine-G. Gouin[11], Nicholas Lunn[12], Evan Richardson[12], David McGeachy[12], Émilie Bouchard[1], Adrián Hernández Ortiz[1], Gustaf Samelius[13], L. Robbin Lindsay[2], Michael Drebot[2], Patricia Gaffney[3], Patrick Leighton[14], Ray Alisauskas, Emily Jenkins[1]

[1]University of Saskatchewan, [2]Public Health Agency of Canada, [3]San Diego Zoo Wildlife Alliance, [4]University of Alaska Fairbanks, [5]Government of Yukon, [6]Ross University School of Veterinary Medicine, [7]Government of the Northwest Territories, [8]Government of British Columbia, [9]University of Calgary, [10]Government of Nunavut, [11]Makivik Corporation, [12]Environment and Climate Change Canada, [13]Snow Leopard Trust, [14]University of Montreal

As northern Canada continues to warm, changes in the diversity and distribution of vectors and pathogens have become a health concern for wildlife and people. California serogroup viruses (CSV) are mosquito-borne viruses of zoonotic importance and wildlife reservoirs in northern ecosystems have yet to be identified. We examined exposure of northern wildlife from multiple ecosystems to CSV. Antibodies were detected in 63% of caribou (n=517; CI¬95 58-67), 4% of Arctic foxes (n=297; CI¬95 2-7), 12% of red foxes (n=77; CI¬95 6-21) and 28% of polar bears (n=377; CI¬95 24-33). Biological factors (sex and age) and summer temperatures were positively associated with polar bear exposure, while sampling location, year and ecotype (migratory tundra, boreal, and mountain) were associated with caribou exposure. This confirms that northern Canadian wildlife have been broadly exposed to CSV and that these viruses are likely emerging as the climate continues to change. In order to determine the reservoir potential of Rangifer (caribou/reindeer) for CSV, captive reindeer at the University of Alaska Fairbanks were exposed to Jamestown Canyon virus (JCV) injected subcutaneously over the shoulders and antibody response, viremia, tissue predilection sites, and health effects were evaluated. All animals were asymptomatic during the study. Naïve animals had a detectable antibody response 5 days post infection and JCV was detected in the blood of animals on day 1 and 5 post infection. Other samples that contained viral RNA included the parotid lymph nodes, spleen, obex, uterus and urine. Viral RNA in the obex suggests that the infection can progress to the nervous system (similar to human infections) and presence in the uterus and urine emphasizes the need for further studies to investigate the impacts on reproductive success and other transmission mechanisms.

Oral Presentation #5

Viral Surveillance in Sanctuary Chimpanzees (Pan troglodytes) Across Africa

Emily Dunay[1], *Leah Owens*[1], *Christopher Dunn*[1], *Joshua Rukundo*[2], *Rebeca Atencia*[3], *Megan Cole*[4], *Averill Cantwell*[5], *Melissa Emery Thompson*[4], *Alexandra Rosati*[6], *Tony Goldberg*[1]
[1]Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, [2]Ngamba Island Chimpanzee Sanctuary/Chimpanzee Trust, [3]Jane Goodall Institute Congo, [4]Department of Anthropology, University of New Mexico, [5]Department of Psychology, University of Michigan, [6]Department of Psychology and Department of Anthropology, University of Michigan

Infectious disease is a major concern in both wild and captive primate populations. Chimpanzee sanctuaries in Africa provide the necessary care and housing for thousands of wild-born, orphaned apes who have been confiscated from the bushmeat or pet trade. Among infectious disease threats to apes, viruses are paramount, considering their historic impacts on wild and captive ape populations and their propensity for anthroponotic transmission. We used metagenomic next-generation sequencing to examine blood samples from chimpanzees (Pan troglodytes) in three sanctuaries across Africa, one in West Africa, one in Central Africa, and one in East Africa. Our goal was to evaluate the degree to which viruses of human origin and other atypical viruses might persistently infect sanctuary chimpanzees. We identified viruses from eight viral families (Anelloviridae, Flaviviridae, Genomoviridae, Hepadnaviridae, Parvoviridae, Picobirnaviridae, Picornaviridae, and Rhabdoviridae). The majority (15/26) of viruses identified are in the family Anelloviridae and represent the genera Alphatorquevirus (torque teno virus) and Betatorquevirus (torque teno mini virus). The only virus identified that has been associated with disease in captive or wild chimpanzees is rhinovirus C (Picornaviridae) in which one individual was infected subsequent to an outbreak of respiratory illness in that population. All other viruses appear to be normal constituents of the chimpanzee virome. Our results suggest that the risk of acquiring persistent, viremic infection with anthroponotic or atypical viruses in sanctuary settings may be low. These results have implications for sanctuary chimpanzee health and management and for captive and wild chimpanzee conservation.

Oral Presentation #6

"Healthy Children, Healthy Chimps": Reducing Reverse Zoonotic Respiratory Virus Transmission from Humans to Chimpanzees in Kibale National Park, Uganda

Taylor Weary[1,2], *Tressa Pappas*[3], *Jim Gern*[3], *Tony Goldberg*[1,2]
[1]University of Wisconsin School of Veterinary Medicine, [2]Kibale EcoHealth Project, [3]University of Wisconsin School of Medicine and Public Health

Reverse zoonotic respiratory diseases threaten wild chimpanzees across Sub-Saharan Africa. In the Kanyawara chimpanzee community in Kibale National Park, Uganda, respiratory disease has caused 59% of deaths over the past 30 years, with mortality rates of up to 10% during outbreaks. Our studies of the Kanyawara and nearby Ngogo communities have identified the causative agents as “common cold” pediatric human pathogens. We hypothesize that respiratory pathogens circulate in children living near chimpanzee habitats, and that adults in those villages become asymptomatically infected and can carry the pathogens into the forest and infect chimpanzees. Our objectives are to characterize respiratory pathogens in local children, forest workers, and chimpanzees using comprehensive molecular diagnostics and metagenomic DNA sequencing, and to examine the reverse zoonotic transmission risk that varies with pathogen type, season, environment, and the individual characteristics of humans and chimpanzees. To date, we have collected respiratory disease symptoms data and 1,900 nasopharyngeal swabs from approximately 250 human study participants and over 700 fecal samples from 141 chimpanzees. Initial data show that children exhibit high frequencies and severities of symptoms while adults are largely asymptomatic and that COVID-19 lockdown significantly decreased symptoms frequencies. Human respiratory symptoms peak in February, just prior to March, the most common month for chimpanzee respiratory disease outbreaks. Our data will inform strategies to reduce transmission of respiratory pathogens, including SARS-CoV-2, to the approximately 1,500 chimpanzees of Kibale and, by extension, to apes across Sub-Saharan Africa. The “Healthy Children, Healthy Chimps” program reflects our hope that reverse zoonotic respiratory disease transmission to chimpanzees can be mitigated through a One Health approach that considers the health of chimpanzees and local people to be linked, and that researches and acts upon evidence-based solutions. Ultimately, improving health outcomes for chimpanzees requires targeted interventions to alleviate respiratory disease burden in children.

Oral Presentation #7

Human Herpesvirus and Mycobacterium tuberculosis Complex in Confiscated and Rescued Neotropical Primates in Peru

Fernando Javier Vilchez Delgado[1,2], A. Patricia Mendoza[3,4], Raul Bello[5,6], Paola Santa[6], Xiomara Zavala Peña[2], Michael Talledo Albujar[2], Marieke H. Rosenbaum[1]
[1]Tufts University, [2]Instituto de Medicina Tropical Alexander von Humboldt, [3]University of Missouri-St. Louis, [4]Neotropical Primate Conservation, [5]Kawsay Biological Station, [6]Taricaya Rescue Center

Neotropical primates (NP) are among the most trafficked wild animals in Peru. This illegal activity involves the extraction and mobilization of NP from forests to densely populated urban areas, enabling opportunities for close human-monkey interactions. Highly prevalent human-associated infectious pathogens such as tuberculosis and herpes simplex pose a serious threat to captive and wild NP populations and often resulted in lethal outcomes. This study aimed to evaluate the presence of Mycobacterium tuberculosis complex (MTBC) and Herpes Simplex Virus 1 and 2 (HSV-1/2) in DNA samples extracted from blood and saliva of NP rescued from trafficking in 4 different Peruvian departments: Lima (n=29), Loreto (n=14), Madre de Dios (n=131), and Piura (n=16). MTBC was detected using a real-time PCR kit targeting IS6110 and MPB genes. HSV-1 and HSV-2 were screened using a Pan-herpesvirus PCR protocol followed by Sanger sequencing of positive amplicons (≈ 180 bp). MTBC was detected in 3% (1/29) monkeys confiscated in Lima and 4% (5/131) confiscated monkeys arriving to rescue centers in Madre de Dios, HSV-1 was detected in 28% (8/29) and 8% (11/131) of them. Only one individual in Lima was infected with HSV-2. Our findings demonstrate the circulation of human-associated pathogens in NP originated in the wildlife trafficking in Peru. Opportune pathogen screening of confiscated animals may prevent the spread of these infections into captive colonies and potential spillover to wild populations.

Oral Presentation #8

Diagnostic Assays to Detect Entomopathogenic Serratia spp. in the Critically Endangered Lord Howe Island Stick Insect (Dryococelus australis)

Nicholas Doidge[1], *Ms. Joanne Allen*[1], *Prof Glenn Browning*[1], *Mr. Rhys Bushell*[3], *Dr. Michael Lynch*[2], *Dr. Marc Marenda*[1]

[1]Asia-Pacific Centre for Animal Health, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, [2]Melbourne Zoo, [3]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne

After seven decades of presumed extinction, the critically endangered Lord Howe Island stick insect (Dryococelus australis) was rediscovered in 2001. Through the concerted efforts of the Melbourne Zoo's captive breeding program and a rodent eradication project carried out by the Lord Howe Island Board, these insects will soon be reintroduced onto Lord Howe Island. One of the most significant challenges facing both the breeding and reintroduction programs for D. australis is the repeated mortality events since 2014 associated with the bacterium Serratia spp. We found that closely related strains of Serratia predominate in affected D. australis, and experimental infections in western honey bees (Apis mellifera) revealed that these strains are pathogenic to insects.

Full genome sequencing of Serratia isolates from stick insects and their environments indicated that diagnostic assays could be developed to specifically detect entomopathogenic Serratia spp. in live and deceased stick insects. We designed two qPCR assays targeting a highly conserved chitinase gene, and a urease gene unique to most insect-associated strains, which can detect and differentiate environmental and entomopathogenic Serratia spp. High resolution melt curve analysis of the amplicons allows us to distinguish between insect-associated strains of Serratia. These assays enable rapid detection of entomopathogenic Serratia from cultures or clinical samples and help establish the significance of different strains in insect populations or environments.

We also developed a loop-mediated isothermal amplification (LAMP) assay to specifically detect entomopathogenic Serratia in the frass produced by live stick insects. The LAMP assay is rapid, simple to perform, and suited to field conditions. This test was applied to screening captive insect populations at Melbourne Zoo, Melbourne Museum and on Lord Howe Island, and we aim to use it in the field prior to releasing stick insects onto Lord Howe Island.

Oral Presentation #9

Black-Legged Ticks (Ixodes scapularis) Harbor and Excrete Chronic Wasting Disease Prions from Infected Blood Meals

Heather N'te Inzalaco[1], Dr. Stuart S. Lichtenberg[2], Francisca Bravo-Risi[3,4], Dr. Rodrigo Morales[3,4], Dr. Dan P. Walsh[5], Dr. Dan J. Storm[6], Dr. Wendy C. Turner[7], Dr. Joel A. Pedersen[8]
[1]Department of Forest and Wildlife Ecology, University of Wisconsin, Madison, [2]Department of Soil Science, University of Wisconsin, Madison, [3]Department of Neurology, The University of Texas Health Science Center at Houston, [4]Centro Integrativo de Biologia y Quimica Aplicada (CIBQA). Universidad Bernardo O'Higgins, [5]US Geological Survey, 'National Wildlife Health Center, [6]Wisconsin Department of Natural Resources, [7]U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, [8]Environmental Health and Engineering, Johns Hopkins University

Transmissible spongiform encephalopathies (TSEs) are a family of fatal neurodegenerative diseases caused by infectious prions —misfolded conformers of the endogenous host prion protein. Chronic wasting disease (CWD) is a TSE affecting wild and domestic cervids (e.g., deer, elk, moose). Indirect transmission events may play a key role in disease dynamics driving geographic spread of CWD. However, indirect transmission modes are not well understood. During disease progression, CWD prions (PrPCWD) are shed via secreta, excreta, and are present blood. The presence of PrPCWD in blood may pose a risk for indirect transmission by way of hematophagous ectoparasites acting as mechanical vectors. Cervids can carry high tick burdens and exhibit allogrooming, a common tick defense strategy between conspecifics. Oral routes of TSE transmission are well documented, and typically involve ingestion of infectious tissues. Ingestion of engorged ticks during allogrooming may expose naïve animals to PrPCWD. This study investigated experimentally and observationally whether black-legged ticks (Ixodes scapularis) can harbor transmission-relevant quantities of PrPCWD by combining experimental tick feeding trials and evaluation of ticks from free-ranging white-tailed deer. Using the real-time quaking-induced conversion (RT-QuIC) assay, we show that I. scapularis fed using artificial membranes and PrPCWD-spiked blood ingest and excrete PrPCWD. Using RT-QuIC and another ultra-sensitive prion detection assay, protein misfolding cyclic amplification, we detected seeding activity in 6 (4 by PMCA, 3 by RT-QuIC, 1 by both) of 15 pooled tick samples removed from wild CWD-infected white-tailed deer, indicating 40% CWD prevalence in black-legged ticks. Seeding activities in ticks were analogous to 10 -1000 ng of CWD-infected retropharyngeal lymph node collected from corresponding deer. Inferred estimates revealed a median infectious dose range of 0.3 – 42.4 per tick, suggesting that black-legged ticks can take up transmission-relevant amounts of PrPCWD and may pose a CWD risk to cervids if consumed

Oral Presentation #10

Laparoscopic Oviductal Artificial Insemination with Frozen Semen for Conservation Management of Endangered Ocelots in Southern Texas

Ashley Reeves[1], *Dr. William F. Swanson*[2], *Dr. Tyler Campbell*[3], *Dr. Clayton D. Hilton*[4], *Dr. Hilary M. Swarts*[5], *Dr. Thomas deMaar*[6], *Dr. Debra L. Miller*[1]

[1]Center for Wildlife Health and College of Veterinary Medicine, University of Tennessee, [2]Center for Conservation and Research of Endangered Wildlife, Cincinnati Zoo and Botanical Garden, [3]East Foundation, [4]Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, [5]Laguna Atascosa National Wildlife Refuge, United States Fish and Wildlife Service, [6]Gladys Porter Zoo

Free-ranging ocelot populations in the United States have declined to just ~50-80 cats in southern Texas. Consequently, increased inbreeding depression may negatively impact their fertility, reduce breeding success and cause regional extinction. In conjunction with semen collection and cryostorage studies, we are exploring the application of laparoscopic oviductal artificial insemination (LO-AI) with frozen semen, previously successful with zoo-housed ocelots, as a conservation tool for wild ocelot populations. In the present study, our goal was to assess the feasibility of LO-AI, using frozen semen sourced from wild Texas ocelots, to produce pregnancies in zoo-based females.

Semen recovered from wild ocelots (n=3) via urethral catheterization during anesthesia or post-mortem after vehicular trauma, was cryopreserved by ultra-rapid freezing and/or traditional straw freezing. Ovarian activity and ovulation of zoo-housed ocelots (n=3) were synchronized for LO-AI using oral progestin treatment (30 days), followed by a 7-day withdrawal period and injection with exogenous gonadotropins (eCG/pLH). At laparoscopy (~38 hours post-pLH), frozen-thawed semen was deposited into oviducts of each ovulatory female, and fecal progestin analysis was used to assess pregnancy status.

All three females ovulated in response to gonadotropin treatment, averaging 4.67 ± 2.03 corpus luteum (CL)/female, and were inseminated with an average of 6.56 ± 2.54 $x10^6$ motile frozen-thawed sperm. No pregnancies resulted, likely due in part to suboptimal post-thaw semen parameters. Additional LO-AI procedures, using newly banked semen samples, are pending to further assess the efficacy of this approach for introducing new founder genes from wild ocelots into zoo-based populations. With further refinement, LO-AI with frozen semen may facilitate ocelot pregnancies using minimal sperm numbers, promote gene flow among isolated populations without requiring translocation of live animals, and re-establish extirpated populations with genetically diverse individuals.

(Assistance of the Albuquerque BioPark, Brookfield Zoo and Pittsburgh Zoo is greatly appreciated).

Oral Presentation #11

Cataloging Retinal Lesions in Asiatic Black Bears (u. thibetanus)

Kylie McDaniel[1], *Dr. Felicia Nutter*[1], *Dr. Rachel Sanki*[2], *Dr. Stephanie Pumphrey*[1]
[1]Cummings School of Veterinary Medicine at Tufts University, [2]Animals Asia

Approximately 17,000 captive bears live on bile farms across Asia. Cardiovascular disease is the third leading cause of death in previously bile-farmed bears, and systemic hypertension is believed to be a common problem. Because blood pressure cannot be measured consistently in rehabilitant bears, evidence of ocular target organ damage (TOD) is one criterion used to diagnose systemic hypertension. However, no published literature characterizes common ocular findings in a large population of bears of any species. This retrospective study of 95 Asiatic black bears (Ursus thibetanus) housed at Animals Asia Vietnamese Bear Rescue Center establishes the prevalence of retinopathy in previously bile-farmed bears, identifies common fundic lesions, and explores the relationship between hypertension and ocular disease. Using a smartphone camera and 40D lens, fundic images were taken during the bears' 2021 health examinations. Lesions were grouped by class and analyzed for associations with history, signalment, and clinical outcomes. Retinal lesions were common in the bears at Animals Asia, with 45% (43/95) of examined bears presenting with a fundic lesion of some kind; 56% (24/43) of these bears had bilateral lesions. Vascular lesions were the most common class (30/95), followed by tapetal (18/95) and optic nerve lesions (7/95). Retinal hemorrhage (21/95) and hypo-reflective tapetal regions (10/95), suspected to indicate chorioretinal infiltrates, were the most common specific lesions identified. These findings emphasize the need for more research on retinopathy in bears as it relates to hypertension. Bears with evidence of ocular TOD, as identified in other species, should be closely monitored for additional signs of cardiovascular disease. Treatment for systemic hypertension may be considered. Furthermore, this non-invasive, inexpensive methodology holds the potential to expand our knowledge of wildlife ophthalmology, particularly in field research settings and the rehabilitation of species where common retinopathies have not been defined.

Oral Presentation #12

Immobilization of Helicopter-Captured Elk (Cervus canadensis) with Butorphanol-Azaperone-Medetomidine versus Nalbuphine-Medetomidine-Azaperone

Kathleen E. Williams[1], *Nathan D. Hooven*[1], *John T. Hast*[2], *Dr. Christine L. Casey*[2], *R. Daniel Crank*[2], *Matthew T. Springer*[1], *John J. Cox*[1]
[1]University of Kentucky, [2]Kentucky Department of Fish and Wildlife Resources

Several reversible compounded immobilization drugs have been developed for use in large mammals, including Butorphanol-Medetomidine-Azaperone (BAM) and Nalbuphine-Medetomidine-Azaperone (NalMed-A). These combination drugs contain opioids that are either unscheduled or Schedule IV, based on potential for abuse, and are thus subject to less regulation than high-potency opioids which have more stringent requirements for acquisition. However, very few studies with large sample sizes have compared the efficacy of these drugs in ungulates under intensive field conditions, such as capture and transport by helicopter prior to sedation. In January 2020 – 2022, we compared these combination drugs in wild elk (Cervus canadensis) captured via helicopter net gun in southeastern Kentucky. During 133 handling events, each animal was physically restrained during transport, then immobilized with a standard dose of BAM (n = 43) or NalMed-A (n = 90) once brought to a central working location. We recorded induction and reversal times as well as physiological responses, including body temperature, heart rate, respiration, and blood oxygen saturation. Mean (± SE) induction and reversal times for BAM (9.42 ± 0.67 and 4.53 ± 0.52 minutes) and NalMed-A (8.8 ± 0.34 and 4.46 ± 0.47 minutes) were not significantly different between drug combinations, but some physiological responses did differ. By the time reversal was administered, elk immobilized with either drug experienced decreased body temperature. Elk immobilized with BAM experienced increased heart rate and respiration, while these vitals remained steady in elk immobilized with NalMed-A. On average, blood oxygen saturation was lower at time of induction in elk immobilized with BAM. However, it eventually increased in elk immobilized with either drug, likely due to supplemental oxygen administration to prevent severe hypoxemia. Despite differences in physiological responses, both BAM and NalMed-A appear to be effective for short-term sedation and could be used interchangeably.

Oral Presentation #13

Multi-Strain Domestic Spillover of Mycoplasma ovipneumoniae and Severe Epizootic Pneumonia Affecting Bighorn Sheep (Ovis canadensis) in Badlands National Park, South Dakota

Treana Mayer[1], Terry Spraker[1], Paul Roghair[3], Chad Lehman[4], Trent Haffley[4], Eddie Childers[3], Nathan Galloway[2], Laurie Baeten[2]

[1]Colorado State University, Veterinary Diagnostic Laboratory, [2]National Park Service, Biological Resources Division, [3]National Park Service, Badlands National Park, [4]South Dakota Department of Game, Fish, & Parks

Epizootic pneumonia complex in bighorn sheep (Ovis canadensis, BHS) is an important disease issue with long-term conservation implications. Contemporary evidence best supports Mycoplasma ovipneumoniae and secondary bacterial pathogens from domestic Caprinae as responsible agents. Here, we describe pathologic findings of epizootic pneumonia in the well-studied, robust BHS herd in Badlands National Park, South Dakota, following documented domestic interactions. On June 4th, 2021, four BHS rams were in proximity to sheep and goat ranches outside park boundaries. Two months later, increased morbidity and mortality was first observed in the herd, followed by a dramatic reduction from 262 to 60 animals between July-December 2021, warranting a thorough outbreak investigation describing pathogenesis and short-term population impacts. Post-mortem findings from necropsy, histopathology, aerobic bacterial culture, PCR, and sequencing are described for up to 11 BHS. Antemortem testing of domestic herd contacts, historical and contemporary BHS survey data provided context and comparison. Pulmonary histopathologic findings included severe pyogranulomatous to suppurative bronchopneumonia with variable pulmonary edema and lymphocytic cuffing. PCR found widespread evidence of M. ovipneumoniae (10/10 BHS, compared to 22/44 sheep, 4/49 goats), some with heavy lungworm burden (4/10), bluetongue virus infection (4/10), and nasal tumor (1/8). Culture isolated Trueperella pyogenes (10/11), and Bibersteinia trehelosi (5/11). Surveys estimated an 80% total population reduction. M. ovipneumoniae strain typing described goat and sheep related strains present in BHS. To our knowledge, this is the first recorded simultaneous spillover of both sheep and goat domestic-origin M. ovipneumoniae strains to BHS, followed by epizootic pneumonia with higher-than-average mortality in an otherwise highly productive population. We discuss the implications of comorbidities, environmental conditions, and historical health status of this herd. This case study highlights the importance of domestic-wildlife spillover prevention and inter-agency collaboration and coordination in controlling BHS pneumonia, with the shared goal of protecting wildlife health into the future.

Oral Presentation #14

Synanthropic Mesomammals and the Peridomestic Transmission Cycle of Trypanosoma Cruzi in Florida

Carson Torhorst[1], *Zoe White*[1], *Michael P. Milleson, Dr. Normal L. Beatty*[2], *Dr. Samantha M. Wisely*[1]
[1]University of Florida Department of Wildlife Ecology and Conservation, [2]University of Florida Department of Medicine, Division of Infectious Diseases and Global Medicine

Trypanosoma cruzi, a parasitic protozoan, is the causative agent of Chagas disease and infects synanthropic wildlife reservoirs across its endemic range. In South America synanthropic reservoirs maintain T. cruzi in peridomestic transmission cycles at a higher prevalence compared to their sylvatic counterparts. In the US, T. cruzi infects raccoons (Procyon lotor) and Virginia opossums (Didelphis virginiana), however, what impact these human-adapted species have in the peridomestic transmission cycle is not understood. We aimed to determine if the prevalence of T. cruzi infected raccoons and opossums changed with ecotype. We hypothesized that raccoons and opossums would have a higher prevalence in peridomestic ecotypes due to higher contact with the human associating triatomine vectors in the peridomestic ecotype. We sampled 5 paired peridomestic and sylvatic sites across North-Central Florida, and from the barrier or key islands of South Florida. DNA was extracted from each sample collected and screened for the presence of T. cruzi nucleic acid using real time PCR methods. In this study raccoons (n=135, 42.2%, 95% CI [34.2-50.7%]) and opossums (n=113, 52.2%, 95% CI [43.1-61.2%]) were infected with T. cruzi within each ecotypes and the prevalence across ecotypes was similar for both raccoons (peridomestic: n= 77, 44.2%, 95% CI [33.6-55.3%], sylvatic: n=58, 39.7%, 95% CI [28.1-52.5%]) and opossums (peridomestic: n=67, 47.7%, 95% CI [36.3-59.5%], sylvatic: n=46, 54.4%, 95% CI [40.4-67.8%]). From the barrier or key island no raccoons were infected with T. cruzi (n=68, 0.0%, 95% CI [0.0-5.3%]). The infection prevalence identified in this study for opossums and raccoons are consistent with previous studies, which used serological methods, from the Southeastern US. Our study does not indicate that peridomestic ecotypes in Florida are maintaining a higher infection prevalence than their sylvatic counterparts; however, ecoregion prevalence differences do exist between North-Central and the barrier or key islands of South Florida.

Oral Presentation #15

Don’t Poop Here! Detection and Genetic Characterization of Toxoplasma gondii in Feral Cat Feces near Southern Sea Otter (Enhydra lutris nereis) Habitat

Sophie Zhu[1], *Dr. Elizabeth VanWormer*[2,3], *Dr. Lauren Camp*[1], *Anika Patel*[1], *Dr. Karen Shapiro*[1]
[1]Department of Pathology, Microbiology, and Immunology, School of Veterinary Medicine, University of California, Davis, [2]School of Veterinary Medicine and Biomedical Sciences, University of Nebraska, [3]School of Natural Resources, University of Nebraska

Toxoplasma gondii is a zoonotic parasite that can cause severe morbidity and mortality in warm-blooded animals, including endangered marine wildlife such as southern sea otters (Enhydra lutris nereis), Hawaiian monk seals (Monachus schauinslandi), and Hector’s dolphins (Cephalorhynchus hectori). Felids, including free-ranging domestic cats, can shed environmentally resistant T. gondii oocysts in their feces. Surface runoff can mobilize oocysts from contaminated soil to water bodies, leading to nearshore contamination. Despite the large populations of feral cats in many areas and their ability to contribute substantial numbers of T. gondii oocysts to diverse environments, there is limited knowledge on the prevalence and genotypes of oocysts shed by free-ranging cats. Our study will determine the prevalence of T. gondii in feces from free-ranging domestic cats in central coastal California and identify parasite genotypes that contaminate watersheds adjacent to the sea otter population range. Utilizing a longitudinal field study design of four free-ranging cat colonies, we are determining oocyst shedding prevalence using microscopy and PCR targeting the ITS1 locus. Samples confirmed as T. gondii using ITS1 are genotyped using multi-locus sequence typing (MLST) at 13 polymorphic loci. Several genotypes of T. gondii have been identified in feral cat feces, including atypical genotypes that were previously associated with fatal infections in sea otters. Preliminary data support the hypothesis that free-ranging domestic cats can be a source of T. gondii oocysts that result in morbidity and mortality in southern sea otters. Environmental pollution of T. gondii oocysts is not only a risk to susceptible wildlife, but also to some human and domestic animal populations. Targeted management of free-ranging domestic cats should be considered as an approach to reduce environmental contamination of oocysts and subsequent T. gondii infection in endangered wildlife and humans globally.

Oral Presentation #16

Are Urban Rookeries Ecological Sources or Sinks? Trade-offs to Urban Nesting in a Wetland Bird

Julia Silva Seixas[1], Sonia Hernandez[1,2], Lindsey Garner[3], Elizabeth Kurimo-Beechuk[1], Katherine Christie[4], William Norfolk[5], Melanie Kunkel[2], Alisia Weyna[2], Michael Yabsley[2], Lisa Shender[6], Robert Cooper[1], Nicole Nemeth[2], Erin Lipp[5], Peter Frederick[3]

[1]Warnell School of Forestry and Natural Resources, The University of Georgia, [2]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, Department of Population Health, The University of Georgia, [3]Wildlife Ecology and Conservation Department, Institute of Food and Agricultural Sciences, University of Florida, [4]Odum School of Ecology, The University of Georgia, [5]Environmental Health Science, The University of Georgia, [6]Florida Fish & Wildlife Conservation Commission, Fish and Wildlife Research Institute

Breeding in urban environments is key for avian species to successfully adapt to anthropogenic landscapes. Species such as House Wrens (Troglodytes aedon) and Northern Ravens (Corvus corax) are highly successful urban breeders. However, nesting in cities can be detrimental to birds, e.g., Great Tits (Parus major), by imposing novel stressors and predators along with increased exposure to pathogens. Highly urbanized populations can also create human-wildlife conflicts, as exemplified by urban Australian White Ibis (Threskiornis molucca) that harass and steal food from people. Ultimately, survival and reproductive success are the two key factors determining the potential for urbanization to produce population-level impacts and subsequent establishment of rookeries as nuisances. As a recent urban colonizer, the White Ibis (Eudocimus albus) provides the ideal model to monitor the potential progression of a novel urban breeder into an abundant urban resident. We investigated productivity, nestling growth, and Salmonella dynamics of one urban and two natural ibis colonies in south Florida (2020-2021), where nests (N=~60/site) were monitored weekly until fledging. Fecal samples were collected weekly (hatch until fledging) from 77 urban (2020-2021) and 39 natural (2021) nestlings. The urban colony had high nest success (70.8-76.4%), however urban nestlings shed Salmonella at a much higher prevalence (52%, N=209 samples) than natural chicks (13%, N=60 samples). In 2020, urban nestlings died suddenly, and 3/4 were diagnosed with West Nile virus (WNV) based on histopathology, immunohistochemistry, virus isolation, and PCR. Sera collected from 4/36 (11%) urban chicks in 2020 had anti-WNV antibodies, which waned over time, indicating maternal transfer. Our results suggest that urban environments are suitable habitats for ibis breeding but with important impacts to nestling health. This study also highlights potential trade-offs for other urban-nesting species of conservation concern (e.g., Wood Stork [Mycteria americana]), and encourages a holistic approach to investigate source-sink relationships of urban breeding.

Oral Presentation #17

Effect of Food Addition and Helminth Removal on Spatial Overlap Networks in Wild Bank Voles (Myodes glareolus)

Janine Mistrick[1], *Shannon M. Kitchen*[2], *Jasmine S.M. Veitch*[3], *Samuel Clague*[3], *Dr. Clayton E. Cressler*[4], *Dr. Richard J. Hall*[5], *Dr. Sarah A. Budischak*[6], *Dr. Kristian M. Forbes*[2], *Dr. Meggan E. Craft*[1]

[1]Department of Ecology, Evolution, and Behavior, University of Minnesota, [2]Department of Biological Sciences, University of Arkansas, [3]W.M. Keck Science Department, Claremont McKenna College, [4]Department of Biological Sciences, University of Nebraska, [5]Odum School of Ecology, University of Georgia, [6]W.M. Keck Science Department, Claremont McKenna, Pitzer, and Scripps Colleges

Variation in space-use overlap between animals in a population can have important effects on the spread of infectious diseases. Food availability and intestinal parasite infection are two factors that often vary across landscapes and are known to affect both space-use and viral transmission dynamics. However, how these affect population spatial structure and the potential for disease transmission have rarely been tested with rigorous experimental designs. The objective of this study was to determine how food addition and helminth removal affect network structure and connectivity in spatial overlap networks of wild bank voles (Myodes glareolus). Importantly, bank voles are the primary wildlife reservoir of Puumala hantavirus, a zoonotic pathogen that fluctuates in prevalence consistent with population cycles of its reservoir host. We conducted a large-scale, factorial field experiment in which populations of wild bank voles were randomized to one of four treatments: food addition, oral anthelmintic, both food and anthelmintic, or neither (control). Each population was monitored from May-October by live-trapping and the capture locations of individual voles were recorded. These locations were used to construct a series of monthly spatial overlap networks for each population. Node- and network-level metrics were calculated to quantify connectivity and network structure. These metrics were then compared across treatments and across time. Food-added populations showed greater network size, density, and increased clustering of nodes compared to populations without food addition, regardless of helminth treatment. These effects were most apparent in August and September when vole densities were highest. Our findings show that food addition increases spatial overlap of wild bank voles, likely by promoting larger, more clustered populations. These effects provide increased opportunities for direct or environmental transmission of pathogens. As such, variation in food availability may be a key driver of variation in Puumala hantavirus prevalence in wild bank voles.

Oral Presentation #18

Hijacking Bat Keratinocytes: Mechanistic Insights into the Early Stages of WNS

Marcos Isidoro-Ayza[1], *Bruce Klein*[1]
[1]Department of Pediatrics, School of Medicine and Public Health, University of Wisconsin-Madison

White-nose Syndrome (WNS) is a devastating emerging disease of North American bats caused by the fungus Pseudogymnoascus destructans (Pd). The little brown bat (Myotis lucifugus) is one of the most susceptible species. During the early phases of WNS, Pd interacts with epidermal keratinocytes by mechanisms that remain unknown. Identifying critical steps in this interaction is essential to find targets for therapies to halt the spread of the disease.

We created a bonafide M. lucifugus keratinocyte cell line that can be challenged with Pd at 12°C (torpor-like) or 37°C (arousal-like). Using electron and confocal microscopy and quantifying apoptosis, we discovered that Pd invades bat keratinocytes by active penetration at 12°C and by induced endocytosis at 37°C without triggering apoptosis of the infected cells. RNAseq analysis of Pd infected keratinocytes uncovered Epidermal Growth Factor Receptor (EGFR) as a regulator of the keratinocyte response to Pd.

We hypothesize that 1) EGFR regulates endocytosis of Pd in bat keratinocytes and 2) Pd inhibits apoptosis of infected bat keratinocytes. To test these hypotheses, we first treated our keratinocyte cell line with inhibitors of EGFR signaling (Gefitinib or PD168393), challenged them with Pd conidia at 37°C, and quantified internalization by confocal microscopy. Both inhibitors reduced the internalization of Pd conidia in a dose-dependent manner. We separately incubated keratinocytes with a pro-apoptotic drug (Staurosporin) in the presence or absence of Pd infection and measured apoptosis by Caspase 3/7 activity and nuclear fragmentation (karyorrhexis). Pd infection prevented Staurosporin-induced apoptosis, as measured by both caspase activity and karyorrhexis.

These findings indicate that during early WNS, Pd invades and colonizes the skin of bats by hijacking the endocytic and apoptotic pathways of keratinocytes. Gefitinib, an FDA-approved inhibitor of EGFR, could prevent Pd infections and be used to control WNS.

Oral Presentation #19

Highly Pathogenic Avian Influenza: Clinical Presentation, Pathology, and Shedding Profiles in a Variety of Southeastern Birds

Chloe Goodwin[1,2], Dr. Rebecca Poulson[2], Dr. Caitlin Burrell[2], Dr. Melanie Kunkel[2], Dr. Rebecca Radisic[1,2], Dr. Alisia Weyna[1,2], Dr. Mark Ruder[2], Dr. David Stallknecht[2], Dr. Mark Cunningham[3], Dr. Rebecca Hardman[3], Dr. Nicole Nemeth[1,2]

[1]Department of Pathology, University of Georgia, [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, University of Georgia, [3]Florida Fish and Wildlife Health Conservation Commission, Fish and Wildlife Research Institute

Waterfowl and shorebirds are natural reservoirs for influenza A viruses (IAV). In North America, highly pathogenic (HP) IAV outbreaks in wild birds have been limited. In January 2022, HP IAV was detected in hunter-harvested waterfowl in the US and has since been detected in moribund birds and carcasses. Subsequently, we diagnostically evaluated wild bird carcasses from throughout the southeastern US.

We performed limited to full necropsies with histopathology and immunohistochemistry on select tissues. Extracted viral RNA from pooled cloacal/choanal swabs was screened with real-time reverse transcriptase polymerase chain reaction (rrt-PCR) tests utilizing primers specific to the clade 2.3.4.4B HP H5 IAV; suspect positives were confirmed at the National Veterinary Services Laboratory. Select tissues from targeted birds were also tested using rrt-PCR.

Seventy birds representing 19 species were diagnosed with HP IAV infection, which were organized into five major species-groups: raptors (46%; 32/70), waterfowl (39%; 27/70), gulls and terns (10%; 7/70), seabirds (3%; 2/70), and herons (1%; 1/70). Twenty eight of the 70 birds were from Florida (40%). Most were adults (60) except for nestling (2), fledgling (1), and juvenile (5) bald eagles and a juvenile laughing gull (1) and ring-billed gull (1). Clinical signs included circling, head shaking, torticollis, limited mobility, altered mentation, and/or lethargy. Distribution and characteristics of lesions varied by species-group. Gross findings often were absent but included cerebral/meningeal vascular congestion, pancreatic/splenic necrosis, and epicardial petechiae. Microscopically, lytic necrosis was common in pancreas, liver, and spleen. Less commonly, perivascular inflammation, sometimes associated with neuronal necrosis and glial nodules, were in the brain. The described lesions labeled immunohistochemically for IAV. rrt-PCR of tissues detected multi-systemic infections.

Diversity in lesions among species-groups may be related to virus-host interactions, infectious dose, and timepoint post-infection. Continued work on varied species susceptibility, pathogenesis, and optimal samples for surveillance is needed.

Oral Presentation #20

Comparison of Natural and Experimental West Nile Virus Infections in Free-Ranging Ruffed Grouse (Bonasa umbellus)

Melanie R. Kunkel[1], *Justin D. Brown*[2], *Lisa Williams*[3], *Kevin D. Niedringhaus*[4], *Heather Fenton*[5], *Mark G. Ruder*[1], *Nicole M. Nemeth*[1]

[1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [2]Department of Veterinary and Biomedical Sciences, Pennsylvania State University, [3]Bureau of Wildlife Management, Pennsylvania Game Commission, [4]Veterinary Medical Teaching Hospital, University of California-Davis, [5]Ross University School of Veterinary Medicine

Ruffed grouse (Bonasa umbellus) population numbers in much of the northeastern USA have declined in recent decades, temporally corresponding to the arrival and establishment of West Nile virus (WNV) in Pennsylvania. Concern over potential impacts of WNV on ruffed grouse prompted research that indicated high rates of morbidity/mortality among experimentally infected ruffed grouse and low statewide WNV seroprevalence concurrent with high WNV vector indices. To further elucidate the potential impacts of WNV on ruffed grouse populations, we describe six cases of natural WNV infection in free-ranging ruffed grouse submitted for necropsy and compare these results to experimentally infected ruffed grouse. Diagnosis was based on gross and microscopic pathology, immunohistochemistry, and virology. All naturally infected grouse were found moribund or dead from August to December 2015-2018 in the northeastern USA, and four of six grouse were juveniles. The most consistent microscopic lesions were myocardial inflammation, degeneration, and/or necrosis, which are consistent with lesions in experimentally infected grouse that succumbed to severe disease at 7-8 days post-inoculation (DPI). Immunohistochemistry was the most useful diagnostic tool in detecting WNV, which was challenged by postmortem sample degradation. While many WNV lesions were severe, all grouse had concurrent evidence of trauma, suggesting infection may have predisposed to trauma (e.g., collision or predation). The lesions and diagnostic findings in half of the naturally infected grouse in our study were consistent with clinically affected, experimentally infected ruffed grouse euthanized on 7-8 DPI, while the findings in the remaining naturally infected grouse were similar to those experimentally infected ruffed grouse that survived to the study endpoint (14 DPI), likely reflecting varied disease manifestation and short-term survivability in naturally infected birds. Collectively, our results support the notion that WNV contributes to morbidity/mortality in ruffed grouse, warranting consideration in population-level management and habitat management for this valuable species.

Oral Presentation #21

House Sparrows and Culex Quinquefasciatus Mosquitos are Capable of Transmitting Usutu Virus

Sarah Kuchinsky[1], *Jeffrey Marano*[1], *Seth Hawks*[1], *Emma Loessberg*[1], *James Weger-Lucarelli*[1], *Nisha Duggal*[1]

[1]Department of Biomedical Sciences and Pathobiology, Virginia-Maryland College of Veterinary Medicine, Virginia Polytechnic Institute and State University

Usutu virus (USUV, Flavivirus) is an emerging zoonotic virus with observed neuroinvasive disease in humans and epizootic events in wild birds. USUV is closely related to West Nile virus (WNV), a virus endemic to the United States. Both USUV and WNV are maintained in a mosquito-bird enzootic cycle, with Culex spp. mosquitos as primary vectors and passerine birds as primary hosts. Whereas the key maintenance bird species have been identified for WNV, this is still unknown for USUV. Due to their ecologic and phylogenetic relatedness, we hypothesized that Culex quinquefasciatus mosquitos and house sparrows (Passer domesticus), two species critical for WNV maintenance in the United States, may also serve in the enzootic cycle of USUV. We assessed the vector competency of Cx. quinquefasciatus mosquitos through artificial bloodmeals spiked with two different USUV strains, Netherlands 2016 and Uganda 2012. We observed a significantly higher infection rate in mosquitos that fed upon a Netherlands 2016 bloodmeal (50%) compared to mosquitos that fed upon a Uganda 2012 bloodmeal (19.1%). We observed limited transmission in saliva, with infectious virus detected in one Netherlands 2016 fed mosquito (1.7%) and none in Uganda 2012 fed mosquitos (0%). To determine host competency of house sparrows, we inoculated groups of house sparrows with either Netherlands 2016 or Uganda 2012 USUV strains. Several individuals reached greater than 5 log10 PFU/mL in the blood. We then fed Cx. quinquefasciatus mosquitos on house sparrows and observed a 22.2% and 29.4% infection rate in mosquitos fed upon Netherlands 2016 and Uganda 2012 infected birds, respectively. Additionally, we detected a significant relationship between avian blood titer and mosquito infection rate. Our results showcase the roles these species may play in perpetuating the enzootic cycle of USUV. Identifying reservoir host and vector speices of USUV is essential to predicting its continued emergence and spread.

Oral Presentation #22

Nowhere to Fly: Ubiquitous Avian Malaria Transmission on O‘ahu

John H. Neddermeyer[1], Katy L. Parise[2], A. Marm Kilpatrick[2], Jeffrey T. Foster[1]
[1]Pathogen and Microbiome Institute, Northern Arizona University, [2]Department of Ecology and Evolutionary Biology, University of California at Santa Cruz

Climate change and invasive species are key threats to biodiversity. Avian malaria in Hawai‘i has been a model system for understanding environmental effects on host, vector, and parasite dynamics. Previous research has shown a clear decrease in malaria infections in native birds with increasing elevation (often attributed to decreasing temperature) and infection has been absent above ~1600 m. However, over the last decade an increase in avian malaria infections has been observed at higher elevations on several islands. The island of O‘ahu, with a maximum elevation of ~1200 m, offers a glimpse into what transmission may look like across the Hawaiian Islands in a warming world. We tested hypotheses about the effects of elevation, temperature, and precipitation on spatial patterns of avian malaria infection on O‘ahu. From May 2015 to November 2017, we collected 1,194 blood samples from birds from seven sites across O‘ahu at elevations ranging from 105–1209 m. Samples were analyzed using real-time PCR to determine Plasmodium relictum infection status and to estimate parasitemia. Malaria infection was widespread across all sites on the island with modeled prevalence across all years of 20.8% with substantial variation among years (8.4%, 33.6% and 21.3% in 2015, 2016, and 2017, respectively). Prevalence in one species increased with monthly maximum temperature but prevalence was not correlated with elevation for any species. These results show that malaria transmission is pervasive at elevations as high as 1200m on O‘ahu and suggest that even higher elevations on other islands may no longer act as a refuge from disease, putting several species at risk of extinction. Climate change may drive species extinct by extending the range of many introduced species, including causes of infectious diseases.

Oral Presentation #23

Avian Haemosporidian Infection and Cloacal Bacterial Diversity in Maine Waterfowl

Olivia Choi[1], *Ann Bryant*[1], *Kelsey Sullivan*[2], *Dr. Pauline Kamath*[1]
[1]University of Maine, [2]Maine Department of Inland Fisheries and Wildlife

Haemosporidian parasites are a diverse group of parasites (Haemoproteus, Leucocytozoon, and Plasmodium spp.) that infect the blood cells of their hosts In birds, these parasites are widespread and typically cause mild symptoms, however, Plasmodium spp. have been attributed to population declines (e.g., Hawaiian honeycreepers). While much is known about their ecology, evolution, and pathology, little is known about their relationship with the microbiome of their avian hosts. Our objectives were to 1) determine the prevalence, diversity, and intensity of haemosporidians in four waterfowl species (American black duck, green-winged teal, mallard duck, and wood duck) found in Maine, 2) evaluate the use of qPCR for parasite detection and quantification in comparison to traditional microscopy, and 3) examine relationships between avian haemosporidian infections and the host-associated bacterial community. For each of 496 birds, we used blood microscopy and molecular approaches to determine haemosporidian infection status and performed 16S rRNA sequencing to characterize the bacterial community from cloacal swabs. With these data, we modeled the relationship between parasite infection and the cloacal bacterial community, accounting for host species and location. Thus far, haemosporidian infection prevalence was 42%, with qPCR detecting parasites in 41% of samples, and microscopy only 19%. We expect to find a predictable relationship between qPCR cycle threshold values (as an index of infection intensity) and parasite load estimated using microscopy. We also expect cloacal bacterial diversity to be decreased in infected birds compared to uninfected birds. The results from this study will improve avian haemosporidian detection methods, provide information on the prevalence and distribution of blood parasites in Maine waterfowl, and further our understanding of the role of the microbiome in host-pathogen interactions.

Oral Presentation #24

Panel: Can We Create Transformative Change in Wildlife Health?

Moderator: LeAnn White
Panelists: Thijs Kuiken, Purnamita Dasgupta, Hans Keune

Oral Presentation #25

The Genome of Rocky Mountain Elk offers insights into their Immunologic Responses to Bucella abortus

Steven Olsen[1], *Rick Massonbrink, David Alt, Darrell Bayles, Paola Boggiatto, Jennifer Wilson-Welder, Andrew Severin*
[1]National Animal Disease Center

The prevalence of brucellosis in Rocky Mountain elk (Cervus canadensis) populations in the Greater Yellowstone Area (GYA) makes the species a possible source of infection for cattle in the GYA area. Naïve pregnant elk have a high level of infection but fewer abortions ($P<0.05$) when compared to bison and cattle experimentally challenged with B. abortus. In addition, vaccinated elk develop poor cellular immune responses and do not demonstrate significant protection against experimental brucellosis challenge. We hypothesized that genomic elements may contribute to the unique immunologic responses of elk to infection or vaccination against brucellosis. To address this hypothesis, we assembled the genome of Cervus canadensis using 686-fold sequencing coverage to generate an assembly of 35 chromosomes. The genome was annotated with 1.5 billion RNA-seq reads, resulting in 18,013 genes and 33,422 mRNAs. To identify putative genomic differences, this assembly was compared to red deer and cattle genome assemblies, confirming previous reports of chromosome fusions and fissions between elk and cattle, but also revealing two large inter-chromosomal translocations between elk and red deer. We further compared the annotations by identifying the presence and absence of cattle-related immunogenic peptides in the elk assembly, revealing the putative absence of 36 genes. These altered genes included the gamma, alpha, and delta chains of the T cell receptor and heavy chains in the immunoglobulin complex. Altogether, we are investigating how these immunologic properties may play a role in the elk's immune response to B. abortus to an provide insights on development of intervention strategies to address brucellosis in this reservoir host.

Oral Presentation #26

Uncovering the Role of Northern Elephant Seals (Mirounga angustirostris) in Maintaining Leptospira in the Marine Ecosystem

Katie Prager[1], *Daniel Costa*[3], *Daniel Crocker*[2], *Ana Carolina Ribeiro Gomez*[1], *Riley Mummah*[4], *Sarah Helman*[1], *Benny Borremans*[1], *James Lloyd-Smith*[1]
[1]University of California Los Angeles, [2]Sonoma State University, [3]Institute of Marine Sciences, University of California Santa Cruz, [4]University of Massachusetts Ahmerst

Over 35 years of data on California sea lions (Zalophus californianus) indicate that they are a reservoir for Leptospira interrogans serovar Pomona in the marine ecosystem. Infections have also been detected in northern elephant seals (Mirounga angustirostris), but their epidemiological role is unknown. Distinguishing between maintenance and non-maintenance hosts of multi-host pathogens such as Leptospira is notoriously challenging. However, an unprecedented pathogen fadeout event, during which Leptospira ceased circulating in the California sea lion population for 4 years (2013-2017), presented a unique opportunity to assess the epidemiological role of elephant seals in the marine-Leptospira system. We used microscopic agglutination testing to measure serum antibody titers from over 900 elephant seals, from three different age classes, sampled between 2008 to 2019. Seroprevalence estimates, analysis of the titer magnitude of individual elephant seals, and analysis of the change in titer magnitude of individual elephant seals sampled repeatedly through time, revealed that there were no new Leptospira infections in elephant seals during the sea lion fadeout period. These findings suggest that elephant seals are not a Leptospira reservoir and did not maintain the pathogen during the 4-year period that Leptospira infections were absent in the sea lion population. However, the first post-fadeout infections detected in the marine ecosystem occurred in elephant seals in May 2017, suggesting that they may have acted as a bridge host, linking an unknown reservoir to CSL.

Oral Presentation #27

Non-Invasive Saliva Collection for Evaluation of Peri-Urban Primate Exposure to Arboviruses of Public Health and Conservation Concern

Tierra Smiley Evans[1], Ohnmar Aung[1], Olivia Cords[1], Lark Coffey[2], Talia Wong[2], Min Thein Maw[3], JoAnn Yee[4], Kodumudi Venkateswaran[5], Neeraja Venkateswaran[5], Peter Nham[4], Koen Van Rompay[4], Marc Valituto[6], Susan Murray[6], Christine Johnson[1]

[1]One Health Institute, School of Veterinary Medicine, University of California, [2]Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California, Davis, [3]Livestock, Breeding and Veterinary Department, [4]California National Primate Research Center, [5]Tetracore, Inc., [6]Global Health Program, Smithsonian Institution

Endemic and emerging arboviruses including chikungunya (CHIKV), Zika (ZIKV), dengue (DENV), yellow fever (YFV), and Japanese encephalitis viruses (JEV) either originated in sylvatic cycles involving non-human primates (NHPs) or utilize NHPs as amplification or "dead end" hosts. These viruses carry significant public health and potential conservation concerns. Despite this, current sampling for arbovirus detection requires invasive approaches requiring chemical immobilization that presents challenges due to difficulties in darting NHPs, restrictions on accessing individuals, arboreal behavior, and/or use of rough terrain. To solve these constraints on sampling, non-invasive methods for detecting exposure to these viruses are needed. We have previously optimized non-invasive saliva collection from semi-habituated NHPs to detect viral pathogens. The goal of this study was to investigate the use of non-invasively collected saliva samples for the detection of arboviral antibodies and to evaluate the potential for peri-urban primates to serve as hosts for arboviruses of significant public health concern. Traditional blood and swab samples and non-invasive saliva samples were collected from rhesus (Macaca mulatta), long-tailed (Macaca fascicularis) and pig-tailed macaques (Macaca nemestrina) in peri-urban areas where NHPs were living in close proximity to humans in Southeast Asia. We employed a multiplex bead-based assay using Luminex xMAP® technology to simultaneously measure total Ig (IgG + IgA + IgM) antibodies against CHIKV envelope (E1) and ZIKV envelope (E) proteins, and non-structural 1 (NS1) protein for ZIKV, DENV 1-4, JEV, West Nile virus, and YFV antigens simultaneously. Antibodies indicating exposure to CHIKV, ZIKV, and JEV were detected, suggesting overlap of sylvatic and urban arbovirus cycles. Importantly, antibodies against these viruses were detected in both serum and saliva samples, demonstrating the utility of non-invasive sampling to detect arbovirus exposure in free-ranging NHPs.

Oral Presentation #28

Urban Host-parasite Dynamics of Two Small Mammals

Kimberly Fake[1,2], Matthew Mulligan[1,2], Mason Fidino[1], Michael Yabsley[3,4], Rachel Santymire[5], Seth Magle[1]

[1]Lincoln Park Zoo, Urban Wildlife Institute, [2]Lincoln Park Zoo, Davee Center for Endocrinology and Epidemiology, [3]Warnell School of Forestry and Natural Resources, University of Georgia, [4]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [5]Department of Biology, Georgia State University

Lyme disease, caused by the bacterial spirochete Borrelia burgdorferi, is the tickborne disease of greatest concern in the United States. Most studies of Lyme disease currently focus on forested areas with little urban development, despite the detection of B. burgdorferi within heavily urbanized areas. Urbanization-driven changes in biodiversity and land use are hypothesized to either increase parasite transmission or result in lack of support for parasitic life cycles, potentially influencing Lyme disease risk in urban greenspaces. Yet, it is largely unknown how urbanization is associated to small mammal tick burdens or Lyme prevalence. Here, we examined the relationship between landscape characteristics and small mammal tick burdens along an urban-to-exurban gradient. We collected ticks from small mammals—primarily meadow voles (Microtus pennsylvanicus) and deer mice (Peromyscus maniculatus)—live-trapped at 10 natural spaces across the Chicago metropolitan area. We identified ticks to species and tested Ixodes ticks via PCR for B. burgdorferi. We found Ixodes scapularis, the primary vector of B. burgdorferi, at 67% of non-urban sites and 25% of urban sites. Dermacentor variabilis ticks were found at 83% of non-urban sites and 25% of urban sites. We found only Ixodes scapularis tick burdens related to urbanization, as meadow voles and deer mice exhibited increasing I. scapularis tick burdens with decreasing urban intensity. Additionally, B. burgdorferi was detected at 50% of non-urban sites and 25% of urban sites. Collectively our results indicate non-urban sites contain greater Lyme disease risk, although there is still risk present within urban areas. Furthermore, this indicates need for further study to determine why some urban sites are suitable for the Lyme pathogen, while others are not. Our results provide guidance to efficiently conduct targeted Lyme disease awareness and prevention campaigns to have the greatest impact on disease mitigation.

Oral Presentation #29

The Wild Life of Ticks: Using Passive Surveillance to Determine the Distribution and Host Range of Ticks and the Exotic Haemaphysalis longicornis, 2010-2021

Michael Yabsley[1], *Alec Thompson*[1], *Seth White*[1], *Emily Doub*[1], *Prisha Sharma*[1], *Kenna Frierson*[1], *David Shaw*[1], *Stacey Vigil*[1], *Mark Ruder*[1]
[1]University of Georgia

Ticks and tick-borne diseases often are best framed in a One Health context, as many ticks utilize multiple hosts, and the pathogens they transmit can be of both veterinary and medical importance. One vector of recent significance in the U.S. is Haemaphysalis longicornis, the Asian longhorned tick. This tick is native to eastern Asia but has become invasive in several countries where it is a major pest to a large range of hosts including livestock, companion animals, wildlife, and humans. To better assess the current distribution of H. longicornis and to identify potential wild host species that are important for maintaining and possibly spreading it, we collected ticks from wildlife using passive surveillance techniques. Passive, region-wide surveillance was conducted in collaboration with state wildlife agencies. Since 2010, we have collected 20,626 ticks from 1,940 hosts from 23 states in the Southeast and Midwest U.S. Our surveillance detected H. longicornis infestations in 8 states (GA, KY, MD, NC, NJ, PA, VA, WV) on 67 mammalian hosts, representing 9 species: white-tailed deer, elk, cow, black bear, coyote, domestic dog, red fox, Virginia opossum, and human. These efforts resulted in numerous new hosts and geographic (state and county) records for H. longicornis and offer insight into the distribution of this exotic tick. In addition, our large-scale passive surveillance network offers valuable information regarding the distribution and host associations for many native tick species of both public health and veterinary importance such as Amblyomma americanum, A. maculatum, Dermacentor albipictus, D. variabilis, and Ixodes scapularis. Collectively our passive surveillance data has determined new established counties for these species which can aid health officials in decision making and active vector and pathogen surveillance programs.

Oral Presentation #30

Assessing the Effects of Saxitoxin Ingestion by Common Murres

Matthew Smith[1], Caroline Van Hemert[1], Robert Dusek[2], Tuula Hollmen[3], Kristen Pelo[3], Aidan Lee[3], Jenna Schlenner[3], Dave Kulis[4], Donald M. Anderson[4], Sherwood Hall[5]
[1]USGS Alaska Science Center, [2]USGS National Wildlife Health Center, [3]Alaska SeaLife Center, [4]Woods Hole Oceanographic Institution, [5]US Food and Drug Administration

Saxitoxins (STXs) are a group of highly potent neurotoxins produced by certain marine dinoflagellate species during harmful algal bloom (HAB) events. These toxins, which are of growing concern in northern waters as temperatures increase, are transferred throughout the marine food web and can cause illness or death in a broad suite of wildlife species, including seabirds and marine mammals. Since 2014, widespread seabird mortality events have occurred annually in Alaska, coincident with anomalously high ocean temperatures. While starvation has often been identified as the proximate cause of death, STXs have been detected in many opportunistically collected carcasses. Due to a lack of knowledge about the toxicity of STXs in seabirds, however, interpretation of these values has proven difficult. To address information gaps and investigate the behavioral effects of sublethal STX exposure on seabirds, we conducted experimental dosing trials with Common Murres (Uria aalge), a seabird species that has been subject to severe die-off events over the past few years. We administered purified saxitoxin (STX-diHCL) and a crude toxin extract from a strain of Alexandrium catenella isolated from the Chukchi Sea to birds via oral gavage. Using a modified up-and-down dose finding scheme, we calculated the median effective dose (ED50) for purified STX-diHCL and the crude toxin extract based on the appearance of ecologically relevant behavior, including vomiting, motor discoordination and paralysis, and death. We also analyzed tissue, serum, and fecal samples from a subset of dosed birds to determine toxin concentrations and congener profiles. These results will help evaluate whether sublethal ingestion of STXs could inhibit birds' mobility or access to food in the wild, thereby compromising seabird health without inducing acute toxicity. Additionally, analysis of tissues from experimental birds will facilitate interpretation of values from field-collected samples, including those associated with ongoing seabird mortality events.

Oral Presentation #31

Impact of Lead Ammunition on Bald Eagle Dynamics in the Northeast United States

Krysten Schuler[1], *Brenda Hanley, André Dhondt, Kevin Hynes, Maria Forzan, Elizabeth Bunting, Mark Pokras*
[1]Cornell University

Bald eagles (Haliaeetus leucocephalus) are one of North America's greatest conservation success stories after rebounding from near extirpation. However, a lingering threat from spent lead (Pb) ammunition fragments continues to cause morbidity and mortality in individual eagles and other scavenging birds and mammals. Therefore, we investigated the impact of lead-associated mortalities on bald eagle population dynamics at an ecological scale. We pooled necropsy and demographic datasets from seven states in the Northeast US from 1990-2018 to determine whether deaths from Pb toxicosis altered the dynamics of the eagle population. With over 1200 necropsy records, we found 78% of tested eagles had exposure to Pb with 37% ingesting enough to be fatal. We adapted a combinatorial optimization algorithm and used it in conjunction with a mathematically symbolic life history to compare population dynamics of eagles under current (Pb) and hypothetical (Pb-free or Pb-reduced) scenarios. We found Pb depressed the long-term growth rate of eagles, altered movement of individuals through their life cycle, and reduced resiliency (the ability to withstand additional threats and still persist) of bald eagles. We estimated that deaths arising from ingestion of Pb was associated with a 4.2% (females) and 6.3% (males) reduction in the asymptotic long-term growth rate. Lead toxicosis was an additive source of mortality and decreased the species ability to withstand additional mortality from other sources. The software we created is freely available for other researchers to use on their own bald eagle data or can be adapted to other species and maladies. Ultimately, we hope that identification of the impacts of lead ammunition on eagles can support a push toward conservation solutions that benefit all species affected by Pb.

Oral Presentation #32

Assessing Neonicotinoids Exposure in Free-Ranging White-Tailed Deer in Minnesota

Michelle Carstensen[1], *Patrick Hagen*[1], *Eric Michel*[1], *John Buchweitz*[2], *Justin Zyskowski*[2], *Jon Lundgren*[3]
[1]Minnesota Department of Natural Resources, [2]Michigan State University, [3]Ecdysis Foundation

Recent research has raised concerns about potential adverse effects of neonicotinoid (neonic) exposure in white-tailed deer (Odocoileus virginianus) including reduced survival and productivity. Our goal was to assess whether free-ranging deer in Minnesota are being exposed to neonics given the potential negative effects of these insecticides on white-tailed deer. We solicited deer hunters to voluntarily submit spleens from harvested animals during the 2019 deer hunting season. Interested hunters signed up to receive a sampling kit (n = 1836) and were asked to submit the spleen of their harvested deer. A total of 770 spleens samples were submitted by hunters throughout Minnesota and 29 additional spleens were collected by agency staff from opportunistic deer (agency culling and sick deer). A subsection of each collected spleen (n = 799) was submitted to the Ecdysis Foundation (Estelline, SD) for analysis of neonic exposure using an ELISA. Sixty-one percent of deer sampled were exposed to at least one neonic. Neonic concentrations were not related to sex, age, or the agricultural intensity ($P \geq 0.313$) associated with the harvest location. We submitted a subset of samples (n = 57) to Michigan State University Veterinary Diagnostic Laboratory (East Lansing, MI) for further analysis using a mass spectrometry test to help confirm the results derived from the ELISA test. We found neonic concentrations derived by ELISA were positively related to neonic concentrations produced by mass spectrometry ($\beta = 0.195$, $P = 0.002$); however, there was low predictability ($R2 = 0.18$). Regardless, our results show that neonicotinoids are widespread throughout Minnesota regardless of region, indicating environmental contamination with neonics from multiple sources.

Oral Presentation #33

Causes of Death and Disease Prevalence in Bottlenose Dolphins (*Tursiops truncatus*) stranding in Alabama Between 2015 and 2020, Following the Deepwater Horizon Oil Spill

Jennifer Bloodgood[1,2], Alissa Deming[3], Kathleen Colegrove[4], Mackenzie Russell[1], Cristina Díaz Clark[1], Ruth Carmichael[1,2]

[1]Dauphin Island Sea Lab, [2]School of Marine and Environmental Sciences, University of South Alabama, [3]Pacific Marine Mammal Center, [4]Zoological Pathology Program, College of Veterinary Medicine, University of Illinois

Between 2010 and 2014 an unusual mortality event (UME) involving bottlenose dolphins (*Tursiops truncatus*) occurred in the northern Gulf of Mexico associated with the Deepwater Horizon oil spill (DWHOS). Cause of death (COD) patterns in bottlenose dolphins stranding in Alabama since that event have not been analyzed, and baseline prevalence data for *Brucella ceti* and cetacean morbillivirus, two pathogens previously reported in bottlenose dolphins in this region, are lacking. We analyzed records (n=233) from bottlenose dolphins stranding in Alabama from 2015 to 2020 to determine COD using gross necropsy and histological findings (both available for 108 cases). This period included another UME in 2019 associated with exposure to low salinity waters. A subset of individuals was selected for molecular testing for *Brucella* spp. and morbillivirus spp. via PCR. Causes of death were grouped into six categories for all age classes, including: 1) human interaction (peracute underwater entrapment, vessel strike, blunt and/or sharp trauma), 2) trauma, 3) infectious disease (*Brucella*, other bacterial, parasitic, fungal, mixed, and unknown), 4) noninfectious disease (prolonged freshwater exposure and degenerative), 5) multifactorial, and 6) unknown. Two additional categories unique to perinates included: [i]in utero[/i] pneumonia and fetal distress. Advanced decomposition limited COD determination in many individuals. Human interaction was the most common COD (27/108, 25.0%), followed by prolonged freshwater exposure (15/108, 13.9%) and infectious disease (15/108, 13.9%). Morbillivirus was not detected in 66 animals tested, and *Brucella* was detected in 18/98 (18.4%) animals tested. *Brucella* was detected in some moderately to severely decomposed carcasses, indicating that it may be feasible to test a broader range of stranded animals than previously assumed. This study provides valuable information on COD in bottlenose dolphins in Alabama since the DWHOS and is the first to examine baseline prevalence of two common infectious diseases in stranded animals from this population.

Oral Presentation #34

Investigating Levels of Per- and Polyfluoroalkyl Substances (PFAS) in Minnesota White-Tailed Deer

Kelsie LaSharr, *Dr. Michelle Carstensen*[1], *Dr. Barbara Keller*[1], *Dr. Eric Michel*[1], *James Kelly*[2], *Sophie Greene*[3]
[1]Minnesota Department of Natural Resources, [2]Minnesota Department of Health, [3]Minnesota Pollution Control Agency

Per- and polyfluoroalkyl substances (PFAS) are a large group of human-created chemicals used to repel water and grease, reduce friction and fire risk, and act as an insulator. These compounds are desirable because of their durability, but they are also of concern because they can move through soils, contaminate drinking water, and bio-accumulate in humans, fish, and wildlife. Exposure to PFAS can lead to adverse health effects in humans and animals. One PFAS compound, perfluorooctane sulfonic acid (PFOS), has been documented in other states at high levels in white-tailed deer liver and muscle tissues; this presents a potential route for PFAS exposure in humans through consumption of wild game. During fall 2020 and 2021, we analyzed PFAS levels in tissues from 116 white-tailed deer (Odocoileus virginianus) taken from 3 study areas where PFAS contamination is either suspected or known to have occurred. We worked with hunters and site managers to collect paired liver and muscle tissue from deer intended for human consumption. We first analyzed the liver, as its function is to filter contaminants. If liver levels were high, we then sampled muscle tissue. We analyzed samples for 40 unique PFAS compounds and detected 19 compounds across 103 livers (results pending from the final 13 deer). PFOS was detected in all white-tailed deer livers and levels ranged from 0.23 - 72.7 ng/g wet weight basis. We subsequently tested muscle tissue from 5 deer that had PFOS levels >20 ng/g wet weigh basis and found PFOS concentrations in the muscle were greatly reduced at 0.22 - 0.43 ng/g wet weigh basis. Minnesota Department of Health has determined that these levels of PFAS are low enough that a consumption advisory is not warranted for deer taken from these particular study areas.

Oral Presentation #35

One Health for All: Advancing Wildlife, Human, and Ecosystem Health in Cities by Integrating an Environmental Justice Lens

Ms. Jacqueline Buckley[1], *Dr. Maureen Murray*[1], *Dr. Kaylee Byers*[2,3], *Ms. Kimberley Fake*[1], *Ms. Elizabeth Lehrer*[1], *Dr. Seth Magle*[1], *Dr. Christopher Stone*[4], *Dr. Holly Tuten*[4], *Dr. Christopher Schell*[5]

[1]Urban Wildlife Institute, Lincoln Park Zoo, [2]School of Population and Public Health, University of British Columbia, [3]Canadian Wildlife Health Cooperative, [4]Illinois Natural History Survey, University of Illinois at Urbana Champaign, [5]Department of Environmental Science, Policy, and Management, University of California Berkeley

We are facing interwoven global threats to public health and ecosystem function, revealing the intrinsic connections between human and wildlife health. These challenges are especially pressing in cities, where income disparities, environmental degradation, and interfaces between humans and wildlife are prevalent. The One Health concept provides an organizing framework that promotes the health and well-being of urban communities and ecosystems by emphasizing the “ecology of health” through the reciprocal interactions between human, wildlife, and environmental health. However, for One Health to be successful, it must incorporate societal disparities and inequities in disamenities, exposures, and policy. Social inequality affects all One Health interfaces including the distribution of ecosystem services and disservices, the nature and frequency of human-wildlife interactions, and legacies of land use. Yet very few studies have explicitly incorporated environmental justice into One Health research. Here we review the current literature on One Health perspectives and environmental justice. We suggest ways to incorporate environmental justice in four One Health issues of growing importance: air quality, disease vectors such as ticks and mosquitos, urban heat as a public health concern, and access to clean water for human and non-human communities. We close with recommendations for future work, such as facilitating interdisciplinary collaborations using social-ecological systems frameworks and active engagement with policymakers to acknowledge health disparities, intersectionality, and the role of policy and governance in One Health research. As cities continue to grow, disparities in race, income and health have become exacerbated. The convergence of global threats – from the COVID-19 pandemic to the climate crisis and social unrest – underscore a dire need for One Health solutions that value all life, making an environmental justice lens necessary to help build healthier, more resilient cities for everyone.

Oral Presentation #36

Wildlife Health as Part of a Transformative Chang to Operationalize One Health Governance in a Post-Pandemic World

Dr. Carlos G. das Neves, *Dr. Knut Madslien*
[1]Norwegian Veterinary Institute

The ongoing COVID-19 pandemic has highlighted the importance of understanding that disease emergence is rooted in human interactions with the biodiversity of microbes and their reservoir host species. As many as 75% of emerging infectious diseases (EID) “jump species” from nonhuman animals to people, with wildlife playing a key role. While microorganisms have their own evolutionary pathways, two recent reports by IPBES and UNEP have highlighted several drivers (pathways) for zoonotic events.

The likely animal origin of many of these viruses allied to the different mechanisms for viral evolution pose a threat for spillover events back to nonhuman animal species (reverse zoonoses). The recent description of SARS-CoV2 infection in white-tailed deer in Northern America across a large geographic area and in animals with little or no contact with humans is a good example.

Monitoring and surveillance is key to prevention, preparedness, response, and recovery. To ensure that prevention is effective, an integrated, multi-systems monitoring and surveillance system for infectious agents and their risk factors is essential, and must be strongly built on synergies between disciplines and the use of innovative technologies and data sharing. Integrated OH surveillance systems should include and connect data that identify risk factors for disease emergence in wildlife, companion animals, livestock, the environment (e.g., soil and water), and humans.

In this presentation we aim to highlight how a truly transdisciplinary integration of wildlife health in ongoing effort to “utilize” a One Health approach to surveillance and emergence preparedness, can lead to transformative changes of behaviours, routines and approaches. We draw from examples related to the implementation of the Norwegian Wildlife Surveillance Programme, its connection to ongoing surveillance systems on both human health and production animal health, and we try to highlight barriers and advantages of the approach now put in place.

Oral Presentation #37

Commodity-Based Trade of Beef: A Holistic Solution for the Future of KAZA's People and Wildlife

Steven A. Osofsky[1,2], Shirley J. Atkinson[1,2], Dr. Mary-Louise Penrith[2,3], Nidhi Ramsden[2], Dr. Gavin R. Thomson[2,4]

[1]Cornell University College of Veterinary Medicine, [2]AHEAD (Animal & Human Health for the Environment and Development) Program, [3]University of Pretoria, Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, [4]Deceased

Co-created by five countries (Angola, Botswana, Namibia, Zambia, and Zimbabwe), the more than 200,000 square-mile Kavango Zambezi Transfrontier Conservation Area (KAZA TFCA) is Africa's largest conservation and development landscape. The vision of KAZA is underpinned by the potential for significant local and regional economic development opportunities. However, the creation of a TFCA like KAZA increases the likelihood of domestic and wild animals coming into ever more intimate contact. This reinforces the need for better scientific knowledge and planning to preclude consequences that can be detrimental on one or both sides of the proverbial fence.

The TFCA concept and prevailing internationally accepted approaches to the management of transboundary animal diseases (TADs) are largely incompatible. The TFCA concept promotes the free movement and re-establishment of migratory patterns of wildlife over large geographic areas and across international boundaries. Conversely, the long-standing internationally accepted approach to the control of TADs (foot and mouth disease in particular) relies on the use of extensive cordon fences to prevent movement of susceptible animals between areas where TADs occur and areas where they do not, and to similarly restrict trade in commodities derived from the former.

Commodity-based trade (CBT) has finally been globally accepted as a way to facilitate the trade of beef even from cattle raised near unfenced wildlife, offering the first opportunity in generations to truly assist southern Africa's livestock sector while simultaneously reopening the habitat corridors that the future of KAZA's wildlife genuinely depends upon. Efforts to mitigate disease risk must evolve, become more holistic. If we fail to take full advantage of CBT and associated conservation benefits soon, there is no question that the region's wildlife will continue to decline in the decades to come, as will the significant economic opportunities tourism and other wildlife-associated activities could and should represent in a post-COVID world.

Oral Presentation #38

Wildlife Health in Environmental Impact Assessments: Are We Missing a Key Metric?

O. Alejandro Aleuy[1], *Susan J. Kutz*[2], *Mark L. Mallory*[3], *Jennifer F. Provencher*[4]
[1]Department of Biological Sciences, University of Notre Dame, [2]Department of Ecosystem and Public Health, University of Calgary, [3]Department of Biology, Acadia University, [4]Environment and Climate Change Canada, Ecotoxicology and Wildlife Health Division

Environmental Impact Assessments (EIA) aim to assess the predicted effects of future projects on the environment, human health and the economic potential of a region. They are an instrumental tool for sustainable development and to reduce the impact of large-scale industrial projects on biodiversity. A common practice in EIAs is to assess the effect of projects using indirect indicators like the predicted changes in the quantity/quality of wildlife habitat and/or in non-specific wildlife population metrics (e.g., relative abundance). In recent decades, the interpretation of wildlife health has moved from the classical dichotomous state of “disease presence/absence’’ to a broader concept that integrates the interaction of biological, social and environmental health determinants. We sought to determine how wildlife health metrics are used in EIAs and propose a framework to characterize, quantify and monitor wildlife health in future EIAs. First, we review EIAs from different jurisdictions in Canada to characterize the relevance and use of ‘wildlife health’. Then, we review case studies to understand wildlife health in different contexts associated with conservation biology and propose a framework to incorporate wildlife health into baselines and mitigation processes in EIAs. Our review illustrates that while wildlife health is often invoked in the main and specific objectives of EIAs, it is rarely tracked and quantified in EIAs and related processes. We identified approaches to effectively incorporate wildlife health in EIAs, including context-specific wildlife health metrics, community-based sampling, and Local Ecological Knowledge. We illustrate how wildlife health can facilitate the inclusion of Indigenous governments and Local Ecological Knowledge into EIAs and into co-management practices of wildlife. Our work highlights the need to move towards incorporating wildlife health into EIAs in order to provide a more holistic perspective on the potential environmental impacts and improve the opportunities for early implementation of mitigation measurements.

Oral Presentation #39

Systems Thinking Applied to Wildlife Health: Building a One Health Framework to Facilitate Adaptive Change Within a State Wildlife Agency and Beyond

Sherri Russell[1], *Lorisa Smith, Sara Parker Pauley, Jason Sumners, Kathi Moore, Jasmine Batten, Maria Anderson*
[1]Missouri Department of Conservation

Post- pandemic awareness of the integration of ecosystem health, animal health and human health may represent an opportunity to connect and establish communities of practice within and outside the field of wildlife health. The Missouri Department of Conservation (MDC) hypothesized that the strength of the One Health approach could be leveraged to improve the quality of life for all species.

This study explored how to integrate the need to acknowledge and support technical experts in the traditional framework while exploring how to use a positive framework to engage broader constituencies in a way that enhances agency relevancy. We utilized network analysis, and principles from systems thinking and report our successes, challenges, and failures in a field report method. State fish and wildlife agencies are complex institutions and we explored mechanisms for change. We iteratively developed a roadmap and executed various strategies to advance the One Health framework inside and outside of MDC.

We conclude that a One Health systems thinking approach can and does leverage the agencies resources and enhance relevance to broader constituencies. Embracing the systems approach expressed as: healthy ecosystems lead to healthy people and that human health and quality of life are dependent on healthy fish and wildlife population (Zinsstag et al, 2011) is a potent lever. One Health as a paradigm can serve as a connector to the mind of the average person, public health agencies and professionals, as well as a diverse set of stakeholders not always reached by traditional conceptualization of Wildlife Health or state fish and wildlife agency missions.

We were challenged by preconceived roles and structural barriers within the state agency endeavoring to change course and adapt. Our conclusion is that it is worth the pain and share surprising partner results using the systems thinking framework.

Oral Presentation #40

A Large-Scale Empirical Study of Hibernating Bat Energetics and Modeled Implications on White-Nose Syndrome Susceptibility

Sarah H. Olson[1], Dan Crowley[2], Brett Dickson[3], Yvonne A. Dzal[4,5], Nathan Fuller[6], Catherine Haase[7], David T. S. Hayman[8], Reed Hranac[8], Emily M. Johnson[6], Emma L. Kunkel[6], Cori L. Lausen[9], Meredith L. McClure[3], Liam P. McGuire[10], Raina K. Plowright[2], Kirk Silas[1], Craig K. R. Willis[4]

[1]Wildlife Conservation Society, Health Program, [2]Montana State University, Department of Microbiology and Immunology, [3]Conservation Science Partners, [4]University of Winnipeg, Department of Biology, [5]Bat Conservation International, [6]Texas Tech University, Department of Biological Sciences, [7]Austin Peay State University, Department of Biology, [8]Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, [9]Wildlife Conservation Society Canada, [10]University of Waterloo, Department of Biology

The fungus, Pseudogymnoascus destructans, causes white-nose syndrome (WNS) and is spreading and infecting new bat populations, species, and their hibernacula across North America. WNS mortality varies considerably among species, populations, and individuals. We hypothesized that this differential mortality is related to species-level bioenergetic traits (morphometric, metabolic, and body composition) and environmental factors (microclimate temperature and humidity). We tested our hypothesis using empirical data and bioenergetic models. Prior to WNS arrival at our sites, located across large latitudinal (~2900 km) and longitudinal (~2100 km) gradients, we measured morphometric traits of 3073 bats, representing 14 species, and collected environmental data within hibernacula. We conducted respirometry (n = 506 bats) and quantitative magnetic resonance (n = 249 bats). We evaluated these new data to create inter- and intraspecific energetic profiles of hibernation physiology for 13 species. Analyses revealed interspecific variation in rates of evaporative water loss formed two species clusters, with high and low rates associated with high and low levels of WNS mortality. These hibernation energetic data allowed us to populate a refined mechanistic WNS survivorship model that now includes evaporative water loss, to make inferences about WNS susceptibility for different species. We incorporated the mechanistic survivorship estimate as a predictor of winter occurrence, along with landscape attributes (e.g., ruggedness, elevation), in an ecological niche model to estimate the pre-WNS occurrence probability of five bat species. We then updated these estimates under conditions of WNS exposure and future climate change predictions to project their combined impacts. These data, analyses, and modeling tools are presented to help inform bat management and mitigation activities, such as species listings, by identifying significant predictors of winter habitat, rate of evaporative water loss as a WNS risk factor, as well as likely susceptible and more resilient species and populations.

Oral Presentation #41

One Health and Wildlife Conservation: Insights from Wood Bison and Beyond

Craig Stephen[1], *Jennifer Provencher*[2], *Alana Wilcox*[2], *Sarah Sine*[2]
[1]McEachran Institute, [2]Environment and Climate Change Canada

Amidst the calls for investment in One Health, are calls for an increased presence of “the environment” in One Health, which often includes wildlife. One Health is largely concerned with threats to human health and agriculture, while conservation of wildlife and ecosystems usually aims to reduce human impacts on a biodiversity from a range of threats. We used a gap analysis on the available peer-review literature from the natural sciences on wood bison (Bison bison athabascae) population health as a model to examine how One Health can be used as a conceptual framework for integrated approaches to wildlife population health for conservation. While none of the articles included in this study provided a definition of bison health, all implicitly looked at health as the absence of deficits and diseases rather than as a capacity for resilience and sustainability. The review found most health assessments via data or analytical approaches in the peer-reviewed literature focused on biophysical determinants of individual animal’s health, but human dimensions of determinants of health predominated discussions about bison health. The breath of determinants of health discussed showed that population health management is a collaborative enterprise that must aim to continually create and improve physical and social environments that allow wildlife to meet their evolved roles and to secure healthy relationship between wildlife and society. Lastly, we combined these findings with recent literature on wildlife health and One Health to propose that the integrated thinking, governance, and methods being developed in One Health could help create population health management strategies that place conservation as the primary goal with co-health benefits for people and ecosystems. Future scoping work will consider grey literature, such as management reports, as well as perspectives from Indigenous communities on concepts related to wildlife population health.

Oral Presentation #42

Landscape of Participatory Surveillance Systems in Wildlife Health

Carrie McNeil[1], *Sarah Verlander*[1], *Nomita Divi*[1], *Mark Smolinski*[1]
[1]Ending Pandemics

Participatory surveillance systems provide innovative ways to augment traditional surveillance through a bi-directional process of receiving and transmitting data for action through direct engagement of the target population. This landscape analysis utilized a combination of systematic literature review, direct outreach and survey to identify and describe 60 participatory surveillance systems across all sectors of One Health. Of the 23 systems collecting data on animals, 16 systems collect data on wildlife including wild birds, mammals, reptiles, amphibians and aquatics/fish. Wildlife health participatory surveillance systems identified span North America, Europe, Asia and Australia with longevities ranging from 2 to 34 years. Ten of the systems self-identify as “One Health” systems. Six systems collect data at a subnational level; 5, national level; and 4, multinational level. Technologies used for reporting most often include email/web reporting (n=14) and smart phone app(n=8). Most systems allow for photo uploading (n=12) and geolocation (n=11). Reported impacts to include earlier detection (n=9), improved community knowledge (n=9), quicker response (n=9), better cross-sector coordination (n=7) and policy and/or funding impact (n=6). The most common types of information shared back to users include training materials (n=12), visualization such as maps (n=9) and newsletters/blogs (n=9). This talk will share a newly launched interactive online map displaying findings from this landscape with the capability of adding additional systems. Participatory surveillance systems are a key component of disease surveillance and provide a unique opportunity for expanding epidemic intelligence while improving community knowledge and awareness of wildlife health issues.

Oral Presentation # 43

What's Happening with Wildlife at the World Organisation for Animal Health?

François Diaz[1], Tiggy Grillo[1], Dharma Shetty[1], Lesa Thompson[3], Sophie Muset[1], Keith Hamilton[1], Paolo Tizzani[2], Chadia Wannous[4]

1. Preparedness and Resilience Department, World Organisation for Animal Health (OIE), Paris, France
2. World Animal Health Information and Analysis Department, World Organisation for Animal Health (OIE), Paris, France
3. Regional Representation for Asia and the Pacific, World Organisation for Animal Health (OIE), Tokyo, Japan
4. Institutional Affairs and Regional Activities, World Organisation for Animal Health (OIE), Paris, France

In the context of disease emergence, wildlife is often seen as a threat, but it is a vital resource, providing essential ecosystem services and a reservoir of biodiversity benefitting everyone. Wildlife is also at risk from emerging infectious diseases. Therefore, managing the risk of disease emergence and protecting wildlife health should be complementary. In response to global trends in disease emergence and biodiversity loss, and the global need to better manage risks from emerging diseases at the human-animal-ecosystem interface, there is recognition of an urgent need to strengthen the wildlife component of One Health.

The World Organisation for Animal Health, as the global authority on animal health, works to ensure the health of animals and their environments across the world, and recognises that animal health, balanced ecosystems, and biodiversity contribute to achieving One Health.

The World Organisation for Animal Health has been working to integrate wildlife health into its policies, with different initiatives including the development of standards and guidelines on the surveillance and control of diseases in wildlife and for wildlife trade; the creation of the OIE Wildlife Working Group in 1994; the support of the expert's network of the Reference Centres working on wildlife; the National Wildlife Focal Points network (created in 2009); the global wildlife diseases notification platform (OIE-WAHIS and WAHIS-Wild) and several OIE publications. Most recently through a collaborative effort involving contributions from the World Organisation for Animal Health's staff, Working Group on Wildlife, Delegates and National Focal Points for Wildlife from 182 Members worldwide, and international partners, a comprehensive Wildlife Health Framework was developed in 2020 and approved by the OIE World Assembly in May 2021, to better integrate wildlife health into the organisation's core activities and reinforce One Health strategies. The resulting framework integrated the views and expectations of Members collected through a survey and two global webinars attended by over 350 stakeholders.

The Wildlife Health Framework's overall goal is to 'protect wildlife health worldwide to achieve One Health'. The framework aims to improve the ability of Members to manage the risk of pathogen emergence in wildlife and transmission at the human-animal-ecosystem interface - whilst taking into account the protection of wildlife - and to improve and strengthen surveillance systems, early detection, National and international notifications, and management of wildlife diseases. This will be achieved through better intersectoral coordination, collaboration and capacity, a fostered political, policy and scientific environment, and a better awareness of risks pathways and best practices.

A series of presentations will be provided by the World Organisation for Animal Health's wildlife team, comprising staff from headquarters (France) and regional office in the Asia and the Pacific. The team is also keen to get to know members of the WDA, so be prepared to be interactive during the sessions.

Oral Presentation #44

Participatory Surveillance System Data Parameters Workshop

Carrie McNeil[1]
[1]Ending Pandemics

Ending Pandemics is leading an international effort to develop a compendium of data parameters for multisector, One Health Participartory Surveillance Systems. With a group of experts, Ending Pandemics has developed a draft list of wildlife health disease parameters and information on how these parameters are being collected. In this workshop, you will have the opportunity to review the current draft and provide feedback. The revised draft from this workshop will inform the fourth International Workshop on Participatory Surveillance (IWOPS IV) in Cambodia in November, 2022. The goal of IWOPS IV is to develop data standards for greater system operability and information sharing.

Oral Presentation #45

Association of Fish and Wildlife Agencies

Sonja Christiansen

Oral Presentation #46

Student Roundtable – Development of a North American Student Section

Marianthis Ioannidis

Oral Presentation #47

Panel: The Power of Collaborations for One Health Outcomes

Moderator: Carlos Goncalo des Neves
Panelists: Casey Barton Behravesh, Catherine Machalaba, Danielle Buttke

Oral Presentation #48

Invasive Corallimorpharians at Palmyra Atoll National Wildlife Refuge are No Match for Lye and Heat

Thierry Work[1], *Renee Breeden, Bob Rameyer, Vernon Born, Tim Clark, Jeremy Raynal, Chris Gillies, Julia Rose, Alex Wegmann, Stefan Kropidlowski*
[1]US Geological Survey

Invasive marine species are well documented but options to manage them are limited. At Palmyra Atoll National Wildlife Refuge (Central North Pacific), native invasive corallimorpharians, Rhodactis howesii, have smothered live native corals since 2007. Laboratory and field trials were conducted evaluating two control methods to remove R. howesii overgrowing native corals at Palmyra Atoll (Palmyra): 1) toothpaste mixed with chlorine, citric acid, or sodium hydroxide (NaOH), and 2) hot water. Paste mixed with NaOH had the most efficacious kill in tank trials and resulted in >90% kill over a 98 m2 area three days after treatment. Hot water at 82C was most effective in mesocosms; in the field hot water was less effective than paste but still resulted in a kill of ca. 75% over 100 m2 three days after treatment. Costs of paste and heat (excluding capital equipment and costs of regulatory approval should this method be deployed large scale) were $70/m2 and $59/m2 respectively. Invasive R. howesii currently occupy ca. 5,800,000 m2 of reef at Palmyra with ca. 276,000 m2 comprising heavily infested areas. Several potential management strategies are discussed based on costs of treatment, area covered, and the biology of the invasion. The methods described here expand the set of tools available to manage invasive species in complex marine habitats.

Oral Presentation #49

Epidemiology of Pathogens in Endangered Peninsular Bighorn Sheep (Ovis canadensis nelsoni)

Jessica N. Sanchez[1], *Dr. Brandon A. Munk*[2], *Janene Colby*[3], *Steve G. Torres*[2], *Dr. Ben J. Gonzales*[2], *James R. DeForge*[4], *Aimee J. Byard*[4], *Lora Konde*[2], *Nicholas J. Shirkey*[2], *Dr. Pranav S. Pandit*[1], *Randy A. Botta*[3], *Dr. Annette Roug*[5], *Dr. Michael H. Ziccardi*[6], *Dr. Christine K. Johnson*[1]
[1]EpiCenter for Disease Dynamics, One Health Institute, School of Veterinary Medicine, University of California at Davis, [2]Wildlife Health Lab, California Department of Fish and Wildlife, [3]California Department of Fish and Wildlife, South Coast Region, [4]Bighorn Institute, [5]Centre for Veterinary Wildlife Research, Department of Production Animal Medicine, Faculty of Veterinary Science, University of Pretoria, [6]One Health Institute, School of Veterinary Medicine, University of California at Davis

Peninsular bighorn sheep (Ovis canadensis nelsoni) are federally endangered due to multiple population threats, including introduced infectious disease. We conducted molecular and serological surveillance for 16 pathogens and estimated population size, adult survival, and lamb recruitment from 1981 – 2017. We used mixed effects regression models to assess the impact of disease at individual and population levels. Infection and/or exposure to pathogens varied spatially and temporally, with the region in which an animal was captured being most associated with pathogen prevalence. These findings suggest that local ecological factors or differences in connectivity among and within herds may be driving pathogen transmission. Respiratory pathogens were relatively common, and most sheep were exposed to, or infected with, multiple pathogens throughout their lives. Higher Mycoplasma ovipneumoniae seropositivity was associated with lower lamb recruitment, consistent with lambs having high rates of pneumonia-associated mortality, but there was no association between M. ovipneumoniae and adult survival. Orf virus seroprevalence was positively associated with adult survival in the previous year, and population size within a region was positively associated with adult survival. We found trends suggestive of higher bighorn sheep survival in years with lower summer temperatures and higher summer rainfall, and observed increasing temperatures and decreasing precipitation over the course of the 36-year study period. These conditions are expected to worsen in southwestern deserts as climate change continues, and environmental stressors may compound population impacts of disease on bighorn sheep through additional physiologic stress and/or behavioral changes leading to increased pathogen transmission. Consideration of environmental factors, such as the distribution of water sources and the impact this has on bighorn sheep contact rates, should be incorporated into future conservation strategies in the face of climate change. Our results will be used to inform bighorn sheep management and ongoing monitoring for disease outbreaks that threaten population recovery.

Oral Presentation #50

Cause of Death, Pathology, and Chronic Wasting Disease Status of White-Tailed Deer Mortalities in Wisconsin

Marie Gilbertson[1], *Ellen Brandell*[1], *Marie Pinkerton*[2], *Nicolette Meaux*[1], *Matthew Hunsaker*[1,3], *Dana Jarosinksi*[3,4], *Wesley Ellarson*[3], *Daniel Walsh*[5], *Daniel Storm*[3], *Wendy Turner*[6]
[1]Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin–Madison, [2]Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin–Madison, [3]Wisconsin Department of Natural Resources, [4]Warnell School of Forestry and Natural Resources, University of Georgia, [5]U.S. Geological Survey, Montana Cooperative Wildlife Research Unit, University of Montana, [6]U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin–Madison

White-tailed deer (WTD; Odocoileus virginianus) are a critical species for ecosystem function and wildlife management. As such, studies of cause-specific mortality among WTD have long been used to understand population dynamics. However, detailed pathological information is rarely documented for free-ranging WTD, especially in regions with high prevalence of chronic wasting disease (CWD). This leaves a gap in understanding how CWD is associated with the prevalence of other disease processes or comorbidities which may subsequently alter broader population dynamics. In this study, we investigated unknown mortalities among collared WTD in southwestern Wisconsin, an area of high CWD prevalence. We tested for associations between CWD and other disease processes and used a network approach to test for clusters of co-occurrences of disease processes. Predation and infectious disease were top causes of death, with high prevalence of CWD (42.4%; n = 245) and pneumonia (51.2%; n = 168) in our sample. CWD prevalence increased with age, before decreasing among older individuals, with more older females than males in our sample. Females were more likely to be CWD positive, and while this was not statistically significant when accounting for age, females were significantly more likely to die with end-stage CWD than were males and may consequently be an underrecognized source of CWD transmission. Diagnosis of CWD was associated with emaciation and atrophy of marrow fat, and tentatively associated with hematopoietic atrophy and ectoparasitism (lice, ticks). Occurrences of severe infectious disease pathologies clustered together (e.g., pneumonia, CWD), as compared to non-infectious or low severity processes (e.g., sarcocystosis). However, pneumonia cases were not fully explained by CWD status. With the prevalence of CWD increasing across North America, our results highlight the critical importance of understanding the role of CWD in favoring or maintaining disease processes of importance for deer population health and dynamics.

Oral Presentation #51

Behavioral Scrapes as a Route of Transmission and Potential Environmental Sentinel for CWD

Miranda Huang[1], Steve Demarais[1], Bronson K. Strickland[1], Anna Grace Welch[1], Alejandro Banda[1], Scoty Hearst[2], Allan Houston[3], Kim Pepin[4], Kurt C. VerCauteren
[1]Mississippi State University, [2]Mississippi College, [3]University of Tennessee, [4]Animal and Plant Health Inspection Service

Chronic Wasting Disease (CWD) has impacted deer populations and upended wildlife management as it spreads across North America. One potential driver of indirect spread is scraping behavior by white-tailed deer (Odocoileus virginianus, hereafter: WTD). Scraping behavior communicates sociosexual status using bodily fluids (urine, saliva, glandular secretions) with the potential to spread infectious material. We used data from 100 camera traps at scrapes over 4 months to document WTD visitation rates of both sexes and to generate a social network of males in an area with high CWD prevalence (50%). We enhanced this analysis by testing prion levels in the soil of and on the licking branch above each scrape. We also determined the CWD status of harvested bucks known to have visited scrapes. Across approximately 10,000 acres, we captured 2,721 scrape interactions by does, fawns, and >200 unique bucks. Bucks interacted with scrapes 3x more often than does and 16x more than fawns. Most WTD visits to scrapes included interactions with the licking branch (59%), while a minority included scraping soil (12%) and urinating or rub-urinating (7%). We used social network measures to identify significant bucks and examined scraping behaviors related to CWD status. Understanding visitation frequency and prion levels at scrapes informs social structures and the potential of scrapes as points for prion transfer. These analyses also show if scrapes could serve as environmental sentinels to identify CWD presence in an area without relying on harvested WTD and strategies for incorporating scrapes into the management of CWD.

Oral Presentation #52

Relatedness of White-Tailed Deer from Culling Efforts Within a Disease Management Zone in Minnesota

Alberto Fameli[1], Jessie Edson[1], Christopher Jennelle[2], W. David Walter[3]
[1]Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University, [2]Minnesota Department of Natural Resources, [3]U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit

Contact between individuals is likely the main process driving chronic wasting disease (CWD) transmission in recently infected areas. In the case of white-tailed deer (Odocoileus virginianus), closely related females form social groups; consequently, infected females are more likely to spread CWD to relatives than non-relatives. Because multiple social groups can overlap spatially, deer culled in a site over weeks/months may represent a collection of unrelated deer from different social groups, however, this assertion has not been evaluated. We assessed the effectiveness of culling operations to remove genetically related deer in three Management Zones (MZ) in Minnesota, USA. We culled 1,053 deer from the MZ during 3 months in 2019 (60 culled groups) and 2 months in 2021 (83 culled groups). We analyzed 11 genetic markers to characterize samples, including hunter-harvested and opportunistically collected samples to better represent genetic diversity (Ntotal=1,256). We calculated mean relatedness between deer of the same culled group (R-intra), and between deer not belonging to the same culled group (R-out). We then calculated the difference between means, assigning significance based on a bootstrapping method as well as between pairs of CWD-positive deer (Rpos-pos), and between pairs of different deer (Rpos-neg/neg-neg) in a MZ. The observed difference between R-intra and R-out was 0.037, while the bootstrapping 95%CI=−0.0033 to 0.0033. Regarding comparisons based on CWD status, the observed difference between Rpos-pos and Rpos-neg/neg-neg was −0.0006, while the bootstrapping 95%CI=−0.0035 to 0.0036. Culling efforts were successful in removing related individuals. We do not discard their capacity to eliminate social groups, a necessary step early on in an epidemic when transmission depends on direct contact. CWD-positive deer were not more related among themselves than the rest of the population in a MZ, likely because most of them were hunter-harvested/opportunistically collected and members of their social group are not represented.

Oral Presentation #53

Monitoring and Surveillance of Unprecedented Wildlife Mortality Due to HPAIV Infections 2020-2022.

Mr. Paul Duff[1], Dr Craig Ross[1], Dr Bart Donato[2], Dr Rowena Hansen[1]
[1]Animal and Plant Health Agency (APHA), [2]Natural England

The severity of HPAIV (highly pathogenic avian influenza virus) infections in both wild waterbirds and poultry has increased in the past two winters in Great Britain culminating in unprecedented mortality in waterbirds during the past winter (2021-2022). HPAIV infections in the Svalbard wintering population of barnacle geese (Branta leucopsis) in the Solway estuary, an SPA (Special Protection Area) was attributed as the cause of death of between 10%-20% of the 40,000 barnacle geese (BG) present, an order of mortality not recorded previously in wild birds since DoWS national wildlife disease surveillance commenced in 1998. This presentation describes multi-pronged investigations into the deaths; including how losses were monitored by 3-weekly transect walks, counting and marking (using dye) carcases, reporting fresh/live birds for testing and sampling at a nearby APHA Veterinary Investigation Centre. Clinical signs were recorded by video. Samples were tested by PCR by the APHA Avian Virology Department and positive cases mapped. A network of 5 organisations performed regular flock counts on the geese populations. Rings from birds were removed and recorded. Reports and data were provided to policy makers by APHA, and advice was provided by local authorities to local stakeholders on the high mortalities. Several isolations of H5N1 virus were made from BG from the estuary area and it was possible to follow an individual goose from clinical disease through pathology to H5N1 isolation. The HPAIV mortality was continuous, for three months, from mid-November 2021 to mid-February 2022. The dense, compact flocking during flight, feeding and roosting in this species may partially explain the persistence of HPAIV infection in the population. This paper also describes investigations by APHA Dept of Virology and DoWS in the past two winters into H5 HPAIV infections in wild mammals (fox and seals) and other wild birds in Great Britain.

Oral Presentation #54

Highly Pathogenic Avian Influenza is Maintained by Conspecific Scavenging in Black Vultures (Coragyps atratus) in Florida

Mark Cunningham[1], Rebecca Hardman[2], Bryan Kluever[3], Nicole Nemeth[4], Rebecca Poulson[4], Lijuan Zhou[5], Trevor Zachariah[6], Kyle Donnelly[6], Michael Milleson[3], Veronica Guzman-Vargas[1], Mark Ruder[4], Y. Reddy Bommineni[5], Dave Stalknecht[4]
[1]Florida Fish and Wildlife Conservation Commission, [2]Florida Fish and Wildlife Conservation Commission, [3]USDA - Wildlife Services, [4]Southeastern Cooperative Wildlife Disease Study, [5]Florida Department of Agriculture and Consumer Services, [6]Brevard Zoo

Highly pathogenic avian influenza (HPAI) H5N1 Gs/Gd 2.3.4.4 was documented in North America in eastern Canada in October 2021. Subsequent surveillance by USDA-Wildlife Services identified the virus in hunter-harvested waterfowl throughout the Atlantic Flyway, including Florida, in the Fall/Winter 2021-2022. Beginning 7 February 2022, increasing numbers of HPAI infected dead or neurologic lesser scaup (Aythya affinis) were documented primarily on Florida's East Coast with fewer reports on the Gulf Coast. Lesser scaup mortalities, estimated to be in the thousands, peaked in late February, and the last recorded mortality was 31 March. As lesser scaup mortalities declined, black vulture (Coragyps atratus) mortalities increased in both number and geographic distribution. Approximately 800 documented mortalities known or suspected to be due to HPAI occurred between 12 February and 14 April 2022 in 20 counties in Florida. Almost 300 black vulture mortalities were observed at one roost site in Volusia County. Water and soil samples collected from this site were negative for HPAI virus; however, conspecific scavenging by black vultures was observed there and in other locations. Samples sequenced from black vultures were confirmed as the HPAI H5N1 Gs/Gd lineage at the National Veterinary Services Laboratory. Infections in black vultures likely originated through scavenging on infected lesser scaup or other infected species, but once in vultures, HPAI infection appears to have been maintained at roost sites by conspecific scavenging. The collection and disposal of >200 carcasses at the Volusia County roost site may have reduced the incidence of infection. Other management actions included public outreach and developing guidelines for wildlife rehabilitators and others. Because of their susceptibility and scavenging behavior, black vultures may serve as an indicator species for HPAI in North America and may sustain an outbreak after infection rates have declined in other species.

Oral Presentation #55

Feline Leukomyelopathy in Florida Panthers and Bobcats

Hollis Stewart[1], *Mark Cunnungham*[1], *Dave Onorato*[1], *Nicole Nemeth*[2]
[1]Florida Fish and Wildlife Conservation Commission, [2]Southeastern Cooperative Wildlife Disease Study – Department of Pathology

Feline leukomyelopathy (FLM) is neuromuscular disorder of Florida panthers (Puma concolor coryi) and bobcats (Lynx rufus). From April 2017 through March 2022, 58 cases (24 panthers, 34 bobcats) have been diagnosed with FLM in peninsular Florida. This includes 14 Confirmed cases (4 panthers, 10 bobcats) and 44 Probable cases (based on remote video, 20 panthers, 24 bobcats). FLM is characterized clinically by mild to severe upper motor neuron signs consisting primarily of hindlimb paresis and ataxia of varying severity. Currently, confirmation is based on histological examination of the spinal cord. Pathologic findings include bilaterally symmetric lesions in the ventral and lateral funiculi that primarily consist of dilated axonal sheaths that occasionally contain myelin debris and gitter cells. To date, non-felids and domestic cats do not appear to be affected. Prevalence data and geographic distribution for the disorder are unknown. The cause of FLM is currently undetermined. Laboratory testing has revealed no viral, nutritional, bacterial, or fungal component. Toxin and heavy metal testing have also been inconclusive or not biologically significant. However, environmental toxins remain a primary suspect. The FLM investigation involves includes 1) video monitoring on public lands, 2) solicitation of observations/video from the public, 3) the capture and radio-instrumentation of bobcats and Florida panthers, and 4) the opportunistic collection, examination and testing of bobcats and panthers euthanized or found dead. Although the impact of the disorder on Florida's wild felid populations is currently unknown, there is potential for FLM to negatively affect the bobcat population and the continued recovery of the Florida panther population.

Oral Presentation #56

Retroviral Infections Affect Survival and Reproduction of Female Wild Turkeys

Stephanie Shea[1], *Matthew Gonnerman*[1], *Erik Blomberg*[1], *Kelsey Sullivan*[2], *Pauline Kamath*[1]
[1]University of Maine, [2]Department of Inland Fisheries and Wildlife

Wild turkeys (Meleagris gallopavo) are a prized upland gamebird that has experienced dramatic increases in population size and range expansion as the result of reintroduction campaigns, which may promote the transmission of diseases. While previous research has focused on factors affecting survival and reproduction in wild turkeys, few studies, if any, have examined the role of pathogen infections on demographic metrics. Lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV) are avian oncogenic retroviruses that infect poultry and wild turkeys, which can result in disease and mortality, though most cases in wild birds appear asymptomatic. Here, we investigate whether retroviral infections influence the fitness of wild turkeys by evaluating the effects of single and dual infections on female survival rate and several reproduction metrics, including daily nest survival rate, clutch size, nesting phenology, nesting propensity, and hatch rate. We live-captured 163 female wild turkeys in central Maine during three winters from 2018–2020. We collected blood for LPDV and REV molecular diagnostics and attached a GPS or VHF transmitter to monitor survival and nesting. We found the weekly survival rate was lower for REV-infected hens than their uninfected counterparts, translating to nearly half the cumulative annual survival probability. Infection with LPDV was a significant predictor of clutch size, with LPDV-infected hens laying an average of 1.43 fewer eggs. We are using these results to inform population growth models to determine population level effects of infection, data which is important for informing management decisions related to translocations, harvest limits, and pathogen transmission between wildlife and poultry operations. These findings demonstrate that retroviral infections can impact survival and reproduction of female wild turkeys, even in the absence of overt disease. Furthermore, our results highlight the importance of considering pathogen infection when assessing factors affecting demographic metrics of free-ranging wildlife.

Oral Presentation #57

A Sarcoptic Mange Outbreak Devastates Wild Camelid Populations in a Protected Area in Argentina

Marcela Uhart[3], Hebe Ferreyra[1], Jaime Rudd[2], Janet Foley[3], Ralph E. T. Vanstreels[3], Ana M. Martin[4], Emiliano Donadio[5]

[1]Administración de Parques Nacionales, [2]California Department of Fish and Wildlife, [3]University of California, Davis, [4]Universidad Catolica de Cordoba, [5]Fundacion Rewilding Argentina

Sarcoptic mange outbreaks often occur as severe epizootics and can devastate wildlife populations. In 2014, mange was first detected in vicuñas (Vicugna vicugna) and guanacos (Lama guanicoe) in San Guillermo National Park (SGNP), Argentina. We investigated the demographic and spatio-temporal dynamics of the outbreak from 2017-2019 and traced the potential source of the epidemic. Between May 2017 and June 2018, density of living vicuñas and guanacos sharply decreased by 68% and 77%, respectively. Both species were nearly extinct in the park by April 2019. Clinical signs of mange were observed in 24% (n = 478) of living vicuñas and 33% (n = 12) of guanacos. Lesions consistent with mange were seen in 94% (n = 124) vicuña and 85% (n = 20) guanaco carcass remains. Mites recovered from carcasses were identified morphologically and molecularly as Sarcoptes scabiei. Microsatellite characterization of mites (n = 13 from 7 vicuña; n = 11 from 3 guanaco) showed low allelic richness (Rvicuña = 1.35, Rguanaco = 1.19), few alleles with a low occurrence of polymorphisms (30% polymorphic loci in vicuña mites and 20% in guanaco mites), and observed (Ho) and expected (He) heterozygosity equilibrium. This suggests a single source and recent origin of the epidemic. Via interviews we identified a governmental livestock incentive program which introduced llamas (Lama glama) in areas adjacent to SGNP as the potential source of mange. Though mange-infested llamas were detected upon arrival in 2009, there were no active cases in remnant herds at the time of this study. However, despite lack of confirmatory testing, multiple evidence points to them as the source host population. Vicuñas and guanacos were the dominant herbivores in PNSG, and this unprecedented event could result in profound cascading effects at the community and ecosystem levels.

Oral Presentation #58

Spatiotemporal Bayesian Model of Pseudogymnoascus destructans Spread

Juan Francisco Mandujano Reyes[1], Anne Ballmann[2], Robin Russell[3], Daniel Walsh[4], Jun Zhu[1]
[1]Department of Statistics, University of Wisconsin-Madison, [2]U.S. Geological Survey, National Wildlife Health Center, [3]U.S. Fish and Wildlife Service, [4]U.S. Geological Survey, Montana Cooperative Wildlife Research Unit

Pseudogymnoascus destructans (Pd), the causative agent of White-nose syndrome (WNS), a devastating infectious fungal disease in bats, was detected for the first time in 2007 in New York, USA. Since then, the evolution of WNS in North America has resulted in a significant decline in bat populations, resulting in threats to ecological and agricultural systems. Identifying areas where Pd is expected to newly arrive is important for prevention, control, and detection of the disease. Additionally, the identification of spatial covariates that may facilitate pathogen transmission is essential for successful surveillance. In this work, we apply a spatiotemporal Bayesian model for prevalence of Pd using georeferenced historical data of infected bats in North America from the USGS's National Wildlife Health Center. We evaluate the effects of spatial covariates such as terrain ruggedness index, linear hydrography (waterway), and tree canopy cover. The R-INLA software is used for model fitting and statistical inference. We present a heat map identifying the areas at the geographic front of disease spread where sampling is suggested, and discuss spatial covariates significant for the propagation of WNS. The results obtained in this study may be helpful for predicting pathogen prevalence at future space-time points, and for facilitating wildlife disease surveillance in general.

Oral Presentation #59

The Importance of Case Definitions in Wildlife Health

E. Jane Parmley[1], Kimberli Miller[3], Julia Lankton[3], Marnie Zimmer[2], Tonia von Hugo[1], Megan Jones[2,4], Anne Ballmann[3], Jennifer Buckner[3], C. LeAnn White[3], Patrick Zimmer[2], Jonathan Sleeman[3]

[1]Ontario Veterinary College, University of Guelph, [2]Canadian Wildlife Health Cooperative, [3]US Geological Survey-National Wildlife Health Center, [4]Atlantic Veterinary College, University of Prince Edward Island

Healthy wildlife populations contribute to economic, cultural, and ecological services and food security. Maintaining healthy wildlife populations during this time of extraordinary social and environmental change is challenging. Effective wildlife disease surveillance programs help guide conservation efforts through their ability to identify on-going and emerging wildlife health threats. Case definitions provide standard sets of criteria for classifying the degree of certainty of a particular diagnosis and effective case definitions improve surveillance data quality and comparability. Better data and standardization allow for improved data sharing, which increases geographic and species surveillance coverage and permits more robust analyses.

In 2018, the USGS National Wildlife Health Center (NWHC) and Canadian Wildlife Health Cooperative (CWHC) created a collaborative working group to develop and maintain wildlife disease case definitions. The group is composed of veterinary pathologists, epidemiologists, and wildlife biologists. Through regular online discussion and one in-person meeting, the group created a charter, case definition template, and definitions for common wildlife diseases. Pathologists from each organization reviewed and finalized the definitions.

The case definition template includes four sections, and each definition provides an overall case classification. Diagnoses are classified as “Confirmed”, “Presumptive”, or “Suspected” and evidence of a pathogen or toxin is classified as “Exposed” or “Present/Detected”. To date, case definitions have been developed for avian botulism, avian cholera, highly pathogenic avian influenza, Newcastle disease, canine distemper, chronic wasting disease, electrocution (avian), lead poisoning (avian), parvovirus, rabies, snake fungal disease, stony coral disease, trichomoniasis, tularemia, West Nile virus, and white-nose syndrome.

Next steps include publication to make the case definitions widely available for others, implementation of case definitions at NWHC and CWHC, and development of additional definitions. Once implemented, we will assess definition use and whether they are contributing to more consistent and comparable data that are easier to share within and between organizations.

Oral Presentation #60

A Field-Deployable Diagnostic Assay for the Visual Detection of Chronic Wasting Disease Prions

Peter Christenson[1,2], Manci Li[2,3], Gage Rowden[2,3], Marc Schwabenlander[2,3], Tiffany Wolf[2,4], Sang-Hyun Oh[1,2], Peter Larsen[2,3]

[1]Department of Electrical and Computer Engineering, University of Minnesota, [2]Minnesota Center for Prion Research and Outreach, University of Minnesota, [3]Department of Veterinary and Biomedical Sciences, University of Minnesota, [4]Department of Veterinary and Population Medicine, University of Minnesota

Diagnostic tools for the rapid and reliable detection of prion diseases are limited. Gold nanoparticles (AuNPs) facilitate sensitive and reliable diagnostic techniques via visual color change for the detection of a variety of targets. In parallel, recently developed quaking-induced conversion (QuIC) assays leverage protein-amplification and fluorescent signaling for the accurate detection of misfolded proteins, especially misfolded prion proteins. Here, we combine AuNP and QuIC technologies for the visual detection of amplified misfolded prion proteins from tissues of wild white-tailed deer infected with chronic wasting disease (CWD), a prion disease of cervids. Our newly developed assay, MN-QuIC™, enables both naked-eye and light-absorbance measurements for the detection of misfolded prions. The MN-QuIC™ assay leverages basic laboratory equipment that is cost-effective and portable, thus facilitating real-time prion diagnostics across a variety of settings. To test the portability of our assay, we deployed to a rural field-station in southeastern Minnesota and tested for CWD on site. We successfully demonstrated that MN-QuIC™ is functional in a non-traditional laboratory setting by performing a blinded analysis in the field and correctly identifying all CWD positive and CWD not detected (independently confirmed with ELISA and/or IHC tests) animals at the field site, thus documenting the portability of the assay. Additionally, we show that electrostatic forces help govern the AuNP/prion interactions and contribute to the differentiation of CWD-prion positive and negative samples. In total, we examined 17 CWD positive and 24 CWD not-detected white-tailed deer tissues that were independently tested using ELISA, IHC, and RT-QuIC technologies and results secured with MN-QuIC™ were 100% consistent with these tests. We conclude that hybrid AuNP and QuIC assays, such as MN-QuIC™, have great potential for sensitive, field-deployable diagnostics of a variety of protein misfolding diseases.

Oral Presentation #61

Histopathology and Genomic Analysis Suggest White-Nose Syndrome / Pseudogymnoascus destructans Evolved from and Maintains Invasion Strategies of Plant Fungal Pathogens

Carol U. Meteyer[1], Julien Y. Dutheil[2], M. Kevin Keel[3], Justin G. Boyles[4], Eva H. Stukenbrock[5]
[1]National Wildlife Health Center, U.S. Geological Survey, [2]Molecular Systems Evolution, Max Planck Institute for Evolutionary Biology, [3]University of California, Davis, School of Veterinary Medicine, Dept of Pathology, Microbiology & Immunology, [4]Cooperative Wildlife Research Laboratory and School of Biological Sciences, Southern Illinois University, [5]Environmental Genomics, Botanical Institute, Christian-Albrechts University of Kiel

Pseudogymnoascus destructans causes the invasive cutaneous ascomycosis responsible for unprecedented deaths of cave hibernating bats in North America. Early in the investigation of WNS, pathology observed in microscopic sections of bat skin was so unique it became the gold standard for diagnosing this disease. This unique 'benign' intraepidermal proliferation of P. destructans hyphae progresses to subsequent deeper invasion suggesting hemibiotrophy. This switch from a biotrophic host relationship without pathology to necrotrophic invasion has previously only been described in plant pathogens. We review of electron micrographs and identified an apparent convergence of P. destructans hyphae at the opening of bat hair follicles, similar to that seen with nutrient tropism in plant-associated fungi. Nutrient tropism, biotrophy, and necrotrophy are often associated with appressoria; structures that have not been reported in vertebrate pathogens. Histopathology of bat skin show penetrating hyphae of P. destructans that resemble appressoria. This evidence led us to investigate the ancestral lineage for P. destructans using a phylogenomic analysis of a taxonomically diverse collection of fungi. Despite gaps in genetic sampling both for prehistoric and contemporary fungal species, P. destructans aligns best with plant-associated fungi, with an 88% probability the ancestral state of the clade containing P. destructans was a plant-associated fungus. Paired with histopathology, these data suggests that P. destructans evolved from ancestral plant-associated fungi pathogens and retained invasion strategies affiliated with fungal pathogens of plants. Collaboration between scientists studying contemporary fungal pathogens of plants in the same clade as P. destructans has the potential to accelerate the understanding of P. destructans, as well as provide a potential new model for pathogenesis in fungi that infect plants. Sharing knowledge of invasion strategies used by pathogens that infect hosts from different kingdoms might also provide more general insight into pathogen emergence from previously unrecognized physical and biological environments.

Oral Presentation #62

WildHealthNet: A One Health Approach to Sustainable Wildlife Health Surveillance

Mathieu Pruvot[1,2], Dr. Sarah H. Olson[2], Khongsy Khammavong[3], Phonesavanh Milavong[3], Alice Porco[5], Dr Sothyra Tum[8], Sokha Chea[5], Sours Sreyem[5], Emily Denstedt[3], Dr Watthana Theppayna[7], Souchinda Phouangsouvanh[3], Dr Sithong Phiphakhavong[7], Dr Phouvong Phommachanh[7], Dr Alice Latinne[4], Dr Phan Thanh Long[6], Nga Nguyen[4], Thanh Vo[4], Ngoc Pham[4], Dr Diego Montecino[2], Dr Amanda Fine[2]

[1]University of Calgary, Faculty of Veterinary Medicine, [2]Wildlife Conservation Society - Health Program, [3]Wildlife Conservation Society Lao PDR, [4]Wildlife Conservation Society Viet Nam, [5]Wildlife Conservation Society Cambodia, [6]Department of Animal Health, Ministry of Agriculture and Rural Development, [7]National Animal Health Laboratory, Department of Livestock and Fisheries, [8]National Animal Health and Production Research Institute

Introduction: Wildlife and their interfaces with people and livestock are essential surveillance targets to monitor the effects of environmental changes on biodiversity and the emergence of new pathogens affecting wildlife, livestock, and human health. However, unbalanced investments in One Health have neglected wildlife health surveillance at national and global scales, particularly in lower and middle income countries (LMICs) where previous efforts have been limited in scope and duration.

Methodology: Building on decades of wildlife health work, and close relationships with environmental sector and One Health partners in over 60 countries, the Wildlife Conservation Society (WCS) has been developing and implementing WildHealthNet, a new locally-scaled multi-pronged One Health approach to establish wildlife health surveillance in LMICs. WildHealthNet utilizes existing capacity in the environmental, animal, and public health sectors, and focuses on iterative field implementation and policy development (WildHealthBuild), capacity building (WildHealthSkills), data collection and management systems (WildHealthTech), and supports management actions (WildHealthRespond).

Results: WildHealthNet has been piloted in Cambodia, Lao PDR, and Viet Nam to support the development of national wildlife health surveillance systems. Networks included protected area rangers, wildlife rescue centers, livestock and human health sector staff and laboratories, and community members. Surveillance activities detected outbreaks of H5N1 highly pathogenic avian influenza in wild birds, African swine fever in wild boar (Sus scrofa), Lumpy skin disease in banteng (Bos javanicus), and other priority endemic zoonotic pathogens. In Cambodia and Lao PDR, national plans for wildlife disease surveillance are being signed by governments.

Conclusion: Cross-sectoral and trans-disciplinary approaches are needed to implement effective and sustainable wildlife health surveillance systems at global scale. WildHealthNet responds to the global needs for wildlife health surveillance and supports the OIE Wildlife Health Framework objectives, but will require further investments and a consortium approach, where key global stakeholders coordinate and align into a coherent workflow.

Oral Presentation #63

Panel: The Future of Training for Wildlife Health Professionals

Moderator: Kirsten Gilardi
Panelists: Mark Ruder, Kelly Straka, Cris Walzer

Oral Presentation #64

Widespread Detection of Batrochochytrium dendrobaditis on Urodele and Anuran Species is Driven by Temperature and Fine-Scale Taxonomy in the United States

Daniel Grear[1], Michael J Adams[2], Adam Baklin[2], William J Barichivich[2], Adrianne B Brand[2], Daniel L Calhoun[2], Robert N Fisher[2], Brad M Glorioso[2], Evan H Campbell Grant[2], Brian J Halstead[2], Blake R Hosack[2], Patrick Kleeman[2], Jeffrey Lorch[1], Brome McCreary[2], Erin Muths[2], Cristopher Pearl[2], Mark F Roth[2], Walt Sandinski[2], Brent Sigafus[2], J Hardin Waddle[2], Susan C Walls[2], Megan E Winzeler[1]

[1]USGS National Wildlife Health Center, [2]USGS Amphibian Research and Monitoring Initiative

Batrachocytrium dendrobaditis (Bd) is a globally distributed pathogen of amphibians and has one of the largest documented impacts on biodiversity of any wildlife pathogen. Bd is regularly viewed through the lens of a global wildlife epizootic because the spread of a highly virulent strain has resulted in well-documented species impacts. However, the current state of Bd occurrence, host range, host impacts, and ecological drivers remains poorly understood outside amphibian species and regions that are affected most negatively by Bd. Our objective was to describe the macro-ecological patterns of Bd occurrence on Urodeles (salamander, newts, and related species) across the United States and to compare these patterns with better-studied Anuran (frogs and toads) species. We sampled amphibians as part of surveillance for the emerging fungal pathogen B. salamandrivorans (Bsal). Species and locations were targeted based on potential susceptibility to and introduction risk of Bsal, but we sampled all amphibians as available. We live-captured apparently healthy amphibians, collected skin swabs, and analyzed the swabs using a quantitative PCR with duplex detection of Bd and Bsal from 2015-2017. We collected swabs from nearly 11,200 amphibians at over 500 sites. We jointly analyzed the prevalence and intensity of Bd detection with covariates of site-level temperature and precipitation, as well as individual characteristics and taxonomy. Bd detection and intensity were most strongly influenced by temperature in the month preceding sampling and variation in taxonomy. We estimated an optimal temperature correlation to Bd detection, indicating that there is strong and non-linear environmental influence on Bd detection and estimating occupancy. Bd detection was widely distributed spatially and detected on nearly every species sampled. However, there was significant variation in the detection prevalence and intensity across both Urodele and Anuran species suggesting that North American Bd has a wider host-range and deeper evolutionary history than previously recognized.

Oral Presentation #65

Using Mosquito Surveillance to Inform Risk of West Nile Virus Exposure to Ruffed Grouse Populations in Pennsylvania

Kristin Bondo[1], Lisa Williams[2], W. David Walter[3]
[1]Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University, [2]Pennsylvania Game Commission, Bureau of Wildlife Management, [3]U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University

Populations of ruffed grouse (Bonasa umbellus) have declined throughout their range in various regions of the United States. Recent evidence suggests that these decreases have been driven by the loss of optimal habitat, and in some regions, the introduction of West Nile virus (WNV). The risk of WNV exposure to ruffed grouse populations is needed to help inform management decisions for this species and other susceptible wildlife populations. Mosquito surveillance is often conducted statewide in several regions but is often collected from anthropogenically-derived habitats. Thus, it is unclear whether these data can be used to help inform the risk of WNV in remote woodlands where ruffed grouse occur. Our objectives were to use Bayesian hierarchical spatial models in R-INLA to make risk maps of potential WNV exposure to ruffed grouse populations in relation to ecological variables (e.g., temperature, precipitation, elevation, and habitat type). From 2018 to 2020, we conducted mosquito surveillance in habitats of ruffed grouse in Pennsylvania. We used gravid traps to focus our trapping on Culex restuans, a known WNV vector that is more common in woodland habitats. Combining Culex restuans data collected in woodland habitats with Culex restuans surveillance collected in human-dominated regions statewide, we built spatial models in R-INLA to identify variables driving high mosquito abundances. We found habitat and climatic variables to be important predictors of mosquito abundance. We also found that statewide mosquito surveillance could be used to help inform the risk of WNV exposure to ruffed grouse populations in Pennsylvania. The results of these efforts could be used as a guide for other states and regions to help conduct conservation and habitat restoration decisions involving wildlife species susceptible to WNV.

Oral Presentation #66

Demographic Risk Factor Variation in an Initial Outbreak of Chronic Wasting Disease in West Virginia

Brian Dugovich[1,2], Ethan Barton[3], James Crum[3], David Stallknecht[1], Mark Ruder[1]
[1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, [2]U.S. Geological Survey, Northern Rocky Mountain Science Center, [3]West Virginia Division of Natural Resources

Following the first detection of chronic wasting disease (CWD) in white-tailed deer (Odocoileus virginianus) in Hampshire County, West Virginia in 2005, we investigated the change of CWD prevalence and potential risk factors promoting infection during the initial stages of the outbreak. For 8 years (2006-2012, 2017) within a 39 mi2 area of central Hampshire County, 853 deer were randomly sampled and tested for CWD by enzyme-linked immunosorbent assay and/or immunohistochemistry. Demographic data measured included sex, age, carcass weight, kidney fat index, and number of fetuses. Risk factors examined with Bayesian logistic regression included birth year, age, and body size approximated from weight residuals of lean body mass. CWD prevalence trended upward with an initial slow growth phase (2006 – 2008) and then entered a fast growth phase thereafter (2009-2017). Although no difference in overall CWD prevalence was found between the sexes, this was confounded by the longevity of females compared to males. With the stronger stochastic dynamics of low prevalence in the slow growth phase (n = 270), age in males was the strongest risk factor but was highly uncertain. However, in the fast phase (n = 371), age, birth year, and body size in males and age and birth year in females were highly certain risk factors. The body size risk found in male deer is plausibly underpinned by behavioral and physiological mechanisms. In this system, older male deer are most likely to be infected with CWD, which supports findings from other studies and highlights concerns over harvest management approaches aimed at increasing the age structure of bucks in CWD-endemic regions.

Oral Presentation #67

Associations of White-Tailed Deer with and Without Chronic Wasting Disease

W. David Walter[1], Dr. Christopher Rosenberry[3], Dr. Alberto Fameli[2], Jessie Edson[2]
[1]U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, 403 Forest Resources Building, The Pennsylvania State University, [2]Pennsylvania Cooperative Fish and Wildlife Research Unit, 403 Forest Resources Building, The Pennsylvania State University, [3]Pennsylvania Game Commission

Chronic wasting disease (CWD) was first detected in white-tailed deer (Odocoileus virginianus) in Pennsylvania in 2012 and has spread within this initial area with prevalence exceeding 5%. Most studies that characterized associations of white-tailed deer infected with CWD used diseased-free deer that were not monitored in an area that had CWD. An understanding of associations of infected deer within an area with CWD is needed to more accurately assess interactions between infected and uninfected white-tailed deer. We analyzed a data set of susceptible and infected deer monitored with global positioning system (GPS) technology from 2018 to 2020. Deer of various sex and ages were monitored to document associations within a threshold of 10 meters and 10 minutes. Combined with genetic analysis of relatedness and 30-minute collection intervals for GPS collars, we derived contact rates based on 25%, 50%, 75%, and 100% of associations being equal to a contact. We found that overall, our infected deer had 704 individual associations with our disease-free deer, mostly female deer. We were also able to confirm with microsatellite data that deer that were captured in close proximity and often traveled together were parent-offspring to identify associations within family groups. This is the first study to collect fine scale spatial and temporal data on white-tailed deer that tested positive for CWD post-mortem for comparison to those that CWD was not detected. This study allowed us to characterize disease transmission between deer that test positive for CWD and deer where CWD was not detected to assess if variability exists between the groups. These results provide novel information to inform levels of association between white-tailed deer infected with CWD to those not infected with CWD in an area experiencing high prevalence of CWD.

Oral Presentation #68

Predicted Probability of Chronic Wasting Disease Infection Among cervids in Kansas Using a Generalized Additive Model

Zoe Koestel[1], Myungsoo Yoo[2], Levi Jaster[3], Shane Hesting[3], Isabella B. Richardson[1], Christopher K. Wikle[2], Ram K. Raghavan[1]

[1]Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, [2]Department of Statistics, College of Arts & Sciences, University of Missouri, [3]Kansas Department of Wildlife and Parks

Chronic wasting disease (CWD) is a fatal prion disease of cervids; and the state of Kansas has seen increase in geographic spread and disease occurrence, accompanied by steady rise in the annual number of cases. The first identification of CWD in Kansas occurred in 2001; and the observed trends since that time could pose problems for cervid populations and outdoor recreation in future generations. Additionally, although CWD prion transmission to humans has not yet been demonstrated, this remains a public health concern given the commonplace consumption of cervid meat by humans, closely shared habitats, and experimental evidence that cross-species transmission is possible. As a first step to assessing the CWD trends in Kansas, surveillance data from 2005-2020 was used to visualize the spatiotemporal patterns in sampling and disease occurrence. Further, a generalized additive model (GAM) was used in fitting two models to predict the probability of CWD infection in Kansas. The smoothed effects of space, time, and space-time interaction were estimated with thin plate regression splines. Both models had significant predictive value, but the space-time interaction term slightly improved precision in the second model. Predicted probability of CWD infection was consistently higher in the northwestern region of the state and increased steadily in the later years of the study period. These findings indicate there may be critical spatiotemporal drivers of disease persistence and propagation in certain areas with high predicted probability of CWD infection; identification of these factors could offer opportunities for disease mitigation. Information from the current study is intended to aid and inform CWD management efforts.

Oral Presentation #69

Sharp Decline in Bald Eagle (Haliaeetus leucocephalus) Nesting Success Associated with Highly Pathogenic Avian Influenza Outbreak

Mark Ruder[1], Bob Sargent[2], Rebecca Poulson[1], David Stallknecht[1], Mark Cunningham[3], Samantha Gibbs[4], Nicole Nemeth[1]

[1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [2]Wildlife Resources Division, Georgia Department of Natural Resources, [3]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, [4]Wildlife Health Office, National Wildlife Refuge System, United States Fish and Wildlife Service

The impact of highly pathogenic avian influenza is well-documented in commercial poultry but less is known regarding population-level consequences in wild birds. The bald eagle (Haliaeetus leucocephalus) is a culturally and ecologically significant species that embodies conservation success. Although delisted (2007) from U.S. Endangered Species Act, bald eagles remain state listed in many states and continue to face threats, including emerging pathogens. Eurasian-origin highly pathogenic (HP) H5 influenza A virus (IAV) of the Goose/Guangdong lineage was confirmed in Newfoundland, Canada in December 2021, and was subsequently detected in wild and domestic birds throughout much of the United States during winter/spring 2022. In the Southeastern U.S., wild bird mortality was most common in waterfowl and raptors and here we show an alarming rate of bald eagle mortality and nest failure attributed to HP IAV outbreaks. In February and March 2022, we confirmed acutely fatal and systemic HP IAV infection in 26 bald eagles (nestlings and adults) from coastal areas of Florida, Georgia, South Carolina and North Carolina. Aerial bald eagle nest surveys of coastal nests conducted by the Georgia Department of Natural Resources during March revealed a 47% (34/73) nest success – a sharp decline from the 78% average (2015-2021). Further, the number of young fledged per occupied territory decreased to 0.7 during 2022, compared with an average of 1.1 (2015-2021). These findings may indicate a negative impact on bald eagle populations through both direct mortality, and decreased recruitment. It is unclear if HP H5 IAV will establish in North America and remain a threat to wild birds; however, recent global trends along with the geographic scope, intensity, and broad host range of the ongoing outbreak in North America are concerning. This new threat to bald eagle health warrants continued vigilance.

Oral Presentation #70

Metagenomic Sequencing to Identify the Etiologic Agent Responsible for Pneumonia-Related Mortality in Wisconsin White-Tailed Deer

Dr. Melanie B. Prentice[1], Dr. Marie Gilbertson[3], Dr. Daniel Storm[4], Dr. Wendy C. Turner[2], Dr. Daniel Walsh[6], Dr. Marie E. Pinkerton[5], Dr. Pauline L. Kamath[1]

[1]School of Food and Agriculture, University of Maine, [2]U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, [3]Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, [4]Wisconsin Department of Natural Resources, [5]Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, [6]Montana Cooperative Wildlife Research Unit, University of Montana

Within the United States, deer represent an important source of recreation, food, and revenue, while also hosting pathogens that put healthy deer populations at risk and potentially jeopardize human and domestic animal health. Developing tools for disease surveillance in important recreational and sustenance species like deer will thus be paramount for detecting and responding to outbreaks and spillover events. In Wisconsin, the Department of Natural Resources has been monitoring the white-tailed deer (Odocoileus virginianus) population for chronic wasting disease (CWD) since 1999. Recently, surveillance efforts have identified additional mortalities in deer attributed to pneumonia. Interestingly, such mortalities have been observed in deer both with and without CWD, suggesting the presence of a yet unknown etiologic agent in this population. We present the results of a pilot study that used metagenomic sequencing of deer lung tissue to identify the etiologic agent responsible for these mortalities. We compared the microbial communities identified from metagenomic sequences of CWD-negative deer that died with pneumonia (n = 21) to those that died without pneumonia (n = 23). Reads were aligned to the white-tailed deer genome to exclude host sequences, and unmapped reads were compared to the NCBI nucleotide database using BLAST. Preliminary results show high prevalence (9.8-41.4% of BLAST-ed reads) of the Gram-negative bacteria Fusobacterium necrophorum in pneumonia-positive individuals, and a lack thereof in control individuals. While F. necrophorum has been previously identified as a cause of mortality in deer, it remains unclear whether it is the direct cause of pneumonia-related mortality in this case or an opportunistic colonizer of already diseased deer. This project is ongoing to confirm the etiologic agent(s) responsible, characterize its distribution, identify risk-factors underlying host mortality, and understand its association with CWD. Ultimately, this information will help inform management strategies and developing disease surveillance systems for the Wisconsin deer population.

Oral Presentation #71

The 2021 Songbird Mortality Event – A Summary of Findings and Discussion of Ongoing Investigations

Sabrina S Greening[7], Bryan Richards[1], Nicole Nemeth[2], Nicole Lewis[3], David Needle[4], Joseph Sevigny[5], Michael Oglesbee[6], Seth Faith[6], Julie Ellis[7]

[1]National Wildlife Health Center, United States Geological Survey, [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [3]New Jersey Fish and Wildlife, [4]Department of Molecular, Cellular and Biomedical Sciences, New Hampshire Veterinary Diagnostic Laboratory, University of New Hampshire, [5]Hubbard Genome Center, College of Life Sciences and Agriculture, University of New Hampshire, [6]Department of Veterinary Biosciences, The Ohio State University, [7]Department of Pathobiology, Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, New Bolton Center

In May 2021, wildlife managers in Washington D.C., Maryland, Virginia, West Virginia, and Kentucky began receiving reports of sick, dying, and dead birds with eye swelling and crusty discharge, some of which also reportedly exhibited neurological behaviors. The public and licensed wildlife rehabilitators provided initial reports, while additional reports were received in Delaware, New Jersey, Pennsylvania, Ohio, Indiana, Tennessee, and Connecticut. The majority of reports involved fledgling common grackles (Quiscalus quiscula), blue jays (Cyanocitta cristata), European starlings (Sturnus vulgaris), and American robins (Turdus migratorius). Early in the event, the involved jurisdictions indicated a collective desire to work together in a regional response with consistent public messaging and collaboration among diagnostic laboratories working to identify the cause(s) of the event. The U.S. Geological Survey National Wildlife Health Center (NWHC) facilitated conversations regarding event response among the affected jurisdictions, and also coordinated with other responding diagnostic laboratories. The laboratories examined numerous carcasses, tissues, and forage items via necropsy, histopathology, virology, microbiology, parasitology, and toxicology. In addition to traditional techniques, transmitting electron microscopy and metagenomics analyses were performed. Despite the exhaustive collective effort of the laboratories, no definitive cause(s) of illness or death have been determined at this time. However, the labs have collectively been able to rule out important diseases and pathogens including salmonellosis, chlamydiosis, avian influenza, West Nile virus, coronaviruses, Newcastle disease, herpesviruses, poxviruses, and Trichomonas parasites. In this presentation, we will provide additional background on the event, summarize the main diagnostic findings, describe lessons learned through the coordinated state agency response and communications with the public, and discuss ongoing metagenomic work on songbirds and cicadas.

Oral Presentation #72

A 20+ year Retrospective of Amphibian and Reptile Disease Events in the United States

Megan Winzeler[1], Daniel Grear[1], Magdalena Twarowski[1], Stephanie Steinfeldt[1], David Green[1]
[1]USGS National Wildlife Health Center

Amphibian and reptile populations have experienced declines over the past 3 decades due to a variety of factors including pathogen emergence, habitat fragmentation, and contaminants. While previous research characterized many amphibian pathogens such as Batrachochytrium dendrobatidis (Bd) and pathogens like Ophiodiomyces ophiodiicola (Oo) in reptiles, most of these studies have focused on specific species, populations, or the mechanisms of disease in isolation. Our goal is to summarize historic amphibian and reptile diagnostic cases collected by the USGS National Wildlife Health Center (USGS NWHC) to identify trends such as the frequency, seasonality, regionality, and/or host diversity of common amphibian and reptile pathogens in the United States. Preliminary data suggests that while a few pathogens are the primary drivers of Anuran die-off events in the United States, many others are present and contributing to die-off events. Pathogens like saprolegnia, ichthyophonus, and clinostomum also cause a proportion of anuran die-off events but are reported much less than other more well-known pathogens. As population stressors change, an understanding of historic trends of pathogen occurrence can provide crucial information to inform natural resource managers and guide research for populations already of conservation concern, like amphibians and reptiles.

Oral Presentation #73

A Mortality Event of Double-Crested Cormorants (Phalacrocorax auritus) in Florida Caused by a Novel Eimeria Species

Lisa Shender[1,2], Constance Roderick[3], Kailyn McKibben[4], Susan Knowles[3], Melanie Kunkel[5], Nicole Nemeth[5], Veronica Guzman-Vargas[2], Heather Walden[6], Rebecca Cole[3]

[1]National Park Service, Biological Resources Division, [2]Fish & Wildlife Research Institute, Florida Fish & Wildlife Conservation Commission, [3]U.S. Geological Survey, National Wildlife Health Center, [4]ACCESS Specialty Animal Hospitals, [5]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [6]University of Florida, College of Veterinary Medicine

In November 2017, a double-crested cormorant (DCC) mortality event at The Villages (Sumter County, FL) was reported to the Florida Fish and Wildlife Conservation Commission. Field signs included listlessness and drooped wings in live birds and ~70 dead cormorants. From three carcasses submitted to the National Wildlife Health Center, severe necrotizing enteritis attributed to a novel eimeriid coccidia was determined as the cause of death. We aimed to characterize this Eimeria spp. and to evaluate a geographically distant population of cormorants to better understand the role of the coccidia in disease and its distribution within a limited area of Florida. Through January 2019, we collected DCC carcasses from recurring mortalities at The Villages and from several wildlife rehabilitation centers ~160 km southwest of the mortality site. To facilitate morphological description and phylogenetic analysis, we processed intestinal content from fresh, non-frozen carcasses using Sheather's solution centrifugation followed by oocyst sporulation in 2.5% potassium dichromate. We examined 15 DCCs from The Villages and 13 from wildlife rehabilitation centers. Necrotizing enteritis, characterized histologically by diffuse blunting and fusion of the jejunal villi, was only observed in DCCs from The Villages. An Eimeria sp. Type A was detected in 10 DCCs from this site. A second Eimeria sp. Type B was found in two DCCs from The Villages and two comparison birds. Molecular sequencing of the partial 18s rRNA gene and query of GenBank revealed that Type A and Type B most closely matched E. hermani (97%; 398/410 bp) and E. phalacoraxae (99%; 383/386 bp and 98%; 380/386bp), respectively. Clinical disease from enteric coccidiosis has not been reported in DCCs, and the original source of the coccidia outbreak at The Villages remains unknown. Pathogen transmission and geographic spread may occur via cormorant migration, and further monitoring is warranted to assess population-level effects.

Oral Presentation #74

Hoiho & Malaria: A Real-Time Avian Malaria Warning System to Aid Yellow-Eyed Penguin Conservation Efforts in New Zealand

Chris Niebuhr[1], *Simon Howard*[1]
[1]Manaaki Whenua – Landcare Research

Avian malaria is a mosquito-borne disease that can negatively impact avifauna in New Zealand and globally. Recent studies in NZ report populations of yellow-eyed penguin, or hoiho (Megadyptes antipodes), the rarest penguin in the world, are declining rapidly due to reduced food abundance and impacts from disease, including avian malaria. In 2018 an increase in malaria mortalities was observed in wild hoiho populations, and as a result, various vector control & monitoring options are being considered. Here we present our work on the development of a real-time avian malaria warning system that identifies and predicts conditions conducive for parasite transmission. The output of which is a free, web-based tool used to predict mosquito vector presence and emergence, as well as conditions suitable for avian malaria transmission. The tool uses existing epidemiological models that incorporate minimum threshold temperatures for vector and pathogen development as well as automatically updated temperature data from local weather stations near penguin nesting sites. Mosquito emergence is predicted by using temperature forecast data (e.g. 30 days), which is estimated using both current and historical data. We hope that by using A) historical temperature data, especially from years that have seen impacts to hoiho from avian malaria, we may be able to identify certain trends, or even predictors of high vector presence or transmission and B) projected temperature data, we may be able to predict mosquito emergence, which could aid in overall management and conservation efforts of the species, especially during more vulnerable times of the year (e.g. fledging or moulting). This work also has the potential to translate to other mosquito species and diseases, some of which may not yet be present in NZ (e.g. Ross River virus, West Nile virus, dengue fever).

Oral Presentation #75

Geographic Risk Assessment of Batrachochytrium salamandrivorans Invasion in Costa Rica

Henry C. Adams[1,5], Katherine E. Markham[2,3], Dr. Marguerite Madden[2,3], Dr. Matthew J. Gray[4], Dr. Sonia M. Hernandez[5,6]

[1]Urban Wildlife Institute, Lincoln Park Zoo, [2]Center for Geospatial Research, University of Georgia, [3]Department of Geography, University of Georgia, [4]Department of Forestry, Wildlife and Fisheries, University of Tennessee, [5]Warnell School of Forestry, University of Georgia, [6]Southeastern Cooperative Wildlife Disease Study, University of Georgia

The emergent fungal pathogen, Batrachochytrium salamandrivorans (Bsal), remains undetected in the Western Hemisphere, but poses an enormous threat to American salamander communities, the most diverse in the world. Pathogen risk assessments, based on factors such as environmental suitability for Bsal and salamander species distributions, have been used to identify areas at high risk of Bsal emergence in the American tropics, specifically within Mexico and Costa Rica, two countries with high salamander diversity and extensive histories of chytridiomycosis related amphibian declines. Additionally, Costa Rica has a multi-million-dollar international ecotourism industry that takes visitors to natural areas, a potential route of chytrid emergence. To further contribute to the proactive mitigation of Bsal's impact, we sought to identify specific areas of high risk in Costa Rica based on Bsal ecological suitability, amphibian distributions, and human visitations. We predicted Bsal suitability would be highest in the Cordillera Central and Talamanca and that these areas of Bsal suitability would overlap with protected areas and areas of high human visitation. We developed an Ecological Niche Model (ENM) using Maxent in TerrSet to identify areas ecologically suitable for Bsal and used data provided by the IUCN and Costa Rican Institute of Tourism to evaluate amphibian distributions and human visitations, respectively. Sites with greatest risk had high environmental suitability for Bsal, high salamander biodiversity, and high human visitation. We found that approximately 23% of Costa Rica's landmass is suitable for Bsal, that 27 salamander species, including 4 endangered species, live in areas suitable for Bsal, and specifically identified eight areas in which high suitability intersected with high biodiversity and/or human visitation. Many high-risk sites were within the Cordillera Central and Cordillera Talamanca, and provide logical points to begin surveillance for Bsal and implementation of other mitigation or outreach strategies.

Oral Presentation #76

Maps, Math, and Models: Data-Driven Decisions to Inform Chronic Wasting Disease Surveillance

Corey Mitchell[1], Brenda Hanley[2], Nicholas Hollingshead[2], Rachel Abbott[2], Cara Them[3], Md Sohel Ahmed[2], Krysten Schuler[2]
[1]Desert Centered Ecology, LLC, [2]Cornell Wildlife Health Lab, Cornell University, [3]Cara Them Consulting, LLC

Chronic wasting disease (CWD) is a contagious, fatal disease of cervids that presents significant challenges for wildlife managers and wildlife disease professionals. Enormous effort has been invested in managing this wildlife disease and disease surveillance is an essential part of these efforts. However, as a disease with a distribution that spans administrative boundaries, there is a pressing need for coordination and collaboration of disease surveillance data collection and data management on a larger, regional scale. Through the multi-institution Surveillance Optimization Project for Chronic Wasting Disease (SOP4CWD), we are bringing North American state and provincial wildlife agencies together to develop data-driven solutions to sample CWD more effectively and efficiently. With the use of data science, mapping, and mathematical modeling we have developed interactive software applications to help managers tackle surveillance challenges. The Positives app maps surveillance sampling data to track the occurrence, persistence, and spread of disease within and across administrative boundaries. The Hazard app displays areas where anthropogenic activities might increase the risk of novel prion introduction and pinpoints locations where the disease is likely to persist, once introduced. The Habitat Risk app can be used to identify areas where targeted removals have better potential to lower CWD prevalence in wild herds. The Optimization app can be used to allocate budgets to specific sampling strategies given a dynamic disease landscape. While the current focus of the project is on CWD surveillance in free ranging cervid populations, the approaches and applications presented can be readily adapted to enhance monitoring efforts for other wildlife diseases and other species.

Oral Presentation #77

Data Collection and Management Tools for Wildlife Health Surveillance

Diego Montecino-Latorre[1], Alice Porco[1], Alice Latinne[1], Emily Denstedt[1], Kevin Brown[2], Bevan Federko[2], Kongsy Khammavong[1], Jonathan Palmer[3], Chris Walzer[1], Sarah H. Olson[1], Mathieu Pruvot[1,4]

[1]Wildlife Conservation Society, Health Program, [2]Canadian Wildlife Health Cooperative, [3]Wildlife Conservation Society, Conservation Technology, [4]University of Calgary - Faculty of Veterinary Medicine

Wildlife Health Surveillance (WHS) requires the generation and management of diverse data. For a WHS system to deliver intelligence for management and response, such data (e.g., geolocation, species involved, animals sampled, necropsies, environmental specimens, and samples) must be standardized, safely and securely stored, and easily shared across stakeholders. Therefore, affordable, flexible, sustainable, and easy-to-use digital tools supporting these processes are key.

As part of the WildHealthNet initiative, we piloted SMART for Health (SfH) in conjunction with the Wildlife Health Intelligence Platform database (WHIP) to support data collection and management. SfH is an adaptation of the Spatial Monitoring and Reporting Tool (SMART), a suite of technological tools originally developed for law enforcement in protected areas. SfH supports the smooth digital recording of wildlife health events using smartphones and their real-time communication. SfH has three versions for users with different expertise.

To centrally manage data we customized WHIP, a database developed by the Canadian Wildlife Health Cooperative. New features expand the hierarchical data structure to include observed-only individuals per species, environmental specimens, and diagnostic tests for individual samples. WHIP was also optimized to accommodate diverse surveillance designs or past surveillance efforts, and structured studies.

The current versions of these tools are the outcome of field testing by stakeholders in recently established WHS networks in Laos, Vietnam, and Cambodia; and iterative design, feedback, and improvement cycles. Network members have successfully integrated them into their workflow. Manuals, data glossaries, and training materials are available and translated.

Data structure in SfH and WHIP are consistent and SMART-to-WHIP data transfer is under development. The long-term expertise embedded in SMART and WHIP, their expected sustainability, the current use of SMART in more than 1,000 protected areas globally, and our successful deployment of these tools, underscore SMART-WHIP as a promising choice to support WHS systems globally.

Oral Presentation #78

What's All the Noise about WHISPers? An Overview of Initial Successes and Future Improvements for the USGS NWHC Wildlife Health Sharing Partnership – Event Reporting System

Katherine Richgels, Bryan Richards, Jonathan Sleeman, C. LeAnn White
United States Geological Survey, National Wildlife Health Center

As the number of emerging diseases affecting wildlife continues to increase alongside other threats to natural ecosystems, timely access to wildlife health information can assist with management decisions, resource allocation, and risk communications. The Wildlife Health Information Sharing Partnership – event reporting system is an online platform that was created to allow the wildlife health community (diagnostic laboratories, wildlife disease experts, and natural resource managers) to share information about wildlife health events in near real-time. The platform has been co-developed with numerous partners including US Fish and Wildlife Service, National Parks Service, and many state natural resource agencies to ensure that it meets partner needs. By providing a collaborative tool for partners along with on-line maps, summary information, reports, and access to nationwide data, WHISPers has contributed to increased situational awareness of wildlife health events. As the number of partners contributing data to the system grows, the platform's utility will also grow. In 2021, 588 mortality or morbidity reports were entered into WHISPers with at least 1 event reported from all 50 US states, 4 Mexican states, and 1 Canadian province. In addition, since July 2019 WHISPers was used to help coordinate an international response to two foreign animal diseases, rabbit hemorrhagic disease virus 2 (RHDV2) and highly pathogenic avian influenza (HPAI) outbreaks. In 2022, WHISPers received funding through the American Recovery Plan Act via USFWS to be expanded to serve the Nation as a centralized data portal. To do this, we envision expanding the current architecture to better capture data on live-animal sampling and disease specific surveillance (beyond mortality or outbreak investigations), improve usability, and add interoperability and porting connections.

Oral Presentation #79

Two Years of Hemorrhagic Disease in North Dakota

Charlie Bahnson[1], William Jensen[1], Bruce Stillings[1], Brent Weston[1], David Stallknecht[2], Mark Ruder[2]

[1]North Dakota Game and Fish, [2]Southeastern Cooperative Wildlife Disease Study

Periodic, substantial hemorrhagic disease-attributed mortality events in white-tailed deer (WTD; Odocoileus virginianus) have been documented in North Dakota since at least the 1960s. In a typical year, nearly all reports are confined to a 14-county area southwest of the Missouri River. After a 9-year period of few reports, a moderate to severe hemorrhagic disease outbreak was documented in 2020 with nearly all cases located within traditional areas. Despite this, impacts to hunter harvest success in the 2020 season appeared minimal. EHDV-2 was the only virus isolated during this outbreak. The following year was characterized by severe to exceptional drought, above average temperatures, and a first frost date that was 4-5 weeks later than normal for much of the state. This coincided with a severe outbreak of hemorrhagic disease in WTD, with most reports located at the fringes or outside the traditionally affected areas in southwestern North Dakota. As in 2020, EHDV-2 was the only virus isolated. In three affected hunting units, there was a 63-79% decrease in the number of WTD harvested per square mile in 2021 compared to 2020. These observations, paired with historical serosurveys, illustrate the impact hemorrhagic disease can have in naïve WTD populations under conducive climatic patterns. Other areas of the Northern Great Plains may be more vulnerable to such impacts than previously appreciated.

Oral Presentation #80

Climate Influenced Disease Expansion of Hemorrhagic Disease

Sonja Christensen[1], Brett Skelly[2], Mark Ruder[3], James Crum[2], David Stallknecht[3]
[1]Michigan State University, [2]West Virginia Division of Natural Resources, [3]Southeastern Cooperative Wildlife Disease Study, The University of Georgia

Hemorrhagic disease (HD) of deer is a vector-borne disease caused by either epizootic hemorrhagic disease virus (EHDV) or bluetongue virus (BTV), and can result in high mortality in white-tailed deer, as well as other wild and domestic ruminants. Outbreaks of HD in deer have been increasing in distribution, frequency, and intensity across the United States in the last 20 years. Climate change has been implicated in the emergence of BTV and EHDV in Europe and may be contributing to emergence in North America. Our objectives were to test whether climatic variation in seasonal precipitation and temperature, predicted landscape-level vector habitat, or host attributes explained the probability of mortality of HD in white-tailed deer in West Virginia over a nearly 40-year period. To assess the patterns of HD from 1981 – 2019, we used historic HD occurrence data and quantified predictor variables on a county-level. We used generalized linear mixed models (glmm) to evaluate the presence of HD in West Virginia relative to a set of hypothesis-driven covariates. Within the time period of the study, we documented 181 HD occurrences across the state of West Virginia, with 94 corresponding virus isolations. The majority of HD outbreaks were from EHDV-2, but EHDV-1, 6, and BTV-3 were also isolated. We found evidence that HD occurrence was driven by precipitation and temperature in West Virginia. Specifically, increased July precipitation followed by decreased August precipitation were significant predictors of HD occurrence. Further, increased spring (March, April, and May) temperature had a significant increase in the probability of HD occurrence. Interestingly, variables such as deer density and wetland cover did not explain observed HD presence in our study. Our research provides a clear relationship between climate factors and emerging wildlife disease and may help inform risk communication for wildlife managers to their stakeholders.

Oral Presentation #81

Using Surveillance to Inform Wildlife Disease Management: Mandatory Chronic Wasting Disease (CWD) Sampling in Missouri as a Case Study

Jasmine Batten[1], *Dr. Sherri Russell*[1]
[1]Missouri Department of Conservation

Complex wildlife disease management challenges are often made in the context of significant uncertainty. Surveillance efforts can effectively inform these decisions but often come with short-falls and competing interests and objectives. We will use the Missouri Department of Conservation's (MDC's) experience implementing a mandatory chronic wasting disease (CWD) sampling regulation as a case study to explore the benefits, challenges and shortfalls of using an intensive wildlife disease surveillance program to inform disease management. Since 2016, hunters in CWD Management Zone counties are required to present their deer harvested opening weekend of the fall firearms hunting season for CWD sampling. Over 700 staff sample as many as 20,000 samples annually during this two-day period, imparting a significant agency cost. The information collected through these efforts is critical in informing management, especially post-season targeted culling. Additionally, these efforts contribute to a valuable dataset and provide unexpected communication and outreach benefits. Despite these benefits and significant agency investment, gaps in data persist, agency staff and the public continue to confuse surveillance with management, and CWD-fatigue may be impacting participation and compliance over time. As CWD detections continue in an increasing number of new areas of Missouri and neighboring states, frequent evaluation of mandatory sampling is necessary. Currently, an in-depth evaluation is underway to inform the revision of Missouri's CWD Response Plan, and the re-shaping of mandatory sampling with be a key component in charting a path forward. Sharing the results of this evaluation will further provide real-word evidence of the important of integrating surveillance and disease management.

Oral Presentation #82

Environmental Transmission of Treponeme-Associated Hoof Disease in Captive Elk

Margaret Wild[1], *Zachary Robinson*[1], *Devendra Shah*[1], *Kyle Taylor*[1]
[1]Washington State University

Treponeme-associated hoof disease (TAHD) is an emerging disease of free-ranging elk (Cervus elaphus) in the northwestern U.S. Although Treponema spp. are associated with lesions, the definitive etiology has not been determined and transmission among elk has not been confirmed. Our objective was to determine whether TAHD was transmissible to captive elk through soil contaminated with hooves from affected elk. Six captive elk were housed in individual concrete-lined stalls. Between October 2020 and March 2021, four treatment elk were exposed to an inoculum prepared with hoof homogenate from TAHD positive elk mixed with soil. An aliquot of the inoculum was applied to an abraded interdigital space (IDS) and held in place temporarily with a light foot wrap. Additionally, inoculum was mixed with pen soil. Two control elk were challenged identically except with inoculum prepared using TAHD-negative hooves. Eight challenges were conducted at 2-4-week intervals. At each challenge, hooves were examined for the development of gross lesions, and IDS scrapings were collected for 16S amplicon sequencing of DNA. IDS biopsies were collected at study termination for histologic examination and 16S amplicon sequencing of DNA. Persistent TAHD lesions were observed grossly in all treatment elk by 4 months and progressed to severe lesions by 5.5 months post-study initiation. Three treatment elk were euthanized when they met humane endpoints, while one recovered. Histologic lesions consistent with TAHD were present in all treatment elk whereas the control elk did not develop lesions. Treponema spp. were detected in IDS scraping and biopsies from all treatment elk but not from control elk. Other bacterial families associated with TAHD in free-ranging elk were also overrepresented in treatment elk. Our results provide evidence that TAHD is a transmissible infectious disease. As such, actions that reduce transmission risk can support disease prevention and management.

Oral Presentation #83

Toward Feasible Control of Sarcoptic Mange in Wombats

Scott Carver[1]
[1]University of Tasmania

The control of wildlife disease remains a major frontier for pathogens of welfare and conservation concern. Successful control programs remain few, and successes are rarely feasible or sustainable. Emblematic of this is sarcoptic mange disease. The etiologic agent of mange disease, the Sarcoptes scabiei mite, occurs worldwide, has been documented to infect >100 species across 10 mammalian orders, is a significant animal welfare and conservation issue, and is among the 30 most prevalent diseases of humans (scabies). In Australia this mite was evidently introduced by European settlers and causes individual welfare issues to wombats, periodic epizootics and population declines. Many people (scientists and non-scientists) are engaged in attempts to manage this disease in wombats, but there are significant hurdles to success. While there remains much to be learned about mange in wombats, a growing body of evidence suggests feasible disease control is achievable. I will summarize the efforts of my research group to uncover the impacts and epidemiology of mange disease in wombats, and our efforts to establish feasible in situ disease control. Our research spans within and between individual effects to population-scales, invasion history, modelling, and applied management.

Oral Presentation #84

Epizootic of Quail Bronchitis Virus in Captive Northern Bobwhite Quail (Colinus virginianus) and Masked Bobwhite (C. virginianus ridgwayi) Reveals Apparent Species Difference in Susceptibility

Anne Justice-Allen[1], Bill Radke[2], Hannah Pierce[2]
[1]Arizona Game and Fish Department, [2]Buenos Aires National Wildlife Refuge

Masked bobwhite quail were one of the original species listed as endangered by the United States Fish and Wildlife Service in 1960. The USFWS has maintained a captive breeding program on the Buenos Aires National Wildlife Refuge (BANWR) for more than 20 years. In 2017 a second captive breeding facility was established at the Sutton Avian Research Center in Oklahoma. No antibodies to quail bronchitis were detected in birds hatched from eggs shipped to Sutton. In 2018, as a result of improved habitat conditions, a release program utilizing vasectomized wild-caught Northern bobwhite quail (NOBO) as foster parents was begun. Northern bobwhites were tested for quail bronchitis virus, and salmonella before being shipped to Arizona from Texas. They were quarantined for at least 30 days and dewormed with ivermectin at 200mcg/kg per os prior to being vasectomized and bonded with captive bred masked bobwhite from Sutton and BANWR. In October 2020, 4 of 12 remaining NOBO that had been at BANWR for several months suddenly died. Over the next 6 weeks, 6 of the 8 remaining NOBO died. There were no mortalities in the masked bobwhite housed in the same flight pens. Quail bronchitis virus DNA was detected in tissues of three of the NOBO. Antibodies to quail bronchitis virus were detected by AGID on a subset of exposed masked bobwhite and one NOBO when testing was done 4 months after the event. Antibodies persisted for more than 11 months after the apparent outbreak. No virus was detected in any tissues of birds euthanized 4, and 11 months after the outbreak. No antibodies were detected in masked bobwhite placed in a pen that 2 weeks previously had held infected bobwhite demonstrating a lack of environmental persistence of the virus.

Oral Presentation #85

SARS-CoV-2 Surveillance of White-Tailed Deer in the United States

Jeffrey Chandler[1], Susan Shriner[1], Kristina Lantz[2], Richard Chipman[3], Kelsey Dawson[4], Jourdan Ringenberg[4], Robert Pleszewski[1], Christopher Quintanal[1], Jeremy Ellis[1], Dennis Kohler[4], Mary Killian[2], Timothy Linder[4], Rachel Tell[2], Mia Torchetti[2], Suelee Robbe-Austerman[2], Thomas DeLiberto[1], Julianna Lenoch[4]

[1]National Wildlife Research Center, USDA/APHIS/WS, [2]National Veterinary Services Laboratories, USDA/APHIS/VS, [3]National Rabies Management Program, USDA/APHIS/WS, [4]National Wildlife Disease Program, USDA/APHIS/WS

In response to the findings that SARS-CoV-2 spillover from humans to white-tailed deer has likely occurred across multiple states, the USDA/APHIS/WS National Wildlife Disease Program initiated SARS-CoV-2 surveillance for white-tailed deer in November 2021. Samples have primarily been collected from a combination of hunter-harvested deer and wildlife damage management activities. For each animal sampled, we collected a paired nasal swab and a Nobuto blood spot. Nasal swabs were collected in molecular transport media. All swabs are being tested by RT-PCR targeting both N1 and N2. Samples positive by RT-PCR with Ct < 35 are being submitted to the National Veterinary Services Laboratories for sequencing. Sequencing and serological testing are ongoing. To date, more than 7,000 swab samples from 25 states have been tested and approximately 100 samples have been sequenced. While prevalence varies spatially, overall prevalence across all samples is approximately 18% with SARS-CoV-2 detections in animals sampled in 19 of 25 states. The majority of viral sequences evaluated have been the delta variant of concern (VoC), but alpha VoC and gamma VoC continue to circulate in white-tailed deer in multiple states. While most sequenced samples were collected prior to the omicron wave in the human population, omicron VoC was identified in deer sampled in February. In contrast to the continued circulation of alpha and gamma VoCs in deer populations, we have not found any evidence of the original Wuhan virus persisting in these populations. Phylogenetic analysis suggests a combination of multiple spillovers from humans to deer and long-term circulation in deer (based on phylogenetic branch lengths and SNP analysis). Understanding the spatial extent of SARS-CoV-2 and patterns of circulation in deer is critical to characterizing the role white-tailed deer may play in SARS-CoV-2 ecology.

Oral Presentation #86

Experimental Infection of Wild Canids with SARS-CoV-2

Stephanie Porter[1], *Airn Hartwig*[2], *Helle Bielefeldt-Ohmann*[3], *Angela Bosco-Lauth*[2], *J. Jeffrey Root*[1]
[1]U.S. Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services, National Wildlife Research Center, [2]Department of Biomedical Sciences, Colorado State University, [3]School of Chemistry & Molecular Biosciences and Australian Infectious Diseases Research Centre, The University of Queensland

Determining the susceptibility of wildlife to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an important component of improving our understanding of the virus and its epidemiology, as SARS-CoV-2 is thought to have an animal origin, and infection of numerous mammalian species has been documented. We evaluated wild canids, specifically red fox (*Vulpes vulpes*) and coyotes (*Canis latrans*), for susceptibility to SARS-CoV-2 as these species are widespread in North America, are often found in close proximity to humans, and given that domestic dogs can be infected with the virus. Following intranasal challenge with SARS-CoV-2 red fox become infected, develop mild clinical signs including sneezing and lethargy, and shed infectious virus in both oral and nasal secretions. No gross lesions were appreciated upon necropsy of the red fox; likewise evaluation of tissue samples did not reveal any histopathological lesions consistent with viral infection, though infectious virus was isolated from the nasal turbinates of two out of three fox necropsied on 3 days post-inoculation (dpi). The remaining red fox were held until 28 dpi, and all developed a neutralizing antibody response. Experimentally challenged coyotes were resistant to infection, and did not shed virus or develop a neutralizing antibody response. These results represent the first evidence that red fox are susceptible to SARS-CoV-2 infection, and suggest that red fox may contribute to transmission of the virus.

Oral Presentation #87

Mobilizing Multiple Sectors, Disciplines and Communities at Varying Levels for Pandemic Primary Prevention: The International Alliance Against Health Risks in Wildlife Trade

Hannah Emde[1], Kathrin Norda[1], Johannes Keil[1], Ulrike Buehler[1], Constanze Riedle[1], PhD Kim Gruetzmacher[1,2]

[1]Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ); Global Program 'Support to the International Alliance against Health Risks in Wildlife Trade', [2]Museum für Naturkunde Berlin; Leibniz Institute for Evolution and Biodiversity Research (MfN)

Wildlife is an important and integral part of biodiversity, which is one of the foundations of the health of human civilization. Wildlife is also a source of pathogens, some of which might have the potential to become pandemic in humans and is therefore integral for pandemic primary prevention. In contrast to its relevance, wildlife and environmental considerations are neglected in health security priorities. That is why a multi stakeholder cooperation is needed to work on a synergistic, multi-solving One Health approach.

To address a major driver of disease emergence the German Government launched the "International Alliance against Health Risks in Wildlife Trade". The goals of the Alliance are to substantially reduce the risks of pathogen spillover from wildlife and step up responses to human and animal health risks caused by direct and indirect contact with wildlife across the wildlife trade spectrum. And to enhance respective international and national awareness, knowledge and policies, thus narrowing the gap between science and implementation, while respecting cultural identity, Indigenous rights and integrating traditional knowledge.

The Alliance offers a venue for communication, exchange and matchmaking to facilitate dialogue, transfer knowledge, integrate diverse expertise and disseminate lessons-learned to improve evidence-based regulation. The members of the Alliance form an international, interdisciplinary, and inclusive multi-stakeholder platform, uniting various disciplines and sectors. With its multi-solving approach and currently 90-member organizations that include research institutions, national decision makers, international political and civil society organizations, the Alliance believes in the power of collaboration for a One Health Outcome. It seeks to involve all actors who may offer additional information, evidence, skills and experience towards the Alliance's goals.

Oral Presentation #88

Using a One Health Approach to Structure Federal Coordination on SARS-CoV-2 Transmission in Wildlife

Ria Ghai[1], Ann Carpenter[1], Danielle Buttke[2], Tom Deliberto[3], Laurie Gage[3], Samantha Gibbs[4], Patrice Klein[5], Steven Rekant[3], Teri Rowles[6], Lisa Shender[2], Sara Taetzsch[1], Jonathan Towner[1], Kate Varela[1], Michelle Verant[2], Casey Barton Behravesh[1], Jonathan Sleeman[7]
[1]HHS Centers for Disease Control and Prevention, [2]DOI National Park Service, [3]USDA Animal and Plan Health Inspection Service, [4]DOI Fish and Wildlife Service, [5]USDA Forest Service, [6]NOAA Fisheries Service, [7]DOI US Geological Survey National Wildlife Health Center

The COVID-19 pandemic has highlighted the importance of taking a One Health approach to address shared health threats across the human-animal-environment interface. In the United States, however, oversight for zoonotic diseases is variable and shared across multiple federal agencies. In early 2020, the CDC One Health Office created the One Health Federal Interagency COVID-19 Coordination group (OH-FICC) to share information on the One Health aspects of COVID-19, facilitate connections of operational personnel, and optimize use of government resources. The OH-FICC presently includes ~150 participants from 23 federal agencies. Five OH-FICC subgroups were also formed to convene subject-matter experts. Here, we focus on one of these subgroups: The Wildlife and Zoo subgroup.

The Wildlife and Zoo subgroup, comprised of members from five federal agencies, met 47 times between January 2020 and March 2022. The primary objective of the subgroup was to spread awareness on the risks of SARS-CoV-2 transmission between people and two animal groups: 1) exotic species in zoological facilities; and 2) free-ranging wildlife. To meet objectives, the subgroup developed guidance, tools, and conducted outreach and training. Specific to wildlife, the subgroup generated resources for CDC's COVID-19 website, including FAQs and wildlife testing recommendations, as well as guidance that used innovative application of an occupational health tool, the Hierarchy of Controls, to provide recommendations to reduce the risk of SARS-CoV-2 transmission between people and wildlife. Up-to-date information and guidance were shared regularly with state officials and public audiences.

Clear successes were demonstrated through the subgroup activities. The subgroup facilitated US government collaboration around a collective mission, resulting in shared COVID-19 strategy, messaging, and deliverables. Further, results from OH-FICC participant surveys indicate the OH-FICC structure increased collaboration and coordination, suggesting this mechanism serves as a valuable model to catalyze response to other One Health issues across US government and partners.

Oral Presentation #89

Structural Biology of Zoonotic Diseases: GM/CA@APS, and a PREVENT Proposal

Michael Becker[1], Stephen Corcoran[1], Dale Ferguson[1], Mark Hilgart[1], David Kissick[1], Oleg Makarov[1], Craig Ogata[1], Sergey Stepanov[1], Nagarajan Venugopalan[1], Qingping Xu[1], Shenglan Xu[1], Kristin Ahrens[1], Robert Fischetti[1], Janet Smith[2]
[1]GM/CA@APS, Argonne National Laboratory, [2]Life Sciences Institute, University of Michigan

The COVID-19 pandemic heightens awareness of the need for expanded molecular studies in wildlife and domestic-animal diseases by the broader scientific community. This includes the field of structural biology, where 3-dimensional biomolecular structures provide a foundation for vaccine and therapeutics development. GM/CA@APS is an NIH-funded national user facility for X-ray crystallographic structure determination of biological macromolecules located at the Advanced Photon Source. GM/CA@APS operates two beamlines (23ID-B and 23ID-D), which provide stable, intense X-ray beams of user-selectable size down to 5-micron diameter, an intuitive user interface for experiment control, and an automated pipeline for data processing. These capabilities have enabled experiments with projects that might otherwise seem impossible. For example, structures of numerous membrane proteins have been determined, where crystals are typically grown in lipidic cubic phase and are small, fragile, and optically invisible. Many targeted structures relate to immunology and infectious diseases, such as COVID-19, influenza, Ebola, and Zika. This presentation provides an overview of GM/CA@APS beamline capabilities, along with a display of selected highlights from beamline users. Scientists working with One Health diseases are encouraged to pursue structural-biology efforts and to apply for beamtime (https://www.gmca.aps.anl.gov). Finally, in an effort to bridge wildlife, domestic-animal, and human research fields and institutions, a nascent proposal called PREVENT (Prevent and React to Emerging Viruses Early Next Time) will be discussed.

Acknowledgments: GM/CA@APS has been funded with Federal funds from the National Cancer Institute (ACB-12002) and the National Institute of General Medical Sciences (AGM-12006). This research used resources of the Advanced Photon Source, a U.S. Department of Energy (DOE) Office of Science User Facility operated for the DOE Office of Science by Argonne National Laboratory under Contract No. DE-AC02-06CH11357. The Eiger 16M detector was funded by an NIH–Office of Research Infrastructure Programs, High-End Instrumentation Grant (1S10OD012289-01A1)

Oral Presentation #90

Experimental infection of Mexican free-tailed bats (Tadarida brasiliensis) with SARS-CoV-2

Jeffrey Hall[1], Udeni Balasuriya[2], Mariano Carossino[2], Elizabeth Falendyz[1], Erik Hofmeister[1], Hon Ip[1], Susan Knowles[1], Ariel Leon[1], Carly Malavé[1], Sean Nashold[1], Tonie Rocke[1]
[1]U.S. Geological Survey, National Wildlife Health Center, [2]Louisiana Animal Disease Diagnostic Laboratory and Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University

The SARS-CoV-2 virus originated in wild bats from Asia, and as the pandemic continues into its third year, concerns have been raised that the virus will expand its host range and infect North American wildlife species, including bats. Mexican free-tailed bats (MFTB, Tadarida brasiliensis) live in large colonies in the southern United States, often in urban areas, and as such, could be exposed to the virus from infected humans. We experimentally challenged wild MFTB with SARS-CoV-2 to determine the susceptibility, reservoir potential, and population impacts of infection in this species. Of nine bats oronasally inoculated with SARS-CoV-2, five became infected and orally excreted moderate amounts of virus for up to 18 days post inoculation. These five subjects all seroconverted and cleared the virus before the end of the study with no obvious clinical signs of disease. We additionally found no evidence of viral transmission to uninoculated subjects. These results indicate that while MFTBs are susceptible to SARS-CoV-2 infection, infection of wild populations of MFTBs would not likely cause mortality. However, the transmission of SARS-CoV-2 from MFTBs to or from humans, or to other animal species, is a distinct possibility requiring further investigation to better define.

Oral Presentation #91

Using Population Genetics to Trace the Origins of Ophidiomyces ophidiicola, the Causative Agent of Snake Fungal Disease, in North America

Jeff Lorch[1], Jason Ladner[2], Jonathan Palmer[3], Cassandra Ettinger[4], Jason Stajich[4], Terence Farrell[5], Brad Glorioso[6], Becki Lawson[7], Steven Price[8], Anne Stengle[9], Daniel Grear[1]
[1]U.S. Geological Survey - National Wildlife Health Center, [2]Northern Arizona University, [3]Genencor Technology Center, [4]University of California-Riverside, [5]Stetson University, [6]U.S. Geological Survey - Wetland and Aquatic Research Center, [7]Institute of Zoology, [8]University of Kentucky, [9]Holyoke Community College

Snake fungal disease (SFD; ophidiomycosis), caused by the pathogen Ophidiomyces ophidiicola (Oo), has been documented in wild snakes in North America and Eurasia, and is considered an emerging disease in the eastern USA. However, a lack of historical disease data has made it challenging to determine whether Oo is a recent arrival to the USA or whether SFD emergence is due to other factors. We examined the genomes of 82 Oo strains to determine the pathogen's history in the eastern USA. Oo strains from the USA formed a clade (Clade II) distinct from European strains (Clade I), and molecular dating indicated that these clades diverged too recently (~2,000 years ago) for transcontinental dispersal of Oo to have occurred via natural snake movements across Beringia. A lack of nonrecombinant intermediates between clonal lineages in Clade II suggests that Oo has actually been introduced multiple times to North America from an unsampled source population, and molecular dating suggests that several of these introductions occurred within the last few hundred years. Molecular dating also indicated that the most common Clade II clonal lineages have expanded recently in the USA, with time of most recent common ancestor mean estimates ranging from 1985-2007 CE. The presence of Clade II in captive snakes worldwide demonstrates a potential mechanism of introduction and highlights that additional incursions are likely unless action is taken to reduce the risk of pathogen translocation and spillover into wild snake populations.

Oral Presentation #92

Wildlife Disease Surveillance - Just the Tip of the Iceberg

Anne Ballmann[1], Daniel Walsh[1,2], Robin Russell[1,3], John Grider[1,4], Kyle George[1], Jeffery Lorch[1], David Blehert[1], Katherine Richgels[1]

[1]USGS-National Wildlife Health Center, [2]USGS Cooperative Fish and Wildlife Research Unit-Univ of Montana, [3]U.S. Fish and Wildlife Service, Species Status Assessment, [4]Colorado State University

Disease surveillance, whether in humans, domestic animals, or free-ranging wildlife, is crucial for monitoring the health of our shared environment. Whereas human and domestic animal health enjoy the benefits of robust, proactive funding because of their recognized economic value, wildlife health, particularly when involving non-game species, remains chronically underfunded. As such, documentation, response, and management of wildlife disease tends to be reactive and often relies on opportunistic observations from wildlife managers, concerned general public, and/or a network of partners pooling their expertise and limited resources. A prime example of this is bat white-nose syndrome (WNS), which emerged in North America over a decade ago. Initial surveillance efforts involved large winter mortality events with visible white fungus on muzzles of multiple species of hibernating bats in the northeastern United States. Surveillance expanded to sampling of subclinical bats once the P. destructans (Pd) pathogen was identified and diagnostic assays were developed for its early detection. As the disease continues to spread, national coordinated surveillance allows for generation of key insights by collation and analysis of surveillance data from across North America. In particular, we have refined and improved surveillance for early detection of Pd by identifying target species to sample, best times to conduct surveys, and developing and optimizing environmental and other non-lethal sampling methods. In addition, collated data have been used to gain insights on the rate of Pd spread and impact of WNS at sites across the country, which has led to better understanding of hibernacula types and risk factors associated with Pd detection. Finally, we have shared the archived samples with other researchers who have gained insights into bat population genetics, viral pathogen discovery/surveillance, host species genetics, and other important ecological and conservation questions for bats faced with WNS.

Oral Presentation #93

Knowledge Basis for the Management of CWD in Norway and Current Status: Will We Manage to Eradicate the Disease?

Bjørnar Ytrehus[1], Dr. Michael A. Tranulis[3], Dr. Maria G. Asmyhr[1], Dr. Danica Grahek-Ogden[1], Dr. Merethe Aasmo-Finne[1]

[1]Norwegian Scientific Committee for Food and Environment (VKM), [2]Department of Biological Medicine and Veterinary Publich Health, Swedish University of Agricultural Sciences, [3]Department of Preclinical Sciences and Pathology, Norwegian University of Life Sciences

The discovery of Chronic Wasting Disease (CWD) in both a wild reindeer population and in two moose in another location in Norway in spring 2016 came as a complete surprise to national environmental and animal health authorities, scientists, the reindeer herding community and nature-interested people in general. The authorities immediately requested the Norwegian Scientific Committee for Food and Environment (VKM) to prepare assessments of food safety, risk factors with regard to disease transmission, and relevant management strategies.
In the following years, VKM has delivered seven more assessments, which serves as the knowledge basis for management of the disease in Norway.

The panels preparing the assessments comprised scientist of varying backgrounds and professions, but their mandates were limited to the biological factors related to the disease and its management. This means that societal, cultural and ethical aspects of the disease response not have been considered in any systematic assessment.

The authorities have implemented a nation-wide and comprehensive surveillance programme and a wide range of measures, among them eradication of the affected reindeer. The cases in moose and cases subsequently detected in red deer are regarded as sporadic cases, and are therefore not met with measures of the same magnitude. The recent (2020) finding of a solitary case of CWD in a new, larger population of wild reindeer do, however, increase uncertainty and highlights the differences in opinions that exist between different authorities, groups of scientists, professions and stakeholders.

In this situation, with a comprehensive, long-lasting, exhaustive and resource-demanding process of wildlife disease management, prominent questions emerge; Which needs and considerations should be emphasized, who should be listened to, who has the right to decide what to do and, will we ever manage to eradicate this disease without creating consequences worse than disease persistence and spread?

Oral Presentation #94

Supplementary Salt Licks as Transmission Hot-Spots Between Wild and Domestic Ruminants

Kjersti Selstad Utaaker[1,2], Bjørnar Ytrehus[2,4], Marie L Davey[2], Olav Strand[1], Per Anders Robertsen[3], Geir Rune Rauset[1], Frode Fossøy[1]
[1]Nord University, [2]Norsk Institutt for Naturforskning, [3]Inland Norway University of Applied Sciences, [4]Swedish University of Agricultural Sciences

Sheep farmers place salt-lick stones on natural pastures to supplement their animals' nutrition. The farmers also use these natural gathering spots for easier monitoring of their animals. Wild and domestic ruminants (e.g. moose, red deer, reindeer, sheep) are also attracted to these stones. As a result, species, which otherwise may not interact, are doing so both directly and indirectly. In addition, they continually contaminate the area with faeces and other bodily fluids, which could turn Salt-lick stone areas into potential "hot-spots" of pathogen transmission, such as parasites and prions.

The first European case of the contagious prion disease of cervids, Chronic Wasting Disease (CWD), was confirmed in a Norwegian wild reindeer in 2016. Since then, a few wild ruminants have been found infected, and the wild reindeer area where CWD was discovered has been stamped out, and will remain free of reindeer for the next year.

As prions can persist for a long period of time in the environment, it is important to understand their transmission potential within the Norwegian environment before reintroducing wild reindeer to this area. Transmission may be particularly high in areas where animals tend to gather, such as salt licks, and although wild reindeer generally range in areas of low animal density in the high mountains, they are attracted to salt-lick stone sites.

By using endoparasites as a proxy, salt-licks` hot-spot potential was investigated using traditional parasitology methods on soil and animal samples, as well as environmental DNA analyses.
Results indicate that salt-licks cumulate pathogens on natural pastures for disease transmission both within and between wild and domestic ruminants, representing possible implications for domestic sheep and wild reindeer health management.

Oral Presentation #95

Chronic Wasting Disease Show and Tell: Gauging Hunters' Willingness to Adopt Management Practices

Sonja Christensen[1], Krysten Schuler[2], Danielle Ufer[1], Nick Pinizzotto[3], David Ortega[1]
[1]Michigan State University, [2]Cornell University, [3]National Deer Association

Chronic wasting disease (CWD) threatens wild cervid populations and the funds available to manage and conserve wildlife. Despite the increasingly widespread apparent prevalence of this disease, few options to control or manage it have been successful. Many of the disease management options available to state wildlife agencies rely on deer hunters complying with new regulations or voluntarily changing behavior following suggested best management practices for harvesting and handling potentially infected animals. Research in behavioral psychology has shown improved success with changing human behavior when subjects are provided with visual demonstrations of the desired action. We created short (< 2 min) videos for deer hunters that demonstrate a series of best management practices for reducing the spread of CWD. We assessed the impact of these videos on hunter intent to accept management actions via a survey before deer season in October 2020, and actual behavior via a follow-up survey of the same individuals in February 2021 (after the deer season). To assess each information treatment against a control, we randomly selected hunters from our total sample to participate in each survey group, including groups that received no information treatment or a placebo treatment. We received 1,450 completed surveys with full baseline, initial intent, and endpoint responses from across the U.S. We evaluated factors including landownership type, region, and CWD proximity. We found that the video treatments had a significant effect on behavioral intent, but not on actual behaviors. Behavioral intent varied based on the behavior being demonstrated in the video treatment. Our survey results and hunter behavior assessment provide critical insight into CWD management adoption and the opportunities for behavior change relative to disease mitigation strategies. Understanding how information campaigns result in differences in hunter behavior is vital for evaluating and targeting successful CWD management options and prioritizing resources.

Oral Presentation #96

Broader Participation in Wildlife Health Research Endeavours: Why Do We Need It, Who Do We Need and What Could It Look Like?

Andew Peters[1,2], Dr Lisa Adams, Dr Scott Carver[3]
[1]Charles Sturt University, [2]Gulbali Institute, [3]University of Tasmania

We have entered the Anthropocene, a period of significant global social and environmental change. Human societies are increasingly subject to the emergence of wicked socio-ecological problems that threaten our values, our ways of life and even our survival. These problems are intractable and refractory to simple, unidimensional solutions. Wildlife health research endeavours that aim to make progress against these problems might look to the transformational changes underway in response to complex socio-ecological problems, with many new systems-based approaches, movements and fields of practice emerging in the past few decades. We identified a common focus on broader participation in the research endeavour amongst these emerging fields of practice.

We explore why broader participation is considered important, and who that participation might extend to in the context of wildlife health. We also imagine what such participation might look like in a wildlife health research endeavour.

We invite each other to reflect on our own role as participants in wildlife health research aiming to 'solve' wildlife health problems and the intersections of our participation with environmental and social justice, and to join us in re-imagining research endeavours that aim to justly deliver tangible responses to the emerging socio-ecological problems we collectively face.

POSTER PRESENTATIONS

Poster Presentation #97

Investigating the Relationship Between Mercury, Urbanization, and Salmonella spp. in the American White Ibis (Eudocimus albus)

Matthew Tatz[1,2], Dr. Sonia Hernandez[1,2,3], Dr. Stacey Lance[1,4,5]
[1]University of Georgia, [2]Daniel B. Warnell School of Forestry and Natural Resources, [3]Southeastern Cooperative Wildlife Disease Study, [4]Savannah River Ecology Laboratory, [5]Odum School of Ecology

In nature, individuals are challenged simultaneously by both contaminants and pathogens, yet avian disease studies have seldom investigated this relationship. Methylmercury (MeHg), the toxic and organic form of mercury (Hg), is a common wetland contaminant that can bioaccumulate in birds and can cause immunosuppression, potentially increasing susceptibility to gastrointestinal colonization with enteric pathogens such as Salmonella. Immunosuppression can lead animals to start shedding Salmonella, shed at higher rates, or develop clinical disease when already infected. Previously, we found American white ibis (Eudocimus albus) that forage in urban habitats shed a higher prevalence of Salmonella and have a less diverse gut microbiome than those that forage in natural wetlands. Florida has high annual atmospheric Hg deposition and unregulated vehicular Hg emissions which may contaminate urban habitats. Therefore, urbanized ibis may have higher Hg exposure and, subsequently, increased immunosuppression. We used a Direct Mercury Analyzer 80 (DMA-80) to analyze the total Hg (THg) concentration of ibis feathers (n=94) from individuals across capture sites (0.00 – 67.6% urbanization) to determine if Hg is positively correlated with urbanization and the Salmonella status (shedding/not shedding) of ibis. We found Hg levels ranged from 0.22 – 8.47 mg/kg dw (PPM), consistent with levels previously found to negatively affect ibis reproduction. Contrary to our expectations, Hg concentrations significantly decreased with increasing urbanization (R^2=0.327, p=0.026, R= -0.608), possibly due to high sulfate concentrations in natural wetlands surrounding the Everglades Agricultural Area. There were no significant differences in Hg concentration between ibis shedding Salmonella and those that were not, among low (p=0.622), high (p=0.758), or overall (p=0.596) urbanization sites, suggesting immunosuppression caused by Hg has no impact on Salmonella infection or colonization. Together, our results indicate that urban water bodies may have less MeHg bioavailability than natural wetlands and that MeHg may not impact avian Salmonella dynamics.

Poster Presentation #98

Lead (Pb) and its Health Effects in Scandinavian Brown Bears (Ursus arctos)

Hydeskov HB[1], Arnemo JM[2], Fuchs B[2], Rodushkin I[3], Boesen AH[2], Evans AL[2], Miller AL[2], Græsli AR[2], Thiel A[2], Lloyd Mills C[4], Gentle LK[1], Zedrosser A[5], Kindberg J[6], Uzal A[1]

[1]Nottingham Trent University, [2]Inland Norway University of Applied Sciences, [3]ALS Scandinavia, [4]Nottingham Trent University, [5]University of South-Eastern Norway, [6]Norwegian Institute for Nature Research

The Scandinavian brown bear (Ursus arctos) is an omnivore that consumes a variety of food items including berries, ants, carrion and ungulates. It lives in areas widely used by large game hunters and it is therefore likely to be exposed to lead (Pb).

We used inductively coupled plasma mass spectrometry (ICP-MS) to study Pb exposure in Scandinavian brown bears in order to assess potential negative health effects. We found a mean blood Pb concentration of 88.9 µg/l (SD: 36.6 µg/l; range: 20.35-220.5 µg/l; n=304), more than seven times higher than the European Food Safety Authority's threshold for developmental neurotoxicity (12 µg/l blood). However, no significant correlations were found between blood Pb concentration and standard haematological or biochemical parameters.

We found significant correlations between blood Pb concentrations of suckling cubs and their mothers, and between blood and milk Pb concentrations of lactating females, indicating that dependent cubs are exposed to Pb in the milk throughout their suckling period. Blood Pb concentration in sub-adult bears (aged 2-3 years, n=16) was significantly higher during hibernation compared to the active period. Although Pb was found in the kidney and liver of hunted bears (N=56), no Pb-associated pathology was identified in these organs by routine histopathology.

The Scandinavian brown bear population is highly exposed to environmental Pb, but the potential negative health effects in this species remain unclear. Likely Pb sources include ammunition residues in gut piles from hunted ungulates and contaminated soil from leaded gasoline and industry. Pb exposure continues to be a global One Health issue and further research into the sources, pathways and potential health effects in wild mammals is needed.

Poster Presentation #99

Stakeholder Attitudes and Perspectives on Wildlife Disease Surveillance as a Component of a One Health Approach in Thailand

Serena George[1], Moniek Smink[1], Nareerat Sangkachai[3,4], Anuwat Wiratsudakul[3,4,5], Walasinee Sakcamduang[3,5], Sarin Suwanpakdee[3,4,5], Jonathan Sleeman[2]
[1]University of Wisconsin-Madison School of Veterinary Medicine, [2]USGS National Wildlife Health Center, [3]Thailand National Wildlife Health Center, Faculty of Veterinary Science, Mahidol University, [4]The Monitoring and Surveillance Center for Zoonotic Diseases in Wildlife and Exotic Animals, Faculty of Veterinary Science, Mahidol University, [5]Department of Clinical Sciences and Public Health, Faculty of Veterinary Science, Mahidol University

Coordinated wildlife disease surveillance (WDS) can help professionals across disciplines effectively safeguard human, animal and environmental health. The aims of this study were to understand how WDS in Thailand is utilized, valued, and can be improved within a One Health framework. An online questionnaire was distributed to 183 professionals (55.7% response rate) across Thailand working in wildlife, marine animal, livestock, zoo animal, environmental, and public health sectors. Twelve semi-structured interviews with key professionals were then performed. Three-quarters of survey respondents use WDS data and information, and sectors agreed that disease control (25.5% of respondents), early threat detection (18%), identification of zoonotic diseases (15.0%), and trust among sectors (14.7%) are the most beneficial outcomes of WDS. Accessing data collected by one's own sector (64.7% of survey respondents) was identified as the most challenging (50%) yet the least difficult to improve (88.3%). Having legal authority to conduct WDS was the second most frequently identified challenge. Interviewees explained that legal documentation required for cross-institutional collaborations poses a barrier to efficient communication and use of human resources. Survey respondents identified allocation of human resources (75.5%), adequate budget (71.6%), and having a clear communication system between sectors (71.6%) as highest priority areas for improvement to WDS in Thailand. Authorization from administrative officials and support from local community members were identified as challenges during the in-person interviews. Future outreach should be directed towards these groups. As 42.9% of marine health professionals had difficulty knowing whom to contact in other sectors and 28.4% of survey respondents indicated that communication with marine health professionals is not applicable to their work, connecting the marine sector with other sectors should be a priority. The information gathered from this study identified priorities for addressing the current challenges in the establishment of a general WDS system and information management system in Thailand.

Poster Presentation #100

Analysis of the Situation of Wild Animals for Pets in Brazil

Victória Lage[1], Rafael Lage[1], Gabriel Lage[1], Ricardo Borovoski[1], PHD Elisângela Sobreira[1]
[1]Volunteer Center for the Rehabilitation of Wild Animals

Wild animals that, through empathy, generate a feeling of admiration and tenderness, with the consequent desire for possession, end up becoming pets. The desire to have wild animals is associated with a feeling of proximity to nature, a place where it transmits peace and invigorates the energies for day-to-day tasks. Regardless of the reason, buying or removing animals from nature, are attitudes that have been triggering a drastic threat to the fauna in general with the consequent decrease in biological diversity, and their abandonment is considered mistreatment of animals prescribed in 9605/98 Law of Environmental Crimes in Brazil. The objective of this work was to understand how the relationship between individuals and wild animals raised as pets occurs, more specifically how this relationship underlies the mistreatment of these animals; Evaluate which species is most sought after to be raised as pets; Evaluate the impacts resulting from the subtraction of these animals within the Ecosystem, regarding the conservation of species and the environment. Data were collected through analysis of IBAMA files. As a result, wild birds led the ranking of animals raised as pets 67%, followed by reptiles 21% and mammals 12%. Birds are easier animals to be raised as a companion due to their ease of handling and containment, as they require less nutritional care, are small in size, can be raised in an apartment, and are easier to domesticate. It is important to emphasize that, however, accustomed these wild animals are to humans, they are not domesticated and may show a certain aggressiveness, arising from the natural behavior of the species, and when they feel threatened, their immune resistance decreases, causing the multiplication of microorganisms. that are part of their natural microbiota. Thus, they will present clinical symptoms and will be able to transmit diseases to their tutors.

Poster Presentation #101

Application of the Heuristic-Systematic Model to Risk Perceptions about Wildlife Disease

Kyle Smith[1,3], Dr. Adam Landon[2,1], Dr. David Fulton[3,1]
[1]University of Minnesota, [2]Minnesota Department of Natural Resources, [3]Minnesota Cooperative Fish and Wildlife Research Unit

The heuristic-systematic model (HSM) suggests that when presented with a choice, individuals will use either heuristic or systematic processing modes, or a combination of both, to arrive at a judgment. While previous studies have demonstrated the merit of the HSM in risk research, it has not been applied in the context of wildlife disease. In this paper, we evaluate the HSM model in the context of hunter perceptions towards chronic wasting disease (CWD), a neurological disease found in members of the family Cervidae. CWD has emerged as a top concern among wildlife managers, as it threatens the health of wild cervid populations and the flow of benefits humans derive from them. Data were obtained from surveys of hunters that harvested inside and outside of Disease Management Areas (DMAs) across the state of Minnesota. Our results have implications for the communication efforts related to CWD management and stakeholder engagement.

Poster Presentation #102

Effects of Filter Paper Strip Storage Duration and Method on Anti-West Nile Virus Antibody Detection in Northern Bobwhite (Colinus virginianus) and Wild Turkeys (Meleagris gallopavo)

Melanie R. Kunkel[1], Roy D. Berghaus[2], Daniel G. Mead[1], Kayla G. Adcock[1], James A. Martin[3], Mark G. Ruder[1], Nicole M. Nemeth[1]

[1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [2]Department of Population Health, University of Georgia, [3]Warnell School of Forestry and Natural Resources and Savannah River Ecology Laboratory, University of Georgia

Blood sample collection utilizing Nobuto filter paper strips is a common sampling method for free-ranging wildlife due to logistical advantages that allow for expanded sampling opportunities. Despite widespread use, there is minimal research evaluating the effects of storage duration and method on the ability to detect antibodies, particularly for West Nile virus (WNV) research in free-ranging avian species. We collected serum and blood-soaked Nobuto filter paper strips from northern bobwhite (Colinus virginianus; n = 20) and wild turkeys (Meleagris gallopavo; n = 23) experimentally infected with WNV to evaluate the influence of different storage methods on plaque reduction neutralization test (PRNT) sensitivity. The storage methods of the filter paper strips included: immediate elution of sample after blood drying, storage at -20°C for 3 months, storage at -20°C for 6 months, storage at room temperature for 3 months, and storage at room temperature for 6 months prior to filter paper strip elution. All eluted samples and serum from each bird were co-titrated via PRNT to determine the endpoint antibody titer of each sample. Antibody titers subsequently were compared between eluted samples and serum and among eluted samples that underwent the various storage conditions. Serum antibody titers for all WNV-inoculated birds ranged from 10 to 5120. Antibody titers decreased 2–16-fold in samples eluted immediately, resulting in 86% sensitivity. Collectively, sensitivity ranged from 44% (room temperature, 6 months) to 84% (-20°C, 3 months), suggesting that the storage duration and method decreases the sensitivity of antibody detection by PRNT, particularly in birds with low serum antibody titers, such as the northern bobwhites in our study. Our results suggest that WNV seroprevalence studies that use filter paper strips may result in biased low seroprevalence results if filter paper strips are stored at room temperature for ≥3 months prior to elution in these two species.

Poster Presentation #103

Spatial Methods for Describing Wildlife Health in Ontario

Daniel Bayley[1], Shoshanah Jacobs[2], Claire Jardine[1,3], Emmanuelle Arnaud[4,5], E Jane Parmley[1,3]
[1]Ontario Veterinary College, University of Guelph, [2]College of Biological Sciences, University of Guelph, [3]Canadian Wildlife Health Cooperative, [4]Ontario Agricultural College, University of Guelph, [5]G360 Groundwater Research Institute

Healthy wildlife provides ecosystem services, cultural value, and food security, and they are also less likely to be a source of pathogens to humans and domestic animals. Determinants of wildlife health have been described but less is known about how wildlife health status varies across the landscape.

The objective of this study was to develop a method for describing wildlife health spatially in Ontario, Canada. Data sources with information about wildlife health were identified, including provincial hunting data, wildlife rehabilitation intake records, wildlife disease surveillance programs and citizen science applications. Data were extracted from these sources and used to identify and develop new health indicators for nine harvestable species: white-tailed deer, moose, black bear, wolf, coyote, raccoon, wild turkey, mallards, and American black ducks. These health indicators were then normalized and combined within and across species, and used to produce maps depicting the state of wildlife health across Ontario.

We found that wildlife health varied spatially across Ontario. For example, indicators of wildlife health scored higher in the southern Canadian shield area, and lower in northwestern Ontario. Indicators of wildlife health also tended to score lower in the most populous regions of the province. Wildlife health also varied by species and data source.

These indicators and maps can be used to direct future research into factors affecting wildlife health. Combining this work with knowledge of the determinants of human health on the same scale may help identify shared health determinants between humans and wildlife, ultimately leading to better health promotion strategies for all species, and a better understanding of how the health of human and wildlife species are connected locally. Through allowing us to identify healthy and unhealthy wildlife populations spatially, this project is the first step in achieving this objective.

Poster Presentation #104

Methods Used to Identify Novel Antigens for Serological Diagnosis of Parelaphostrongylus tenuis Infections in Cervid Hosts

Jessie Richards[1], *Stephen Kania*[1], *Katherine Kurth*[1], *Brad Miller*[2], *Lisa Muller*[1], *Richard Gerhold*[1]
[1]University of Tennessee, [2]Tennessee Wildlife Resource Agency

Parelaphostrongylus tenuis is an important parasitic nematode causing neurologic impairment in a variety of ungulates both domestic and wild. This parasite has been particularly detrimental to moose and elk populations across North America where their ranges increasingly overlap with the definitive host, white-tailed deer. Antigen identification for development of an antemortem serological assay was accomplished using previously undescribed methods. Proteins extracted from P. tenuis organisms were bound to polyclonal antibodies purified from seropositive moose. These complexes were then analyzed using mass spectrometry and liquid chromatography to obtain amino acid sequences that were then cross-referenced to an assembled transcriptome. An antigen of interest was assessed for immunogenic epitopes and subsequently synthesized into 10-mer synthetic overlapping peptides to represent these regions. This antigen was coated onto plates and used to detect antibodies in collected sera in an enzyme-linked immunosorbent assay. This serological assay was applied to a well-observed subset of Tennessee elk revealing presence of P. tenuis antibodies in an estimated 41% (n=11) of Tennessee elk. Application of this assay to elk herds across North America will help direct the management of wild cervid populations and better inform us of this parasite's geographic distribution.

Poster Presentation #105

Comprehensive, Fine-Scale Spatial Models Predict the Presence and Abundance of Blacklegged Ticks in Ohio

Allison Williams[1], PhD Risa Pesapane[1], PhD Bill Peterman[1]
[1]The Ohio State University

Lyme disease was first identified in 1975 in Lyme, Connecticut, USA and has since increased in incidence and distribution at an alarming rate. In the present day, Lyme disease is the most common vector-borne disease in the United States with over 400,000 estimated cases per year. The increase in Lyme disease incidence is attributed to the expansion of the vector, Ixodes scapularis (blacklegged tick). Blacklegged ticks have increased in presence and abundance across much of the eastern United States and southern Canada due to a confluence of environmental factors, including the expansion of host availability, increased forested habitat, and climate change. Local health departments are able to inform Lyme disease risk in counties and townships by active surveillance of ticks throughout the year, however, the funds, time, and personnel to do so effectively are often unavailable. Predictive models can reduce the efforts required to assess tick and pathogen presence by predetermining where ticks are likely to be. Despite this, previously developed predictive models for blacklegged ticks over the past two decades have failed to predict the widespread invasion of blacklegged ticks seen today. Additionally, due to data limitations, these models often predict at the county resolution when a finer scale would benefit targeted surveillance efforts. The recent availability of fine-scale climate and landscape data as well as more accurate, spatially explicit modeling techniques have the potential to improve efforts to model the presence and abundance of blacklegged ticks. I have developed fine-scale (< 1 km2), comprehensive spatial models predicting the presence and abundance of blacklegged ticks in Ohio using R-INLA, incorporating climate, host, and landscape characteristics. These results can direct future modeling efforts in other regions and for other tick species, better informing local health departments and communities of their vector-borne disease risk.

Poster Presentation #106

Viral Copy Number Detected by a Novel Diplex Probe-Hybridizization Quantitative PCR For Miroungine Gammaherpesvirus 3 Significantly Correlates with Lymphoma in Northern Elephant Seals (Mirounga Angustirostris)

Molly Horgan[1], Dr. Margaret Martinez[2], Linda Archer[1], Dr. Pádraig Duignan[2], Dr. James Wellehan[1]
[1]Department of Comparative, Diagnostic, and Population Medicine, University of Florida, College of Veterinary Medicine, [2]The Marine Mammal Center, 2000 Bunker Road

Recently, a novel gammaherpesvirus, Miroungine gammaherpesvirus 3 (MirGHV3), was described in two juvenile elephant seals (Mirounga angustirostris) with diffuse large B cell lymphoma. This is the third herpesvirus described in elephant seals. The goals of this study were to develop and validate a quantitative PCR for rapid detection of MirGHV3, and to look at association with lymphoma. We developed a duplex probe-hybridization quantitative PCR with MirGHV3 DNA polymerase (pol) as the target gene. Each primer-probe combination was cross-validated against the other. Interference was not seen when they were run in the same well as a duplex assay. Twenty-three samples from five northern elephant seals were run using the duplex assay. Viral DNA was detected by the assay in 9/9 (100%) of tissues affected by lymphoma, and in 6/14 (42.9%) of samples from tissues unaffected by lymphoma. There was a strong correlation between viral copies detected with each of the assays ($p=0.0002$). Viral load was significantly higher in tissues affected by lymphoma than those unaffected ($P < 0.0001$). This is consistent with a role of MirGHV3 in oncogenesis in northern elephant seals. The qPCR developed has utility for further investigations of MirGHV3.

Poster Presentation #107

Investigating Viruses Associated with Freshwater Mussel Mass Mortality Events

Jordan Richard[1,2], Eric Leis[3], Christopher Dunn[1], Cleyo Harris[5], Rose Agbalog, Lewis Campbell, Susan Knowles, Diane Waller, Joel Putnam[4], Tony Goldberg[1]

[1]Department of Pathobiological Sciences and Freshwater & Marine Sciences, University of Wisconsin-Madison, [2]Southwestern Virginia Field Office, US Fish and Wildlife Service, [3]La Crosse Fish Health Center, Midwest Fisheries Center, US Fish and Wildlife Service, [4]Upper Midwest Environmental Sciences Center, U.S. Geological Survey, [5]Michigan Department of Natural Resources, [6]National Wildlife Health Center, U.S. Geological Survey

Freshwater mussels (Unionida) are among the world's most imperiled taxa, but the relationship between freshwater mussel mortality events and infectious disease is largely unstudied. We surveyed viromes of a widespread and abundant species (mucket, Actinonaias ligamentina) expe-riencing a mortality event of unknown etiology in the Huron River, Michigan, in 2019-2020 and compared them to viromes from mucket in a healthy population in the St. Croix River, Wisconsin and a population from the Clinch River, Virginia and Tennessee, where a mortality event was affecting the congeneric pheasantshell (A. pectorosa) population. We identified 38 novel viruses, most of which were associated with mussels collected during the mortality event. Viral richness and cumulative viral load were significantly higher in moribund mussels from the Huron River than in healthy controls from each of the three populations. Our results demonstrate significant increases in the number and intensity of viral infections for freshwater mussels experiencing mortality events, whereas individuals from healthy populations have a substantially reduced virome comprising a limited number of species at low viral loads.

Poster Presentation #108

Evaluating the Effectiveness of Using Water Filtration Methods to Detect the Chytrid Fungus, Batrachochytrium dendrobatidis

Leah Joyce[1], Dr Dan Grear[2], Dr Angie Luis[1], Dr Winsor Lowe[1]
[1]University of Montana, [2]USGS National Wildlife Health Center

The chytrid fungus, Batrachochytrium dendrobatidis, has been implicated as one of the main drivers of global amphibian declines since its discovery two decades ago. Current monitoring initiatives of chytrid presence in the field rely on catching, handling, and swabbing amphibians, then processing the skin swabs in a lab to detect the fungus DNA via qPCR. Water filtration methods coupled with highly-sensitive molecular methods to detect environmental DNA are a relatively recent development for monitoring presences of organisms in the environment. Chytrid fungus can be detected in the absence of amphibians sampling because it has a free-living life stage. Previous studies have detected chytrid fungus DNA in water samples, however, the factors that influence detection probability and occupancy is largely unknown, so the implementation of these methods has been limited compared to the more common swabbing method. Following a multi-year USGS chytrid fungus survey across the US, we analyzed detection data from 3 years of water filtration efforts to understand the detection probability of filters in the field, as well as that of their qPCR counterparts in the lab. We found that the detection probability of filters increases with the volume of water filtered. In addition, we found that Bd occupancy is affected by temperatures over the week leading up to sampling, as well as hydroperiod and flow. This study provides a vital insight to the use of filtration methods to detect chytrid fungus, particularly as their use would save time and effort compared to swabbing methods and assist in the re-introduction of amphibians that have gone extinct in the wild due to chytrid fungus.

Poster Presentation #109

Assessing Sampling Technique for Mycoplasma bovis in American Bison (Bison bison)

Katherine Schwartz[1], Erin Schwalbe[1], Maggie Johnson[2], Tesia Lin[1], Danielle Buttke[3], Tom Bragg[4], Kerry Sondgeroth[1,5], Jennifer Malmberg[1,5]

[1]University of Wyoming, Department of Veterinary Sciences, [2]Wyoming Game and Fish Department, Wildlife Health Laboratory, [3]National Park Service Biological Resources Division, [4]Turner Institute of Ecoagriculture, [5]Wyoming State Veterinary Laboratory

Mycoplasma bovis (M. bovis) is an important bacterial pathogen of cattle that most commonly causes pneumonia, mastitis, arthritis, and otitis media. M. bovis has more recently emerged as a primary pathogen in American bison (Bison bison), causing significant morbidity and mortality. Bison rarely show clinical signs until the disease is quite advanced, and some evidence suggests that M. bovis can be carried asymptomatically in bison at low prevalence. Asymptomatic infections could be important sources of outbreaks, and thus detection of such infections is critical to disease management. However, little is known about the optimal sampling technique for ante-mortem detection of M. bovis in bison. While nasopharyngeal swabbing is recommended in cattle, support for this technique has not been established in bison. Our research addresses the need for a standardized sampling technique for M. bovis detection in bison. We compared paired superficial nasal swabs to deep nasopharyngeal swabs in opportunistically sampled sick and apparently healthy bison screened in triplicate by PCR. Thus far, we have detected M. bovis in 35 out of 535 (6.5%) bison from eleven herds, seven of which had a recent history of clinical signs consistent with mycoplasmosis. Of bison testing positive on either sample type, M. bovis was detected in 85.7% of nasopharyngeal swabs (n=30) and 42.8% of nasal swabs (n=15). Agreement between swabs for positive bison was 28.6% (n=10), and the kappa coefficient was 0.42 (95% CI 0.239 to 0.607), interpreted as moderate agreement between sampling methods. These preliminary results suggest that nasopharyngeal swabs may be recommended for ante-mortem detection of M. bovis in bison, though additional research is needed. With increasing concern for the impact of M. bovis on bison, standardized sampling and detection methods will be necessary to minimize both economic loss and ecological threats to this iconic wildlife species.

Poster Presentation #110

Integrative Conservation of the Baird's Tapir as a Flagship Species to Protect a Fragmented Landscape in Northwestern, Costa Rica

Jorge Rojas[1,2], Dr. Sonia M. Hernandez[1,3], Dr. Richard Chandler[1], Dr. Jeffrey Hepinstall-Cymerman[1], Dr. Theodore Gragson[4], Dr. Christopher Jordan[5]

[1]Warnell School of Forestry and Natural Resources, The University of Georgia, [2]Costa Rica Wildlife Foundation, [3]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, [4]Department of Anthropology, [5]Re: Wild

Biological Corridors such as the Tenorio-Miravalles (TMBC), in Northwestern Costa Rica, exhibit frequent human-wildlife interactions. In this Corridor, the endangered and elusive Central American tapir (Tapirus bairdii) has shifted its behavior, with tapirs moving outside protected areas, and traveling through small-scale farms, interacting with people and domestic animals while consuming crops during the day. Although infectious diseases have not been a significant concern for free-living tapirs, this shift in behavior may change their pathogen dynamics and has led to negative interactions with people (vehicular accidents, retaliation poaching etc). We aimed to: 1) monitor tapir locations, movement patterns, resource selection and hotspots of human-tapir conflict by outfitting tapirs with radiocollars, 2) develop a community-based camera trap network to evaluate the impact of conservation actions, and 3) reduce conflicts by implementing and assessing mitigation strategies across TMBC. Since July 2021, we have radiocollared 5 tapirs and thus far have found high individual variation of home ranges size and habitat use including primary forests, regeneration patches, rivers, crops and pasture use in the TMBC. Through both radiocollar and camera data, we have determined human-tapir interaction hotspots and camera traps have also documented 20 species of mammals utilizing the TMBC, some of which are also endangered (e.g. puma, Puma concolor; red-brocket deer, Mazama temama). We documented tapir-friendly practices already implemented by local farmers including selective fencing, crop rotation, etc., and are currently implementing and assessing the response of tapirs to electric fencing and natural repellents. After one-year, electric fencing appears as the most efficient method for excluding tapirs from crops. Conservation of tapirs has been focused on protection of large, protected areas, but viable, connected populations will require research and protection in adjacent corridors.

Poster Presentation #111

A Preliminary Evaluation for Subclinical Renal Disease using Serum Creatinine in California Sea Lions, Zalophus californianus, exposed to Domoic Acid

Dr. Ami Krasner, Dr. Padraig Duignan, Dr. Cara Field, Dr. Spencer Fire, Dr. Kelli Hunsucker, Dr. Maggie Martinez, Dr Glenn Miller
[1]Florida Institute of Technology

Harmful algal blooms are increasingly identified worldwide as agents responsible for acute and chronic health effects in species that contact or consume contaminated water or prey. Since 1998, California sea lions (CSL), Zalophus californianus, have stranded due to the neurotoxic effects of domoic acid (DA). Research has historically focused on the characterization and management of the severe central nervous system (CNS) symptomology. Recent publications suggest that further exploration of the kidneys as sites of DA-related pathology is warranted. While overt kidney toxicity is not evident in CSL after acute or chronic DA exposure, there are no focused studies evaluating for subclinical kidney damage in marine wildlife. Serum creatinine is a commonly measured renal biomarker in a variety of species where minor changes within or above the reference interval can signify declining function. Retrospective datasets provided by The Marine Mammal Center (TMMC), Sausalito, CA, were utilized to evaluate serial serum creatinine measurements, along with blood eosinophil counts (an established biomarker for DA exposure), in CSL undergoing rehabilitation. CSL diagnosed with DA toxicosis (DA group) were compared to CSL with trauma-related injuries or other illness. CSL with known Leptospirosis infection or amyloidosis were excluded from the study. Statistical analysis, including RMANOVA, determined serum creatinine values increased temporally and were higher in the DA group than the control group. There was also a strong negative relationship between initial eosinophil counts on admit to TMMC and percentage change in serum creatinine during rehabilitation. Further research is recommended to elucidate if increased serum creatinine over time in CSL with DA toxicosis is related to subclinical renal pathology versus other causes, and whether eosinophilia may have a prognostic role in CSL with DA. Unappreciated kidney insufficiency may impact individual and population health and fitness.

Poster Presentation #112

Risky Business: Deer Behavior and Chronic Wasting Disease

Samantha Courtney[1], Dr. Dwayne Etter[2], Dr. Sonja Christensen[3], Dr. David Williams[1]
[1]Boone and Crockett Quantitative Wildlife Center-Michigan State University, [2]Michigan Department of Natural Resources, [3]Christensen Lab for Wildlife Population Health-Michigan State University

Since the discovery of chronic wasting disease (CWD) in cervids in the 1960s, and despite management efforts, this fatal disease continues to expand its range in North America. White-tailed deer (Odocoileus virginianus) are projected to have long-term population impacts as a direct result of CWD. Transmission pathways for CWD have been well characterized, but we do not fully understand one of the most important factors for transmission: direct physical contact. Previous studies have made assumptions of how frequently deer come into direct physical contact based on the proximity of radio-collared individuals, but this information is not precise and does not account for potential contacts among uncollared deer. Additionally, deer behavior likely differs depending on group size and composition, and proximity to food resources. Our goal was to provide a more accurate representation of direct physical contact frequency among deer to help evaluate disease transmission risk. Our objective was to quantify group size and composition, behavior types, and direct physical contact rates among deer at congregation areas including baited sites, food plots, and natural forage. We used camera trapping and direct observation along road-based surveys during the post-breeding period (January-April) when deer congregate into larger groups and more easily observed. Over 550 road-based surveys have been conducted and over 15 TB of video data have been processed. Road-based surveys produced over 1,800 deer observations and over 1,200 individuals in video surveys. The median number of groups and individuals observed on a road transect was 14.5 and 35.5, respectively. Using a two-proportions z-test in R, we found deer exhibited significantly more risky behaviors (non-contact, contact) proportionally at baited sites (0.92, 0.13) compared to food plots (0.87, 0.06) and natural forage (0.77, 0.10). Results from our research will improve the accuracy and efficacy of epidemiological models to help create more effective management approaches.

Poster Presentation #113

Surveillance of Parasites and Canine Distemper Virus in Free-Ranging Canada Lynx (Lynx canadensis) and Fishers (Pekania pennanti) from Maine, USA

Michael Yabsley[1,2], Natalie Heyward[1,2], Corinna Hazelrig[1], Shevenell Webb[3], Jennifer Vashon[3], Kayla Garrett[1], David Needle[4], Christopher Cleveland[1]

[1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [2]Warnell School of Forestry and Natural Resources, University of Georgia, [3]Maine Department of Inland Fisheries & Wildlife, [4]New Hampshire Diagnostic Laboratory, University of New Hampshire

Data on diseases of Canada lynx (Lynx canadensis) and fishers (Pekania pennanti) from the northeastern US is limited. Canine Distemper Virus (CDV) infects many carnivore species and can be an important cause of mortality directly or secondarily through immunosuppression. The goal of this study was to survey lynx and fishers for CDV and selected parasites including lungworms (Metastrongyloidea), Hepatozoon spp., Babesia spp., and Cytauxzoon felis. Tissues were collected from 62 lynx and 104 fishers that were trapped, found dead, or killed by vehicle collision in 2020 and 2021 in Maine, USA. DNA/RNA extracted from tissues were tested for lungworms using 18s rRNA conventional PCR, apicomplexans (e.g., Hepatozoon, Babesia, and Cytauxzoon spp.) using both 18s rRNA and ITS gene targets, and CDV by P gene RT-PCR. For lynx, three species of lungworms were detected. Overall prevalence was 47% (n=29/62) and Troglostrongylus wilsoni was the most commonly detected lungworm. Three apicomplexans were detected in lynx including Hepatozoon spp. (60%), Sarcocystis spp. (11%), and Toxoplasma gondii (3%). Regarding fishers, 34% (n=35/104) were infected with lungworm with Crenosoma spp. being most commonly detected. One fisher was PCR positive for Hepatozoon spp. and 16% were positive for Cystoisospora spp. We did not detect Cytauxzoon, Babesia spp. or CDV. No demographic variables (sex, age, weight, location, cause of death, and body condition) were associated with infection using binomial generalized linear models and pairwise comparison which, for lungworms, maybe because the surveillance was not conducted in a robust fashion (i.e., PCR of a small lung section vs. complete helminth recovery) due to the sample design. Regardless, the relatively high prevalence of lungworms in both host species, despite our low sensitivity testing scheme, and the high prevalence of Hepatozoon spp. in lynx indicates additional research is needed to confirm parasite identities, clinical relevance, and potential impacts on management.

Poster Presentation #114

Surveillance and Assessment of Skin Keratin Abundance Associated with Batrachochytrium dendrobatidis Prevalence in Red-Spotted Newts (Notophthalmus viridescens viridescens) and Mole Salamanders (Ambystoma talpoideum)

Michael Yabsley[1,2], Corinna Hazelrig[1,2], Kayla Garrett[1,2], Corrie Navis[2], John Maerz[2], Nicole Nemeth[1,3]

[1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [2]Warnell School of Forestry and Natural Resources, University of Georgia, [3]Department of Pathology, College of Veterinary Medicine, University of Georgia

Surveillance for Batrachochytrium dendrobatidis (Bd) in amphibians and understanding risk factors associated with detection and infection are necessary for mitigating the potential detrimental impacts of Bd on amphibian populations. The prevalence of Bd at two sites in Georgia, USA, Whitehall Experimental Forest in the Piedmont region and Sandhills Wildlife Management Area in the Upper Coastal Plain region, was investigated from September 2020 – April 2021. The potential association between Bd detection prevalence and skin keratin abundance between the red-spotted newt (Notophthalmus viridescens viridescens) and mole salamander (Ambystoma talpoideum) was also investigated. The prevalence of Bd detection varied by season, location, male sexual characteristics, and species sampled. The overall prevalence of Bd detection was 25.1% (n=553) with the highest prevalence in adult red-spotted newts (39.1%, n=220) and paedomorphic mole salamanders (27.7%, n=94). Marked seasonality was noted from a low in September 2020 (n=21, 0%) to a peak in December 2020 (n=84, 44.0%). The skin keratin abundance was scored (scale 0-3) based on histologic examination of skin samples from the caudal abdominal cavity and hindlimbs. Keratin abundance was higher in adult red-spotted newts (score=1.69) compared to paedomorphic mole salamanders (score=0). These data support the purported role of red-spotted newts as a reservoir of Bd, along with seasonality of Bd detections, and higher association between skin keratin abundance and Bd detection prevalence. The novel finding of relatively high Bd prevalence in mole salamanders not only suggests that they may be reservoirs, but warrants additional investigation into their susceptibility to associated morbidity and mortality.

Poster Presentation #115

Parasitic Infections an Energetic Burden for River Otter (Lontra canadensis) and Mink (Neogale vison) in Western Canada.

Kyle Shanebeck[1], *Dr. Stephanie Green*[1], *Dr. Clement Lagrue*[1,2]
[1]University of Alberta, [2]New Zealand Department of Conservation

We assessed the energetic (body) condition of river otter (Lontra canadensis, n=101) and mink (Neogale vison, n=58) in relation to parasitic infection by helminths (cestodes, nematodes, trematodes, and acanthocephalans) in Alberta and British Columbia. Mink and river otter carcasses were obtained from licensed fur trappers during the winter of 2020-2021. Gross necropsies were performed to determine overall health and energetic condition, based on fat deposits (both internal and external), reproductive organ mass, liver somatic index (LSI), splenic mass index (SMI), and body mass index (BMI). Age and sex were determined, and the respiratory tract, heart, gastrointestinal tract, liver, spleen, pancreas, omentum, kidney, adrenal gland, and bladder evaluated for health of the tissues and the presence of parasites. Multiple parasites were found, including some zoonotic species of concern (Versteria sp.), and novel infections of a marine acanthocephalan (Corynosoma strumosum) in coastal foraging mink and otter on Vancouver Island, which led to peritonitis and death in a juvenile mink. Most prevalent was infection by metacercaria (third larval stage) of Diplostomid (Digenea) parasites with over 80% of necropsied animals infected. Metacercariae burrowed into the intestinal or stomach wall, often migrating to the pancreas (most commonly), liver, kidneys, diaphragm, or abdominal musculature. Animals with moderate or severe infections showed classic signs of peritonitis and were in poorer condition, especially in terms of internal fat stores, than animals with mild or no infection. While many Diplostomids are generally not reported as serious threats to wild mammals, our findings show that infection with the metacercarial stage can be a significant burden on energetic condition. This is especially concerning for mustelids, which have high energetic demands. Continued monitoring of aquatic mammals, which are particularly susceptible to parasitic infection, is needed as this may have serious implications for individual health and population dynamics.

Poster Presentation #116

Co-Infection of Anaplasma Bacteria and Winter Ticks Decreases Moose Calf Survival in Maine

Alaina Woods[1], Lee Kantar[2], James Elliott[1], Sandra De Urioste-Stone[1], Pauline Kamath[1]
[1]University of Maine, [2]Maine Department of Inland Fisheries and Wildlife

Parasite coinfection has been shown to increase host susceptibility to other pathogens and decrease host fitness. Winter ticks (Dermacentor albipictus) are negatively impacting the Maine moose (Alces alces) population, causing hair loss, reduced fecundity, anemia, and even death. Furthermore, a bacterial blood parasite from the genus Anaplasma has recently been detected in Maine moose, with prevalence increasing over the study period (54% 2014-2018; 93% in 2021). Prior phylogenetic work has shown the moose Anaplasma to be specific to cervids, sharing a common ancestor with A. marginale, which is known to cause weight loss, abortion, and death in cattle. However, the effects of Anaplasma infection on moose survival, as well as the compounding impacts of winter tick and Anaplasma co-infections remains unknown. Here, we examine the impact Anaplasma infection and co-infection with winter ticks has on moose calf survival in Maine. We utilize five years of live capture data (2017-2019; 2021-2022), from moose to model calf overwintering survival probability (using the Kaplan-Meir estimator) as a function of winter tick load and/or Anaplasma infection status. Our results show that moose with heavy winter tick loads have a significantly lower survival probability than their moderately and lightly infected counterparts. Furthermore, for moose calves with heavy winter tick infestations, the survival probability of those infected with Anaplasma is 22% lower ($p < 0.05$) than those that are uninfected. Given our results showing additional negative effects of co-infection with Anaplasma and winter ticks, there is an urgent need to further understand the effects of co-infecting parasites on calf survival as previous research suggests the moose populations in the Northeastern United States are in decline.

Poster Presentation #117

Use of Implants for Terbinafine Administration to Prevent Chytridiomycosis in Greater Sirens (Siren lacertina)

Anastasia Towe[1], Dr. Rebecca Hardman[1], Dr. Wesley Sheley[1], Joseph DeMarchi[1], E. Davis Carter[1], Debra Miller[1]
[1]University of Tennessee

Batrachochytrium dendrobatidis (Bd) is a chytrid fungus that infects amphibians and is present in habitats worldwide. Bd chytridiomycosis has been documented to cause mortalities in sirens (Siren lacertina). This study evaluated the efficacy and safety of an anti-fungal drug (Terbinafine) along with a novel delivery method, a Terbinafine-impregnated intracoelomic implant, in prevention and clearance of Bd infection in sirens. Four sirens received Terbinafine implants and four received blank implants. They were exposed to Bd zoospores at one-and two-months post-implant placement. Blood was collected monthly for plasma terbinafine levels, and skin swabs performed weekly for Bd PCR. Animals with terbinafine implants showed increased levels of terbinafine in plasma; however, treatment did not prevent infection and the clearance rate of Bd infection was not different from control animals. These findings indicate that intracoelomic drug implants are a safe method for antifungal drug delivery in amphibians; however, Terbinafine efficacy remains unclear.

Poster Presentation #118

Fatal Gastric Amoebiasis in a Linnaeus's Two-Toed Sloth (Choloepus didactylus)

Jeongha Lee[1], Anibal Armien[2], Daniel Paulsen[1]
[1]Department of Pathobiological Science, School of Veterinary Medicine, Louisiana State University, Louisiana Animal Disease Diagnostic Laboratory, [2]California Animal Health & Food Safety Laboratory System (CAHFS), School of Veterinary Medicine, University of California, Davis

Gastric amoebiasis has been reported sporadically in macropods including kangaroos and wallabies and in leaf-eating monkeys, including colobus monkeys and silver-leafed monkeys, which have a sacculated stomach where vegetation is fermented. Gastric amoebiasis has not been reported in sloths, which also have a sacculated stomach.

An 11-month-old Linnaeus's two-toed sloth (Choloepus didactylus) was submitted for necropsy with a history of weight loss and intermittent diarrhea for 18 days. The sloth was emaciated with mild hydrothorax and ascites. The stomach was markedly distended with fluid. The mucosa of the cardiac glandular region was multifocally reddened and raised, occasionally covered by fibrinonecrotic membranes. On microscopic examination, severe multifocal necrotizing gastritis was noted in the cardiac glandular region with intralesional amoebic trophozoites and cysts. Transmission electron microscopy confirmed the presence of trophozoite and cyst stages of an amoeboid organism, most consistent with a free-living Amoebozoa in the family Acanthamoebidae. The presence of mitochondria ruled out Amoebozoa of the family Entamoebidae, and PCR for Entamoeba was negative in formalin fixed paraffin embedded stomach tissue. Further, the lack of flagellate forms, a third stage seen in some amoeboid pathogens, exclude Percolozoa of the genus Naegleria.

Gastric amoebiasis in macropods and leaf-eating monkeys is caused by Entamoeba histolytica, which causes necrotizing colitis in humans and nonhuman primates. Free-living amoeboid pathogens, including Acanthamoeba, Balamuthia, Naegleria sp., most commonly cause encephalitis in humans and non-human animal species and are not primarily associated with gastrointestinal diseases. To our knowledge, this is the first report of gastric amoebiasis caused by a pathogenic free-living Amoebozoa in a sloth.

Poster Presentation #119

Novel Avibacterium Species Associated with Sinusitis and Conjunctivitis in a Merriam's Wild Turkey (Meleagris Gallopavo Merriam) Flock in Colorado, USA

Jayne Ellis[1], Christopher MacGlover[2], Kerry Sondgeroth[2,3], Derek Brown[4], Joshua Daniels[5], Karen Fox[6]

[1]Department of Pathobiology, Veterinary Diagnostic Laboratory, Michigan State University, [2]Department of Veterinary Sciences, University of Wyoming, [3]Wyoming State Veterinary Laboratory, [4]Pueblo Area Office, Colorado Parks and Wildlife, [5]Department of Microbiology, Immunology, and Pathology, Colorado State University, [6]Wildlife Health Laboratory, Colorado Parks and Wildlife

A sick Merriam's wild turkey (Meleagris gallopavo) from Pueblo County, Colorado, USA with periocular swelling and periocular skin crusting was diagnosed with severe lesions of catarrhal and fibrinous sinusitis and conjunctivitis. A novel species of Avibacterium was detected in the exudates from this bird. While eight additional turkeys culled from the flock did not have clinical signs or gross lesions, histologically all had mild to moderate chronic sinusitis, and infraorbital cultures yielded the same novel clade of Avibacterium that was found in the sick turkey. Analysis of the novel clade isolates using a MALDI dendogram, 16s rDNA sequencing, whole genome sequencing, and phylogenetics denoted a novel species within the genus Aivbacterium (proposed Avibacterium gallopavo). The presence of this Avibacterium species in the absence of significant disease in some birds suggests that other factors may have been involved in the development of severe sinusitis and conjunctivitis in the sick wild turkey. Negative culture results from a distant flock of wild turkeys, acquired with similar methods to the affected flock, suggest that this novel species of Avibacterium is not widespread throughout wild turkeys in Colorado.

Poster Presentation #120

Risk of Bacteremia Associated with Probiotic Treatment of Batrachochytrium salamandrivorans

Anastasia Towe[1], *Dr. Debra Miller*[1], *Dr. Wesley Sheley*[1], *Dr. Sree Rajeev*[1], *E. Davis Carter*[1], *Joseph DeMarchi*[1], *Dr. Matthew Gray*[1]
[1]University of Tennessee

Batrachochytrium salamandrivorans (Bsal) is a recently described fungal pathogen that has caused declines of wild salamanders and been detected in captive populations in Europe. One potential preventative and/or treatment option for Bsal is the use of probiotic bacteria. Previous studies have shown that certain bacteria present on amphibian skin can be protective against fungal pathogens. This study aimed to determine the safety and efficacy of using probiotic bacteria (Pseudomonas fluorescens) in order to prevent and treat chytridiomycosis. A secondary aim was to further our understanding of the pathogenesis of this disease through determining if bacteremia may play a role in morbidity and mortality caused by chytridiomycosis. Eastern newts (Notophthalmus viridescens) were exposed either to Bsal, probiotic bacteria, pathogenic bacteria (Aeromonas hydrophila), or a combination of Bsal and one of the bacterial species. They were monitored throughout the course of disease and samples were collected for PCR, blood cultures, and histopathology. Preliminary results of this completed study indicate that Bsal loads on the skin measured by qPCR were not lower in groups that were exposed to probiotic bacteria, and mortality ranged from 67-100% and did not differ among treatment groups. We also found evidence of bacterial infiltration into the blood and organs in animals that were exposed to Bsal in probiotic-exposed and -unexposed newts. Our results suggest that use of probiotics to treat animals with Bsal chytridiomycosis may facilitate bacteremia, and bacteremia may contribute to Bsal pathogenesis.

Poster Presentation #121

Widespread Hepatozoon sp. Infection in Southeastern Coyotes

Eliza Baker[1], Dr. Richard Gerhold[1], Dr. Debra Miller[1], Alex Jensen[2]
[1]University of Tennessee College of Veterinary Medicine, [2]Clemson University, Department of Forestry and Environmental Conservation

Hepatozoon is a genus of apicomplexan parasites known to cause musculoskeletal disease in numerous species. There are two species reported in canids: Hepatozoon americanum, the agent of American canine hepatozoonosis (ACH), and Hepatozoon canis. ACH is an emerging disease known to cause severe muscle pain, osteoproliferation, and occasionally death in domestic dogs in the United States. ACH is restricted to the range of its vector, the Gulf Coast tick (Ambylomma maculatum), which historically occurred in a 150-mile range around the Gulf of Mexico. However, in recent years, the tick has been documented as far north as Delaware, and it is expected to continue its expansion due to various factors. To assess the prevalence of ACH in the southeast, whole blood was opportunistically collected from free-ranging coyotes from South Carolina (n=53), Tennessee (n=25), and Virginia (n=13). Carcasses were collected when available for necropsy and histopathology (n=50). DNA was extracted from whole blood, and PCR targeting the 18s rRNA gene was performed. 43% of coyotes from South Carolina, 23% of coyotes from Virginia, and no Tennessee coyotes were positive for Hepatozoon sp. on whole blood PCR. 85% of positives were most closely related to H. americanum with the remaining 15% sequencing to H. canis. When histology was available, it matched PCR findings in all cases. This study revealed a high prevalence of Hepatozoon infection in coyotes from South Carolina and Virginia but found no evidence of the disease in east Tennessee. PCR of whole blood was shown to be a sensitive and specific method for the detection of the infection in coyotes. The potential impacts of this disease on wild and domestic canid populations remain an important area of investigation.

Poster Presentation #122

Finding Normal in a Warming World: Baseline PCV and TS Data and its Relation to Incubation Temperature in Leatherback Sea Turtle Hatchlings and Post Hatchlings

Samantha Kuschke[1], Debra Miller[1,3], Jeanette Wyneken[2]
[1]Department of Biomedical and Diagnostic Services, College of Veterinary Medicine, University of Tennessee, [2]Department of Biological Sciences, Florida Atlantic University, [3]Center for Wildlife Health, University of Tennessee

There are seven extant species of sea turtles, all of which are imperiled. As such, large efforts are aimed at understanding the effects of climate change on these animals to aid conservation efforts. Currently, a large knowledge gap exists across hatchling and post hatchling baseline blood values and the potential impact of elevated incubation temperatures. Filling these knowledge gaps is critical for these imperiled species, especially leatherbacks. All leatherback populations are considered endangered, but isolated populations of leatherbacks are at higher risk of extinction. The Eastern Pacific population is anticipated to become extinct within the next 100 years. As such, maintaining this population of leatherbacks in a temporary human managed setting may be necessary to rescue the population. But to do this successfully, we need to have baseline information, including baseline blood parameters. Here we present preliminary data gathered to establish reference ranges for packed cell volume (PCV) and total solids (TS) in leatherback hatchlings and post hatchlings. In hatchlings we found a mean PCV of 24.78 (n = 50) and mean TS of 3.4 (n=47), while post hatchlings (3-4 weeks) had a mean PCV of 20 (n=30) and a mean TS of 1.9 (n=26). Additionally, we analyzed the effects of incubation temperature on PCV and TS at emergence and found that as incubation temperature increases so do both PCV and TS. Both values are likely elevated due to dehydration, a suboptimal physiologic state that has the potential to negatively impact a hatchling's overall fitness and survival. These data provide baseline values to assess hatchling health and possibly an explanation for decreased survival in hatchlings incubated at higher temperatures. Additionally, these findings can be used in the development of management strategies to mitigate the effects of elevated incubation temperatures in nature.

Poster Presentation #123

Landscape Feature Determinants of Parelaphostrongylus Tenuis Transmission in Northeastern Minnesota

Tyler Garwood[1], Dr. Seth Moore[2], Dr Nicholas Fountain-Jones[3], Dr. Peter Larsen[4], Dr. Tiffany Wolf[1]
[1]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota-Twin Cities, [2]Department of Biology and Environment, Grand Portage Band of Lake Superior Chippewa, [3]Department of Mathematics and Physics, School of Natural Resources, University of Tasmania, [4]Department of Veterinary and Biomedical Sciences, College of Veterinary Medicine, University of Minnesota-Twin Cities

Parelaphostrongylus tenuis infection is the leading cause of death among adults in Minnesota's declining moose (Alces alces) population. Lowering densities of white-tailed deer (Odocoileus virginianus), P. tenuis's natural definitive host, is currently the only management option for reducing transmission to moose. Since reducing deer densities can be politically infeasible and varies in efficacy, new options are needed. Habitat management to reduce transmission is less controversial, and previous research found that increased moose use of certain forest types predicts P. tenuis infection probabilities. However, whether those forest types or other landscape features serve as barriers or corridors for P. tenuis transmission remains unexplored. To address this question, we used a landscape genomics framework in which we measured gene flow between P. tenuis sample locations. By layering geo-labeled, pairwise measures of genetic variability of P. tenuis samples on the landscape we can quantify the effect of different landscape variables on P. tenuis transmission. To that end, we collected a spatially stratified set of 139 P. tenuis larval samples from Grand Portage Indian Reservation (GPIR) in Minnesota, USA. We then used restriction site associated DNA sequencing to identify 109,562 single nucleotide polymorphisms, which we used to measure gene flow and delineate five genetically distinct clusters of P. tenuis on GPIR. By the time of the conference, we will test which habitat features best explain the gene flow patterns we observed. Ultimately, these results can be used to predict and enhance the efficacy of habitat management plans aimed at reducing P. tenuis transmission to moose. This study is particularly relevant to the 1854 Ceded Territory, an area of nearly 5 million acres in northeastern MN where the Grand Portage Band and other Chippewa tribes retain treaty-reserved rights to preserve their culture and subsist through moose hunting and other forms of hunting, fishing, and gathering.

Poster Presentation #124

A Multiplexed Magnetic-Capture Tool for Monitoring Polar Bear Health and Wildlife Disease Surveillance

Christina Tschritter[1], Marsha Branigan[2], Peter V. C. de Groot[1], Markus Dyck[3], Zhengxin Sun[1], Kayla Buhler[4], Dr. Emily Jenkins[4], Dr. Stephen C. Lougheed[1]

[1]Queen's University, [2]Department of Environment and Natural Resources, Government of the Northwest Territories, [3]Department of Environment, Government of Nunavut, [4]Western College of Veterinary Medicine

The Arctic is experiencing unprecedented change, warming at a rate more than twice the global average. This is causing large-scale environmental changes, including the distributions of pathogens, vector and host-species, and subsequently impacting northern species' exposure to disease. Advancements in diagnostic technologies are enhancing our ability to develop novel, community-based, disease surveillance protocols. Hunter/ harvester-based monitoring systems allow for sample acquisition, greater geographic and temporal coverage, and diminished overall cost of monitoring. The goal of this work is to quantify the geographical distribution of focal pathogens and assess the correlation between various environmental stressors, diet, and our focal pathogens. Polar bear tissue sets (n= 68; skeletal muscle, liver, colon, and fecal) provided from annual harvest facilitate the monitoring of pathogens relevant to the health and economy of the Northern people; providing baseline pathogen presence data and allowing us to assess change over time. The immediate objectives of our study were to: (i) Firstly, develop a novel multiplexed magnetic-capture ddPCR protocol to assess the presence of focal pathogens (Toxoplasma gondii, Trichinella spp., Sarcocystis spp., Pasteurella multocida, Erysipelothrix rhusiopathiae, Francisella tularensis, and Mycobacteria spp) in hunter/harvester collected samples; (ii) Secondly, observe the seroprevalence of Toxoplasma gondii, Trichinella spp., and Francisella tularensis using meat juice collected from the tissues. Future validation of these tests on feces will enable us to non-invasively monitor for pathogens through field collected fecal samples. The BearWatch project is collaborating with northern Canadian governments and Inuit communities to generate a scat-based non-invasive monitoring toolkit. A harvest and scat-based surveillance program could form a passive and real-time screening for new and emerging infectious diseases, allowing monitoring of the occurrence and distribution of pathogens of economic, food security, and health relevance, while simultaneously monitoring the health of polar bears and the impact that climate change is having on pathogen distributions.

Poster Presentation #125

Challenges to IUCN Guideline Implementation in theRehabilitation and Release of Trafficked Primates in Peru

Siena Mitman[1], Marieke Rosenbaum[1], Raul Bello[2], Cambrey Knapp[1], Felicia Nutter[1], Patricia Mendoza[3,4]
[1]Cummings School of Veterinary Medicine at Tufts University, [2]Kawsay Biological Station, [3]University of Missouri- St. Louis, [4]Asociación Neotropical Primate Conservation Peru

The rehabilitation and release of nonhuman primates after confiscation, surrender, or abandonment during illegal wildlife trafficking has implications for conservation, animal welfare, and public health. Risks associated with primate release include ecosystem disruption, inability of released primates to engage in normal foraging and social behaviors, and pathogen spillover. The International Union for the Conservation of Nature (IUCN) has several guidelines for the rehabilitation and release of trafficked primates intended to minimize such risks, though little is known about the use of these guidelines during primate confiscation, rehabilitation, and release or about the challenges faced by those who attempt to implement such guidelines in specific contexts. As one of the leading sources of Neotropical primate trade in the world, Peru has a primate population particularly vulnerable to the negative consequences of trafficked primate release. This study used semi-structured interviews and structured questionnaires of 19 people involved in primate confiscation, rehabilitation, and/or release in Peru and found that awareness and implementation of the IUCN guidelines are minimal. Opportunities to increase guideline implementation in Peru include expanding government involvement and support, adapting guidelines to specific contexts and locations, and establishing a platform for increased communication, cooperation, and research amongst those performing this work.

Poster Presentation #126

Mange and Microbes: Microbial Changes Associated with Sarcoptic Mange in Bare-Nosed Wombats (Vombatus ursinus)

Christina Næsborg-Nielsen[1], Dr. Raphael Eisenhofer[2,3], Dr. Tamieka A. Fraser[1,4], Vicky Wilkinson[1], Dr. Christopher Burridge[1], Dr. Scott Carver[1]

[1]Department of Biological Sciences, University of Tasmania, [2]Center of Evolutionary Hologenomics, GLOBE Institute, University of Copenhagen, [3]School of Biological Sciences, University of Adelaide, [4]Center for Animal Health Innovation, Faculty of Science, Health, Education and Engineering, University of the Sunshine Coast

Sarcoptes scabiei is one of the most impactful mammalian ectoparasites globally with significant health implications. Sarcoptic mange causes major disruption of the epidermis which can have microbial impacts such as reduced diversity and accumulation of pathogenic microbes that can lead to secondary infections, this however has not been studied in marsupials. Until now, research have primarily focused on bacterial microbiota changes, but there is little to no knowledge about the fungal microbial changes with mange. Here, we aimed to (1) examine bacterial and fungal microbiota changes associated with mange in wild bare-nosed wombats (BNWs); and (2) evaluate whether potentially pathogenic microbes are facilitated by S. scabiei infection.

We sequenced epidermal bacterial and fungal microbial communities from healthy and mange affected BNWs. Severely affected BNWs had lower microbial richness and altered community structure compared to healthy individuals. Potentially pathogenic microbial taxa increased in mange affected BNWs: bacteria Staphylococcus spp., Corynebacterium spp., Brevibacterium and Brachybacterium; and fungi from Pseudogymnascus spp. and Debaryomyces.

This study represents the first microbial investigation of sarcoptic mange in a marsupial host, as well as the first investigation in fungal microbial changes on the skin in any host affected by sarcoptic mange. Our results are broadly consistent with bacterial microbiota changes observed in humans, pigs, canids, and ibex, suggesting the epidermal microbial impacts of mange disease may be generalisable across host species. We recommend that future studies investigating the skin microbiota changes include both bacterial and fungal data to gain a more complete picture of skin microbiota.

Poster Presentation #127

Persistence of Low Pathogenic Avian Influenza Viruses in Artificial Streams Mimicking Natural Conditions of Waterfowl Habitats

Albert Perlas Puente[2], Dr. Kateri Bertran[1], Dr. Xavier Abad[1], Dr. Carles M. Borrego[3], Dr. Miquel Nofrarías[1], Rosa Valle[1], Dr. Antonio Ramis[2], Dr. Martí Cortey[2], Dr. Vicenç Acuña[3], Dr. Natàlia Majó[1]

[1]Unitat mixta d'Investigació IRTA-UAB en Sanitat Animal. Centre de Recerca en Sanitat Animal (CReSA). Campus de la Universitat Autònoma de Barcelona (UAB)., [2]Departament de Sanitat i Anatomia animals. Facultat de Veterinària. Campus de la Universitat Autònoma de Barcelona (UAB)., [3]Catalan Institute for Water Research (ICRA).

Avian influenza viruses (AIV) can affect wildlife, poultry, and humans, so a One Health perspective is needed to tackle them. Furthermore, migratory waterfowl are not only just Trojans that globally spread low pathogenic AIV (LPAIV) over long distances, but they can also suffer from high mortality rates by highly pathogenic AIV (HPAIV) infections. Therefore, the study of AIV persistence in waterfowl rest areas is key to understand their transmission dynamics and control strategies. Here, we used an artificial stream facility that mimics the behaviour of natural waterbodies where waterfowl live (day/night cycles of photosynthetic active radiation (PAR), recirculating flow, etc.) to investigate LPAIV persistence. We used 12 artificial streams to assess the effects of temperature (10-13°C vs. 16-18°C) and sediments (presence vs. absence) on the persistence of a H1N1 LPAIV that was spiked in the streams (5.3 $\log_{10}$ $TCID_{50}$). We collected water samples from all 12 streams (three replicates by temperature and sediment condition) at different time points until 15 days after viral spike to quantify viral RNA by qPCR and to detect infectious particles by virus isolation in eggs. Viral RNA was detected until the end of the experiment and we observed a significant combined effect of temperature and sediments in viral decay, with higher viral genome loads in colder streams without sediments. In contrast to laboratory-controlled studies, infectious H1N1 LPAIV was isolated in only seven streams at 24h, one stream at 48h, and none beyond that. Colder temperatures seemed to favour infectious virus persistence, but not the presence of sediment. We hypothesize that experiments as the aforementioned, closer to natural conditions, provide a more realistic approach to AIV infectious persistence decays due to the effect of factors such as water kinetics and PAR effects.

Poster Presentation #128

Investigating SARS-CoV-2 Infection and Exposure in Norway Rats (Rattus norvegicus) from Ontario, Canada

Sarah Robinson[1], Jonathon Kotwa[2], Simon Jeeves[1], Chelsea Himsworth[3], David Pearl[4], J. Scott Weese[1], L. Robbin Lindsay[5], Antonia Dibernardo[5], Bradley Pickering[6,7,8], Melissa Goolia[6], Hsien-Yao Chee[2,9], Juliette Blais-Savoie, Emily Chien[2], Winfield Yim[2], Lily Yip[2], Samira Mubareka[2,10], Claire Jardine[1,11]

[1]Department of Pathobiology, Ontario Veterinary College, University of Guelph, [2]Sunnybrook Research Institute, [3]School of Population and Public Health, University of British Columbia, [4]Department of Population Medicine, Ontario Veterinary College, University of Guelph, [5]Public Health Agency of Canada, National Microbiology Laboratory, [6]National Centre for Foreign Animal Disease, Canadian Food Inspection Agency, [7]Department of Medical Microbiology and Infectious Diseases, University of Manitoba, [8]Department of Veterinary Microbiology and Preventative Medicine, College of Veterinary Medicine, Iowa State University, [9]Global Health Research Center and Division of Natural and Applied Sciences, Duke Kunshan University, [10]Faculty of Medicine, University of Toronto, [11]Canadian Wildlife Health Cooperative, Ontario Veterinary College, University of Guelph

Emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has raised concerns about spillover from humans to animals, the establishment of wildlife reservoirs, and the potential for future outbreaks caused by variants of wildlife origin. Norway rats (Rattus norvegicus) are abundant in urban areas and live in close proximity to humans, providing the opportunity for spillover of SARS-CoV-2. Cryptic SARS-CoV-2 lineages have been detected in New York City wastewater, which may indicate the presence of animal reservoirs in the urban environment. However, there is no evidence of natural SARS-CoV-2 infection in rats and experimental studies suggest rats are likely not susceptible to wild-type SARS-CoV-2, but as variants emerge, host ranges are likely shifting, as demonstrated by the susceptibility of rats to the Alpha (B.1.1.7) variant. We investigated SARS-CoV-2 infection and exposure in Norway rats from southern Ontario, Canada. From October 2019 to June 2021, 224 rats were submitted by collaborating pest control companies. The majority of samples were collected in Windsor (79.9%; n=179), Hamilton (13.8%; n=31), and the Greater Toronto Area (5.8%; n=13). Overall, 50.0% (n=112) were female and most rats were sexually mature (55.8%; n=125). Nasal turbinate (n=164) and small intestinal (n=213) tissue samples were analyzed for SARS-CoV-2 RNA by RT-PCR. Thoracic cavity fluid samples (n=213) were tested for neutralizing antibodies using GenScript cPass; positive samples (n=11) were further tested using a plaque reduction neutralization test (PRNT). We did not detect SARS-CoV-2 RNA in any samples tested. However, two samples were serological reactors (PRNT70). Most of our samples were collected pre-emergence of variants, while 22 samples were collected while B.1.1.7. was the predominant circulating variant in humans. It is imperative that efforts to control and monitor SARS-CoV-2 include surveillance of rats and other relevant wildlife species as novel variants continue to emerge.

Poster Presentation #129

No Abstract Assigned

Poster Presentation #130

Pathogen Surveillance and Discovery in Vampire Bats (Desmodus rotundus) Distributed Across Ecologically Distinct Regions of Guyana, South America

Lexi Frank[1], Marissa Milstein[1], Evan Kipp[1], Roxanne Larsen[1], Laramie Lindsey[1], Elisha Marawanaru[2], Christopher Shaffer[3], Phillip Suse[2], Tiffany Wolf[4], Peter Larsen[1]
[1]Department of Veterinary and Biomedical Sciences, University of Minnesota, [2]Masakenari Village, Konashen Indigenous District, Region 9, [3]Department of Anthropology, Grand Valley State University, [4]Department of Population Veterinary Medicine, University of Minnesota

The diversity and frequency of zoonotic pathogen spillover from wildlife has steadily increased over the past century. Neotropical bats have been identified as significant hosts/reservoirs for a number of zoonoses, and are a potential source for emerging pathogens. The common vampire bat (Desmodus rotundus) is endemic to the Neotropics and is particularly interesting with respect to the zoonotic potential of its metacommunity. This highly social bat is an obligate blood feeder (e.g., livestock, wildlife, and infrequently humans) and, as such, they are exposed to blood-borne pathogens daily. Guyana, South America is ideal for studying D. rotundus, given their abundance and distribution across ecologically distinct sites. The potential for negative human and animal health impacts highlights the importance of researching the zoonotic disease capacity of Desmodus. The aims of this study are (1) collect tissues of D. rotundus from two ecologically distinct regions in Guyana, South America, (2) characterize metagenomic and metatranscriptomic communities of D. rotundus using advanced next-generation sequencing technologies, (3) compare bat-pathogen communities across both sites, including putative zoonoses. Our study sites consist of one characterized by dense human and livestock populations with frequent human disturbance activities, and a second that is an expansive, intact forest with no livestock and low-levels of human disturbance. Potentially pathogenic bacteria, viruses, and macro/micro-parasites will be characterized using de novo metagenomic and metatranscriptomic approaches. Our work within a predicted Neotropical zoonotic disease hotspot will help elucidate the drivers of bat-related zoonotic pathogen emergence. This research lays the foundation for broader next-generation pathogen surveillance and discovery initiatives that will help to predict future zoonotic disease outbreaks, while providing opportunities to mitigate or prevent future spillover events.

Poster Presentation #131

The Impacts of Resource Provisioning on the Frequency and Diversity of Antimicrobial Resistance Genes Carried by the White Stork (Ciconia ciconia) in Madrid, Spain

Raquel Francisco[1,2], Dr. Sonia Hernandez[1,2], Dr. Jose Aguirre[3], PhD Canidate Alejandro Lopez-Garcia[3], Dr. Irene Sacristan[4], Dr. Fernando Esperon[4]

[1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [2]Warnell School of Forestry and Natural Resources, University of Georgia, [3]Department of Zoology and Physical Anthropology, Faculty of Biology, Complutense University of Madrid, [4]Veterinary Department, School of Biomedical and Health Sciences, Universidad Europea de Madrid

Anthropogenic environments are hotspots for the emergence and maintenance of antimicrobial resistance. Agricultural pastures and landfills are of particular interest due to their complex microbial communities and abundant wildlife visitation, which could facilitate the exchange of antimicrobial resistance genes (ARGs) via horizontal transfer. Wild birds that occupy these environments may become both reservoirs and transporters of ARGs. The White Stork is a highly urbanized wading bird that has significantly changed its ecology due to shifts in Spanish waste management toward open-air landfills. This species now heavily forages at landfills, which provide abundant food and allow for improved reproductive success. Birds that are dependent on anthropogenic resources, such as storks, provide the ideal opportunity to understand the emergence and spread of AMR. We evaluated the diversity and quantity of ARGs in storks during three periods of the breeding season (defined by distinct foraging strategies). A total of 31 nests at Prado Herrero were sampled between March-July (2020-2021). Fresh feces were collected from 31 nests to evaluate the presence of 23 important ARGs affecting eight antibiotic classes via quantitative PCR. All nests carried multiple ARGs. Over 70% of nests had multi-drug resistance to at least 3 antibiotic classes during at least one time-period. Generalized Linear Mixed Models revealed that increased diversity in antibiotic class resistance, amount of ARGs present in a sample, and multi-drug resistance were associated with increased adult age, later sample periods (i.e., older chicks), and decreased landfill use. Our results suggest that landfills may not be contributing significantly to the emergence and maintenance of AMR in this system. Little literature exists on the relationship between stork habitat selection and health outside of landfill use in Spain. Future efforts in stork AMR research should focus on exploring the relationship between agricultural land use and health.

Poster Presentation #132

Streamlining Mitochondrial Genome Assembly and Bloodmeal Identification in Hematophagous Insects Using Nanopore Adaptive Sampling

Evan Kipp[1], Laramie Lindsey[1], Cristina Blanco[2], Julia Baker[2], Marissa Milstein[1], Christopher Faulk[3], Jonathan Oliver[4], Peter Larsen[1]

[1]Department of Veterinary and Biomedical Sciences, University of Minnesota, [2]College of Veterinary Medicine, University of Minnesota, [3]Department of Animal Science, University of Minnesota, [4]Division of Environmental Health Sciences – School of Public Health, University of Minnesota

Globally, hematophagous (i.e., blood-feeding) insects are capable of vectoring a vast array of human and animal pathogens. Despite their well-documented medical and veterinary importance, molecular and genomic resources for many blood-feeding insect taxa remain limited. Recently, advancements in next-generation sequencing technologies have opened the door for exciting new approaches to help characterize these important disease vectors and disentangle complex pathways of the pathogens they transmit. Here, we set out to demonstrate the utility of nanopore adaptive sampling (NAS)—a “cutting-edge” next-generation sequencing approach—for the dual purposes of whole mitochondrial genome assembly and determination of host bloodmeal sources among a diverse group of blood-feeding arthropod species. In brief, NAS utilizes an advanced bioinformatic software to enable investigators to enrich their sequencing libraries based on real-time mapping results to targets of their choosing. We hypothesized that by targeting NAS for enrichment across all available metazoan mitochondrial genomes, we could leverage this method to ‘phylogenetically capture’ sequences in related hematophagous insect species for which complete mitochondrial genomes are lacking. We also hypothesized that this approach could simultaneously be leveraged to allow us to obtain host mitochondrial genome sequences contained within insect bloodmeals to rapidly determine their sources. By using NAS, we were successfully able to sequence and assemble mitochondrial genomes of four mosquito species: Aedes vexans, Culex restuans, and Cu. territans; and the deer fly, Chrysops niger. Importantly, these represent the first mitochondrial genome assemblies for these insect species, and document the efficacy of NAS for phylogenetic capture. Importantly, we were also successful in dually identifying vertebrate bloodmeal sources in Cu. restuans, A. trivittatus, and Ch. niger specimens. Our findings suggest that NAS holds great promise across a wide variety of molecular systematic applications in hematophagous arthropods, and will help inform a variety of global One Health and vector-borne disease initiatives.

Poster Presentation #133

Proximal Land-use Drives Salmonella Population Dynamics in Surface Water

Jared Smith[1]
[1]Jared C. Smith, [2]Nikki W. Shariat

Salmonella is ubiquitous in natural environments, such as surface water; however, an understanding of factors influencing the prevalence and diversity of Salmonella in these settings is incomplete. There are over 2500 genetically distinct Salmonella serovars, which gives rise to enormous phenotypic diversity, including host restriction and environmental persistence. To add to this complexity, Salmonella populations can be comprised of multiple serovars, often not realized by conventional methods that only characterize a few colonies, representing only the most abundant serovars present in a mixed population. We hypothesized that proximal land-use drives the types of Salmonella found in water. Over six-months, 10L water samples were collected each month from both the headwaters and downstream sites in four distinct creek systems in Georgia (95 overall samples). One creek was embedded within a National Forest, two were surrounded by commercial livestock and poultry operations, and one was within an urban neighborhood. After determining Salmonella prevalence by culture, a deep serotyping approach using CRISPR-SeroSeq was used to analyze Salmonella serovar populations. The overall Salmonella prevalence was 84.2% and was highest following precipitation events. Despite most often being associated with food animal production, Salmonella prevalence was highest in the National Forest watershed (all sites positive over all trips) and lowest in the urban watershed. We identified 24 different serovars and 83.3% of samples contained multiple serovars, averaging 3.1 serovars per sample (range 1-9 serovars). We identified distinct Salmonella signatures for each watershed; within the National Forest sites, we found serovars Muenchen, Rubislaw, and Montevideo, among others, and these are also often found in wildlife in the same geographical region. Future work will involve PCR-based analyses to attribute animal sources of Salmonella. In summary, our data indicates that Salmonella in water is driven by proximal land usage and overall Salmonella prevalence is influenced by weather.

Poster Presentation #134

Legacy and Contaminants of Emerging Concern (CECs) in Tree Swallows Nesting in Three Drainages of the Milwaukee Estuary, WI

Christine Custer[1], Thomas Custer[1], Paul Dummer[1], Natalie Karouna-Renier[2], Chi-yen Tseng[3], Cole Matson[3]
[1]U.S. Geological Survey, [2]U.S. Geological Survey, [3]Baylor University

There are often few data for birds, either on exposure to or effects from many emerging contaminants (CECs). This Great Lakes Restoration Initiative (GLRI) project provides new data on legacy contaminants and CECs for a model species, the tree swallow (Tachycineta bicolor). Exposure to multiple classes of contaminants was assessed in tree swallow food and in their tissues by sampling birds nesting along three drainages, with differing land use patterns, in the Milwaukee Estuary, WI. Samples were also collected from a remote lake in northern Wisconsin for comparison. Exposure to bioaccumulative contaminants, such as polychlorinated biphenyls (PCBs), polybrominated diphenyl ethers (PBDEs), and per- and polyfluorinated substances (PFAS), was generally below concentrations that have been linked with reproductive effects or physiological responses. Only a few pharmaceutical and personal care products (PPCPs, e.g., amphetamines, azithromycin, DEET, and iopamidol) and non-organochlorine pesticides (N-OCs, e.g., atrazine and desethylatrazine) were detected. Desethylatrazine was found in most samples (eggs and nestling carcasses), but its parent compound, atrazine, was rarely detected. The PPCPs were detected more frequently in liver than in egg tissue. Both DEET and amphetamines were also detected in the remote lake, which probably reflects the wide-spread use of DEET as an insect repellent. Concentrations of polycyclic aromatic hydrocarbons (PAHs) in tree swallow diet samples were higher in all three drainages compared to the remote lake, however, within the Milwaukee Estuary, the Menomonee River was 10 times more contaminated with PAHs than the other two drainages in the estuary. Associations of biomarker assessments with contaminant exposure, both legacy and emerging contaminants, will be presented. Sediment, the only abiotic matrix sample, was not necessarily predictive of exposure in birds.

Poster Presentation #135

Bald Eagles as Indicators of Emerging Contaminants and Ecosystem Health

Sean Strom[1]
[1]Wisconsin Department of Natural Resources

The Wisconsin Bald Eagle Bio-sentinel Program is a collaborative program that has monitored bald eagle contaminant levels in WI since 1990. The purpose of this project is to monitor exposure patterns of both legacy and emerging contaminants in nestling bald eagles as well as illustrate the utility of bald eagles as monitoring tools for contaminant exposure and ecosystem health. Data from this monitoring program suggest eaglets along the middle section of the Wisconsin River have elevated levels of per- and polyfluoroalkyl substances (PFAS) compared to other populations. Other emerging contaminants that have been detected include industrial compounds (phthalates) and endocrine disrupting chemicals (Bisphenol-A). This project provides natural resource managers with a snapshot of chemical exposure within a given ecosystem. We have illustrated that bald eagles can be useful and reliable indicators of contaminant exposure, environmental change, and ecosystem health.

Poster Presentation #136

A Comparative Burden of Lead in Virginia Opossums in Illinois

Alysha McDaniel[1], *Will Sander*
[1]University of Illinois

The Virginia opossum (Didelphis virginiana), the only marsupial in North America, is widespread in Illinois. The lifestyle of opossums is such that they are foragers, making them in frequent contact with soil, suggesting they are exposed to heavy metal contaminants in terrestrial environments. Additionally, they thrive in human-altered ecosystems including peri-urban environments. Lead is a naturally occurring, highly toxic metal that is abundant in the soil, primarily due to anthropogenic factors such as fossil fuel use and industrial facilities. Surprisingly, there are few studies on lead toxicity in the Virginia opossum. This is a pilot study to evaluate the blood lead burden of 15 opossums that presented to a wildlife medical clinic (WMC) compared to 15 wild-caught opossums trapped in grassland, maintained forest, or mixed ecotones. We hypothesize that the opossums presenting to the WMC will have significantly higher blood lead levels compared to their free-roaming counterparts due to symptoms of lead toxicity increasing their likelihood of trauma and injury. To date, 7 opossums have been evaluated for lead toxicity at the WMC and 5 opossums in the field, although it is expected to achieve the desired number of samples by the end of summer 2022. The average blood lead levels of the opossums at the wildlife medical clinic were three times higher than the levels of the wild-caught opossums, supporting the hypothesis that Virginia opossums are susceptible to lead-toxicity-induced physical ailments. In addition, collaboration with sites in Minnesota across various ecotones is ongoing as well as another wildlife medical clinic all to look at lead levels in this marsupial.

Poster Presentation #137

Osteofluorosis in a Free Ranging California Sea Lion

Margaret Martinez[1], Michelle Rivard[1], Jaclyn Isbell[1], Chelsea Sykes[2], Robert Poppenga[2], Padraig Duignan[1]

[1]The Marine Mammal Center, [2]California Animal Health and Food Safety Laboratory, School of Veterinary Medicine, University of California

A free ranging subadult male California sea lion (CSL) was admitted to The Marine Mammal Center with a primary clinical differential of a musculoskeletal disease. Radiographs demonstrated periosteal new bone proliferation on the mandible and both humeri. Despite care, the animal continued to decline, and euthanasia was elected. Necropsy revealed segmental circumferential periosteal new bone proliferation on the diaphysis of both femurs and humeri. New bone proliferation was also on both mandibles and the cranium. Histopathology established that the periosteal woven bone was formed from endochondral, and a lesser extent, intramembranous ossification radiating perpendicular to the pre-existing cortical bone, entrapping atrophied muscle bundles at the periphery, and with remodeling of the inner two thirds of the new bone trabeculae. Differentials for hyperostosis included a toxicosis, congenital disease, and hypertrophic osteopathy. Total fluoride levels within various bones of the case ranged from 4,000 – 9,700 ppm dw. Ribs from 4 unaffected CSLs of various ages and both sexes had an average total fluoride of 1,575 ppm dw, which is 6x lower than the rib fluoride levels in the present case. In comparison to known levels in cattle, the average total fluoride levels in the unaffected CSLs were almost twice as high as the bone fluoride levels of normal adult cattle. Meanwhile, the present case had 2.5x higher total fluoride levels than those found to cause hyperostosis in adult cattle. Therefore, this is the first case of osteofluorosis in a free ranging marine mammal. As the growth plates and teeth were not affected, this animal was likely exposed later in life; however, the exact source is not known as male CSLs have a large range and varied diet.

Poster Presentation #138

Disorders of Sexual Development in Free Ranging California Sea Lions

Margaret Martinez[1], Barbie Halaska[1], Robert Foster[2], Padraig Duignan[1]
[1]The Marine Mammal Center, [2]Department of Pathobiology, Ontario Veterinary College, University of Guelph

Disorders of sexual development (DSD) are extensively reported in domestic animals but are not documented in free ranging California sea lions (CSLs). Since 2016, 4 cases of disorder of sexual development were recorded at The Marine Mammal Center. This was out of 1,349 postmortems (prevalence of 0.3%). The cases included two phenotypically juvenile males and two adult females. The males had normal prepubertal testes and internal and external genitalia. There was one with a persistent penile frenulum and the other had a persistent paramesonephric duct (rudimentary uterus). The females had normal ovaries and external genitalia but internally one was completely bicornual with a persistent uterine septum (nonunion) and the other, segmental aplasia of the paramesonephric duct with no cervix and uterine body, and unilateral horn. Three of the cases were incidental findings; the male with a persistent paramesonephric duct (uterus) had posthitis, endometritis, cystitis, and pyelonephritis as the cause of death. DSDs occur due to sex chromosome and genetic abnormalities, hormonal or receptor disruptions, or exogenous substances such as endocrine disrupting chemicals in the environment. The cause of DSDs in these sea lions is unknown; further investigation is ongoing to characterize the sex chromosomes and presence of SRY. It is possible that pollutants within the food chain could be responsible for the lesions, as endocrine disrupting chemicals within the environment are shown to induce DSDs in fish and other wildlife; and several chemicals that cause significant disease, such as PCBs and DDTs, have already been detected in CSLs.

Poster Presentation #139

Mercury (Hg) Concentrations of Adult and Nestling Red-Shouldered Hawks (Buteo lineatus) in Central and Northeastern Wisconsin

Matthew Hanneman[1], PhD Cady Sartini[1], PhD Shelli Dubay[1], PhD Marie Perkins[1], PhD Jason Riddle[1], Eugene Jacobs[2], John Jacobs[3]
[1]University of Wisconsin - Stevens Point, [2]Linwood Springs Research Station, [3]N/A

Red-shouldered Hawks (Buteo lineatus) are forest-dwelling raptors that are threatened in Wisconsin and a species of conservation concern throughout much of the Great Lakes region. As top predators that forage on semi-aquatic prey, and commonly select for breeding territories in floodplain forests, Red-shouldered Hawks may be at an elevated risk of mercury (Hg) contamination. However, little is known about mercury exposure in the species. In June 2020, we collected blood and feather samples to investigate Hg concentrations in adult and nestling Red-shouldered Hawks in central and northeastern Wisconsin. The average raw (± SE) total mercury (THg) concentration (blood) in adults (n = 4) was 0.43 ± 0.05 µg/g and was 0.02 ± 0.003 µg/g in nestlings (n = 17). The average THg concentrations (feathers) for adults were 1.88 ± 0.21 µg/g (breast, n = 10), 2.21 ± 0.22 µg/g (back, n = 8), and 3.81 ± 0.70 µg/g (secondary 1 [s1], n = 8). THg concentrations (breast) did not differ significantly between sexes ($t_{0.05(2), 8} = 1.03$, $p = 0.34$), or between study sites ($t_{0.05(2), 8} = -0.32$, $p = 0.76$). Nestlings exhibited very low THg concentrations likely due to the dilution effect. Average inter-nest blood THg concentrations in nestlings ranged from 0.003-0.042 µg/g. Inter- and intra-tract feather THg concentrations were highly variable with the highest concentrations and variability found in s1 (3.81 µg/g, range: 1.57-7.48 µg/g). Percentage of inter-tract feather THg variability ranged from 16 – 86% across individuals. Based on these results and previous research, it is difficult to conclude whether Hg is adversely affecting Red-shouldered Hawks in Wisconsin.

Poster Presentation #140

Developing a Large Volume Filtration Method to Recover Infectious Avian Influenza Virus from the Aquatic Environment

Laura Hubbard[1], Carrie Givens[2], Erin Stelzer[3], Dana Kolpin[4], Rebecca Poulson[5]
[1]U.S. Geological Survey, [2]U.S. Geological Survey, [3]U.S. Geological Survey, [4]U.S. Geological Survey, [5]University of Georgia

Avian influenza virus (AIV) infects and sickens both wild birds and domestic poultry (e.g., turkey and chicken), that can result in economically devastating outbreaks. Currently, there are information gaps regarding how wild birds may contract AIV; whether aquatic habitat is a reservoir and source of AIV; and how AIV moves from migratory birds to poultry operations. While previous studies have examined methods to determine molecular AIV presence in water, few studies have examined recovery of infectious virus. To date, there is no widely accepted method to recover infectious AIV from environmental samples such as surface water. With the recent (i.e., 2022) highly pathogenic avian influenza (HPAI) A(H5N1) virus detections in the United States and Canada, incorporating environmental sampling of infectious HPAI into current surveillance is a critical, immediate need. The U.S. Geological Survey, along with partners at the Center for Disease Control and University of Georgia Southeastern Cooperative Wildlife Disease Study developed a method to recover infectious AIV from large-volume water filtration. Known titers of AIV H3N8 were spiked into 20 L carboys and various water matrices, pump speeds, filtering types, elution solutions, and concentration approaches were tested during methods development. The concentrated samples were inoculated into eggs and confirmed by polymerase chain reaction. The method was developed in two stages: 1) determine the most promising procedure (combination of pump speed, filtering type, elution solution, and concentration) to recover infectious AIV; 2) determine the minimum concentration for infectious AIV recovery and if biotic components significantly affect infectious AIV recovery. Confirmed AIV was isolated from all procedures tested in stage 1 and viral recovery efficiencies ranged from 5.07% to 165%. The final laboratory method will be field tested in 2022 to: (1) detect and recover naturally occurring infectious AIV in wetlands, and (2) examine persistence of these infectious AIVs.

Poster Presentation #141

Profiling Research on PFAS in Wildlife: A Systematic Map and bibliometric Analysis

Catharina Vendl[1], Dr Matthew D. Taylor[2], Dr. Jennifer Bräunig[3], Mr Matthew J. Gibson[4], Prof Daniel Hesselson[5], Prof G. Gregory Neely[6], Dr Malgorzata Lagisz[1], Prof Shinichi Nakagawa[1]
[1]University of New South Wales, [2]Port Stephens Fisheries Institute, New South Wales Department of Primary Industries, [3]Queensland Alliance for Environmental Health Sciences, Faculty of Health and Behavioural Sciences, The University of Queensland, [4]School of Computer Science and Engineering, University of New South Wales Sydney, [5]Centenary Institute and Faculty of Medicine and Health, The University of Sydney, [6]Dr. John and Anne Chong Lab for Functional Genomics, Charles Perkins Centre, Centenary Institute, and School of Life and Environmental Sciences, University of Sydney

Per- and polyfluoroalkyl substances (PFAS) are a group of 5000–10,000 organic chemicals that are exclusively synthetic. Due to their high persistence, PFAS are ubiquitous in the environment, humans, and wildlife. Chronic exposure or high levels of PFAS can lead to numerous adverse health effects such as reduced hatching success in birds and immunosuppression in mammals. Further, PFAS exposure can impact the conservation status of already threatened wildlife species. Since the early 2000s, hundreds of studies on PFAS in wildlife have been published. However, this plethora of published evidence makes it difficult to gain a comprehensive overview. Therefore, we collated and characterized the available evidence in a systematic evidence map and bibliometric analysis, enabling fast identification of emerging trends, evidence gaps and clusters. After systematic database searches and screening, we identified 598 documents as eligible for the systematic map. The most examined group was fish with Cyprinus carpio being the overall most frequently studied species, featuring in 6% of all studies. Interestingly, the second most studied were polar bears (Ursus maritimus) (4%). Temperate habitats were targeted in half of all studies and then, remote polar habitat came second, providing additional evidence that these areas are of significant interest. Popular topics included the bioaccumulation of PFAS within food webs, maternal transfer to the fetus and other adverse effects of PFAS. Notably, the legacy PFAS compounds, PFOS and PFOA, were the most researched, featuring in almost 100% of studies. Whereas new generation compounds like GenX, ADONA and PFECHS have become more researched, they are still not nearly as ‘popular’. In summary, large efforts have gone into research on PFAS in wildlife, yet terrestrial species other than birds and tropical regions are still highly underrepresented. Importantly, more detailed evidence is needed on how PFAS exposure threatens wildlife.

Poster Presentation #142

Thermal Processing Reduces PFAS Concentrations in Blue Food – Asystematic Review and Meta-Analysis

Catharina Vendl[1], Mr Patrice Pottier[1], Dr Matthew D. Taylor[2], Dr Jennifer Bräunig[3], Mr Matthew J. Gibson[4], Prof Daniel Hesselson[5], Prof G. Gregory Neely[6]

[1]Evolution and Ecology Research Centre and School of Biology Earth & Environmental Sciences, University of New South Wales Sydney, [2]Port Stephens Fisheries Institute, New South Wales Department of Primary Industries, [3]Queensland Alliance for Environmental Health Sciences, Faculty of Health and Behavioural Sciences, The University of Queensland, [4]School of Computer Science and Engineering, University of New South Wales Sydney, [5]Centenary Institute and Faculty of Medicine and Health, The University of Sydney, [6]Dr. John and Anne Chong Lab for Functional Genomics, Charles Perkins Centre, Centenary Institute, And School of Life and Environmental Sciences, University of Sydney

Per- and polyfluoroalkyl substances (PFAS) are ubiquitous in the environment and often ingested with food. PFAS exposure in people can have detrimental health consequences. Therefore, reducing PFAS burdens in food items is of great importance to public health. Here, we investigated whether cooking reduces PFAS concentrations in animal-derived food products by synthesizing experimental studies. Further, we examined the moderating effects of the following five variables: cooking time, liquid/animal tissue ratio, cooking temperature, carbon chain length of PFAS and the cooking category (oil-based, water-based & no-liquid cooking). In our systematic review searches, we obtained 512 effect sizes (relative differences in PFAS concentration between raw and cooked samples) from 10 relevant studies. These studies exclusively explored changes in PFAS concentrations in cooked seafood and freshwater fish. Our multilevel-meta-analysis has revealed that, on average, cooking reduced PFAS concentrations by 29%, although heterogeneity among effect sizes was very high (I2 = 94.65%). Our five moderators cumulatively explained 49% of the observed heterogeneity. Specifically, an increase in cooking time and liquid/animal tissue ratio, as well as shorter carbon chain length of PFAS (when cooked with oil) were associated with significant reductions in PFAS concentrations. The effects of different ways of cooking depended on the other moderators, while the effect of cooking temperature itself was not significant. Overall, cooking can reduce PFAS concentrations in blue food (seafood and freshwater fish). However, it is important to
note that complete PFAS elimination requires unrealistically long cooking times and large liquid/animal tissue ratios. Currently, literature on the impact of cooking of terrestrial animal produce on PFAS concentrations is lacking, which limits the inference and generalization of our meta-analysis. However, our work represents the first step towards developing guidelines to reduce PFAS in food via cooking exclusively with common kitchen items and techniques.

Poster Presentation #143

Biological Collections as a Resource in Wildlife Contaminant Research

Marie Perkins[1]
[1]University of Wisconsin - Stevens Point

Exposure to environmental contaminants is well known to negatively affect wildlife health. Understanding temporal and spatial exposure patterns of both emerging and legacy contaminants is a challenge. There are large knowledge gaps across species, regions, and time for even the most well-studied contaminants. Biological specimens stored in natural history collections offer an underused resource for wildlife health researchers. Wildlife specimens within these collections date as far back as the mid-1800s and up to the present day. Retrospective analyses of these specimens for contaminant exposure can provide important trends related to changes in contaminant releases and the efficacy of policies or regulations. Historic samples may prove particularly important to better understanding wildlife exposure to many emerging contaminants. Commonly, these substances were first released to the environment decades ago, however, the negative effects of exposure have only recently been determined (i.e. per- and polyfluoroalkyl substances; PFAS). Analyses of collection specimens can provide a sort of hindsight to better understand wildlife exposures when these contaminants were initially released. Biological collections also represent wildlife specimens from across vast areas of the globe, providing a resource for under-represented regions in wildlife exposure science such as the southern hemisphere. Collection specimens are often dried skins, comprised of tissues commonly analyzed for contaminants such as feathers, fur, bone, claws, and teeth, as well as wet (preserved in fluid) and frozen tissues or specimens. For many contaminants destructive analysis is often used (i.e. spectrophotometry methods) but new, non-destructive methods are emerging (i.e. X-ray fluorescence). Additionally, specimen information is available to researchers in a public database complied of >400 collections. Here I provide examples of recent research utilizing biological collections to better understand contaminant exposure in wildlife and I highlight how researchers can take better advantage of these collections moving forward.

Poster Presentation #144

How Will the End of Bear Bile Farming in Vietnam Influence Consumer Choice?

Dr Elizabeth Davis[1], Dr Diogo Verissimo[2], Mr Brian Crudge[3], Mr Son Sam[4], Mr Dung Cao[4], Mr Po Ho[4], Ms Nhung Dang[4], Mr Hien Nguyen[4], Prof Trung Cao[4], Dr Jenny Glikman[5]
[1]San Diego Zoo Wildlife Alliance, [2]Department of Zoology, University of Oxford, [3]Free the Bears, [4]Vinh University, [5]Instituto de Estudios Sociales Avanzados

The Vietnamese Government committed to closing all bear farms in the country by 2022. Some researchers have expressed concerns that ending the commercial farming of bears, while demand for bear bile persists, could lead to increased hunting pressure on wild bear populations. In this article, we used mixed methods of questionnaires, Discrete Choice Experiments (DCEs), and interviews to investigate current consumer demand for bear bile in Vietnam, with a specific aim of understanding the potential for consumers to seek out wild bear bile. We sampled at seven areas across the country of Vietnam (total respondents = 2,463). We found low use of farmed and wild bear bile. Despite widespread belief in farmed and wild bear bile's efficacy, we found that individuals were apathetic about continuing to use bear bile. Coupled with a strong preference for using synthetic bear bile over wild and farmed bear bile found in the DCEs, we posit that bear bile consumers in Vietnam will be willing to use non-animal-based products, including bear bile plant and Western medicine, to treat future ailments.

Poster Presentation #145

Impacts of the COVID-19 Pandemic on Wildlife Rehabilitation in the United States

Ellen Haynes[2], Lindsey Guerra[1], Dr. Kyle Woosnam[1], Dr. Michael Yabsley[1,2]
[1]Warnell School of Forestry and Natural Resources, University of Georgia, [2]Southeastern Cooperative Wildlife Disease Study, University of Georgia College of Veterinary Medicine

Efforts to limit the spread of the SARS-CoV-2 virus following the World Health Organization's declaration of a global pandemic on March 11, 2020 led to numerous societal changes. The potential role of wildlife in transmission resulted in wildlife rehabilitators assuming responsibility for keeping both wildlife and people safe. We constructed and disseminated a 33-question online survey instrument to wildlife rehabilitators to characterize the impact of the pandemic on their caseloads, learn what measures they had taken to protect wildlife and humans, and assess their knowledge of SARS-CoV-2. The survey was available from October to December 2020, and we received 122 responses: 119 from 38 US states and three from two Canadian provinces. Respondents had an average of 15 years of experience, with 47.9% working out of their homes and 57.9% working for an organization. Of the responses, 91.4% said that the COVID-19 pandemic impacted their rehabilitation activities; some centers closed completely or partially and, of those that remained open, many saw an increase in their caseloads, with the total number of admissions 66.4% greater in 2020 than in 2019. However, there was variation among rehabilitators, with 29.5% reporting a decrease in admissions in 2020 and 15% reporting no change. Increased admissions may be explained by people spending more time outdoors during the lockdown and encountering animals in need of assistance more frequently. Rehabilitation centers modified procedures to protect both animals and humans, including quarantining animals, instituting curbside animal pick-up, and cleaning shared spaces more often. Personal protective equipment was also used more frequently. Funding for half of the respondents decreased due to event cancellations and economic uncertainty. Knowledge of SARS-CoV-2 varied amongst rehabilitators; in early stages of the pandemic, lack of scientific research about the virus resulted in wildlife rehabilitators relying on their personal experience and general pandemic guidelines.

Poster Presentation #146

Wilderness City: Health Surveillance in Urban Red Foxes Reveals Implications for Public Health in Whitehorse, Yukon, Canada

Cassandra Andrew[2], N. Jane Harms[1], Maud Henaff[1], Kristenn Magnusson[1], Jodie Pongracz[1], Emily Jenkins[3], Cody Malone[3], Temitope Kolapo[3]

[1]Department of Environment, Yukon Government, [2]School of Population and Public Health, University of British Columbia, [3]Zoonotic Parasite Research Unit, Department of Microbiology, Western College of Veterinary Medicine

Interactions with wildlife can have health benefits for people, however, potential public health risks associated with living in close proximity to wildlife can include exposure to zoonotic pathogens. The red fox (Vulpes vulpes) population living within Whitehorse, Yukon, Canada is increasing. Their urban presence has raised concerns about Echinococcus multilocularis, a zoonotic parasite, as well as other pathogens, such as rabies, that may affect human health. A pilot project was initiated using samples from opportunistically-collected carcasses found throughout Whitehorse to better understand which pathogens, including those of zoonotic importance, foxes carry. Red fox carcasses (n=38) from neighbourhoods in Whitehorse were collected between 2014-2021. The majority of foxes had been hit by a vehicle (n=25), other causes of death included gunshot, drowning, and predation. Additionally, red fox scat samples (n=100) were collected from den sites in Whitehorse between May-August, 2021. Samples collected from carcasses were tested for Echinococcus spp. (0/12 positive), Trichinella spp. (2/13 positive), distemper virus (0/14 positive), and rabies virus (0/29 positive). Fecal analysis revealed a low prevalence of Toxascaris spp. (4/11 positive), Taeniid spp. (1/11 positive), and coccidia spp. (1/11 positive) in the sampled animals. All samples were negative for Uncinaria spp.. Analysis of the scat samples revealed a similar range and prevalence of infections for Toxascaris spp. (27/100 positive), Taeniid spp. (21/100 positive), coccidia spp. (Cytoisospora spp.) (20/100 positive) and Uncinaria spp. (1/100 positive). Giardia (1/28 positive) and cryptosporidium (2/28 positive) were detected in a subset of scat samples. None of the scat samples were positive for Echinococcus spp. on copro-PCR. While several of the parasites detected in urban foxes are of zoonotic importance, we found no evidence of E. multilocularis or rabies virus in this subsample of Whitehorse red foxes.

Poster Presentation #147

Causes of Wildlife Morbidity and Mortality Identified Using Wildlife Rehabilitation and Post-Mortem Data in Canada

Claire Jardine[2], Meagan King[1,2], Jolene Giacinti[2], Sara Dubois[3,4], Stéphane Lair[5], Jane Parmley[2]
[1]University of Manitoba, [2]University of Guelph, [3]University of British Columbia, [4]British Columbia Society for the Prevention of Cruelty to Animals, [5]Université de Montréal

The health and welfare of wild animals are of increasing concern, yet there are very few large-scale data syntheses examining how causes of wildlife mortality and morbidity vary across time, space, and taxa. Our objectives were to: 1) identify the main causes of morbidity and mortality for Canadian wildlife detected through the Canadian Wildlife Health Cooperative (CWHC) and wildlife rehabilitation centers (WRC), and 2) assess the utility and complementarity of these data sources to further our understanding of wildlife health. Records for 18,540 animals submitted to the CWHC (2009-2019) and 144,846 animals admitted to 19 WRC (2015-2019) are described. CWHC cases (mortality) were examined by pathologists and grouped by the presence/absence of 5 diagnostic categories (trauma, emaciation, infection/inflammation, toxicity, other). CWHC animals could also be classified as 'killed due to real or perceived human-wildlife conflict' based on finder history. WRC admissions were categorized by health issue (according to initial intake records) and based on reported/observed situational reasons for admission (parental loss, unsafe/unsuitable location, nest/habitat disturbance, illegal possession, and abnormal behavior). For both CWHC and WRC datasets, the main reason for submission/admission was trauma (44 and 48% of animals, respectively), especially vehicle collisions (7 and 11%) and window/building strikes (5 and 7%). Many other WRC admissions were due to parental loss (28%), cat attacks (6%), and immature animals being found in unsafe/unsuitable locations (6%). Most other CWHC mortalities were caused by infections (27%) and emaciation (23%). Relatively few birds, amphibians, and reptiles submitted to CWHC were killed due to human-wildlife conflict but 22% of mammals were killed for this reason, highlighting the taxonomic differences in the perceived threat of wildlife to finders, and, therefore, their response. Together, these data sources highlight key issues impacting the health and welfare of wild animals in Canada.

Poster Presentation #148

Asymptomatic Carriers of Beak and Feather Disease Virus: Lessons Learnt from Infection in a Wild Parrot Population

Berta Blanch-Lázaro[1,2], Dr Anthony Chamings[2,3], Dr Raoul F.H. Ribot[1], Dr Mathew L. Berg[1,4], Prof Soren Alexandersen[2,3,5,6], Prof Andrew T.D. Bennett[1]

[1]Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, [2]Geelong Centre for Emerging Infectious Diseases, [3]School of Medicine, Deakin University, [4]Parks Victoria, [5]Barwon Health, University Hospital Geelong, [6]Statens Serum Institut (SSI)

Screening for infectious diseases is a major part of biosecurity – both in conservation programs and the pet trade – and is critical to prevent their spread. This is particularly important when infection is not always associated with clinical disease. Beak and feather disease virus (BFDV) is a circovirus that mostly affects Psittaciformes. To date, limited attention has been given to the pathogenesis and epidemiology of BFDV in asymptomatic carrier species. Crimson rosellas (Platycercus elegans) are abundant parrots in south-east Australia, which have high BFDV prevalence without showing clinical signs. However, seroconversion with low antibody titres and clearing BFDV from blood has been described in this species, suggesting they may have evolved mechanisms to tolerate BFDV infection. We investigated: [1] if BFDV persisted in tissues, similarly to other circoviruses, [2] if BFDV showed a particular tissue tropism, and [3] if BFDV antibodies stored long-term on filter-paper at room temperature – a widespread practice in BFDV serology – degraded. We sampled 66 wild P. elegans that were culled for pest control purposes, quantified BFDV load in 10-12 tissues per bird using qPCR and tested for antibodies at different storage durations using haemagglutination inhibition (gold standard test). We revealed that while BFDV replicated to high levels in subadult birds, in adults it was detected at much lower levels and fewer tissues (and never in blood). Adults had antibodies against BFDV more often than subadults. Highest loads were detected in bursa (subadults only), spleen and skin. Antibody detection on filter-paper decreased over time, suggesting degradation of antibodies in storage. Our study provides important insights into the current screening practices (mostly done on blood), and has major implications for future assessments of BFDV-status and associated conservation programs worldwide. We highlight the need for new BFDV screening guidelines to improve the reliability of future studies.

Poster Presentation #149

Quantitative Measurements of Chronic Wasting Disease Prions Recovered from Swab Samples and Environmentally Relevant Surfaces

Qi Yuan[1], Gage Rowden[2], Peter Larsen[2], Shannon Bartelt-Hunt[3], Jason Bartz[1]
[1]Creighton University, [2]University of Minnesota, [3]University of Nebraska-Lincoln

Chronic wasting disease (CWD) has been identified in 26 states in the United States, three provinces in Canada, and recently emerged in Scandinavia. The association of CWD prions with environmental materials such as soil, plants, and surfaces may enhance the persistence of CWD prion infectivity in the environment exacerbating disease transmission. Identifying and quantifying CWD prions in the environment is significant for prion monitoring and disease transmission control. A systematic method for CWD prion quantification from associated environmental materials, however, does not exist. In this study, we developed a rapid method for extracting prions from swabs and quantifying swab-recovered CWD prions from different types of surfaces including glass, stainless steel, and wood. We found that samples dried on swabs were unfavorable for prion extraction, with the greatest prion recovery from wet swabs. Using this swabbing technique, the recovery of CWD prions dried to glass and stainless steel were approximately 30% in most cases, whereas that from wood was undetectable by the conventional techniques for prion detection. Using real time-quake induced conversion (RT-QuIC), an ultrasensitive method, the detection limit of CWD prion from stainless steel was increased by 4 orders of magnitude. More importantly, the RT-QuIC detectability of CWD prion recovered from stainless steel surface using this rapid method was similar (< 1 Log) to the original CWD prion load. Our findings provide a rapid, ultrasensitive method for prion detection from contaminated surfaces which can be applied to identify and quantify prion contamination in natural settings.

Poster Presentation #150

Assessment of Standardization for Data Analysis for RT-QuIC-based detection of Chronic Wasting Disease

Gage Rowden[1,2], Dr. Catalina Picasso-Risso[2,3], Manci Li[1,2], Marc Schwabenlander[1,2], Dr. Tiffany Wolf[2,3], Dr. Peter Larsen[1,2]

[1]Department of Veterinary and Biomedical Sciences, University of Minnesota, [2]Minnesota Center for Prion Research and Outreach, University of Minnesota, [3]Department of Veterinary Population Medicine, University of Minnesota

CWD is a transmissible spongiform encephalopathy affecting cervids caused by prions accumulating as amyloid fibrils in lymphoid and CNS tissues. Recently, real-time quaking-induced conversion (RT-QuIC), which quantifies amyloid formation as relative fluorescent units (RFU), has rapidly become a viable option for CWD diagnosis. However, there is little consensus on the best approach to interpret RT-QuIC data. Data are typically assessed by a predetermined number of replicates crossing a threshold some number of standard deviations above the average RFU of the entire plate, and replicates are given a rate of amyloid formation (RAF) based on the time to threshold. Given the potential use of RT-QuIC for CWD regulatory testing, it is imperative to identify a standardized method for determining CWD status in a sample from RT-QuIC data. Here, we assessed variabilities in RT-QuIC substrate batches and plate readers and explored the potential use of Maxpoint Ratios (MPR: maximumRFU/backgroundRFU) to improve consistency in RT-QuIC results by retrospectively analyzing RT-QuIC results from 773 white-tailed deer lymph node samples. Our results reveal a distinct MPR threshold of two (i.e. twice the background RFU) for dichotomizing RT-QuIC runs. Differences of MPRs in control samples were observed between plate readers (P-value < 0.001) while none were observed between substrate batches (P-value > 0.4). RAF vs. MPR showed little correlation (r: 0.5449, 95%CI: 0.494-0.592). MPR results showed excellent concordance (κ: 0.957, 95%CI: 0.875-1.000) with ELISA results. Our findings suggest that MPR is a viable option for future diagnostic purposes using RT-QuIC without the need for multiple comparisons analysis.

Poster Presentation #151

Detection of an Enzootic Mycoplasma ovipneumoniae Strain in Alaska, USA, Wildlife

Kimberlee Beckmen[1], Camilla Lieske[1], Robert Gerlach[2], Marla Francis[3], Kimberly R. Andrews[4], E. Frances Cassirer[5]
[1]Alaska Department of Fish and Game, [2]Alaska Department of Environmental Conservation, [3]Washington Animal Disease Diagnostic Laboratory, [4]University of Idaho, [5]Idaho Department of Fish and Game

In 2018, Mycoplasma ovipneumoniae was detected in free-ranging caribou (Rangifer tarandus grantii) and Dall's sheep (Ovis dalli dalli) in Alaska, USA. Evaluation of additional nasal swabs and archived tissues from 2004 onward for M. ovipneumoniae suggested that this bacterium was widespread geographically and temporally in populations of both species. Furthermore, most detections by PCR and culture were from presumably healthy hunter harvested and live capture release animals without evidence of mass mortality events or reduced lamb survival associated with M. ovipneumoniae in bighorn sheep (Ovis canadensis). Multilocus sequence typing (MLST) of four loci identified a single novel apparently stable strain type of M. ovipneumoniae in 11 Dall's sheep and 15 caribou in multiple populations across Alaska sampled over a period of 15 years (2004-2019). This strain type differs from those detected to date from wild or domestic sheep (Ovis aries) or goats (Capra aegagrus hircus) tested in Alaska or the lower 48 USA states. Evaluation of the genomic differences through full genome sequencing placed the Alaska strain in a lineage that is separate from, but closely related to, other sheep strains. This strain has a substantially lower number of genes resulting in a smaller genome size of around 400 fewer genes compared to other sheep or goat strains. While the population health implications of this strain are unknown, it has not been associated with population-wide mortality events or declines. The presence of this strain does not decrease the potential risk from the introduction of a pathogenic M. ovipneumoniae strain associated with severe disease in other wildlife populations, therefore continued monitoring for signs of disease and additional strains is important.

Poster Presentation #152

Detection of Chronic Wasting Disease (CWD) Prion in Blood by Real-Time Quaking-Induced Conversion (RT-QuIC)

Estela Kobashigawa[1], Shuping Zhang[1], Michael Zhang[1], Sherri Russell[2], Jasmine Batten[2]
[1]University of Missouri, [2]Missouri Department of Conservation

Introduction: CWD is a progressive, fatal, neurological disease of cervids. The mechanism of disease involves the conversion of a native, protease-sensitive cellular protein (PrP-C) to a protease-resistant, self-replicating conformation, denoted PRP-Sc. Early diagnosis is the key to successful control and prevention of CWD. Postmortem diagnosis relies heavily on IHC or ELISA screening followed by IHC confirmation of positive results. For live-animal testing, IHC on rectal mucosa associated lymphoid tissue has been proposed as a useful, but imperfect method. RT-QuIC exploits the ability of PrP-C to induce the conversion of PrP-C to PrP-Sc. RT-QuIC is highly sensitive and allows real-time detection of PrPSc as the conversion takes place. The goal of this project is to optimize RT-QuIC assay for the detection of PrP-Sc in samples that are easy to obtain but have a low prion concentration.

Material and methods: postmortem blood samples were collected from 13 CWD IHC positive and 94 CWD negative animals. Platelet-rich plasma were analyzed by RT-QuIC using a buffer system with NaCl or NaI. Blood samples from IHC-positive animals were further analyzed by RT-QuIC with or without ASR1 pre-concentration. RT-QuIC reactions were carried in FLUOstar Omega Microplate Reader under the following conditions: 95 µL master mix (320 mM NaCl or NaI, 20mM Na2HPO4, 1mM EDTA and 0.1 mg/mL rPrP), 3µL sample at 10-1 to 10-3 dilutions, 42℃, reading every 15 min, gain at 1800, 1 min shaking at 700 rpm and 1 min resting, and 188 cycles.
Results: RT-QuIC positive rate on blood samples from CWD positive animals were 82.05% (ASR1/NaI), 74.36% (ARS1/NaCl), 66.67% (NaI) and 51.28% (NaCl). RT-QuIC positive rate on blood samples from CWD negative animals was 4.25% using NaI without ASR1 pre-concentration.

Conclusions: Introduction of ASR1 pre-concentration and NaI improves RT-QuIC sensitivity and blood may be used for CWD testing.

Poster Presentation #153

Implementing a Veterinary Forensics Approach to Investigate Chronic Wasting Disease at a Deer Carcass Disposal Site

Marc Schwabenlander[1], Gage Rowden[1], Suzanne Stone[1], Rachel Shoemaker[1], Laramie L. Lindsey[1], Jonathan D. Oliver[2], Linda Glaser[3], Michelle Carstensen[4], Jason C. Bartz[5], W. David Walter[6], Roxanne J. Larsen[1], Tiffany M. Wolf[7], Peter A. Larsen[1]

[1]Department of Veterinary and Biomedical Sciences, College of Veterinary Medicine, University of Minnesota, [2]Division of Environmental Health Sciences, School of Public Health, University of Minnesota, [3]Minnesota Board of Animal Health, [4] Minnesota Department of Natural Resources, [5] Department of Medical Microbiology and Immunology, School of Medicine, Creighton University, [6]U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, [7]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota

Chronic wasting disease (CWD) has been confirmed in 30 US states, three Canadian provinces, Sweden, Norway, Finland, and South Korea. Although its geographic origin is speculative, much of the disease spread in North America over the past seven decades is attributed to human activities that include the movement of live cervids and cervid carcasses. Given the potential for CWD-causing prions to remain infectious within the environment, disposal of CWD-positive animal remains, whether from free-ranging or captive sources, can play an important role in the transmission of CWD. Regulatory agencies provide guidance and proper disposal opportunities of cervid carcasses for the control of CWD in endemic areas and to reduce the risk of introduction to new areas. We employed a veterinary forensics approach to investigate the existence of CWD-positive materials at an illegal carcass dumping site in connection with a CWD-positive captive cervid facility. Animal remains were examined to determine species, age, sex, relatedness, and CWD status. We utilized advanced anatomic, entomologic, genetic, and prion amplification methods to discover CWD-positive remains across multiple age classes of white-tailed deer (Odocoileus virginianus). Carcass remains appeared to be present at the site for weeks to years. CWD prions were detected via RT-QuIC in 13 of 49 carcass samples with 9 of 13 from fawns, 1 of 13 from a yearling, 2 of 13 from adults, and 1 of 13 from a deer of unknown age. We also identified CWD-positive fly larvae associated with positive remains. Our multi-methods approach provides the foundation for veterinary forensic investigation of CWD spread by means of cervid carcasses.

Poster Presentation #154

CWD Sentinels: Detecting Environmental Prion Protein (ePrP) Via Surfaces for the Early Discovery of Chronic Wasting Disease

Marc Schwabenlander[1], Gage Rowden[1], Qi Yuan[2], Erik Hildebrand[3], Patrick Hagen[3], Shannon L. Bartelt-Hunt[4], Jason C. Bartz[2], Tiffany M. Wolf[5], Peter A. Larsen[1]

[1] Department of Veterinary and Biomedical Sciences, College of Veterinary Medicine, University of Minnesota, [2]Department of Medical Microbiology and Immunology, School of Medicine, Creighton University, [3] Minnesota Department of Natural Resources, [4]Department of Civil and Environmental Engineering, University of Nebraska-Lincoln, [5]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota

Chronic wasting disease (CWD) continues to be detected in new regions throughout North America utilizing traditional diagnostic tests (e.g., immunohistochemistry (IHC) and enzyme-linked immunosorbent assay (ELISA)) on post-mortem tissue samples. Although IHC and ELISA platforms are accurate for such purposes, scientists are developing highly sensitive prion detection methodologies that can utilize non-tissue samples to fight the war against CWD in new ways. Real-time quaking-induced conversion (RT-QuIC) is one such assay proven to be a more sensitive tool for CWD prion (PrPsc) detection than current antibody-based methods. Similar to environmental DNA (eDNA) advances for the detection of pathogens and discovery of invasive and rare species in aquatic and terrestrial environments, our work investigates a rapid method for extracting prions from swabs of environmental surfaces to detect PrPsc when paired with the RT-QuIC assay. Laboratory investigation of the methods demonstrated recovery of PrPsc at 25% to 99%, with the majority around 30%. We deployed particular surfaces shown to effectively bind misfolded prions as environmental prion protein (ePrP) sentinels in food sources of captive and free-ranging herds known to have CWD at various prevalence. We were able to detect PrPsc in natural settings using the swabbing and extraction methods in conjunction with RT-QuIC. Additionally, CWD prevalence of the animals interacting with the sentinels coincided with intensity of PrPsc detection - in a herd with 1 of 12 IHC positive animals, 1 of 16 swabs were RT-QuIC positive, and in a herd with 13 of 19 IHC positive animals, 19 of 34 swabs were RT-QuIC positive. Our findings open the possibility for ePrP detection through non-invasive methods for real-time surveillance and discovery of CWD and other protein misfolding diseases.

Poster Presentation #155

Sentinels of Emerging Infectious Diseases in South American Wildlife: The Role of Zoos and Rescue Centers in Identifying Health Threats to Pudu (Pudu puda) in Chile

Ezequiel Hidalgo-hermoso[1], Javier Cabello[2], Francisco Ruiz Fons, Sebastián Muñoz, Galaxia Cortes, Frank Vera, Carolina Valencia, Sebastián Celis, Dario Moreira, Paulina Sepúlveda, Jose Pizarro Lucero, Victor Neira, Adriana Santodomingo, Sofia Robbiano, Rocio Vicencio, Juan Verasay, Nour Abuhadba Medrano, Carolina Ortiz[4], Ronni Atencio, Belén Bustamante, Ignacio Kemec[4], Rocio Lagos[5], Galia Ramirez, Pedro Abalos, Barbara Parra, Antonio Garnham, Ananda Muller, Fernando Esperon

[1]Fundacion Buin Zoo, [2]Centro de conservación de la biodiversidad, Chiloé-Silvestre. Nal Bajo, [3]Health & Biotechnology (SaBio) group, Instituto de Investigación en Recursos Cinegéticos IREC (CSIC-UCLM-JCCM), [4]Departamento de Ciencia Animal, Facultad de Ciencias Veterinarias, Universidad de Concepción, [5] Escuela de Medicina Veterinaria, Facultad de Agronomía e Ingeniería Forestal, Facultad de Ciencias Biológicas y Facultad de Medicina, Pontificia Universidad Católica de Chile, Avenida Vicuña Mackenna 4860, Santiago, Chile

Wildlife pathogens surveillance is essential for an early identification of emerging diseases/threats that pose a health risk to animal and human populations. Collateral benefits of this activity are the improvement of regional preparedness, estimating the impact of the pathogens on ecosystems, and identifying areas that should be prioritized for funding. However, Chile lacks of Governmental funding to monitor diseases that affect wild animals and scientific literature regarding the susceptibility of native wildlife to infectious pathogens is rather limited. Here we present the findings of 10 years of surveillance on the Southern pudu (Pudu puda) using laboratory diagnosis, clinical records and pathological findings to detect the presence and quantify the impact of viral, bacterial and protozoan agents in Chile. In order to assess whether infectious diseases are underdiagnosed in Southern pudus from Chile, samples from wild (140) and captive pudus (55) were tested through genetic screenings (blood/stool/tissues) and serological assays targeting adenovirus, herpesvirus, pestivirus, rotavirus, hepatitis E, circovirus, Sars-Cov 2, Brucella abortus, Leptospira interrogans, Mycobacterium bovis, Mycobacterium avium paratuberculosis, Chlamydia abortus, Coxiella burnetii, Bartonella spp., hemoplasmas, Anaplasma spp., Piroplams, Neospora caninum and Toxoplasma gondii. We found evidence of exposure or infection to 12 infectious agents including the first report of CaHV-2, Mycoplasma ovis-like, Anaplasma sp. and Babesia sp. in Chile, and the first report of Chlamydophilla abortus in Chilean wildlife. Clinical and pathological findings suggest that viral pathogens could be causing infectious abortions and malignant catarrhal fever in pudu. Furthermore, our results point that infectious diseases are an emerging and neglected threat for wild and captive pudus in Chile, and that this cervid species has the potential to host zoonotic agents. More epidemiologic and pathology studies are urgently needed to understand the role of infectious diseases in the cases of dog attacks and runovers in free-ranging populations of pudu in Chile.

Poster Presentation #156

No Abstract Assigned

Poster Presentation #157

Proposing a New Approach for CSFV Detection Using Environmental Samples and Swabs Wiped on the Skin

Kei Nabeshima[1], Mayumi Yokoyama[2], Shun Takagi[2], Taro Sugimoto[2], Takeo Kuriyama[2], Manabu Onuma[1]

[1]National Institute for Environmental Studies, Japan, [2]Institute of Natural and Environmental Sciences, University of Hyogo

Classical swine fever virus (CSFV) is one of the most seriously damaging epizootic viruses in swine production. This virus infects only pigs and wild boars and is highly contagious and virulent. Nationwide survey of CSFV have been conducting using tonsils or blood correcting from dead bodies or controlled killed individuals. However, the sample number often did not reach minimum requirement (299 samples per each prefecture). One of the causes is the difficulty of sampling of tonsils or blood. Thus, utilization of other sample for surveillance materials such as a swab wiped over skin surface and environmental material (water and soil) were evaluated. We confirmed that a swab wiped on the skin of a positive individual showed CSFV positive with qPCR and conventilal PCR. In addition, water and soil collected around the dead body of a CSFV positive individual also showed positive results. Then, 180 swabs wiped over skin surface obtained from controlled killed wild boars and 106 water samples were collected from Hyogo prefecture showed CSFV prevalence of 13.2% (100/760). 8 swabs out of 180 showed CSFV positive. On the other hand, there were no positive in water samples. The results suggest that the swabs wiped on the skin can be used for materials of CSFV surveillance. However, further methodological improvement should be needed when utilizing water. This research was performed by the Environment Research and Technology Development Fund (JPMEERF20204G01) of the Environmental Restoration and Conservation Agency of Japan.

Poster Presentation #158

No Abstract Assigned

Poster Presentation #159

Detection of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) Utilizing Reverse transcriptase Real-Time Polymerase Chain Reaction (RT-rtPCR) on Alternative Sample Types

Katie Luukkonen[1], Jessica Jennings-Gaines[1], Kara Robbins[1], Nadine Vogt[2], Adam Vogt, William Edwards[1], Dr. Samantha Allen[1]
[1]Wyoming Game and Fish Department, [2]University of Guelph

Rabbit hemorrhagic disease Virus 2 (RHDV2) can cause acute fatal disease in lagomorphs resulting in devastating impacts on some wild populations. This disease is relatively new to North America, and was detected in Wyoming, USA, in December of 2020. Detection of this disease primarily relies on ELISA and RT-rtPCR utilizing liver tissue. For flexibility in sampling as well as providing a safer means of sample collection, we validated two alternative sample types for the detection of RHDV2. Filter paper (n=77) and ear punch biopsies (n=66) were evaluated using RT-rtPCR, in comparison to liver (as the gold standard for comparison). From December 2020 to July 2021, samples (ears, filter blood and liver) were collected from wild lagomorphs (cottontails and jackrabbits) as part of the Wyoming game and fish RHDV2 surveillance program. Each sample was tested and compared at initial sampling as well as over time (e.g., ear punches - 1, 3, 5, and 7 weeks post-sampling; filter paper - 2, 4, 6 weeks post-sampling). Both filter paper and ear punch biopsies had 100% sensitivity and specificity at initial sampling. Ear punches were evaluated over time and remained at 100% sensitivity where filter paper evaluated over time had a sensitivity over 96%. The maximum mean difference in Ct value (6.0) of both alternative methods still resulted in a PCR positive test with the average Ct values of liver samples at 15.1 (95% CI: 14.7-15.5). We determined that filter paper and ear punches are adequate sample alternatives to liver for RHDV2 surveillance in wildlife populations. These alternative samples will provide flexibility in surveillance, increase opportunity for sample submissions and provide a safer approach to sample collection in areas with zoonotic disease risk. Further research into alternative sample types for additional diseases could increase the success of future wildlife surveillance and monitoring programs.

Poster Presentation #160

Nested and RT-PCR Assays for Detection of Elaeophora schneideri from Infected Host Tissues in Wyoming, USA

Kara Robbins[1], *Samantha Allen*[1,2]
[1]Wyoming Game and Fish Department (Veterinary Services), [2]University of Wyoming (Department of Veterinary Sciences)

Elaeophora schneideri, the arterial worm, is a parasitic filarial nematode that infects a variety of domestic and wild ruminants. Mule and black-tailed deer are thought to be the definitive hosts for this parasite and are often not adversely impacted by infection. Aberrant hosts of the parasite include a number of wildlife species, such as moose (*Alces alces*). Infection in aberrant hosts can cause significant morbidity and mortality. Historically, Wyoming has relied on post-mortem tissues and visual identification of worms in moose carcasses to determine cause of mortality and to assess the distribution of *E. schneideri*. While these data have contributed to an overall understanding of disease epidemiology, moose in Wyoming are still impacted by *E. schneideri* and, due to the parasite's pathenogenesis, it is often difficult to identify and confirm infections. Previously published molecular tools are not sensitive enough to detect low level *Elaeophora* infections. Therefore, developing new molecular tools can assist in identifying the parasite in different tissues and at different stages of infection. We used adult *E. schneideri* samples and primers designed to detect filarial nematode CO1 DNA and the subsequent sequencing data to design a nested PCR and a RT-PCR for detecting *E. schneideri* DNA in infected tissues. Use of primers specific to *E. schneideri* have increased the sensitivity of PCR testing in multiple tissue types (e.g. brain, carotid artery, tongue, nasal cavity, forehead skin, and ear tips). These PCR assays can improve detection in post-mortem samples and have the potential for use in ante-mortem sampling. This would allow opportunities for improved herd health surveillance and, in the long run, provide field managers with additional tools to discern disease and make conservation decisions.

Poster Presentation #161

Agreement of Point-of-Care Blood Uric Acid Meter and Benchtop Chemistry Analyzer in Eastern Box Turtles (Terrapene Carolina Carolina)

Carly Clark[1], Matthew C Allender[1,2,3], Laura Adamovicz[1,2], Julie Sheldon[4], Kaitlin Moorhead[1], Kelcie Fredrickson[1]

[1]Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois, [2]Veterinary Diagnostic Laboratory, College of Veterinary Medicine, University of Illinois, [3]Chicago Zoological Society/Brookfield Zoo, [4]Small Animal Clinical Sciences, College of Veterinary Medicine, University of Tennessee

Uricotelic reptiles excrete uric acid as the primary product of protein metabolism and elevated plasma uric acid concentrations can indicate renal compromise in these species. Plasma uric acid concentrations can be measured using point-of-care (POC) meters or gold-standard benchtop chemistry analyzers. POC meters are relatively inexpensive, readily accessible, and require a smaller blood volume than benchtop analyzers, making them an attractive option for renal health screening. However, their performance has not been compared to benchtop analyzers in reptiles. The objective of this study was to assess agreement in uric acid concentration between a POC meter and a benchtop chemistry analyzer in eastern box turtles (EBT, Terrapene carolina carolina). We hypothesized that method agreement would be poor, consistent with findings in avian species with similar renal physiology. Whole blood samples were collected from 56 wild EBTs in Tennessee and Illinois, USA. Uric acid concentrations were measured on a POC meter using whole blood (WB POC), frozen-thawed plasma (Plasma POC), and on a benchtop analyzer using frozen-thawed plasma (Plasma Benchtop). Agreement between methods and sample types was assessed using Kendall's tau, general linear mixed models, Passing-Bablok regression, and Bland-Altman plots. Poor to moderate correlation was present between each of the methods and sample types (tau: -0.06 – 0.46). Mixed models revealed systemic bias between all measurement methods ($p < 0.0001$). Proportional error was present when comparing WB POC vs. Plasma POC and Plasma POC vs. Plasma Benchtop. Differences between methods fell outside of clinically acceptable limits, indicating that the POC meter is an inadequate substitute for the benchtop analyzer in EBTs. Our findings amplify concerns with POC measurement found in Magellanic penguins (Spheniscus magellanicus) and American flamingos (Phoenicopterus ruber), suggesting that POC meter uric acid determination may not be accurate in non-mammalian species.

Poster Presentation #162

Application of Precision Medicine to Detect Age-Related Changes in the Immunome of Black Rhinoceros (Diceros bicornis)

AA Aguirre[1], Molly Corder[1,2], Weidong Zhou, Timothy P. Cleland, Parker Penningtom, Jennifer Nagashima, Emanuel Petricoin, Budhan Pukazhenthi
[1]George Mason University, [2]Smithsonian Conservation Biology Institute, [3]Smithsonian Museum Conservation Institute

The black rhinoceros (Diceros bicornis) is critically endangered due to poaching pressures in-situ. The ex-situ population serves as a genetic reservoir against impending extinction threats. However, many black rhinoceroses in human care (zoos) display unusual disease syndromes related to immune-metabolic dysfunction not typically observed among their wild counterparts. The etiology of these disease syndromes remains poorly understood. Further, older animals have a higher risk for developing these disease syndromes.

We analyzed the proteome of peripheral blood mononuclear cells (PBMCs) to investigate the physiological underpinnings of age as it relates to disease. PBMCs were isolated using a Ficoll® density gradient from whole blood (n = 38 samples) collected from 14 rhinoceroses housed in the US. Extra cellular proteins were extracted, digested with Trypsin, and processed for mass spectrometry. The resulting mass spectral profiles were mapped against the Uniprot black rhinoceros proteomic database with MetaMorpheus. Spectral intensities were log transformed, fold change calculated (>1.5-fold and <0.5-fold) and analyzed for statistical significance ($P < 0.05$) using Student's t-test.

We identified 30 differentially expressed proteins based on age: adult (8-25 yr) vs senior (26+ yr). Of those, 2 were down-regulated in the senior cohort 1) core histone macro-H2A: involved in DNA binding and 2) inactive serine/threonine-protein kinase: involved in ATP binding, protein phosphate binding, and regulation of phosphoprotein phosphatase activity. Twenty-eight proteins were up regulated in the senior cohort. These up-regulated proteins display a wide range of functions including roles in inflammation, innate immune response, phosphorylation, signal transduction, and cell proliferation.

Several of these proteins are involved in immune function regulation and aging in humans and animal models. This study reveals that black rhinoceros, like humans, may be susceptible to age-related immune dysfunction, "immune senescence". Findings demonstrate that aging may contribute to dysregulation of immune function in ex-situ managed southern black rhinos.

Poster Presentation #163

Isolation, Characterization, and Antimicrobial Susceptibility of Bacteria Isolated from Sea Lion Pups (Zalophus californianus) in Northwestern Mexico

AA Aguirre[1], Alan A Zavala-Norzagaray[2], Uriel A Angulo-Zamudio, Cesar Paul Ley-Quiñonez, Hector Flores-Villaseñor, Nidia León-Sicairos, Jorge Velázquez-Román, Fernando R Elorriaga-Verplancken, Kevin Zavala-Félix, Catherine E Hart, Adrian Canizalez-Román
[1]George Mason University, [2]CIIDIR-SINALOA, [3]Autonomous University of Sinaloa, [4]Sinaloa State Public Health Laboratory, [5]CICIMAR, [6]ICSAS A.C., [7]The Women's Hospital

Bacterial infections have been documented in marine mammals for decades and some are considered emerging pathogens with zoonotic potential. The aerobic oral (n=16) and rectal (n=17) bacterial microbiota and their antimicrobial resistance were characterized for 17 apparently healthy California sea lion pups (Zalophus californianus) captured using a hoop net in Farallon Island, Sinaloa, Mexico. Bacteriological cultures, API and PCR were used to identify bacterial species. Moreover, the Escherichia coli (E. coli) phylogenetic groups were identified by PCR, Salmonella serotypes and resistance to antibiotics was evaluated. Overall, 39 bacterial species were isolated including in the same proportion E. coli and Salmonella spp. (35.9%) and Pseudomonas aeruginosa (28.2%). E. coli with UNKNOW phylogroup was the most prevalent (57.7%), followed by A (37.1%). Most Salmonella serotypes were identified as Newport (92.8%) while serotype Sant Paul was also identified (7.2%). Moreover, sea lions with bacterial co-colonization including 24.2% presenting two bacterial species and 3% with three species. A total of 59% of bacteria were resistant to any antibiotic tested and 25.6% were XDR. Overall, bacteria were more resistant to ampicillin and cefotaxime. This study demonstrates the importance of characterizing the microbiome of sea lions and the potential impact on wildlife conservation and public health.

Poster Presentation #164

Drivers of Contact Rates in Wintering Elk and Methods for Assessing Disease Risk

William Janousek[1], *Tabitha Graves*[1]
[1]U.S. Geological Survey, Northern Rocky Mountain Science Center

Degree of sociality and aggregation can drive disease transmission, but it can be challenging to measure and disentangle causes of aggregation in wildlife populations. Chronic wasting disease has been found in 28 US states and 3 Canadian provinces over the last 40 years and has direct effects on populations and indirect effects on outdoor recreation industries. In Wyoming, supplemental feeding of wintering elk occurs on 23 feedgrounds, including the National Elk Refuge (NER). Concern that feeding increases elk aggregation and thus disease spread has been rising. However, the comparison of feeding to other factors, including known abiotic drivers of aggregation such as snow levels has been underexplored. The winter of 2017-2018 had ample forage and little snow leading to a rare non-feeding year on the NER and providing a unique opportunity to evaluate the role of feeding in aggregation relative to other conditions. We examined data from 2016 to 2019 for 68 elk fitted with GPS collars (227,370 elk relocations). We used a proximity index to assess daily joint space use of elk and modeled contact rates as a function of 13 variables including abiotic weather-related effects, biotic effects such as supplemental feeding and hunting pressure, and aggregation from the prior day. Daily contact rate between elk was 2.6 times higher during winters with feeding but was also strongly regulated by snow cover and hunting pressure. To support future assessments and adaptive management of ungulate populations and other wildlife we developed the R package ‘wildagg’ to streamline analysis of wildlife aggregation metrics using location information like GPS collar data. The framework we present supports the evaluation of temporally varying management actions that influence aggregation broadly and can be easily implemented to answer a range of questions about disease transmission, human-wildlife conflict, and inter-species competition.

Poster Presentation #165

An Update on Utilizing Test and Cull to clear M. ovi from a Bighorn Sheep Herd in Nevada

Dr. Nate LaHue[1], *Mike Cox*[1], *Matt Jeffress*[1], *Ed Partee*[1], *Chris Morris*[1]
[1]Nevada Department of Wildlife

Pneumonia in Bighorn sheep caused by Mycoplasma ovipneumoniae (M. ovi) was the major cause of bighorn declines across their range. Post initial die-off some animals become persistently infected and continue to shed the bacteria. This continued shedding of the bacteria, especially in ewes, leads to yearly lamb die-offs and a severe reduction in lamb recruitment in some herds. Over time this leads to population declines or stagnation. Removing this small percentage of persistently infected sheep has the potential to clear a herd of M. ovi and restore lamb recruitment. This effort, known as test and cull, involves identifying persistently infected animals and removing them from the herd. This was originally pioneered in Hells Canyon to great success. Nevada has attempted to replicate this success in several herds. Nevada conducted multiple rounds of testing and removals starting in 2016 in one herd and expanded to a second herd in 2020. While this effort is ongoing, lamb recruitment has improved in the initial herd. During this time, we have improved the way we conduct operations and identified several pitfalls. In addition, we have found that rams play a more important role in maintaining infection that previously thought. We will give an update on our efforts and lessons learned. In addition, we will discuss preliminary findings on the potential role of sinus tumor in persistently infected animals.

Poster Presentation #166

Evaluation of RT-QuIC Detection for CWD Prion Seeding Activity in Soil

Stephanie Katircioglu[1,2], Dr. Stuart Lichtenberg[3], Heather Inzalaco[3], Dr. Allen Herbst[2], Dr. Paul Cross[4], Dr. Brant Schumaker[1], Dr. Daniel Walsh[5]
[1]University of Wyoming, [2]U.S. Geological Survey, National Wildlife Health Research Center, [3]University of Wisconsin-Madison, [4]U.S. Geological Survey, Northern Rocky Mountain Science Center, [5]U.S. Geological Survey, Montana Cooperative Wildlife Research Unit

Chronic Wasting Disease (CWD) is a contagious fatal disease caused by a misfolded prion that is known to affect cervids, including white-tailed deer, elk, moose, mule deer, and caribou. To date, CWD has been detected in 27 States, three Canadian Provinces, and three countries in northern Europe. CWD spreads through direct contact or indirectly through environmental contamination. Data has shown that the CWD prion can bind to various soil types, which can potentially increase infectivity and permit persistence in the environment for years. To understand the epidemiology of CWD and the contribution of environmental transmission in that process, there is a need to detect CWD in the environment. Real-time quaking-induced conversion (RT-QuIC) is a highly sensitive and specific assay amplifying misfolded CWD prions in vitro. It has been used to detect prions from a variety of matrices such as tissues and feces. Here we evaluate the compatibility of RT-QuIC with various soil types. We demonstrate the ability of RT-QuIC to detect prions bound to different soil types in a laboratory and field setting. Our data suggests that RT-QuIC can be used as a tool for research and management programs to help monitor and detect CWD in the environment.

Poster Presentation #167

Hellbender Mortality Post Captive-to-Wild Translocation Involves Bd, but it's Complicated

Rebecca Hardman[1,2], Sherri Reinsch[3], Wesley Sheley[1], Marley Machara[4], Heather Schwartz[3], Sandy Skeba[3], Dale McGinnity[3], Debra Miller[2], William Sutton[4]
[1]Center for Wildlife Health, University of Tennessee, [2]Florida Fish and Wildlife Conservation Commission, [3]Nashville Zoo at Grassmere, [4]Tennessee State University Wildlife Ecology Laboratory

Hellbenders, Cryptobranchus alleganiensis, are large fully aquatic salamanders found in rivers and streams in the eastern United States. They are declining throughout their range and captive head-starting programs are becoming necessary to augment populations. We implemented the first captive to wild release in Tennessee of zoo-raised adult hellbenders during the summer of 2021. To prevent potential chytridiomycosis due to expected Batrachochytrium dendrobatidis (Bd) exposure in released animals, we placed terbinafine - impregnated slow-release implants subcutaneously in half of individuals. Other factors implemented to reduce stress of release into wild streams included introduction of river water weekly 3-month pre-release, and introduction of the common wild food item, crayfish, 1-month pre- release. All animals were also surgically implanted coloemically with radio transmitters and monitored weekly for movements and signs of disease. Within 6 weeks of release, we observed severe disease and mortality in a majority of individuals. In several individuals, we were able to collect antemortem and/or postmortem samples including skin swabs, blood work, skin peptide washes, and full necropsies with histopathology and pathogen testing. A notable finding was that although terbinafine implants did significantly reduce Bd load they had no effect on disease manifestation or survival. Clinicopathological findings of this syndrome and plans to reduce future disease risk in 2022 releases will be discussed.

Poster Presentation #168

Barcoding Approaches to Characterizing the Parasites and Pathogens of Endangered Hawaiian Land Snails

Bonnie Derne[1], *Dr. David Sischo*[2], *Dr. Norine Yeung*[1], *Dr. Kenneth Hayes*[1]
[1]Bernice Pauahi Bishop Museum, [2]Department of Land and Natural Resources

Parasites and pathogens can negatively impact host populations, impede conservation efforts, and potentially drive vulnerable species to extinction. Despite these threats, very little research has been published about the parasites, pathogens, and other symbionts of threatened and endangered species, including some of the most threatened groups in the world, such as Hawaiian land snails. This group once comprised more than 750 species, nearly all endemic to the Hawaiian Islands, but species extinctions over the last 200 years have been among the highest of any animal group recorded. As much as 95% of some endemic families are already lost. Active management includes captive rearing, predator-proof enclosures, and translocation planning to mitigate further extinctions. Disease outbreaks of unknown etiology have periodically caused mortalities among captive populations. This project focuses on characterizing the parasites, pathogens and other symbionts of Hawaiian land snails to inform more effective conservation strategies. DNA-based techniques such as metagenomic barcoding present opportunities to conduct taxonomically broad and minimally invasive screening of host 'parasitomes', with less specialist taxonomic knowledge than required by traditional parasitology and microbiology methods. However, optimization is needed to overcome obstacles such as barcoding- and sequencing biases. Preliminary results enable a comparison of gut microbiota communities among several invasive gastropods sympatric to Hawaiian landsnails, and also the identification of some potential pathogens and parasites found in captive rearing environments. The subsequent metagenomic barcoding of land snail gut contents from a range of native wild and captive specimens will provide insights into the identity of symbiotic organisms, and understanding of their underlying host-symbiont relationships. Such knowledge will inform the development of targeted disease screening tools, disease prevention measures in captive rearing, and the optimization of conservation practices that encourage the maintenance of healthy symbiotic communities, ultimately resulting in fitness gains for the hosts.

Poster Presentation #169

Parasite Genotyping Yields Insights into Post-Translocation Transmission in an Endangered Lizard

Bonnie Derne[1,2], Dr. Stephanie Godfrey[3], Dr. Mark Hutchinson[2,4], Prof. Philip Weinstein[5], Prof. Michael Gardner[2,4]

[1]Bernice Pauahi Bishop Museum, [2]College of Science & Engineering, Flinders University, [3]Department of Zoology, University of Otago, [4]South Australian Museum, [5]School of Public Health, University of Adelaide

Wildlife translocations are increasingly necessary conservation tools to mitigate biodiversity loss arising from anthropogenic environmental and climate change. Translocations, however, entail risks, including that of parasite and pathogen transmission among stressed and/or immunologically naïve animals, which may negate conservation gains. The pygmy bluetongue lizard (Tiliqua adelaidensis) is an endangered skink endemic to grassland patches of South Australia. It is predicted to face extinction later this century without translocations to more temperate habitats. Here, we asked if genetic structuring for the two known parasites of this skink; the mite Ophiomegistus michaeli and the nematode Pharyngodon wandillahensis, occurred among three isolated host populations united by an experimental translocation we conducted. Any inter-population genetic differences would allow us to measure the extent of transmission among lizard hosts of different origins for the two-year post-translocation monitoring period. Genotyping using single nucleotide polymorphisms (SNPs) showed genetic structuring among isolated host populations for both parasites. Mean relatedness between nematode individuals following translocation increased over time for nematodes from different host individuals. Conversely, inter-nematode relatedness decreased over time for nematodes found on the same host individual. These gradual changes in mean relatedness over two years suggest a slow mixing of different nematode lineages, i.e. that the transmission of non-local parasites is occurring as hosts from different population origins share habitat. This temporality is consistent with the host's solitary lifestyle, and suggests that the disease transmission risk posed by translocation is generally low, particularly in the early, establishment phase immediately following a translocation, where heightened host stress and movement are most likely. More generally, this work highlights the knowledge gaps on parasite lifecycles and host-parasite ecology typical of wildlife parasites, and the potential use of novel methods to fill these gaps and provide recommendations for better-informed conservation management.

Poster Presentation #170

Protocols for Human Exposure to Opioids and Concentrated Medetomidine Used in Field Applications

Jenny Powers[1], James McCue[2], Geoff Stroh[2], William Lance[3]
[1]National Park Service, [2]University of California San Francisco, [3]Wyoming Wildlife Veterinary Consulting, LLC

Wildlife veterinarians and biologists routinely use potent sedatives and anesthetics when chemically immobilizing wildlife and zoo species. While accidental human exposure to these drugs is rare, the effects could be life threatening if appropriate medical care is not immediately available. Two of the most important categories of drugs used in wildlife medicine are opioids and α2-adrenoreceptor agonists. The effects of these drug classes can be reversed with specific antagonists. A search of the literature using key words 'human reversal, medetomidine, potentiated opioids' produced a dearth of protocols for emergency field response to human exposure of these drugs in remote settings; only one of which was medically endorsed for the use of α2-adrenoreceptor antagonists. We have created a protocol that can be used by wildlife health professionals with basic human emergency medical response training in a field setting. Key components include, building local relationships between human Emergency Medical Services (EMS) and wildlife professionals, focused EMS training which includes artificial respiratory support for wildlife professionals, and recommendations for delivery of specific α2-adrenergic and narcotic antagonists in humans, in addition to local evacuation procedures. This framework could be adopted by wildlife management agencies or zoos as a template for responding to human exposures to commonly used drug combinations that include opioids or concentrated medetomidine.

Poster Presentation #171

No Abstrat Assigned

Poster Presentation #172

Beachcast Seabird Investigation Reveals Bycatch in the Purse Seine Fishery

Bjørnar Ytrehus[1], Dr. Signe Christensen-Dalsgaard[2], Magdalena Langset[2], Jørgen Ree Wiig[3], Dr. Kim Magnus Bærum[4]
[1]Department of Biomedical Sciences and Veterinary Public Health, Swedish University of Agricultural Sciences (SLU), [2]Norwegian Institute for Nature Research (NINA), [3]Directorate of Fisheries, Sea Surveillance Unit, [4]Norwegian Institute for Nature Research (NINA)

Multiple beachcast events involving large numbers of seabirds were observed in Northern Norway from 2015 to 2020. We used a transdisciplinary and applied approach to elucidate the etiology of these events, starting with collection of field observations and necropsies of bird carcasses. Necropsy of carcasses from an event in 2017 showed that the birds were in good condition and had no signs of acute infection or intoxication that could explain the mortality, but that they most probably had drowned more or less simultaneously. From having no clear hypothesis of what could have led to the first episode, this led us to suspect bycatch in the purse seine fishery as the cause of these increases in at-sea mortality. Monitoring of the purse seine fishery was consequently initiated, and it was observed that most fishing events resulted in zero bycatch, but that some hauls resulted in drowning of large number of gulls within the seine. Necropsies performed after an event in 2019 confirmed the findings of simultaneous drowning of large number of birds and the association with purse seine fishery. Beachcast events where a large number of seabird carcases drift ashore, occur with irregular intervals. These events are due to specific situations where mass mortality of seabirds have occurred. Disentangling the cause of these events can provide valuable information on stressors that may have an impact on seabird populations.

The highly episodic and unpredictable nature of these events makes it demanding to achieve solid estimates of the occurrence and extent of bycatch without a very high monitoring effort. Our study shows that systematic investigation following beachcast events can shed light on the occurrence of such extreme events. Further investigations are needed to get inference on how preventive measurements and awareness can mitigate this problem.

Poster Presentation #173

Evaluation of a Vaccine for Chronic Wasting Disease Based on Measurements of Serologic Responses in Captive Rocky Mountain Elk (Cervus canadensis nelsoni)

Peach Van Wick[1,2], Andrew Fang[4], Samantha Allen[1,2,3], Holger Wille[4]
[1]Tom Thorne/Beth Williams Wildlife Research Center, Wyoming Game and Fish Department, [2]Veterinary Services, Wyoming Game and Fish Department, [3]Department of Veterinary Sciences, University of Wyoming, [4]Centre for Prions and Protein Folding Diseases, University of Alberta

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy and results in a fatal, neurodegenerative disease of cervids. CWD was first identified in a captive cervid facility in the United States in the 1960's and has continued to spread across the USA, Canada, and in other parts of the world. The spread of this prion disease is a cause for concern among wildlife health professionals, outdoor recreationalists, and others, as there is no effective treatment for CWD. Due to the lack of available treatment, wildlife managers are forced to consider other tools for the mitigation of disease spread. Vaccination remains on the forefront of disease prevention and control, and although vaccinating free-ranging wildlife poses certain challenges, targeted vaccine efforts have yielded promising results in some cases (e.g., terrestrial rabies).

Our study aimed at quantifying an immune response in captive Rocky Mountain elk (Cervus canadensis nelsoni) after being vaccinated with a novel prion vaccine developed at the University of Alberta. From August-October 2021, we vaccinated 12 elk held at the Tom Thorne/Beth Williams Wildlife Research Center in Wheatland, Wyoming. Elk were grouped in a double-blinded manner in either a control group, a low dose vaccine group, or a high dose vaccine group. After initial vaccination, elk were vaccinated every three weeks for a total of three boosters per individual. Serum was collected prior to the initial vaccination, prior to each subsequent vaccine administration, and three weeks after the final booster was administered. Serum samples were analyzed at the University of Alberta using ELISAs.

A prion-specific immune response was identified in most elk who were administered a vaccination in comparison to the control group. Future work needs to determine if the immune response elicited by this novel vaccine could act as a preventative tool against chronic wasting disease in cervids.

Poster Presentation #174

Protecting Endangered Riparian Brush Rabbits from RHDV2 in California

Megan Moriarty[1,2], Deana Clifford[1,2], Jaime Rudd[1], Daniel Applebee[3], Fumika Takahashi[4], Eric Hopson[4], Kim Forrest[4], Colleen Kinzley[5], Darren Minier[5], Alex Herman[5], Andrea Mikolon[6], Tristan Edgarian[7], Patrick Kelly[8], Beate Crossley[9], Ashley Hill[9]

[1]Wildlife Health Laboratory, California Department of Fish and Wildlife, , [2]Department of Medicine and Epidemiology Karen C. Drayer Wildlife Health Center, School of Veterinary Medicine, University of California, [3]Wildlife Diversity Program, California Department of Fish and Wildlife, [4]San Luis National Wildlife Refuge Complex, United States Fish and Wildlife Service, [5]Department of Animal Care, Conservation and Research, Oakland Zoo - Conservation Society of California, [6]Animal Health Branch, California Department of Food and Agriculture, [7]USGS Western Ecological Research Center, [8]Endangered Species Recovery Program, California State University, Stanislaus, [9]California Animal Health and Food Safety Laboratory, University of California, Davis

Rabbit hemorrhagic disease virus serotype 2 (RHDV2), the cause of a highly transmissible and fatal lagomorph disease, has spread rapidly through North America, resulting in significant mortality in domestic and wild rabbits. The disease was initially detected in California in May 2020, prompting the formation of an ad hoc interagency team to implement emergency conservation actions to protect the endangered riparian brush rabbit (Sylvilagus bachmani riparius) from RHDV2. Riparian brush rabbits are endemic to California's San Joaquin Valley, with an estimated population size of 2,200-3,500. They face threats from habitat loss, flooding, wildfire, drought, and disease. The team first implemented a vaccine safety trial by giving a subcutaneous dose of Filavac VHD K C+V® vaccine (Filavie, France) to 19 wild riparian brush rabbits temporarily held in captivity. Rabbits were monitored for side effects, including inappetence, lethargy, and swelling at the injection site. Serum was collected prior to, and at 7-10-, 14-20-, and 60-days post-vaccination to determine antibody response. No adverse effects from vaccination were observed. The team then initiated a large-scale, ongoing field effort in September 2020, with the goal of keeping 15% of the wild population vaccinated to reduce extinction risk. Population estimation via remote camera transects and predictive modeling were used to inform vaccination goals. Serologic testing to determine optimal booster frequency by examining duration of antibody response to vaccination is in progress. To date, 586 individuals have been vaccinated at least once and surveillance via RT-PCR of rectal swab samples from riparian brush rabbits and sympatric desert cottontails (S. audubonii) indicates RHDV2 has not reached core habitat as of December 2021. Vaccination campaigns of free-ranging populations may be the only effective management tool to protect threatened and endangered lagomorphs against RHDV2, at least until long-term conservation efforts are implemented to improve resiliency in small, geographically restricted species.

Poster Presentation #175

Management and Ecological Effects of High Pathogenicity Avian Influenza on Southern African Seabirds

David Roberts[1], Laura Roberts[2,3], Azwianewi Makhado[4,5], Pierre De Villiers[6]
[1]Southern African Foundation for the Conservation of Coastal Birds, [2]Western Cape Government, [3]University of Pretoria, [4]University of Cape Town, [5]Department of Forestry, Fisheries and the Environmnent, [6]CapeNature

Wild seabirds in Southern Africa were severely affected by two outbreaks of high pathogenicity avian influenza between 2018 and 2022. It is challenging to respond to disease outbreaks in endangered wild birds in their natural habitat or in rehabilitation centres, where the traditional disease control and quarantine recommendations designed for farms and zoos are not appropriate.
The outbreak response was complex and included disease diagnosis, the collection of epidemiological data, biosecurity measures, and the management of symptomatic and dead birds. Affected birds were identified, counted, and removed daily by field personnel and rehabilitation centres and reported to the state veterinary services.

Rehabilitation centres were instrumental in detecting the disease in wild seabirds, fostering a coordinated and appropriate response, and assisting with disease surveillance and the euthanasia of affected birds. Increased biosecurity measures, including the establishment of an off-site quarantine area, were necessary to ensure continued functioning of the rehabilitation centre.

The effect of the disease on endangered seabirds was significant. In 2018 and 2019, approximately 600 African penguin (Spheniscus demersus) deaths were officially attributed to avian influenza. In 2021, over 230 African penguins and 24 000 Cape cormorants (Phalacrocorax capensis) were reported to have died. At the peak of the outbreak, over 500 affected birds were collected per day. The actual number of mortalities may be far higher than those reported. The population level effect was of an unprecedented scale, especially in cape cormorants. Even at conservative estimates, more than fifteen percent of the South African population of cape cormorants died from avian influenza in less than four months, showing that disease can play a significant role in population decline in endangered species. The management strategies, monitoring tools and contingency plans developed during these outbreaks can be used to manage similar future outbreaks.

Poster Presentation #176

Survey of Haemosporidian Parasites from Lesser Prairie Chickens (Tympanuchus pallidicinctus) from Texas and Kansas

E. Morgan Tolliver[1], Nubia Salinas[1], Nicolas Triana[2], Dr Kristin Bondo[3], Blake Grisham[3], D. S. Sullins[4], Whitney Kistler[2]

[1]College of Veterinary Medicine, Lincoln Memorial University, [2]School of Mathematics and Sciences, Lincoln Memorial University, [3]Llano River Field Station and Department of Natural Resources Management, Texas Tech University, [4]Department of Horticulture and Natural Resources, Kansas State University

The lesser prairie-chicken (Tympanuchus pallidicinctus) is a grassland grouse species with a declining population. The main driver of the population decline is loss of sand sagebrush and shinnery oak rangeland habitat across their historic range. This has led the United States Fish and Wildlife Service to propose protection under the Endangered Species Act (ESA). Their declining population makes this species especially vulnerable to infectious diseases. Therefore, we screened blood samples collected from 2008-2010 in Texas (n=110) and in 2019 from Kansas (n=17) using a nested polymerase chain reaction to detect infection of haemosporidian parasites. Then, we bi-directionally sequenced positive samples. We amplified and sequenced a 995 base pair region of the cytochrome b gene from six (5.4%) of the samples from Texas and two (11.8%) of the samples from Kansas. We detected infected lesser prairie-chickens every year. These sequences matched 100% with Plasmodium homopolare from a California Condor (Gymnogyps californianus). This is the first report of P. homopolare in lesser prairie-chickens from Texas and Kansas. A previous study identified P. pedioecetii infections in lesser prairie-chickens from New Mexico; however, that study only used morphology for species identification. Plasmodium homopolare is a recently described species that has broad host and geographic ranges in the western hemisphere. Although no reports of pathogenicity have been documented with P. homopolare infections, haemosproidian parasites are known to have negative effects on wild bird populations. Additionally, this parasite has been documented in two species protected under the ESA, highlighting the need for further research into the effects this parasite can have on these populations.

Poster Presentation #177

Terrestrial Gastropod Species-Specific Responses to Forest Management: Implications for Parelaphostrongylus tenuis Transmission to Moose

William Severud[1], Matt Petz Giguere[2], Tyler Walters, Tyler Garwood[1], Kim Teager[3], Katherine Marchetto[1], L. Gustavo R. Oliveira-Santos[1], Seth A. Moore[2], Tiffany M. Wolf[1]
[1]University of Minnesota, [2]Grand Portage Band of Lake Superior Chippewa, [3]Lakehead University

Moose (Alces alces) are an important subsistence species to the Grand Portage Band of Lake Superior Chippewa. Recent studies in Minnesota have implicated the parasitic nematode Parelaphostrongylus tenuis in moose mortality and population decline. Multiple taxa of terrestrial gastropods are important intermediate hosts in the lifecycle of P. tenuis, for which white-tailed deer (Odocoileus virginianus) are definitive hosts. Moose become infected with P. tenuis when they incidentally ingest gastropod intermediate hosts, leading to morbidity and mortality. Landscape management can influence the abundance and diversity of terrestrial gastropods that host P. tenuis. We investigated the role of forest management on the terrestrial gastropod community, and specifically known intermediate host species of P. tenuis, on the Grand Portage Indian Reservation in northeastern Minnesota, USA. Field crews surveyed gastropods through timed searches of soil and litter. We digested all identified gastropods to determine prevalence of P. tenuis infection. We examined gastropod community responses to management and forest structure using multivariate regressions. We additionally used regressions to examine total gastropod richness and abundance, as well as P. tenuis intermediate host responses to forest structure, soil moisture class, canopy cover, treatment, and years since treatment. Digestions detected no infected gastropods. Gastropod community assemblages shifted with recent understory treatment, but no other predictors. Total gastropod abundance and host abundance were lower in sites treated ≤5 years. For known intermediate host taxa, we observed species-specific responses to forestry treatments through time. Specifically, Deroceras spp. recolonized sites post-treatment (0–30 years), Discus cronkhitei were higher in abundance immediately following treatment, and the Succinea ovalis group, along with pooled intermediate hosts, displayed no discernable patterns. Our results underscore the complexity of P. tenuis transmission dynamics, the importance of management disturbance in regulating gastropod populations, and the potential of additional post-harvest treatments to reduce P. tenuis infection in moose.

Poster Presentation #178

Retrospective Study of Tumors in Wild and Captive Virginia Opossums (Didelphis Virginiana)

Dr. Elizabeth Howerth[1], Dr. Rita McManamon[1,2], Dr. Nicole Gottdenker[1], Dr. Brittany McHale[2]
[1]Department of Pathology, College of Vet Med, [2]Infectious Disease Laboratory, College of Vet Med

Pathology reports of 54 Virginia opossums whose tissues were submitted for histopathology to a single diagnostic laboratory between 2011 and 2022 were reviewed for the presence of neoplasia, particularly lung tumors, as they had previously been seen in wild opossums from another diagnostic laboratory. Slides were reviewed and immunohistochemistry was done to confirm tumor diagnoses. Animals were from multiple sources and included 32 captive, 19 wild, and 4 of unknown origin. Seventeen animals, all captive, had tumors. Several had more than one tumor for a total of 26 tumors. Tumors included pulmonary adenomas/adenocarcinomas (n=12), lipomas (n=3), lymphomas (n=2), and 1 each hemangiosarcoma, hemangioma, mammary carcinoma, squamous cell carcinoma, renal carcinoma, adrenocortical adenoma, trichoblastoma, apocrine adenoma, pheochromocytoma, and pituitary adenoma. Animals ranged in age from 1-3.5 years and most were females. Animals with pulmonary tumors were 2.6-3.5 yrs and mostly female. These pulmonary tumors were from animals originating from multiple sources, were often multiple, ranged from benign to malignant, and two had metastasized. The high incidence of pulmonary tumors suggests a viral etiology similar to pulmonary tumors seen in sheep due to a retrovirus and needs further exploration. Although exact age of the wild animals was unknown, several were juvenile, so failure to find lung tumors in the wild animals may be related to them being a younger cohort.

Poster Presentation #179

Pilot Study Investigating Shiras Moose Mortalities in Jackson and Sublette County, Wyoming

Virginia Stout[1], Benjamin Wise, Alyson Courtemanch, Hank Edwards, Dr. Jacqueline Kurz, Troy Koser, Dr. Deborah McCauley
[1]Veterinary Initiative for Endangered Wildlife

Shiras moose (Alces alces shiras) in the western United States are suspected to be declining due to parasitism (winter ticks, arterial worm), climactic variables, predation, and other factors. This trend reflects declines in moose across eastern North America at the southern extent of their range. In the winter of 2018-2019, a moose mortality event occurred in and around Jackson, WY. Since little is known about the population-wide health of the Jackson and Sublette herds, a pilot study was performed on moose heath using opportunistic necropsies. During the study period, 2019-2021, thirty moose died, 17/30 (56%) were adults and 13/30 (43%) were calves. Through rigorous necropsies, several mortality factors emerged. Dermacenter albipictus (winter ticks) were found in varying loads on all necropsied moose 30/30 (100%) but affected calves more severely with hair loss and emaciation. Elaeophora schneideri (arterial worm) was present in 5/30 (16%) moose, with low parasite loads. Septicemia was identified in several individuals 3/30 (10%) with bacterial pericarditis and pneumonia. Evidence of trauma, including vehicular, occurred in 6/30 (20%) of moose. Cyanide toxicity due to a plant, pesticide, or fertilizer was one cause of mortality. Adenovirus hemorrhagic disease (AHD) was confirmed as a novel pathogen in one individual. No single factor associated with moose mortalities was identified in this study; rather, mortality appears to be multifactorial in many moose. Further investigation into mortalities and host- parasite interactions will continue in the region.

Poster Presentation #180

Detection and Identification of Coronaviruses in North American Bats from Environmental Guano

Tyler Mclaughlin[1], *Kathryn Griffin*[1], *Hon Ip*[1], *Anne Ballmann*[1]
[1]U.S. Geological Survey National Wildlife Health Center

Bat species are known carriers of alpha- and beta-coronaviruses (CoVs) which can include pathogens of zoonotic significance. Screening bat populations for circulating CoVs is needed to understand the spatial and temporal distribution of variants across the landscape. Our goal is to catalog CoV variants in North American bat populations by leveraging composite (“community”) guano collected at summer roost sites across the United States originally collected for the surveillance of white-nose syndrome fungus Pseudogymnoascus destructans (Pd) responsible for significant population declines in several North American bat species over the past decade. Overall, 219 environmental samples (99 individual guano pellets, 120 composite guano) from 17 states were analyzed for presence/absence of CoVs between the 2018-2021 Pd surveillance seasons, representing both pre- and post-SARS-CoV-2 (a beta-CoV) emergence in the U. S. Using a nested qPCR targeting the conserved RNA-dependent RNA polymerase (RdRp) gene for the detection of pan-coronaviruses, 47% of samples (n=103) were shown to be presumptively positive for CoVs. Both guano sample types yielded similar CoV detection rates at the single site where both sample types were available for comparison. Thus far, sequencing has been performed on six individual pellet samples. Two different alpha-CoVs were identified in two samples. A third sample contained an amplicon of the expected size but was bacterial in nature. Sequence quality did not allow for identification from the remaining three presumptive positive samples. Additional sequence analysis is needed to identify CoVs among the remaining samples. Next steps for this project include analyzing host DNA from guano samples to determine which North American bat species are associated with the various strains of CoVs identified.

Poster Presentation #181

Comparison of Attachment Methods for Passive Integrated Transponder (PIT) tags in Big Brown Bats (*Eptesicus fuscus*) and Little Brown Bats (*Myotis lucifugus*) used in White Nose Syndrome Research

Elizabeth Falendysz[1], Connor Whalen[1], Harrison Lamb[1], Dr. Ariel Leon[1], Dana Calhoun[1], Dr. Tonie Rocke[1]
[1]US Geological Survey, National Wildlife Health Center

The study of White Nose Syndrome in insectivorous bats often requires the ability to track individual bats in a study population, ideally without handling individuals. Passive integrated transponder (PIT) tags, used in concert with strategically placed RFID readers, allows the registration of individual bats as they pass in and out of hibernacula. However, concerns have been raised about the effects of subcutaneously injected PIT tags on the health and fitness of bats. In this study, we tested two methods for applying PIT tags to captive big brown bats ([i]Eptesicus fuscus[i], EPFU): topical application using a surgical adhesive and subcutaneous injection. We measured tag retention and recorded skin irritation, infection, and alopecia at the application site. We monitored bats for 1 month in euthermic conditions and 5 months in hibernation. After 6 months of observation of captive EPFU, 3.1% of subcutaneous tags and 96.3% of topical tags were lost. In the captive EPFU, topically adhered tags in were 88.6 times more likely to be lost compared to subcutaneous tags ($p < 0.01$). We also report resighting data observed in PIT-tagged little brown bats ([i]Myotis lucifugus[i]; MYLU) in the field, over 2 field seasons at the same location, one in which topical PIT tag attachment was used and subsequent field season in which tags were injected subcutaneously. Subcutaneously injected tags were resighted at spring emergence at 40.7%, whereas 21.7% of glued tags were resighted, although other factors may also have contributed to his difference. Injected tags also allowed for multi-year surveillance of individual animals, with 30% of MYLU resighted during fall swarm at hibernacula entrances the year following injection. Subcutaneously injected PIT tags have higher rates of retention and resightings in big brown and little brown bats than externally applied PIT tags, with no increased risks of injury or disease.

Poster Presentation #182

Suppurative Polyarthritis in Wild-Caught Big Brown Bats (*Eptesicus fuscus*) at Two Institutions in Wisconsin, Caused by a Novel *Mycoplasma* Species

Elizabeth Falendysz[1], Dr. Mary Thurber[2], Dr. Valerie Shearn-Bochsler[1], Dr. Jeffrey Lorch[1], Dr. Jenna Motz[1]
[1]US Geological Survey, National Wildlife Health Center, [2]University of Wisconsin, School of Veterinary Medicine

Diseases of free-ranging insectivorous bats are poorly described in the literature, except for rabies and white-nose syndrome. This presentation describes a suspected novel *Mycoplasma* sp.-induced polyarthritis in big brown bats ([i]Eptesicus fuscus[i], EPFU). In 2018, three cases of severe polyarthropathy occurred in wild-caught EPFU at the USGS National Wildlife Health Center (NWHC). Initial treatment with enrofloxacin, amoxicillin-clavulanic acid, ketoconazole, and meloxicam was ineffective and 2/3 bats died. Necropsy revealed chronic suppurative and lymphoplasmacytic polyarthritis. The third case was treated successfully with doxycycline. Ten additional cases occurred between 2018-2021; 8/10 cases were successfully treated with meloxicam and doxycycline. Joint culture of a euthanized bat revealed a novel *Mycoplasma* species. Similar EPFU polyarthropathy cases were seen at a nearby institution, the Dane County Humane Society's Wildlife Center (DCHS-WC), starting in 2018. These cases were initially treated with meloxicam and sulfamethoxazole-trimethoprim or clindamycin, with mixed success. After the NWHC's report of a novel *Mycoplasma* species, bats with polyarthropathy at DCHS-WC were treated with doxycycline. A retrospective analysis of 454 bat submissions at DCHS-WC from 2015-2020 revealed eight cases of polyathropathy in EPFU (1.7% prevalence). At both institutions, 100% (15/15) of affected bats treated with at least 4 weeks of doxycycline had complete resolution of clinical signs. In comparison, only 2/6 (33.3%) resolved with other treatments. The success of doxycycline treatment, along with the detection of a novel *Mycoplasma* species from an affected joint, supports the conclusion that a novel *Mycoplasma* species is the cause of polyarthritis in wild EPFU.

Poster Presentation #183

Evaluation of the Efficacy of Carbon Dioxide for Euthanasia of Big Brown Bats (*Eptesicus fuscus*) as Compared to Isoflurane

Elizabeth Falendysz[1], Dr. Michelle Verant[2], Dr. Emma Brown[3], Carly Malave[1], Dr. Ariel Leon[1], Dana Calhoun[1], Harrison Lamb[1], Dr. Devin Tunseth[1], Rachel Lambert[1], Dr. Tonie Rocke[1]
[1]US Geological Survey, National Wildlife Health Center, [2]National Park Service, Biological Resources Division, Wildlife Health Branch, [3]National Park Service, Natural Sounds & Night Skies Division

Inhalant anesthetics, such as carbon dioxide (CO_2) and isoflurane are used for euthanasia of small animals including laboratory, domesticated and wildlife species. To meet the definition of euthanasia, the method should cause rapid unconsciousness and painless death. There has been concern that CO_2 may be an inappropriate method of euthanasia of insectivorous bats, as they may have higher tolerance to elevated serum CO_2. However, isoflurane, the more common inhalant euthanasia method of bats, requires veterinary oversight and may not be safely used in confined spaces such as hibernacula. We evaluated the efficacy of CO_2 compared to isoflurane for euthanasia of big brown bats (*Eptesicus fuscus*). Ten bats were euthanized with CO_2 administered at a 50% displacement rate, and twelve bats were euthanized with 5% isoflurane. Video and acoustic recordings were made during all euthanasia events. Live and recorded videos were scored by blinded observers. Acoustic recordings were analyzed for bat calls using acoustic processing software. We assessed time to cessation of movement as a proxy of consciousness, time to cessation of breathing, and frequency and duration of potential indicators of distress such flapping, open-mouth breathing, and vocalizations. The time to cessation of respirations was significantly shorter in bats euthanized by CO_2, and all bats in the isoflurane group were still breathing at the cutoff time of ten minutes. The frequency and duration of movement, such as wing flapping, were significantly higher in the isoflurane group. A total of five bats called when placed in the chamber, but only one bat in the isoflurane group called after initiation of gas flow. We conclude that CO_2 delivered at a 50% displacement rate is a more rapid method of euthanasia for insectivorous bats compared to isoflurane, without behavioral evidence of increased negative affective states (distress).

Poster Presentation #184

Avian Influenza A Virus Transmission to Quail from a Flocking Passerine

Jeff Root[1], *Jeremy Ellis*[1], *Susan Shriner*[1]
[1]USDA/APHIS/WS/National Wildlife Research Center

The effects of flock size of European starlings were experimentally manipulated to assess the potential of influenza A virus (IAV) transmission from a flocking passerine to bobwhite quail through shared resources. Three starling flock sizes were tested (n = 30, n = 20, and n =10). All flock treatments successfully transmitted the virus to all or most of the quail in each animal room, as determined by serology and/or viral RNA detections. This study has provided evidence that relatively small flocks (i.e., 10 or possibly a smaller number) of starlings can collectively transmit IAV to a highly susceptible gallinaceous bird species. Future work should assess if starlings can transmit IAVs to additional poultry species commonly found in backyard or free-range settings.

Poster Presentation #185

Current Antimicrobial and Probiotic Use in Wildlife Rehabilitation Facilities in the United States

Irene Bueno, Elizabeth A. Miller, Rachel Amato, Julia B. Ponder
University of Minnesota

Antimicrobial resistance (AMR) is a global health concern. As such, there have been increased efforts to monitor and standardize antimicrobial prescribing practices in humans and domestic animals. Despite the wide use of antimicrobials to treat captive wildlife, there is relatively little known about specific prescribing practices. Therefore, the goal of this study was to examine current antimicrobial and probiotic use from a cross-section of wildlife rehabilitation facilities in the United States. An anonymous electronic survey was administered to 106 U.S. permitted wildlife facilities to collect information about admissions, current antimicrobial and probiotic practices, and current staff knowledge and attitudes about AMR risk and probiotic use. Survey response rate was 45%. The majority of facilities (38%) treated between 101-500 animals per year. Birds were the most common wildlife group treated (40%), and within birds, raptors were the most prevalent (30%). All facilities (100%) used antimicrobials for treatment, with enrofloxacin as the most frequently used, followed by amoxicillin-clavulanic acid and trimethoprim/sulfamethoxazole. When making decisions about whether to use an antimicrobial, treatment success (17%) and previous experience with a drug (16%) were the main indicators, while recommended duration of the drug (25%) and resolution of clinical signs (21%) were the main factors considered when stopping treatment. For probiotics, 64% of facilities used them in some capacity for a variety of circumstances ranging from diarrhea to being used as a calming agent. In terms of knowledge and attitudes, 28% of facilities reported to have a good understanding of AMR in relation to antimicrobial use, 10% stated that AMR was a problem at their facility, and 44% thought that probiotics may improve clinical outcomes. The results of this survey are a first step towards understanding antimicrobial prescribing practices in the treatment of captive wildlife and developing an antimicrobial stewardship program for wildlife rehabilitation.

Poster Presentation #186

Strain Types for Chronic Wasting Disease and a Plea for a National Tissue Repository

Chia-Hua Lue[1], *W. David Walter*[2]
[1]Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University, University Park, [2]U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University, University Park

Chronic wasting disease (CWD) is a prion disease that affects Cervidae species and is a prominent transmissible spongiform encephalopathy (TSE) in wildlife. Since CWD was first identified in the 1960s in the United States, it has been documented in 29 states in captive and wild cervids. Movement of captive cervids resulted in CWD introductions into Canada and South Korea and more recently, Scandinavian countries have detected CWD in wild cervids from an unknown origin. When normal cellular prion protein (PrPc) misfolds to an abnormal conformation (PrPsc) it causes CWD infections. Different conformations of PrPsc result in various disease phenotypes with regard to pathogenicity, incubation time, and host range and others. These different phenotypes characterize different prion strains. The types of CWD strains are crucial to tracking distributions and progression of the CWD, which has been a challenge in North America. The first aim of this project is to summarize the known CWD strains in North America and to expand our general knowledge of the CWD strains. One of the main obstacles in CWD research is a lack of a centralized collection of wild CWD-positive tissues. The second aim will overcome this obstacle by introducing a national repository for CWD. There are multiple benefits of this national repository. First, with tissues collected on a large geographic scale in North America, we can assess the distribution, frequency, and strain types to their point of origin. Second, along with collection metadata, we can learn interactions among host range, strains, and their environments. Third, the repository can provide standardized CWD-infected and uninfected tissue resources for the development of diagnostic and testing methods for multiple research purposes. Finally, implementations of the repository will serve as a centralized platform to facilitate cooperation and the sharing of resources between state agencies and research institutes.

Poster Presentation #187

Staphylococcal Arthritis and Osteomyelitis with Sandspur-Associated Injury in Immature Black Skimmers (Rynchops niger) in Southwest Florida

Dr. Nicole Nemeth[1], Michelle van Deventer[2], Brittney Piersma[2], Veronica Guzman-Vargas[3], Dr. Heather Barron[4], Dr. Alexandro Troiano[4], Dr. Alisia Weyna[1], Dr. Melanie Kunkel[1], Dr. Andrew Allison[5], Dr. Lisa Shender[3,6], Dr. Rebecca Hardman[7], Dr. Susan Sanchez[8]

[1]Southeastern Cooperative Wildlife Disease Study, [2]Florida Fish and Wildlife Conservation Commission, [3]Florida Fish and Wildlife Conservation Commission, [4]Clinic for the Rehabilitation of Wildlife, [5]Department of Comparative, Diagnostic & Population Medicine, University of Florida, [6]National Park Service, Biological Resources Division Wildlife Health Branch, [7]Florida Fish and Wildlife Conservation Commission, [8]Athens Veterinary Diagnostic Laboratory, University of Georgia

The black skimmer (Rynchops niger) is a state threatened species in Florida that nests in colonies ranging in size from a few to several hundred pairs. Conservation threats include habitat modification, disturbance by humans, severe weather events, and elevated predation levels. During sequential nesting seasons (July-September 2020 and 2021), black skimmer nestlings and fledglings at colonies on Fort Myers and Marco Island beaches had multiple, often severely swollen joints. We characterized field, clinical, radiographical, and pathological findings to determine the likely pathogenesis as well as risk of an ongoing health threat. Clinically, affected skimmers were thin to emaciated, dehydrated, dyspneic and weak; attitude was alert to lethargic and some were unable to stand. Many skimmers had sandspurs penetrating the skin associated with ulceration and mild hemorrhage. Joints were variably swollen, including combinations of stifle, hock, interphalangeal, and less commonly, elbow and carpus. Postmortem evaluation of 18 immature skimmers revealed gram-positive, coccoid, bacterial dermatitis, tenosynovitis and/or osteomyelitis. Staphylococcus aureus was cultured from affected joints of 14/15 skimmers and from 8/10 lung/kidney samples. West Nile virus was isolated from 2/13 skimmers tested. There was no evidence of avian influenza viruses or paramyxoviruses by PCR test, nor Bisgaard Taxon 40 by culture. No brevetoxins were detected in kidney/liver by ELISA in 15 skimmers tested. Our evaluation revealed severe staphylococcal joint disease in which the bacteria likely entered via sandspur-induced skin breaks with hematogenous dissemination to other joints and internal organs. Disease severity likely was facilitated by age-associated, underdeveloped immune systems. Additional investigation is recommended to determine if there are higher levels of S. aureus in these skimmer colonies relative to other nesting sites. Also, to improve nesting outcomes, we recommend site managers employ vegetation management techniques that reduce the risk of sandspur interaction with chicks and fledglings during the late nesting season.

Poster Presentation #188

Batrachochytrium salamandrivorans Lesions in Larval Northern Two-Lined Salamanders (Eurycea bislineata)

Debra Miller[1], *E. Davis Carter*[1], *Wesley Sheley*[1], *Anastasia Towe*[1], *Matthew Gray*[1]
[1]University of Tennessee Center for Wildlife Health

Batrachocytrium salamandrivorans (Bsal) is a chytrid fungus that infects amphibians, often causing devastating skin lesions and eventually death. As part of a larger study involving multiple species, two Eurycea bislineata larvae were exposed to a dose of Bsal known to infect adult salamanders (5x106). Larvae do not typically develop lesions despite testing positive for Bsal on PCR, so we hypothesized that these two animals would not develop lesions. They were swabbed for PCR every sixth day of the experiment starting on day 4 and were both positive for Bsal on the first swab and continued to be positive throughout the 60-day experiment. Interestingly, these larvae did develop lesions on the feet. Both survived the duration of the experiment. These findings highlight the potential for Bsal to negatively impact a greater portion of amphibian populations, dealing an even harsher blow to biodiversity.

Poster Presentation #189

Evaluation Tolazoline or Vatinoxan for Alleviating Adverse Effect of Butorphanol-azaperone-medetomidine Immobilization in Rocky Mountain Elk

Annette Roug[1], *Pauline Nol*[2], *Khursheed Mama*[3]
[1]Centre for Veterinary Wildlife Research, University of Pretoria, [2]Foothills Wildlife Research Center, [3]Department of Clinical Sciences, Colorado State University

A mixture of butorphanol, azaperone, and medetomidine (BAM) is frequently used for immobilization of North American hoofstock. Common adverse effects include respiratory depression, hypoxia, and bradycardia. In this study we evaluated the efficacy of the alpha-adrenergic antagonist tolazoline and peripheral alpha-2 antagonist vatinoxan in alleviating adverse effects of BAM in Rocky Mountain elk. Eight female elk aged 7-20 years and weighing 224-284 kg were immobilized 3 times with BAM at a dose of 0.15 mg/kg butorphanol, 0.05 mg/kg azaperone, and 0.06 mg/kg medetomidine in a cross-over study. Tolazoline at 2 mg/kg or vatinoxan at 3 mg per mg medetomidine was administered 20 minutes after recumbency. All elk exhibited hypoxemia, bradycardia, and moderate hypertension, and because of the severe hypoxemia observed, all animals received intra-tracheal oxygen (3 L/min) throughout the immobilization. Intramuscular tolazoline had no significant effect on heart rate or respiratory rate, however, the blood pressure dropped by a mean of 14 mmHg (standard deviation (SD) = 9.8 mmHg) in the first 5 minutes post administration. Intravenous vatinoxan caused a mean (SD) drop in blood pressure of 34 (8.5) mmHg and mean (SD) increase in heart rate of 20 (10.4) beats per minute in the first 5 minutes post administration but no significant change in respiration. Neither tolazoline nor vatinoxan had a significant impact on PaO2 or PaCO2 and the depth of sedation was unchanged after administration.

Poster Presentation #190

Amphibian Infection Tolerance and Resistance in the Context of Chytridiomycosis

Laura Grogan[1], *Matthew Mangan*[1], *Hamish McCallum*[1]
[1]Griffith University

Animal defenses against infection involve two distinct but complementary mechanisms: tolerance and resistance. Tolerance measures the animal host's ability to limit detrimental effects from a given infection, whereas resistance is the ability to limit the intensity of that infection. Tolerance is a valuable defense for highly prevalent, chronic, persistent or endemic infections where mitigation strategies based on traditional resistance mechanisms are less likely to be effective, or less evolutionarily stable. Selective breeding of amphibians for enhanced tolerance to Batrachochytrium dendrobatidis (hereafter Bd) has been suggested as a valuable alternative approach in the context of mitigating the impacts of the devastating fungal disease, chytridiomycosis, longer term. Here, we (1) define infection tolerance and resistance in the context of chytridiomycosis, (2) synthesize current research on tolerance and resistance to chytridiomycosis including across different scales and study types, study limitations and challenges, and avenues for future research, (3) evaluate current evidence for variation in tolerance versus resistance to Bd, (4) explore evidence for mechanisms underlying tolerance versus resistance to Bd, (5) outline ecological, epidemiological and evolutionary implications of tolerance versus resistance to chytridiomycosis across life stages, species, and between populations and individuals, and (6) explore outstanding questions including whether a negative correlation between resistance and tolerance should occur, the relative importance of tolerance versus resistance in defense against Bd, and potential costs of both tolerance and resistance. Improving our understanding of infection tolerance and resistance greatly broadens our repertoire of strategies for mitigating the ongoing impacts of emerging infectious diseases such as chytridiomycosis.

Poster Presentation #191

Host Genomic Variation and Beak and Feather Disease Virus Infection in Crimson Rosellas (Platycercus elegans)

Candice Lachenicht[1], Dr Flavia Garcia-Termignoni[2], Miss Berta Blanch-Lázaro[1,3], Dr. Raoul Ribot[1], Dr Mathew Berg[1], Prof Soren Alexandersen[3], Prof Scott Edwards[2], Prof Andrew Bennett[1]
[1]Deakin University, [2]Harvard University, [3]Geelong Centre for Emerging Infectious Diseases

Beak and feather disease virus (BFDV) is a global threat to parrots (Psittaciformes). In Australia, BFDV is considered a “key threatening process to biodiversity” by the Australian government’s EPBC Act. The outcomes of BFDV infection vary across species, with some showing severe signs leading to death, whilst others are relatively unaffected, like the crimson rosella (Platycercus elegans). Host genetics may play a fundamental role in determining differences in disease outcomes within and across species. The aim of this study was to determine the relationship between BFDV infection and genomic variation in crimson rosellas, with particular attention to the immune genes of the major histocompatibility complex (MHC). After producing a reference genome, genome resequencing was performed on 54 crimson rosellas whose BFDV infection status was determined by real-time quantitative PCR. Genotype likelihoods were obtained from the resequenced individuals for variant discovery to perform population genomic analyses such as admixture, principal component analyses (PCA) and scan for selection. The first four principle components (PCs) explained about 9% of the total variability. The data clustered into 2 to 4 groups depending on the PCA figure. Genomes were annotated and used to identify genes under selection, particularly with relation to BFDV infection, and candidate genes in the MHC. The MHC class I, class II genes and toll-like receptors were mapped to scaffolds of the crimson rosella genome. Understanding associations between host genomics and BFDV infection status should benefit conservation efforts for vulnerable Psittaciforme populations.

Poster Presentation #192

Treponeme-Associated Hoof Disease in Free-Ranging Wild Elk in Southwestern Washington USA: Correlation of Bacterial Community and Visual Disease Progression

Jenny Wilson-Welder[1], David Alt[1], Darrel Bayles[1], Kristin Mansfield[2], Sushan Han[3]
[1]USDA-Agricultural Research Service, National Animal Disese Center, Infectious Bacterial Disease Research Unit, [2]Washington Department of Fish and Wildlife, [3]Colorado State University Diagnostic Medicine Center

Treponeme-Associated Hoof Disease (TAHD) is a polybacterial, multifactorial disease affecting free-roaming wild elk (Cervus elaphus) in the Pacific Northwest. Previous studies have indicated bacterial etiology similar to digital dermatitis, including isolation of Treponema species from lesions. The lesions appear to progress rapidly from ulcerative areas in the interdigital space or along the coronary band to severe, ulcerative, necrotic, proliferative lesions under-running the hoof wall, perforating the sole, contributing to hoof elongation, deformity, and overgrowth. Eventually the lesions undermine the entire laminal structure leading to sloughing of the hoof horn capsule. The objective of this study was to determine the bacterial community associated with hoof lesion categorized into 5 stages or disease grade severities with 0 being unaffected tissue and 4 being sloughed hoof capsule. The goal was to determine if TAHD continued to be bacterial driven disease through the morphological changes observed and was dominated by Treponema bacteria, similar to the livestock diseases. Bacterial 16S rRNA gene was sequenced from 66 hoof skin biopsy samples representing the 5 lesion grades from feet collected by Washington Department of Fish and Wildlife as part of a voluntary hunter program. Analysis of the relative abundance of bacterial sequences showed that lesions were dominated by members of the bacterial phyla Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria. In lesioned samples, members of the genus Treponema, Porphyromonas, Mycoplasma, and Faucicola increased with lesion severity. Confirming lesion status with Treponeme species specific PCR and histopathology, the bacterial 16S rRNA sequencing confirms the presence of Treponema species in lesion development and persistence, as well as the presence and persistence of other pathogenic anaerobic bacteria associated with other hoof infections. Understanding the bacteria involved, and their persistence in the lesions, will provide evidence for science-based management decisions in TAHD infected elk populations.

Poster Presentation #193

Canine Distemper Virus Ecology: Insights from a Longitudinal Serological Study in Wild Raccoons (Procyon lotor)

Jolene Giacinti[1], David Pearl[2], Davor Ojkic[3], Kristin Bondo[4], Claire Jardine[5]
[1]Department of Pathobiology, Ontario Veterinary College, University of Guelph, [2]Department of Population Medicine, Ontario Veterinary College, University of Guelph, [3]Animal Health Laboratory, University of Guelph, [4]Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University, [5]Canadian Wildlife Health Cooperative, Ontario Veterinary College, University of Guelph

Increasing reports of canine distemper virus (CDV) in a variety of hosts and changing CDV dynamics have led to renewed interest in understanding the ecology of CDV infections in wildlife. Longitudinal repeat sampling serological studies can provide valuable insights into intra–population and intra–individual pathogen dynamics, but few studies in wildlife have been conducted. We used data from 235 raccoons captured on more than one occasion between May 2011–November 2013 to investigate CDV dynamics in raccoons in Ontario, Canada. In examining variables associated with CDV seropositivity using mixed multivariable logistic regression, we identified a significant interaction between age and sex. Specifically, juvenile raccoons were more likely to be seronegative from August–November compared to May–July. Furthermore, using paired titres from individuals exposed to CDV during the study period, we determined that the winter breeding season, when there is high intraspecific contact among raccoons and an increase in susceptible juveniles, may be a period of high risk for CDV exposure. Interestingly, adult raccoons seropositive for CDV on one capture had non–detectable titres ranging from one month–one year later, which is notable and inconsistent with the accepted notion that immunity against CDV is lifelong. Based on our preliminary investigation using two different statistical approaches, CDV exposure was associated with a decrease in parvovirus titre. This result raises important questions about whether virus–induced immune amnesia occurs following CDV exposure, which has been described for measles virus, a closely related pathogen. Overall, our results provide significant insights into individual and population level CDV disease dynamics. Further research is needed to investigate whether CDV induced immune amnesia occurs in raccoons and to determine the potential impacts of a reduced population immunity that may occur secondary to CDV exposure in raccoons and other wildlife particularly as it relates to rabies control efforts.

Poster Presentation #194

No Abstract Assigned

Poster Presentation #195

Hepatitis and Hepatic Necrosis Associated with Chlamydiales sp. in the Endangered Santa Cruz Long-Toed Salamander (Ambystoma macrodactylum croceum)

Valerie Shearn-Bochsler, Jeffrey Lorch
U.S. Geological Survey National Wildlife Health Center

The Santa Cruz Long-toed salamander (SCLS) is an endangered subspecies of the long-toed salamander. The range of the SCLS is limited to a few locations near ponds and freshwater marshes in Santa Cruz and Monterey Counties in California. A single SCLS was found excessively bloated in the wild in January of 2022 and was brought into captivity, where it continued to swell and eventually died. The salamander was submitted chilled to the U. S. Geological Survey National Wildlife Health Center for cause of death determination. Skin swabs were PCR negative for Batrachochytrium dendrobatidis and Batrachochytrium salamandrivorans. On macroscopic exam, the animal was emaciated with marked ascites. No significant bacterial pathogens were isolated on aerobic culture from a swab of the coelomic fluid. On parasitological examination of the gastrointestinal tract, many live symbiotic flagellates were seen: no helminths were present. Pooled liver, spleen, and kidney were PCR negative for ranavirus.
On microscopic exam, acute multifocal hepatic necrosis affecting approximately one-half of the liver was seen, accompanied by mild lymphoplasmacytic infiltrates and increased numbers of melanomacrophages. No other significant abnormalities were seen. Small numbers of hepatocytes contained basophilic cytoplasmic inclusions less than 1 µm in diameter, which stained positively with Giemsa stain, consistent with chlamydial reticulate or elementary bodies. A pooled sample of the liver, kidney, and spleen was positive for Chlamydiales using a pan-Chlamydiales end-point PCR targeting the 16S rRNA gene. Subsequent sequencing of the PCR product indicated the organism was most similar to Candidatus Amphibiichlamydia salamandrae which has been previously reported from captive salamanders in Europe, in which the infection caused hepatitis and was 100% fatal. Knowledge of the diseases of wild salamanders is limited, and the significance of this infection to the SCLS population is currently unknown.

Poster Presentation #196

Comparative Response of Smallmouth Bass (Micropterus dolomieu) and Largemouth Bass (Micropterus salmoides) to a Short-Term Poly I:C challenge

Jessica Leet[1], Dr. John Hansen[2], Dr. Catherine Richter[1], Dr. Donald Tillitt[1], Dr. Justin Greer[2], Dr. Luke Iwanowicz[3]
[1]US Geological Survey, Columbia Environmental Research Center, [2]US Geological Survey, Western Fisheries Research Center, [3]US Geological Survey, Eastern Ecological Science Center

Disease outbreaks, skin lesions, fish kill events, and reproductive abnormalities have been observed in wild populations of Centrarchids in the Chesapeake Bay watershed (CBW). These adverse effects occur more predominantly in smallmouth bass (SMB; (Micropterus dolomieu) populations than largemouth bass (LMB; Micropterus salmoides) populations, suggesting a potential species difference in sensitivity to stressors that impact the immune response. To date there have been no comparative studies to identify differences in immune response between these two species. To investigate the physiological and molecular mechanisms of antiviral immune response in bass, polyinosinic: polycytidylic acid (poly I:C) was administered in vivo to juvenile SMB and LMB to mimic a viral infection. Thirty fish per species were intraperitoneally injected with 10 µl g-1 fish of poly I:C or sterile phosphate-buffered saline (PBS), and this was repeated for three replicates per treatment and species. Ten fish were sampled at each time point of 24 h, 48 h, or 72 h post-injection to evaluate gene expression changes in a suite of immune related genes over time. At 72 h post-injection, blood smears were also collected for differential blood cell analysis. Our results indicated a shift in leukocyte profile in the poly I:C challenged groups in both species to a higher neutrophil: lymphocyte ratio compared to the PBS control groups, indicating a stress response was induced. Differential expression was observed in the spleen at 24 h post-injection, with more genes downregulated in SMB relative to LMB. The comparison suggests a trend toward greater magnitude of the immune response in LMB relative to SMB. To our knowledge this is the first study to compare the antiviral immune response of smallmouth and largemouth bass.

Poster Presentation #197

No Abstract Assigned

Poster Presentation #198

Host Immune Responses to Enzootic and Invasive Pathogen Lineages Vary in Magnitude, Timing, and Efficacy

Coby Mcdonald[1], C. Guilherme Becker, Carolina Lambertini, Felipe Toledo, Célio Haddad, Kelly Zamudio
[1]Colorado State University, [2]Pennsylvania State University, [3]UNICAMP, [4]UNICAMP, [5]UNESP, [6]University of Texas, Austin

Infectious diseases of wildlife continue to pose a threat to biodiversity worldwide, yet pathogens are far from monolithic in virulence. Within the same pathogen species, virulence can vary depending on strain or lineage, in turn eliciting variable host responses. One pathogen that has caused extensive biodiversity loss is the amphibian-killing fungus, Batrachochytrium dendrobatidis (Bd), which is comprised of a globally widespread hypervirulent lineage (Bd-GPL), and multiple geographically restricted lineages. Whereas host immunogenomic responses to Bd-GPL have been characterized in a number of amphibian species, immunogenomic responses to geographically-restricted, enzootic Bd lineages are unknown. To examine lineage-specific host immune responses to Bd, we exposed the pumpkin toadlet (Brachycephalus pitanga), which is endemic to Brazil's Southern Atlantic Forest, to either the Bd-GPL or the enzootic Bd-Asia-2/Brazil lineage. We quantified functional immunogenomic responses over the course of infection using differential gene expression tests and coexpression network analyses. Host immune responses varied significantly with Bd lineage. Toadlet responses to Bd-Brazil were weak at early infection, peaked by mid-stage infection, and were nearly fully resolved by late-stage disease. In contrast, responses to Bd-GPL were magnified and delayed. Given that infection intensity did not vary between mid- and late-stage disease, this suggests that pumpkin toadlets may be at least partially tolerant to the geographically-restricted Bd-Brazil lineage. In contrast, mortality was higher in Bd-GPL-infected toadlets, suggesting that late-stage immune activation against Bd-GPL was not protective and was consistent with immune dysregulation previously observed in other species. Our results demonstrate that both the timing of immune response and the particular immune pathways activated are specific to Bd lineage. Within regions where multiple Bd lineages co-occur, and given continued global Bd movement, these differential host responses may influence not only individual disease outcome, but transmission dynamics at the population and community levels.

Poster Presentation #199

Nasopulmonary Mites (Acari: Halarachnidae) as Potential Vectors of Bacterial Pathogens, including Streptococcus phocae, in Marine Mammals

Risa Pesapane[1], Andrea Chaves[2], Janet Foley[2], Nadia Javeed[2], Samantha Barnum[2], Katherine Greenwald[3], Erin Dodd[3], Christine Fontaine[4], Padraig Duignan[4], Michael Murray[5], Melissa Miller[3]
[1]Ohio State University, [2]University of California Davis, [3]Marine Wildlife Veterinary Care and Research Center, [4]The Marine Mammal Center, [5]Monterey Bay Aquarium

Nasopulmonary mites (NPMs) of the family Halarachnidae are obligate endoparasites that colonize the respiratory tracts of mammals. NPMs damage surface epithelium resulting in mucosal irritation, respiratory illness, and secondary infection, yet the role of NPMs in facilitating pathogen invasion or dissemination between hosts remains unclear. Using 16S rRNA massively parallel amplicon sequencing of six hypervariable regions (or “16S profiling”), we characterized the bacterial community of NPMs from 4 southern sea otters (Enhydra lutris nereis). This data was paired with detection of a priority pathogen, Streptococcus phocae, from NPMs infesting 16 southern sea otters and 9 California sea lions (Zalophus californianus) using conventional polymerase chain reaction (cPCR). The bacteriome of assessed NPMs was dominated by Mycoplasmataceae and Vibrionaceae, but at least 16 organisms with pathogenic potential were detected as well. Importantly, S. phocae was detected in 37% of NPM by cPCR and was also detected by 16S profiling. Detection of multiple organisms with pathogenic potential in or on NPMs suggests they may act as mechanical vectors of bacterial infection for marine mammals.

Poster Presentation #200

One Health Community-Based Wildlife Mortality Surveillance for Ebola

Sarah H. Olson[2], Alain U. Ondzie[1], Marc-Joël Akongo[1], Trent Bushmaker[3], Kenneth N. Cameron[1], Morgane Cournarie[1], Dania M. Figueroa[3], Robert J. Fischer[3], Cynthia Goma-Nkoua[4], Serge D. Kaba[1], William B. Karesh[5], Eeva Kuisma[1], M. Jeremiah Matson[3], Jean-Vivien Mombouli[4], Vincent J. Munster[3], Patricia E. Reed[1], Stephanie N. Seifert[6], Chris Walzer[2]

[1]Wildlife Conservation Society Congo, Wildlife Health Program, [2]Wildlife Conservation Society, Health Program, [3]Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Disease, National Institutes of Health, [4]Laboratoire National de Santé Publique, Service d'Epidémiologie Moléculaire, [5]EcoHealth Alliance, [6]Washington State University, Paul G. Allen School for Global Health

Central Africa remains a high-risk Ebolavirus (EBOV) region, but the Republic of Congo (RoC), home to the largest remaining populations of great apes, has not had an epidemic since 2005. EBOV ecology is not fully understood but infected wildlife and consumption of animal carcasses have been linked to human outbreaks, especially in the Congo Basin. Since 2005, our One Health community-based wildlife mortality surveillance for EBOV has partnered with the Congolese Ministry of Health to reach communities and protected areas in northern RoC where people and great apes have died from past Ebola virus disease outbreaks. The outreach and surveillance is designed as an intervention to prevent contact between humans and infected animals and as an early warning system to locate carcasses or diseased animals and enable rapid detection of EBOV epizootics. Between April 2008 and September 2022, we conducted a total of 641 visits to 328 villages spread over 34 separate missions in four departments in the North of the RoC. We delivered the educational message to a total of 8,503 hunters, and to thousands of women and children who frequently visit the forest to gather food. Many villages were revisited each year. We achieved specimen collection by training project staff on a safe sampling protocol and equipping geographically distributed bases with sampling kits. We established in-country diagnostics, including recent deployment of mobile field-based platforms for EBOV testing, reducing diagnostic turnaround time to hours and days and demonstrated the absence of EBOV in 80 carcasses.

Poster Presentation #201

Developing a Wildlife Health Information System: Insights and Opportunities

Sabrina S Greening[1], Katie Haman[2], Lowell Ballard[3], Stephanie Herman[3], Chris Lutz[3], Julie Ellis[1]
[1]Department of Pathobiology, Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, New Bolton Center, [2]Wildlife Program, Washington Department of Fish and Wildlife, [3]Timmons Group

Globalization, population growth, and landscape changes are intensifying interactions at the animal-human-environment interface, and facilitate the transmission of infectious diseases. Wildlife disease surveillance at this interface is crucial for protecting public health, animal health, and biodiversity. However, despite its importance, many state and federal wildlife agencies tasked with managing wildlife populations lack the resources to respond efficiently to wildlife health events. For example, many agencies still rely on paper-based methods or simple spreadsheets to record wildlife health data; making it difficult to detect emerging diseases or track changes in the frequency, magnitude, and geographic extent of known disease threats. In this presentation, we show how an iterative delivery approach is being used to develop the Shared Wildlife Health Information System (SWHIS) - an online database tool designed to facilitate the organization, visualization, analysis, and sharing of wildlife health data. Throughout the development process, it has become clear that design flexibility and data integrity are crucial to safeguard the value and longevity of the database structure. Frequent feedback loops have helped to refine requirements across different states and ensure the system will not only support wildlife management agencies in making timely and informed decisions but also facilitate cross-agency communication. State feedback has also helped to prioritize system attributes that would be useful to agencies in the future, such as having access to resource libraries, building existing data into disease surveillance plans, and integrating diagnostic laboratory reporting systems. By outlining the design and development process used for SWHIS, we hope to inspire further discussions on what is needed to develop a successful agency-based wildlife health information system that can be used by states to help inform management decisions, strengthen regional and national responses to disease threats, engage the public in disease prevention, and promote the stewardship of animal, human and environmental health.

Poster Presentation #202

Avian Vibriosis: A Rising Barometer for One Health

Andrea Ayala[1], Miles Goldenberg[1], Salvador Almagro-Moreno[2,3], C. Brandon Ogbunugafor[1,4]
[1]Department of Ecology and Evolutionary Biology, Yale University, [2]Burnett School of Biomedical Sciences, University of Central Florida, [3]National Center for Integrated Coastal Research, University of Central Florida, [4]Public Health Modeling Unit, Yale School of Public Health

Avian vibriosis is an emerging disease of waterfowl, shorebirds, and terrestrial ground-foraging species caused by bacteria within the Vibrio genus, categorized in the family Vibrionaceae. As climate-sensitive prokaryotes, these marine and estuarine inhabitants are experiencing a period of unprecedented global change. As water temperatures rise and precipitation increases, pathogenic Vibrio species are expanding their distribution and abundance. To determine their emergence in avian species, we utilized the databases Web of Science and Google Scholar to perform a meta-analysis of the literature, documenting that eleven Vibrio species, including V. cholerae, V. parahaemolyticus, V. vulnificus and V. metschnikovii, have been increasingly isolated from birds since 1965. In total, we identified 76 studies from the primary literature which report on or examine, birds as hosts for these pathogenic Vibrio species. In our meta-analysis, we documented studies from 29 countries, constituting all continents except for Antarctica. We further report that the burden of disease in birds is most commonly associated with V. cholerae, followed by V. metschnikovii and V. parahaemolyticus. Meta-analysis wide prevalences of the Vibrio pathogens across avian species varied from 19% for V. parahaemolyticus to 1% for V. mimicus. Of note, 41 of 76 studies investigated the prevalence or pathogenesis of V. cholerae in avian species, representing both O1 and non-O1/O139 serotypes. In addition, we document that pathogenic Vibrio species were recovered from both wild and domestic birds throughout the world. This finding not only has implications for the conservation of wild birds, but also for the agriculturally associated birds raised by subsistence farmers. Given our documentation of avian vibriosis, further research into the correlation between Vibrio pathogen shedding and avian pathogenesis remains a crucial avenue of research. Additional studies should investigate the community-level effects of Vibrio colonization within our imperiled coastal and marine-dwelling wild birds.

Poster Presentation #203

Fish Eating Birds Can Spread Bacterial Diseases Between Catfish Ponds

Fred Cunningham[1], 2 Lorelei Ford[2], Larry Hanson[2]
[1]USDA/APHIS/WS/NWRC, [2]Mississippi State University-College of Veterinary Medicine

Severe outbreaks of Motile Aeromonad Septicemia disease in commercial catfish aquaculture ponds have been associated with a virulent Aeromonas hydrophila strain (vAh) that is genetically distinct from less virulent strains. We demonstrated that Great Egrets (Ardea alba), Double-crested Cormorants (Phalacrocorax auritus), American White Pelicans (Pelecanus erythrorhynchos), and Wood Storks (Mycteria americana) can carry and shed viable vAh after consuming fish infected with vAh.

In a separate study, Great Egrets were fed fish injected with vAh on days 0, 3, 7, 10 and placed on enclosed ponds that contained naive catfish fingerlings. In pond 1 (treated) fish and water samples were positive for vAh on days 17 and 21. Samples of fish, water, chironomids, invertebrates, snails, and mud, from pond 3 (treated) were positive for vAh days 15-29 and experienced fish mortalities from days 15-29.

Edwardsiella ictaluri and E. tarda are considered the primary species of Edwardsiella to cause disease outbreaks in North American catfish aquaculture. Genetic analysis has determined that most isolates designated as E. tarda were a new species, E. piscicida. There has been an increase in E. piscicida diagnostic cases in recent years. We conducted a study to determine if Great Egrets (Ardea alba) shed viable E. piscicida when fed catfish infected with the bacteria.

Great Egrets fed infected fish shed viable E. piscicida bacteria for multiple days, (Table 1), after last consuming infected fish on day 2 of the study. Great Egrets in the control group did not shed the bacteria. Given that Great Egrets can shed viable E. piscicida after consuming diseased fish, we hypothesize that they could also serve as a reservoir for E. piscicida and could spread the pathogen while predating fish in catfish ponds. Additional research is needed to determine if this shedding could cause disease in catfish ponds.

Poster Presentation #204

Epistylid Infestation Resulting in Morbidity in Two Species of Mud Turtles (Kinosternon spp.) in the American Southwest

Audrey Owens[1], Jennifer Smith[2], Rebecca Cole[3], Jeffrey Lorch[3], Anne Justice-allen[1], Daniel Grear[3]
[1]Arizona Game and Fish Department, [2]New Mexico State University, [3]USGS National Wildlife Health Center

The protistan genus Epistylis contains freshwater colonial species that attach to aquatic organisms in an epibiotic relationship. They are known to attach to the epidermis and shells of aquatic turtles (Bishop and Jahn 1941; Bovee 1976; Germano 2000), but have not been reported to cause heavy infestations or morbidity in turtles. Here, we document heavy infestations of Epistylis spp. in several populations of Sonoran mud turtles (Kinosternon sonoriense) inhabiting livestock ponds in Arizona and rough-footed mud turtles (K. hirtipes) from livestock ponds in Texas over the course of several years. We observed severe Epistylis sp. infestations on mud turtles that appeared to alter normal diving and foraging behavior when compared to uninfested individuals, leading to anorexia and malnutrition. Infestations were cleared using chlorinated tap water or a 10 % salt solution, and the turtles had no permanent damage to their shell or epidermis upon clearing. Several of the turtles we observed would have likely succumbed to the infestation without intervention, given their behavioral limitations and severe muscle wasting. We suggest that heavy infestations of Epistylis spp. could be an important source of morbidity or mortality in Kinosternon spp. where mud turtles inhabit warm, shallow, eutrophic aquatic habitats,
such as livestock ponds.

Poster Presentation #205

Erysipelothrix rhusiopathiae: An Increasingly Significant Pathogen for Critically Endangered Cook Inlet Beluga Whales

Natalie Rouse[1, 2], DVM, DACVP Kathy Burek-Huntington[1,2]
[1]University of Alaska Anchorage, [2]Alaska Veterinary Pathology Services

Cook Inlet beluga whales (CIB) are a critically endangered, non-migrating, distinct population of beluga whales, located in Southcentral Alaska (O'Corry-Crowe et al. 1997). Erysipelothrix rhusiopathiae (ER) is a zoonotic gram-positive bacillus that affects marine mammals and other wild and domestic animals (Waltzek et al. 2012, Keatts et al. 2021). ER is known to cause skin disease, infectious endocarditis, systemic infection and, in some cases, death (Ceccolini et al. 2021) (Brock et al. 2020). In 2019 and 2021 ER was found in the vast majority of dead stranded CIB in one or more internal organs (8/9 or 89%). This is a drastic increase from prior years. From 2014-2018 no more than one animal per year was found infected with ER in Cook Inlet and ER was not detected at all before 2014. Due to the critically endangered status of CIB, the increased frequency of detection of ER in CIB, and the zoonotic nature of this pathogen, an increased understanding of the relationship of this pathogen with CIB is warranted. This is a critical examination of all known cases of ER in CIB over the last 10 years, including retrospective analyses of archived tissues by PCR when samples were available. We also compiled data on ER detections in other marine mammals from Cook Inlet and attempted to acquire information regarding ER detection in terrestrial wildlife and in the environment in and around Cook Inlet.

Poster Presentation #206

Causes of Morbidity and Mortality in Free-Ranging Sea Turtles Found on St. Kitts and Nevis (2015-2022)

Heather Fenton[1], Angela Picknell[1], Michelle Dennis[3], Maria-Jose Navarrete[1], Pompei Bolfa[1], Kimberly Stewart[2]
[1]Ross University School of Veterinary Medicine, [2]St. Kitts Sea Turtle Monitoring Network, [3]University of Tennessee

Between 2015 and 2022, 17 free-ranging sea turtles that were found on beaches on the islands of St. Kitts and Nevis, West Indies underwent full post-mortem and histopathological examination. Of the 17 individuals, two sea turtle species were represented: critically endangered hawksbill (Eretmochelys imbricata, n = 2) and endangered green (Chelonia mydas, n = 15) sea turtles. The age distribution included juveniles (n = 8; 47 %), one post-hatchling (5%), one subadult (5%), and seven adults (41%). When the sex could be determined, slightly more males (n = 8), were represented than females (n = 4). Anthropogenic causes of death were reported in five cases (29%) and included watercraft-related injury (n = 3) and fisheries interactions (n = 2). Suspected antemortem predation by sharks was documented in 4/17 (23%) of cases. The cause of mortality could not be determined in six cases (35%). Potential negative impacts associated with Sargassum sp. seaweed have been implicated in morbidity and mortality of marine species in the eastern Caribbean region although the pathogenesis is not understood. Sargassum sp. ingestion was documented in four cases with no other obvious cause of mortality. Severe systemic coccidiosis (likely Caryospora sp.) was considered to have been the ultimate cause of death in one case. Additional subclinical findings included evidence of systemic spirorchiasis and intestinal trematodiasis (presumably Diachistorchis pandus). Although the current sample size is low, the species are of high conservation importance. Literature on causes of disease and mortality in juvenile to adult free-ranging sea turtles from the Caribbean region is limited. These findings highlight potentially important mitigation targets for anthropogenically-caused mortalities, such as public awareness campaigns targeted at fisheries regulations, monofilament fishing line management, and watercraft activities.

Poster Presentation #207

Diet-Induced Thiamine Deficiency in Canada Geese (Branta canadensis) Recovered from Low-Head Dam Site in Iowa

Rachel Ruden[1,2], Dr. Jenni Boonjakuakul[3], Dr. Yuko Sato[2]
[1]Wildlife Bureau, Iowa Department of Natural Resources, [2]Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, [3]Iowa Bird Rehabilitation

Between 15 February and 22 February 2021, approximately 150-200 Canada geese (Branta canadensis) and at least two mallard ducks (Anas platyrhynchos) were found acutely dead or neurologic below a low-head dam site in Iowa City, Iowa. This event shortly followed a polar vortex that left eastern Iowa in heavy ice cover, with birds reported to be actively feeding on gizzard shad containing the enzyme thiaminase. One adult mallard and one adult Canada goose were dispatched by Iowa Department of Natural Resources personnel on 18 February in excellent body condition. In both birds, the brain had no diagnostic findings but there were gross and histopathologic lesions in the heart. Live birds were admitted by four individual wildlife rehabilitators or rehabilitation networks, with most birds (n = 52) entering Iowa Bird Rehabilitation (IBR) in Des Moines, Iowa. Clinical signs included ataxia, torticollis, and somnolence. Birds at IBR received 30-50 mg/kg thiamine mononitrate orally each day for 3-7 days depending on clinical improvement with most making a rapid recovery and being releasable within 2 weeks. On four birds, whole blood was collected on day 0 at admission prior to treatment, and then again on days 8 and 15 for thiamine testing. Thiamine values rose 3-7-fold higher with supportive care, consistent with the field observations and necropsy findings that a diet-induced thiamine deficiency, likely exacerbated by the weather, drove this health incident.

Poster Presentation #208

White-Tailed Deer Lung Cells are Susceptible to Japanese Encephalitis Virus

Leela Noronha[1], Emily Hedden[1], Jeana Owens[1], Dana Mitzel[1]
[1]National Bio and Agro-Defense Facility, Agricultural Research Service, United States Department of Agriculture

Japanese encephalitis virus (JEV) is a zoonotic mosquito-borne flavivirus maintained in an enzootic transmission cycle between mosquitoes, mammals, and birds primarily in Southeast Asia and the Western Pacific. JEV has a wide host range and some wildlife species have been implicated. North American white-tailed deer (WTD; Odocoileus virginianus) can be infected by a closely related flavivirus, West Nile virus, as well as other significant zoonotic pathogens such as those that cause tuberculosis, brucellosis, and COVID-19. Here, we investigated the in vitro susceptibility of primary white-tailed deer lung cells (WTDLg) to an attenuated strain of JEV, SA14-14-2. In duplicate experiments, WTDLg cells were infected with SA14-14-2, with JEV-susceptible baby hamster kidney cells (BHK-21) used as positive controls. An indirect immunofluorescence assay was used to detect the presence of JEV NS1 antigens in cells infected at 1 multiplicity of infection (MOI) for 48 hours. NS1 antigens were observed in infected WTDLg and BHK cells, but not mock-infected cells. To examine virus replication, the cells were infected with SA14-14-2 at a 0.1 MOI and observed for 120 hours. Monolayers were photographed, cytopathic effects (CPE) were noted, and supernatants were collected every 24 hours between 0 and 120 hours post infection (hpi). Plaque assays were used to quantify the number of infectious virus particles in cell supernatants. In initial studies, virus was detected in the supernatants of infected WTDLg cells by 24 hpi, with peak titers comparable to BHK cells and occurring between 48 and 72 hpi. Infected WTDLg cells showed signs of CPE at 72 hpi, onward. Our results indicate that WTDLg cells are susceptible to JEV SA14-14-2. This may imply a broader host range for JEV than previously described. These results warrant further investigation into the susceptibility of WTD to JEV and their potential role in the maintenance of JEV in nature.

Poster Presentation #209

Evidence of Tick-borne Virus Circulation in Virginia via Serosurveillance in Wildlife Species

Gillian Eastwood[1], Dr Alexandra Cumbie[1], Peter Schiff[1], Ahmed Garba[1], Rebecca Trimble[1], Dr Jen Riley[2]
[1]Virginia Tech, [2]Blue Ridge Wildlife Center

Emerging tick-borne viruses such as Bourbon virus (genus: Thogotovirus), Heartland virus (genus: Phlebovirus) are recently discovered pathogenic agents which have caused fatal human cases, yet little is known about their distribution or enzootic maintenance. The infection exposure of potential vertebrate host species is important to understand the prevalence and transmission of arboviral pathogens. Blood sera was obtained from a combination of wildlife specimens either as patients admitted to wildlife rehabilitation centers, samples from local harvested deer, or road kill. Plaque reduction neutralization assays were used to test for the presence of antibodies against each tick-borne virus. In addition, tick species were collected from ten counties of Virginia and screened for Bourbon, Heartland, and Powassan virus (genus: flavivirus) via RT-PCR. We corroborate evidence that Bourbon and Powassan virus are circulating in several counties of western Virginia through detection of the virus in locally collected ticks and seropositive wildlife species. No evidence of Heartland virus was found in ticks tested to date, however seropositivity in wildlife suggest this virus has also now emerged in the region. Seroprevalence studies to determine infection exposure to arboviral pathogens are ongoing. Taking a One Health approach, serosurveys of wild and domestic animal species, as well as continued vector surveillance, can demonstrate the introduction and expansion of novel arboviral pathogens.

Poster Presentation #210

Parasites of the Invasive North American Raccoons (Procyon lotor) in Central Spain

Michael Yabsley[1,4], Carlos García[2], Jose Aguirre[2], Silvia Villaverde, Eva Banda[2], Sonia Hernandez[1,4]

[1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [2]Departamento de Biodiversidad, Ecología y Evolución, Universidad Complutense de Madrid, [3]Centro de Recuperación de Animales Silvestres de la Comunidad de Madrid (CRAS), Tres Cantos, [4]Warnell School of Forestry and Natural Resources, University of Georgia

The American raccoon (Procyon lotor) is an invasive meso-carnivore which has been introduced and established in many European countries. Although the presence of the raccoon in the Iberian Peninsula was confirmed around 20 years ago, there are few data on pathogens of these animals in this region. For this work, 72 American raccoons from two subpopulations in the central region of the Iberian Peninsula were examined for selected parasites. Ectoparasite species richness (both fleas and ticks) increased during the sampling season and was highest in the Henares subpopulation and on males. Similarly, ectoparasite abundance increased during the sampling season and was highest in Henares and on adult raccoons. Four species of ticks were detected including Rhipicephalus pusillus (71%), followed by R. turanicus (24%), Ixodes ventalloi (3%), and Dermacentor marginatus (1.4%). Three species of fleas were detected including Pulex irritans (44%), Ctenocephalides felis (3%) and C. canis (1.4%) infestations. A subset of raccoons (n=56) were examined for intestinal parasites. A low prevalence and diversity were founding including Strongyloides procyonis (4%), Dilepis sp. (5%), Plagiorchis sp. (2%), and Moniliformis moniliformis (2%). Importantly, Baylisascaris procyonis was not found. Finally, no subcutaneous nematodes (i.e., Dracunculus and Dirofilaria spp.) were found in the 56 raccoons examined. The results of this work show that the invasive North American raccoons currently are infected with few endoparasites but are commonly infested with native ectoparasites, several of which can transmit pathogens relevant for public and veterinary health. However, the geographically distinct populations of raccoons in Spain have different introduction histories, thus additional surveillance for parasites is warranted.

Poster Presentation #211

Echinococcus Species Infections Among Wild Canids in Pennsylvania, USA

Christopher Cleveland[1], Kayla Garrett[1,2], Dr. Justin Brown[3], Ryan Grunert[1], Jonathan Hunte[4], Dr. Mark Ruder[1], Kyle Van Why[5], Dr. Michael Yabsley[1,2]

[1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, [2]Warnell School of Forestry and Natural Resources, University of Georgia, [3]Department of Veterinary and Biomedical Sciences, Pennsylvania State University, [4]University of Georgia College of Veterinary Medicine, [5]USDA Wildlife Services

Echinococcus species are zoonotic tapeworms of veterinary/medical concern, and can cause disease in wildlife, domestic/agricultural animals and humans (cystic or alveolar echinococcosis). Two species of interest in North America are Echinococcus multilocularis and E. granulosus canadensis. The primary wildlife definitive hosts for E. multilocularis and E. canadensis are red foxes (Vulpes vulpes), gray foxes (Urocyon cinereoargenteus), coyotes (Canis latrans), and wolves (Canis lupus); while intermediate hosts for E. multilocularis and E. canadensis are rodents and cervid species, respectively. Historically absent in the eastern US, E. multilocularis was recently reported in a domestic dog in Virginia, a human in Vermont, and a domestic dog in Missouri, while E. canadensis has been reported in coyotes in Maine and translocated elk in Tennessee. These findings highlight the need for Echinococcus surveillance in the eastern US. During 2019-2020, gastrointestinal tracts (GIT) were collected from wild canids in Pennsylvania. A total of 307 canid GITs were screened. Two coyotes (2/154) were positive with both E. multilocularis and E. canadensis species. No red foxes (n=137) or gray foxes (n=16) had evidence of Echinococcus species infection. Our data indicate that Echinococcus species are present in wild canids in Pennsylvania and the threat to humans, wildlife, and domestic/agricultural animals in this region remains unknown. Further evaluation of both the definitive and intermediate hosts is needed for a better understanding of Echinococcus in Pennsylvania and neighboring regions.

Poster Presentation #212

Francisella Tularensis Exposure in Arctic Wildlife: A Need for Renewed Surveillance in Alaska?

Matthew Smith[1], Caroline Van Hemert[1], Todd C. Atwood[1], David R. Sinnett[2], Jerry W. Hupp[1], Brandt W. Meixell[1,3], David D. Gustine[1,4], Layne G. Adams[1], Andrew M. Ramey[1]
[1]USGS Alaska Science Center, [2]USDA APHIS Wildlife Services, [3]US Forest Service, [4]US Fish and Wildlife Service

Infections by Francisella tularensis, the causative agent of tularemia, are ubiquitous in the northern hemisphere, including in Alaska where the pathogen was first identified in 1938. This highly infectious zoonotic bacterium, which can cause severe disease in some hosts, has been identified in a broad suite of taxa including insects, birds, and mammals. Few recent studies have been conducted in Alaska, however, and knowledge about the distribution of F. tularensis in Arctic wildlife is limited, including among species that are frequently harvested for subsistence or personal use. To assess the seroprevalence of F. tularensis antibodies in wildlife from the Arctic Coastal Plain of Alaska and its nearshore marine region, we screened serum samples collected from mammals and tundra-nesting geese using a commercially available slide agglutination test. We detected antibodies in 14.8% of all individuals sampled (n=724), with titers ranging from 1:20 to 1:320. Arctic foxes (Vulpes lagopus) and small mammal species had the highest seroprevalence at 21.3% and 21.2%, respectively, followed by polar bears (Ursus maritimus) at 14.5%. Caribou (Rangifer tarandus) had comparatively low seroprevalence at 6.5%. Antibodies were detected in all three species of geese sampled, with Black Brant (Branta bernicla nigricans) having the highest seroprevalence at 13.6%. The detection of F. tularensis antibodies across multiple taxa from the Arctic Coastal Plain, an area that is undergoing rapid environmental change due to climate warming, provides evidence of widespread exposure to this pathogen throughout the region and highlights the need for renewed surveillance in Alaska.

Poster Presentation #213

Plague-Positive Mouse Fleas on Prairie Dog Colonies: Flea Blood Meal Identification by Amplicon Deep Sequencing

Gebbiena Bron[1,2,3], Leah A. Owens[2], Chris D. Dunn[2], Professor Tony L. Goldberg[2], Dr. Tonie E. Rocke[3]

[1]Wageningen University & Research, [2]University of Wisconsin - Madison, [3]U.S. Geological Survey National Wildlife Health Center

Increased DNA sequencing power created the opportunity to further decipher vector-borne pathogen transmission by elucidating feeding relationships of vectors and hosts. Plague, associated with rodents worldwide and primarily transmitted by fleas, can extirpate prairie dog (Cynomys spp.) colonies in the western United States. However, it is unclear where the causative agent, Yersinia pestis, persists between plague outbreaks and how the disease re-emerges on prairie dog colonies. Short-lived rodents have been hypothesized to play a role in plague dynamics on prairie dog colonies; potentially serving as a source of plague infection for prairie dogs or as a spillover host for the pathogen during a plague outbreak in prairie dogs. For either scenario, we would expect infectious fleas to be shared between prairie dogs and mice. During a field study we discovered two deer mice and one grasshopper mouse with plague-positive fleas before plague-induced prairie dog die-offs in Montana black-tailed and Utah white-tailed prairie dog colonies, respectively. This provided evidence for mouse involvement in the plague cycle but did not show a direct link between prairie dogs and mice. We developed universal primers targeting part of the rodent cytochrome B gene, then sequenced the target amplicon using the Illumina platform to assess possible cryptic feeding relationships of the fleas. The plague positive fleas contained primarily DNA from their most recent host species; no prairie dog DNA was detected. Interestingly, one pool collected from a deer mouse contained <0.01% prairie vole (Microtus ochrogaster) DNA. However, we cannot exclude other host sources of Y. pestis infection, because the bacterium can persist in fleas longer than blood meal DNA can. We anticipate that our blood meal analysis protocol can be used to evaluate other predator-prey relationships of vectors and hosts.

Poster Presentation #214

Investigating Host Ecology of Lyme Disease Causative Agent Borrelia burgdorferi in Ohio

Ningzhu Bai[1], Dr. Andreas Chavez[2], Dr. Risa Pesapane[1,3]
[1]School of Environment and Natural Resources, College of Food, Agricultural, and Environmental Sciences, The Ohio State University, [2]Department of Evolution, Ecology, and Organismal Biology, College of Arts and Sciences, The Ohio State University, [3]Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University

Lyme disease is rapidly expanding and is of a great public health concern in the United States. The emergence is the consequence of a confluence of the causative agent, Borrelia burgdorferi, Ixodes tick vectors, hosts, and the ecological and climatic conditions supporting tick and host populations. Little is known about how B. burgdorferi prevalence in the blacklegged tick population has changed in Coshocton County since its initial establishment in 2010 or the pathogen-tick-host relationships of Ohio's small mammal community.

This study aims to: (1) determine the current prevalence of B. burgdorferi among questing blacklegged ticks, (2) investigate pathogen-tick-host relationships, like tick infestation and B. burgdorferi infection prevalence among different host species. The current infection prevalence among ticks is expected to increase and various hosts species are parasitized. We revisited the original sites of establishment to collect ticks and small mammals in 2021. Real-time PCR was used to detect the presence of pathogens in tick and host DNA extracts. High B. burgdorferi infection prevalence was detected in questing blacklegged ticks and field-caught white-footed mice (Peromyscus leucopus) and eastern chipmunks (Tamias striatus). Compared to the data from the initial study in 2010, B. burgdorferi infection prevalence has increased significantly in ticks and hosts. Various small mammal species were used by blacklegged ticks, including white-footed mouse, eastern chipmunk, short-tailed shrew (Blarina brevicauda), American red squirrel (Tamiasciurus hudsonicus), house mouse (Mus musculus), and southern flying squirrel (Glaucomys volans).

Our study detected an increase in the overall prevalence of B. burgdorferi and the risk of Lyme disease in Coshocton County, Ohio. Our study generated new insights on the involvement of non-Peromyscus small mammals in Lyme disease transmission cycle. Understanding host ecology is valuable for designing effective host-targeted control and surveillance activities as well as making accurate predictions of the continued geographic expansion of Lyme Disease.

Poster Presentation #215

SARS-CoV-2 in White Tail Deer in Pennsylvania

Roderick Gagne[2], Andrew Marques[1], Scott Sherrill-Mix[1], John Everett[1], Hriju Adikhari[1], Shantan Reddy[1], Julie Ellis, Haley Zeliff[3], Sabrina S. Greening[2], Carolyn Cannuscio[4,5], Katherine Strelau[4,5], Ron Collman[6], Brendan J. Kelly[7], Kyle Rodino[8], Frederic D. Bushman[1], Eman Anis[3]

[1]Department of Microbiology, Perelman School of Medicine, University of Pennsylvania, [2]Department of Pathobiology, Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, [3]Department of Pathobiology, University of Pennsylvania School of Veterinary Medicine, New Bolton Center, [4]Leonard Davis Institute of Health Economics, University of Pennsylvania, [5]Department of Family Medicine and Community Health, University of Pennsylvania, [6]Pulmonary, Allergy and Critical Care Division; Department of Medicine; University of Pennsylvania Perelman School of Medicine, [7]Division of Infectious Diseases; Department of Medicine & Department of Biostatistics, Epidemiology, and Informatics; Perelman School of Medicine, University of Pennsylvania, [8]8Department of Pathology and Laboratory Medicine, Perelman School of Medicine, University of Pennsylvania

The SARS-CoV-2 pandemic began by a spillover event from an animal host into humans. Subsequently, animals in contact with infected humans have been infected with SARS-CoV-2 via ‘reverse zoonosis’. White-tail deer, Odocoileus virginianus in North America are infected at substantial levels, raising concerns about the formation of a new animal reservoir. A reservoir species could result in accelerate evolution of the virus, with the potential for strain divergence. Subsequent infection of humans could propagate new strains with potential different pathogenicity, transmission potential, or capacity for immune escape. We tested 123 nasal swabs from Pennsylvania deer with RT-qPCR, and found 20 (16%) were positive for SARS-CoV-2. Seven whole-genome sequences were obtained, which were annotated as alpha and delta, the first reported observations of these lineages in deer. The alpha lineage persisted in deer after its displacement by delta in humans, and deer-derived alpha variants diverged significantly from those in humans, consistent with a distinctive evolutionary trajectory in deer. Further analyses identified multiple independent jumps from humans to deer and showed persistence within deer populations over several months.

Poster Presentation #216

Genetic Detection of Sin Nombre Virus in Rodent Assemblages of East New Mexico, A Region with No Known Human Infection

Jaecy Banther-McConnell[1], Thanchira Suriyamongkol[2], Robert Nofchissey[3], Samuel Goodfellow[3], Steven Bradfute[3], Ivana Mali[1]
[1]Eastern New Mexico University, [2]Southern Illinois University, [3]University of New Mexico Health Sciences Center

Orthohantaviruses cause two zoonotic diseases in humans: hemorrhagic fever with renal syndrome (HFRS) and hantavirus cardiopulmonary syndrome (HCPS). HCPS occurs primarily in North America, with Cricetid rodents, such as deer mice (Peromyscus maniculatus), serving as the primary reservoir of Sin Nombre virus (SNV). In the United States, New Mexico (NM) is leading the nation in the number of HCPS cases. However, no reported cases of HCPS have occurred within eastern NM. The objective of our study was to assess SNV seroprevalence and genetically confirm SNV in rodent communities across this portion of the state. Our primary focus was to assess how the overall rodent community composition and habitat affects prevalence in Peromyscus sp. In 2020 and 2021, we surveyed 20 sites over 30,000 trap nights and collected blood and lung samples from 740 rodents. We captured Peromyscus sp. at 17 sites and they constituted 24% (180/740) of all captures. Blood samples from all rodent captures were tested through enzyme-linked immunosorbent assays (ELISAs) for detection of IgG antibodies against a full-length SNV nucleocapsid antigen. All Peromyscus lung samples were tested through RT qPCR using SNV specific primers. In total, 11 Peromyscus samples tested seropositive, and 51 samples were positive in the SNV qPCR assay. Both laboratory analyses indicate presence of SNV in eastern New Mexico, with RT qPCR techniques detecting more positive individuals than ELISA. PCR analysis on non-Peromyscus lung samples is still ongoing, but testing to date shows SNV detection in three additional species not yet reported in the literature. Abundance of SNV positive Peromyscus per site was positively correlated to the proportion of male Peromyscus and the abundance of all known competent hosts, but negatively correlated to species richness. This ongoing study can aid in predicting future HCPS outbreaks and expand our understanding of hantavirus prevalence within eastern NM.

Poster Presentation #217

Complex Virus Diversity Among Wild-Caught Rodents in Sierra Leone – Insights into Virus Ecology at High-Risk Interfaces

Bruno Ghersi[1,2], James Bangura[1,3], Matej Vucak[4], Emmanuel Amara[3], Marilyn Kanu[3], Victor Lungay[3], Edwin Lavalie[3], Willie Robert[3], Jenna Nichols[4], David Wolking[1], Corina Monagin[1], UC Davis PREEMPT consortium, Andrew Davison[4], Brian Bird[1]

[1]One Health Institute, School of Veterinary Medicine, University of California, Davis, [2]Tufts University, [3]University of Makeni, [4]MRC University of Glasgow center for virus research

Abundant rodent and naturally co-evolved endemic virus species diversity is a hallmark across tropical West Africa. Among this rodent community, the multimammate rat (Mastomys natalensis) is widely distributed and the natural reservoir of a significant human pathogen, Lassa virus (LASV, Arenaviridae). M. natalensis occupies multiple environments (houses, agricultural croplands, grasslands, and brush areas) depending on food availability. To understand rodent and virus dynamics more fully, we conducted longitudinal surveillance in 17 communities found across Sierra Leone from 2019 to 2021 at high-risk interfaces (e.g., in and near dwellings, granaries, croplands). Over 16,269 trap nights we captured 718 small mammals representing 18 different species. Mastomys natalensis was the most abundant small mammal captured and was present in 94% of the visited communities. Overall, LASV genome was detected in 4.2% (30/718) of tested individuals. Somewhat surprisingly, and in marked contrast with the reported distribution of human LF cases, LASV positive rodents were found in both the north and south of the country, demonstrating a wider distribution than previously recorded. Seasonal detection of LASV was higher during wet season (6.3%) vs. dry season (2.14%) months. LASV positive rodents were detected in all environmental types with the highest proportion of infected rodents found inside dwellings (4.7%). Further findings include the detection of an entirely new species of rodent-borne arenavirus (Seli virus) in Mus minutoides (the African pygmy mouse), and among M. natalensis multiple cytomegaloviruses (Herpesviridae) were detected. Serologic testing for LASV and CMVs is underway. Taken together, our data identifies new potential risk areas for LF and highlights the complex and rich rodent and virus species diversity present in Sierra Leone.

Poster Presentation #218

Salmonella Environmental Persistence Informs Management Relevant to Avian and Public Health

Kimberly Perez[1], Sonia Hernandez[2,3], Olivia Seiverts[2], William Norfolk[1], Raquel Francisco[2,3], Susan Sanchez[4], Erin Lipp[1]

[1]Environmental Health, College of Public Health, University of Georgia, [2]Warnell School of Forestry and Natural Resources, University of Georgia, [3]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, [4]Bacteriology, Athens Diagnostic Lab, College of Veterinary Medicine, University of Georgia

Globally, salmonellosis outbreaks are common in aquatic and songbird populations and Salmonella continues to be a significant pathogen for public health. Notably, in 2021 a Salmonella Typhimurium outbreak in people was associated with the use and handling of bird feeders. Research is needed to understand the interaction between humans, birds, and their interface. Key to preventing outbreaks is understanding transmission dynamics, specifically, how long Salmonella persists on various materials. Persistence has been studied in food systems and commercial poultry operations—neither are relevant to free-living birds or people in contact with bird feeders. To fill these gaps, we conducted two experiments. First, white ibis in South Florida were encouraged to feed on wooden picnic tables until they deposited fresh feces, which were collected every day for 8 days to determine prevalence and persistence. Second, 4 types of feeders in Georgia (cedar, plastic, cedar + antimicrobial coating, and plastic + antimicrobial coating) were seeded with sterile chicken feces inoculated with 10^6 CFU of S. Typhimurium and swabbed at regular intervals for a month. For both experiments, fecal swabs were processed using a standard Salmonella culturing protocol with primary enrichment in dulcitol selenite broth, secondary enrichment in Rappaport-Vassiliadis broth, and presumptive identification on XLT-4 agar. Of 96 deposited feces, we obtained 27% positive. Salmonella persisted for an average of 3 days, and maximum of 4 days. On feeders, Salmonella persisted longer on coated and uncoated plastic feeders (27%; first 5 days) compared to coated and uncoated cedar feeders (3%; first 5 days). The antimicrobial coating used did not lower Salmonella persistence. Our studies suggest that Salmonella can have prolonged persistence on shared spaces, persistence depends on surface material, and precautionary measures (i.e., increased hygiene) should be adopted to reduce human exposure.

Poster Presentation #219

Cryptococcus Gatii Infections in Oregon Roosevelt Elk (Cervus Canadadensis RooseveltI).

Julia Burco[1], Deborah Chong[2], Emilio DeBess[3]
[1]ODFW, Wildlife Health and Population Laboratory, [2]Oregon State University, [3]Oregon Health Authority

Cryptococuccus gattii is an emerging fungal pathogen affecting humans, domestic pets and wildlife in the pacific northwest. Historically (C. gatii) has been endemic to the tropics and subtropical regions (Australasia, southeast Asia, and parts of Latin America). However, in the early 2000's cases started to crop in in Canada on Vancouver Island and then have moved down into the pacific northwest including Oregon and Washington. Here the fungus appears to be largely associated with Coastal Douglas Fir and Coastal Western Hemlock biogeoclimatic zones. Variant type IIa predominates in these Pacific Northwest cases and it as an emerging infectious disease of concern in this area as it can cause clinical disease (often fatal) in both immunocompromised and immunocompetent hosts. In addition to the emergence of human and domestic pet cases, wildlife cases have been increasingly documented which have primarily included porpoises and Roosevelt elk. Since the early 2000's at least 8 clinical cases have been confirmed in Roosevelt elk from the mid-Willamette valley to central and north-coast regions of Oregon. Localization of lesions range from cutaneous presentations, pneumonia, meningioencephalitis to bone infections. Roosevelt elk cases in order to better understand the epidemiology of this disease in the northwest as elk appear to be a sentinel species of infection of this fungus that poses a significant risk to humans and animals in the region. Preliminary passive surveillance results have yielded one positive nasal PCR result and 44 negative culture and serologic results on a recent live elk capture, suggesting that infections are still relatively rare and difficult to evaluate on a landscape level. Nevertheless, Roosevelt elk appear to be a good sentinel species for infections and case distribution helps elucidate the environment in which this fungus thrives.

Poster Presentation #220

Development and Implementation of a Strategic Bio-Risk Management Plan in the Context of Viral Zoonoses

Tristan Burgess[1,3], Dr Katie Prager[2], Dr Bruno Gerci[3], Dr Jonathan Gass[3], Dr Felicia Nutter[3], Ms Colleen Cronin[5], Dr David Brett-Major[4], Dr Deborah Kochevar[3]
[1]Center for Wildlife Studies, [2]University of California Los Angeles, [3]Tufts University, [4]University of Nebraska Medical Center, [5]University of Washington, Institute for Risk Analysis and Risk Communication

Bio-risk management (and biosafety in particular) is a critical topic in any wildlife health work, especially research focused on emerging zoonoses which often involves handling and sampling wildlife with unknown infection status. The potential transmission of known and unknown high consequence pathogens such as filoviruses and coronaviruses necessitates clear guidelines to safely conduct this vital work. While literature and institutional policies and practices exist regarding bio-risk management from a general perspective, especially in laboratory biosafety, surprisingly little published work explicitly addresses biosafety and bio-risk management in the context of wildlife fieldwork. Existing laboratory biosafety practices are generally designed to protect against known and understood hazards of working with documented pathogens at designated biosafety levels. Exposure to such threats in a controlled setting can be considered 'Preventable Risks' – the hazards are documented, understood and effectively mitigated by rules and protocols governing operator behavior. Wildlife fieldwork, on the other hand, is dynamic with myriad factors that cannot always be completely documented, understood and anticipated beforehand, making exposures in that setting more akin to 'Strategic Risks.' This increases the necessity to develop risk management approaches that continually adapt to exposure, as well as environmental, risks. High precautionary levels of hazard control, potentially inappropriate to the setting (e.g. very high levels of PPE for relatively low-risk activities), could do more harm than good by causing overheating or decreased mobility in the field or discouraging adherence to protocols perceived as impractical. In this context, we describe USAID STOP Spillover Tufts University Consortium's strategy for creating a biosafety and bio-risk management plan for a multi-country project involving high-consequence zoonotic viruses. In developing our approach, we draw not only on the traditional biosafety literature, but also on processes and concepts from other disciplines including Strategic Risk Management and Infection Prevention and Control.

A

Aasmo-Finne, Merethe 93
Abad, Xavier 127
Abalos, Pedro 155
Abbott, Rachel 76
Abuhadba Medrano, Nour 155
Acuña, Vicenç 127
Adamovicz, Laura 161
Adams, Henry C. 75
Adams, Layne G. 212
Adams, Lisa 96
Adams, Michael J 64
Adcock, Kayla G. 102
Adikhari, Hriju 215
Agbalog, Rose 107
Aguirre, AA 162, 163
Aguirre, Jose 131, 210
Ahmed, Md Sohel 76
Ahrens, Kristin 194
Akongo, Marc-Joël 200
Aleuy, O. Alejandro 38
Alexandersen, Soren 148, 191
Alisauskas, Ray 129
Alisauskas, Ray 137
Allan, Elizabeth 158
Allen, Joanne 8
Allen, Samantha 159, 160, 173
Allender, Matthew C 161
Allison, Andrew 187
Almagro-Moreno, Salvador 202
Alt, David 25, 192
Amara, Emmanuel 217
Amato, Rachel 185
Anderson, Donald M. 30
Anderson, Maria 39
Andrew, Cassandra 146
Andrews, Kimberly R. 151
Angulo-Zamudio, Uriel A 163
Anis, Eman 215
Applebee, Daniel 174
Archer, Linda 106
Armien, Anibal 118
Arnaud, Emmanuelle 103
Arnemo JM, 98
Asmyhr, Maria G. 93
Atencia, Rebeca 5
Atencio, Ronni 155
Atkinson, Shirley J. 37
Atwood, Todd C. 212
Aung, Ohnmar 27
Ayala, Andrea 202

B

Bærum, Kim Magnus 172
Baeten, Laurie 13
Bahnson, Charlie 79
Bai, Ningzhu 214
Baker, Eliza 121
Baker, Julia 132
Baklin, Adam 64
Balasuriya, Udeni 90
Ballard, Lowell 201
Ballmann, Anne 58, 59, 92, 156, 180
Banda, Alejandro 51
Bolfa, Pompei 206
Bommineni, Y. Reddy 54
Bondo, Kristin 65, 176, 193
Boonjakuakul, Jenni 207
Born, Vernon 48
Borovoski, Ricardo 100
Borremans, Benny 26
Bosco-Lauth, Angela 86
Botta, Randy A. 49
Bouchard, Émilie 137
Boyles, Justin G. 61

Banda, Eva 210
Bangura, James 217
Banther-McConnell, Jaecy 216
Barichivich, William J 64
Barnum, Samantha 199
Barron, Heather 187
Bartelt-Hunt, Shannon 149
Bartelt-Hunt, Shannon L. 154
Barton, Ethan 66
Barton Behravesh, Casey 88
Bartz, Jason 149
Bartz, Jason C. 153, 154
Batten, Jasmine 39, 81
Batten, Jasmine 152
Bayles, Darrel 192
Bayles, Darrell 25
Bayley, Daniel 103
Beatty, Normal L. 14
Becker, C. Guilherme 198
Becker, Michael 194
Beckmen, Kimberlee 151
Bello, Raul 7, 125
Bennett, Andrew 191
Bennett, Andrew T.D. 148
Berg, Mathew 191
Berg, Mathew L. 148
Berghaus, Roy D. 102
Bertran, Kateri 127
Bielefeldt-Ohmann, Helle 86
Bird, Brian 217
Blais-Savoie, Juliette 128
Blake, John 137
Blanch-Lázaro, Berta 148, 191
Blanco, Cristina 132
Blehert, David 92
Blomberg, Erik 56
Bloodgood, Jennifer 33
Boesen AH, 98
Boggiatto, Paola 25
Bradfute, Steven 216
Bragg, Tom 109
Brand, Adrianne B 64
Brandell, Ellen 50
Branigan, Marsha 124
Bräunig, Jennifer 141, 142
Bravo-Risi, Francisca 9
Breeden, Renee 48
Brett-Major, David 220
Bron, Gebbiena 213
Brown, Derek 119
Brown, Emma 183
Brown, Justin 211
Brown, Justin D. 20
Brown, Kevin 77
Browning, Glenn 8
Bryant, Ann 23
Buchweitz, John 32
Buckley, Jacqueline 35
Buckner, Jennifer 59
Budischak, Sarah A. 17
Buehler, Ulrike 87
Bueno, Irene 185
Buhler, Kayla 124, 129, 137
Bunting, Elizabeth 31
Burco, Julia 219
Burek-Huntington, Kathy 205
Burgess, Tristan 220
Burrell, Caitlin 19
Burridge, Christopher 126
Bushell, Rhys 8
Bushmaker, Trent 200
Bushman, Frederic D. 215
Buss, Peter E. 4
Bustamante, Belén 155
Buttke, Danielle 88, 109
Byard, Aimee J. 49
Byers, Kaylee 35

C

Cabello, Javier 155
Calhoun, Dana 181, 183
Calhoun, Daniel L 64
Cameron, Kenneth N. 200
Camp, Lauren 15
Campbell, Lewis 107
Campbell, Tyler 10
Campbell Grant, Evan H 64
Canizalez-Román, Adrian 163
Cannuscio, Carolyn 215
Cantwell, Averill 5
Cao, Dung 144
Cao, Trung 144
Carmichael, Ruth 33
Carossino, Mariano 90
Carpenter, Ann 88
Carriere, Suzanne 137
Carstensen, Michelle 32, 34, 153
Carter, E. Davis 117, 120, 188
Carver, Scott 83, 96, 126
Casey, Christine L. 12
Cassirer, E. Frances 151
Celis, Sebastián 155
Chamings, Anthony 148
Chandler, Jeffrey 85
Chandler, Richard 110
Chase, Dorothy 158
Chaves, Andrea 199
Chavez, Andreas 214
Chea, Sokha 62
Chee, Hsien-Yao 128
Chien, Emily 128
Childers, Eddie 13
Chipman, Richard 85
Choi, Olivia 23
Chong, Deborah 219
Christensen, Sonja 80, 95, 112
Christensen-Dalsgaard, Signe 172
Christenson, Peter 60
Christie, Katherine 16
Clague, Samuel 17
Clark, Carly 161
Clark, Tim 48
Cleland, Timothy P. 162
Cleveland, Christopher 113, 211
Clifford, Deana 174
Coffey, Lark 27
Colby, Janene 49
Cole, Megan 5
Cole, Rebecca 73, 204
Colegrove, Kathleen 33
Collman, Ron 215
Cooper, David 4
Cooper, Robert 16
Corcoran, Stephen 194
Corder, Molly 162
Cords, Olivia 27
Cortes, Galaxia 155
Cortey, Martí 127
Costa, Daniel 26
Cournarie, Morgane 200
Courtemanch, Alyson 179
Courtney, Samantha 112
Cox, John J. 12
Cox, Mike 165
Craft, Meggan E. 17
Crank, R. Daniel 12
Cressler, Clayton E. 17
Crocker, Daniel 26
Cronin, Colleen 220
Cross, Paul 166
Crossley, Beate 174
Crowley, Dan 40
Crudge, Brian 144
Crum, James 66, 80
Cumbie, Alexandra 209
Cunningham, Fred 203
Cunningham, Mark 19, 54, 69
CUNNINGHAM, MARK 55
Custer, Christine 134
Custer, Thomas 134

D

D'Agnese, Erin 158
Dang, Nhung 144
D'Angelo, Gino 83
Daniels, Joshua 119
Davey, Marie L 94
Davidson, Rebecca 129
Davis, Elizabeth 144
Davison, Andrew 217
Dawson, Kelsey 85
De Urioste-Stone, Sandra 116
De Villiers, Pierre 175
DeBess, Emilio 219
DeForge, James R. 49
Deliberto, Tom 88
DeLiberto, Thomas 85
Demarais, Steve 51
DeMarchi, Joseph 117
DeMarchi, Joseph 120
Deming, Alissa 33
Dennis, Michelle 206
Denstedt, Emily 62, 77
Derne, Bonnie 168, 169
Dhondt, André 31
Diaz, François 228
Díaz Clark, Cristina 33
Dibernardo, Antonia 128
Dibernardo, Antonia 137
Dickson, Brett 40
Divi, Nomita 42
Dodd, Erin 199
Doidge, Nicholas 8
Donadio, Emiliano 57
Donato, Bart 53
Donnelly, Kyle 54
Doub, Emily 29
Drebot, Michael 137
Dubay, Shelli 139
Dubois, Sara 147
Duff, Paul 53
Duggal, Nisha 21
Dugovich, Brian 66
Duignan, Padraig 111, 137, 138, 199
Duignan, Pádraig 106
Dummer, Paul 134
Dunay, Emily 5
Dunn, Chris D. 213
Dunn, Christopher 5, 107
Dusek, Robert 30
Dutheil, Julien Y. 61
Dyck, Markus 124
Dzal, Yvonne A. 40

d

das Neves, Carlos G. 36
de Groot, Peter V. C. 124
deMaar, Thomas 10

E

Eastwood, Gillian 209
Edgarian, Tristan 174
Edson, Jessie 52, 67
Edwards, Hank 179
Edwards, Scott 191
Edwards, William 159
Eisenhofer, Raphael 126
Elkin, Brett 1
Ellarson, Wesley 50
Ellis, Jeremy 85, 184
Ellis, Julie 197, 201, 215
Elorriaga-Verplancken, Fernando R 163
Emde, Hannah 87
Emery Thompson, Melissa 5
Esperon, Fernando 131, 155
Etter, Dwayne 112
Ettinger, Cassandra 91
Evans AL, 98

Elliott, James 116
Ellis, Jayne 119
Everett, John 215

F

Faith, Seth 197
Fake, Kimberley 35
Fake, Kimberly 28
Falendysz, Elizabeth 181, 182, 183
Falendyz, Elizabeth 90
Fameli, Alberto 52, 67
Fang, Andrew 173
Farrell, Terence 91
Faulk, Christopher 132
Federko, Bevan 77
Fenton, Heather 20, 206
Fenton, Heather 137
Ferguson, Dale 194
Fernandez Aguilar, Xavier 137
Ferreyra, Hebe 57
Fidino, Mason 28
Field, Cara 111
Figueroa, Dania M. 200
Fine, Amanda 62
Fire, Spencer 111
Fischer, Robert J. 200
Fischetti, Robert 194
Fisher, Robert N 64
Flores-Villaseñor, Hector 163
Foley, Janet 57, 199
Fontaine, Christine 199
Forbes, Kristian M. 17
Ford, Lorelei 203
Forrest, Kim 174
Forzan, Maria 31
Fossøy, Frode 94
Foster, Jeffrey T. 22
Foster, Robert 138
Fountain-Jones, Nicholas 123
Fox, Karen 119
Francis, Marla 151
Francisco, Raquel 131, 218
Frank, Lexi 130
Fraser, Tamieka A. 126
Frederick, Peter 16
Fredrickson, Kelcie 161
Frierson, Kenna 29
Fuchs B, 98
Fuglei, Eva 129
Fuller, Nathan 40
Fulton, David 101

G

Gaffney, Patricia 137
Gage, Laurie 88
Gagne, Roderick 215
Galloway, Nathan 13
Galloway, Terry 129
Garba, Ahmed 209
García, Carlos 210
Garcia-Termignoni, Flavia 191
Gardner, Michael 169
Garner, Lindsey 16
Garnham, Antonio 155
Garrett, Kayla 113, 114
Garrett, Kayla 211
Garwood, Tyler 123, 177
Goldberg, Tony 5
Goldberg, Tony L. 213
Goldenberg, Miles 202
Goma-Nkoua, Cynthia 200
Gonnerman, Matthew 56
Gonzales, Ben J. 49
Goodfellow, Samuel 216
Goodwin, Chloe 19
Goolia, Melissa 128
Goosen, Wynand 4
Gottdenker, Nicole 178
Gouin, Geraldine-G. 137
Græsli AR, 98
Gragson, Theodore 110

Gass, Jonathan 220
Gentle LK, 98
George, Kyle 92, 156
George, Serena 99
Gerci, Bruno 220
Gerhold, Richard 104, 121
Gerlach, Robert 151
Gern, Jim 6
Ghai, Ria 88
Ghersi, Bruno 217
Giacinti, Jolene 193
Giacinti, Jolene 147
Gibbs, Samantha 69
Gibbs, Samantha 88
Gibson, Matthew J. 141, 142
Gilbertson, Marie 50
Gilbertson, Marie 70
Gillies, Chris 48
Givens, Carrie 140
Glaser, Linda 153
Glikman, Jenny 144
Glorioso, Brad 91
Glorioso, Brad M 64
Godfrey, Stephanie 169
Goldberg, Tony 6, 107
Grahek-Ogden, Danica 93
Graves, Tabitha 164
Gray, Matthew 120, 188
Gray, Matthew J. 75
Grear, Dan 108
Grear, Daniel 64, 72, 91, 204
Green, David 72
Green, Stephanie 115
Greene, Sophie 34
Greening, Sabrina S 197, 201
Greening, Sabrina S. 215
Greenwald, Katherine 199
Greer, Justin 196
Grider, John 92
Griffin, Kathryn 180
Grillo, Tiggy 228
Grisham, Blake 176
Grogan, Laura 190
Gruetzmacher, Kim 87
Grunert, Ryan 211
Guerra, Lindsey 145
Gustine, David D. 212
Guzman-Vargas, Veronica 54, 73
Guzman-Vargas, Veronica 187

H

Haase, Catherine 40
Haddad, Célio 198
Haffley, Trent 13
Hagen, Patrick 32, 154
Halaska, Barbie 138
Hall, Jeffrey 90
Hall, Richard J. 17
Hall, Sherwood 30
Halstead, Brian J 64
Haman, Katie 201
Hamilton, Keith 228
Han, Sushan 192
Hanley, Brenda 76
Hanley, Brenda 31
Herbst, Allen 166
Herman, Alex 174
Herman, Stephanie 201
Hernandez, Sonia 16, 97, 131, 210, 218
Hernandez, Sonia M. 75, 110
Hernández Ortiz, Adrián 137
Hesselson, Daniel 141, 142
Hesting, Shane 68
Heyward, Natalie 113
Hidalgo-hermoso, Ezequiel 155
Hildebrand, Erik 154
Hilgart, Mark 194
Hill, Ashley 174
Hilton, Clayton D. 10

Hanneman, Matthew 139
Hansen, John 196
Hansen, Rowena 53
Hanson, Larry 203
Hardman, Rebecca 19, 54, 117, 167
Hardman, Rebecca 187
Harms, N. Jane 146
Harms, N. Jane 137
Harris, Cleyo 107
Hart, Catherine E 163
Hartwig, Airn 86
Hast, John T. 12
Hawks, Seth 21
Hayes, Kenneth 168
Hayman, David T. S. 40
Haynes, Ellen 145
Hazelrig, Corinna 113, 114
Hearst, Scoty 51
Hedden, Emily 208
Helman, Sarah 26
Henaff, Maud 146
Hepinstall-Cymerman, Jeffrey 110
Himsworth, Chelsea 128
Ho, Po 144
Hofmeister, Erik 90
Hollingshead, Nicholas 76
Hollmen, Tuula 30
Hooven, Nathan D. 12
Hopson, Eric 174
Horgan, Molly 106
Hosack, Blake R 64
Houston, Allan 51
Howard, Simon 74
Howerth, Elizabeth 178
Hranac, Reed 40
Huang, Miranda 51
Hubbard, Laura 140
Hunsaker, Matthew 50
Hunsucker, Kelli 111
Hunte, Jonathan 211
Hupp, Jerry W. 212
Hutchinson, Mark 169
Hydeskov HB, 98
Hynes, Kevin 31

I

Inzalaco, Heather 166
Inzalaco, Heather N'te 9
Ip, Hon 90, 180
Isbell, Jaclyn 137
Isidoro-Ayza, Marcos 18
Iwanowicz, Luke 196

J

Jacobs, Eugene 139
Jacobs, John 139
Jacobs, Shoshanah 103
Janousek, William 164
Jardine, Claire 103, 128, 147, 193
Jarosinksi, Dana 50
Jaster, Levi 68
Javeed, Nadia 199
Jeeves, Simon 128
Jeffress, Matt 165
Jenkins, Emily 146
Jenkins, Emily 124
Jenkins, Emily 129, 137
Jennelle, Christopher 52
Jennings-Gaines, Jessica 159
Jensen, Alex 121
Jensen, William 79
Johnson, Christine 27
Johnson, Christine K. 49
Johnson, Emily M. 40
Johnson, Maggie 109
Jones, Megan 59
Jordan, Christopher 110
Joyce, Leah 108
Justice-allen, Anne 84, 204

K

Kaba, Serge D. 200
Kailing, Macy 156
Kamath, Pauline 23, 56, 116
Kamath, Pauline L. 70
Kania, Stephen 104
Kantar, Lee 116
Kanu, Marilyn 217
Kapur, Vivek 225
Karesh, William B. 200
Karouna-Renier, Natalie 134
Katircioglu, Stephanie 166
Keel, M. Kevin 61
Keil, Johannes 87
Keller, Barbara 34
Kelly, Allicia 137
Kelly, Brendan J. 215
Kelly, James 34
Kelly, Patrick 174
Kelly, Ryan 158
Kemec, Ignacio 155
Kerr, Tanya J. 4
Khammavong, Khongsy 62
Khammavong, Kongsy 77
Killian, Mary 85
Kilpatrick, A. Marm 22
Kindberg J, 98
King, Meagan 147
Kinzley, Colleen 174
Kipp, Evan 130, 132
Kissick, David 194
Kistler, Whitney 176
Kitchen, Shannon M. 17
Kleeman, Patrick 64
Klein, Bruce 18
Klein, Patrice 88
Kleynhans-Cornelissen, Leanie 4
Kluever, Bryan 54
Knapp, Cambrey 125
Knowles, Susan 73, 90, 107
Kobashigawa, Estela 152
Kochevar, Deborah 220
Koestel, Zoe 68
Kohl, Michel 83
Kohler, Dennis 85
Kolapo, Temitope 146
Kolpin, Dana 140
Konde, Lora 49
Koser, Troy 179
Kotwa, Jonathon 128
Krasner, Ami 111
Kropidlowski, Stefan 48
Kuchinsky, Sarah 21
Kudla, Nathan 156
Kuiken, Thijs 24
Kuisma, Eeva 200
Kulis, Dave 30
Kunkel, Emma L. 40
Kunkel, Melanie 16, 19, 73, 187
Kunkel, Melanie R. 20, 102
Kurimo-Beechuk, Elizabeth 16
Kuriyama, Takeo 157
Kurth, Katherine 104
Kurz, Jacqueline 179
Kuschke, Samantha 122
Kutz, Susan J. 38

L

Lachenicht, Candice 191
Ladner, Jason 91
Lage, Gabriel 100
Lage, Rafael 100
Lenoch, Julianna 85
Leon, Ariel 90, 181, 183
León-Sicairos, Nidia 163
Lewis, Nicole 197

Lage, Victória 100
Lagisz, Malgorzata 141
Lagos, Rocio 155
Lagrue, Clement 115
LaHue, Nate 165
Lair, Stéphane 147
Lamb, Harrison 181, 183
Lambert, Rachel 183
Lambertini, Carolina 198
Lance, Stacey 97
Lance, William 170
Landon, Adam 101
Langset, Magdalena 172
Lankton, Julia 59
Lantz, Kristina 85
Larsen, Peter 60, 123, 130, 132, 149, 150
Larsen, Peter A. 153, 154
Larsen, Roxanne 130
Larsen, Roxanne J. 153
LaSharr, Kelsie 34
Latinne, Alice 62, 77
Lausen, Cori L. 40
Lavalie, Edwin 217
Lawson, Becki 91
Leclerc, Lisa-Marie 137
Lee, Aidan 30
Lee, Jeongha 118
Leet, Jessica 196
Lehman, Chad 13
Lehrer, Elizabeth 35
Leighton, Patrick 137
Leis, Eric 107
Ley-Quiñonez, Cesar Paul 163
Li, Manci 60, 150
Lichtenberg, Stuart 166
Lichtenberg, Stuart S. 9
Lieske, Camilla 151
Lin, Tesia 109
Linder, Timothy 85
Lindsay, L. Robbin 128
Lindsay, L. Robbin 137
Lindsey, Laramie 130, 132
Lindsey, Laramie L. 153
Lipp, Erin 16, 218
Lloyd Mills C, 98
Lloyd-Smith, James 26
Loessberg, Emma 21
Long, Phan Thanh 62
Lopez-Garcia, Alejandro 131
Lorch, Jeff 91
Lorch, Jeffery 92
Lorch, Jeffrey 64, 182, 195, 204
Lougheed, Stephen C. 124
Lowe, Winsor 108
Lucero, Jose Pizarro 155
Lue, Chia-Hua 186
Luis, Angie 108
Lundgren, Jon 32
Lungay, Victor 217
Lunn, Nicholas 137
Lutz, Chris 201
Luukkonen, Katie 159
Lynch, Michael 8

M

M. Borrego, Carles 127
MacGlover, Christopher 119
Machara, Marley 167
Madden, Marguerite 75
Madslien, Knut 36
Maerz, John 114
Magle, Seth 28, 35
Meaux, Nicolette 50
Meixell, Brandt W. 212
Mendoza, A. Patricia 7
Mendoza, Patricia 125
Meteyer, Carol U. 61
Michel, Eric 34
Michel, Eric 32

Magnusson, Kristenn 146
Majó, Natàlia 127
Makarov, Oleg 194
Makhado, Azwianewi 175
Malave, Carly 183
Malavé, Carly 90
Mali, Ivana 216
Mallory, Mark L. 38
Malmberg, Jennifer 109
Malone, Cody 146
Mama, Khursheed 189
Mandujano Reyes, Juan Francisco 58
Mangan, Matthew 190
Mansfield, Kristin 192
Marano, Jeffrey 21
Marawanaru, Elisha 130
Marchetto, Katherine 177
Marenda, Marc 8
Markham, Katherine E. 75
Marques, Andrew 215
Martin, Ana M. 57
Martin, James A. 102
Martinez, Maggie 111
Martinez, Margaret 106, 137, 138
Massonbrink, Rick 25
Matson, Cole 134
Matson, M. Jeremiah 200
Maw, Min Thein 27
Mayer, Treana 13
McCallum, Hamish 190
McCauley, Deborah 179
McClure, Meredith L. 40
McCreary, Brome 64
McCue, James 170
McDaniel, Alysha 136
McDaniel, Kylie 11
Mcdonald, Coby 198
McGeachy, David 137
McGinnity, Dale 167
McGuire, Liam P. 40
McHale, Brittany 178
McKibben, Kailyn 73
Mikolon, Andrea 174
Milavong, Phonesavanh 62
Miller, Brad 104
Miller, Debra 117, 120, 121, 122, 167, 188
Miller, Debra L. 10
Miller, Elizabeth A. 185
Miller, Glenn 111
Miller, Kimberli 59
Miller, Melissa 199
Miller, Michele A. 4
Miller AL, 98
Milleson, Michael 54
Milleson, Michael P. 14
Milstein, Marissa 130, 132
Minier, Darren 174
Mistrick, Janine 17
Mitchell, Corey 76
Mitman, Siena 125
Mitzel, Dana 208
Mombouli, Jean-Vivien 200
Monagin, Corina 217
Montecino, Diego 62
Montecino-Latorre, Diego 77
Moore, Kathi 39
Moore, Seth 123
Moore, Seth A. 177
Moorhead, Kaitlin 161
Morales, Rodrigo 9
Moreira, Dario 155
Moriarty, Megan 174
Morris, Chris 165
Motz, Jenna 182
Mubareka, Samira 128
Muller, Ananda 155
Muller, Lisa 104
Mulligan, Matthew 28
Mummah, Riley 26
Munk, Brandon A. 49
Muñoz, Sebastián 155
Munster, Vincent J. 200
Murray, Maureen 35
Murray, Michael 199

Mclaughlin, Tyler 180
McManamon, Rita 178
McNeil, Carrie 42
Mead, Daniel G. 102
Murray, Susan 27
Muset, Sophie 228
Muths, Erin 64

N

Nabeshima, Kei 157
Næsborg-Nielsen, Christina 126
Nagashima, Jennifer 162
Nakagawa, Shinichi 141
Nashold, Sean 90
Navarrete, Maria-Jose 206
Navis, Corrie 114
Neddermeyer, John H. 22
Needle, David 113, 197
Neely, G. Gregory 141, 142
Neira, Victor 155
Nemeth, Nicole 16, 19, 54, 69, 73, 114, 187, 197
Nemeth, Nicole M. 20, 102
NEMETH, NICOLE 55
Nguyen, Hien 144
Nguyen, Nga 62
Nham, Peter 27
Nichols, Jenna 217
Niebuhr, Chris 74
Niedringhaus, Kevin D. 20
Nofchissey, Robert 216
Nofrarías, Miquel 127
Nol, Pauline 189
Norda, Kathrin 87
Norfolk, William 16, 218
Noronha, Leela 208
Nutter, Felicia 11, 125, 220

O

Ogata, Craig 194
Ogbunugafor, C. Brandon 202
Oglesbee, Michael 197
Oh, Sang-Hyun 60
Ojkic, Davor 193
Oliveira-Santos, L. Gustavo R. 177
Oliver, Jonathan 132
Oliver, Jonathan D. 153
Olsen, Steven 25
Olson, Sarah H. 40, 62, 77, 200
Ondzie, Alain U. 200
ONORATO, DAVE 55
Onuma, Manabu 157
Ortega, David 95
Ortiz, Carolina 155
Osofsky, Steven A. 37
Ostenberg, Carl 158
Owens, Audrey 204
Owens, Jeana 208
Owens, Leah 5
Owens, Leah A. 213

P

Palmer, Jonathan 77, 91
Pandit, Pranav S. 49
Pappas, Tressa 6
Parise, Katy L. 22
Parmley, E Jane 103
Parmley, E. Jane 59
Parmley, Jane 147
Picasso-Risso, Catalina 150
Pickering, Bradley 128
Picknell, Angela 206
Pienaar, Elizabeth 83
Pierce, Hannah 84
Piersma, Brittney 187
Pilfold, Nicholas 137

Parra, Barbara 155
Partee, Ed 165
Patel, Anika 15
Pauley, Sara Parker 39
Paulsen, Daniel 118
Pearl, Cristopher 64
Pearl, David 128, 193
Pedersen, Joel A. 9
Pelo, Kristen 30
Pennington, Parker 162
Penrith, Mary-Louise 37
Pepin, Kim 51
Perez, Kimberly 218
Perkins, Marie 139, 143
Perlas Puente, Albert 127
Pesapane, Risa 105, 199, 214
Peterman, Bill 105
Peters, Andew 96
Petricoin, Emanuel 162
Petz Giguere, Matt 177
Pham, Ngoc 62
Phiphakhavong, Sithong 62
Phommachanh, Phouvong 62
Phouangsouvanh, Souchinda 62

Q

Quintanal, Christopher 85

R

Radisic, Rebecca 19
Radke, Bill 84
Raghavan, Ram K. 68
Rajeev, Sree 120
Ramey, Andrew M. 212
Rameyer, Bob 48
Ramirez, Galia 155
Ramis, Antonio 127
Ramsden, Nidhi 37
Rauset, Geir Rune 94
Raynal, Jeremy 48
Reddy, Shantan 215
Pinizzotto, Nick 95
Pinkerton, Marie 50
Pinkerton, Marie E. 70
Pleszewski, Robert 85
Plowright, Raina K. 40
Pokras, Mark 31
Ponder, Julia B. 185
Pongracz, Jodie 146
Poppenga, Robert 137
Porco, Alice 62, 77
Porter, Stephanie 86
Pottier, Patrice 142
Poulson, Rebecca 19, 54, 69, 140
Powers, Jenny 170
Prager, Katie 26, 220
Prentice, Melanie B. 70
Price, Steven 91
Provencher, Jennifer 41, 38
Pruvot, Mathieu 62, 77
Ptochos, Sokratis 129
Pukazhenthi, Budhan 162
Pumphrey, Stephanie 11
Putnam, Joel 107
Roberts, Laura 175
Robertsen, Per Anders 94
Robinson, Sarah 128
Robinson, Zachary 82
Rocke, Tonie 90, 181, 183
Rocke, Tonie E. 213
Roderick, Constance 73
Rodino, Kyle 215
Rodushkin I, 98
Roghair, Paul 13
Rojas, Jorge 110
Root, J. Jeffrey 86

Reed, Patricia E. 200
Reeves, Ashley 10
Reinsch, Sherri 167
Rekant, Steven 88
Ribeiro Gomez, Ana Carolina 26
Ribot, Raoul 191
Ribot, Raoul F.H. 148
Richard, Jordan 107
Richards, Bryan 78, 197
Richards, Jessie 104
Richardson, Isabella B. 68
Richardson, Evan 137
Richgels, Katherine 78, 92
Richter, Catherine 196
Riddle, Jason 139
Riedle, Constanze 87
Riley, Jen 209
Ringenberg, Jourdan 85
Rivard, Michelle 137
Robbe-Austerman, Suelee 85
Robbiano, Sofia 155
Robbins, Kara 159, 160
Robert, Willie 217
Roberts, David 175
Root, Jeff 184
Rosati, Alexandra 5
Rose, Julia 48
Rosenbaum, Marieke 125
Rosenbaum, Marieke H. 7
Rosenberry, Christopher 67
Ross, Craig 53
Roth, Mark F 64
Roug, Annette 49, 189
Rouse, Natalie 205
Rowden, Gage 60, 149, 150, 153, 154
Rowles, Teri 88
Rudd, Jaime 57, 174
Ruden, Rachel 207
Ruder, Mark 19, 29, 54, 66, 69, 79, 80, 83, 211
Ruder, Mark G. 20
Ruder, Mark G. 102
Ruiz Fons, Francisco 155
Rukundo, Joshua 5
Russell, Mackenzie 33
Russell, Robin 92
Russell, Robin 58
Russell, Sherri 39, 81, 152

S

Sacristan, Irene 131
Sage, Abigail 156
Sakcamduang, Walasinee 99
Salinas, Nubia 176
Sam, Son 144
Samelius, Gustaf 137
Samelius, Gustaf 129
Sanchez, Jessica N. 49
Sanchez, Susan 187, 218
Sander, Will 136
Sandinski, Walt 64
Sangkachai, Nareerat 99
Sanki, Rachel 11
Santa, Paola 7
Sinnett, David R. 212
Sischo, David 168
Skeba, Sandy 167
Skelly, Brett 80
Sleeman, Jonathan 59, 78, 88, 99
Smiley Evans, Tierra 27
Smink, Moniek 99
Smith, Janet 194
Smith, Jared 133
Smith, Jennifer 204
Smith, Kyle 101
Smith, Lorisa 39
Smith, Matthew 30, 212
Smolinski, Mark 42

Santodomingo, Adriana 155
Santymire, Rachel 28
Sargent, Bob 69
Sartini, Cady 139
Sato, Yuko 207
Schell, Christopher 35
Schiff, Peter 209
Schlenner, Jenna 30
Schuler, Krysten 31, 76, 95
Schumaker, Brant 166
Schwabenlander, Marc 60, 150, 153, 154
Schwalbe, Erin 109
Schwantje, Helen 137
Schwartz, Heather 167
Schwartz, Katherine 109
Seifert, Stephanie N. 200
Seiverts, Olivia 218
Sepúlveda, Paulina 155
Severin, Andrew 25
Severud, William 177
Sevigny, Joseph 197
Shaffer, Christopher 130
Shah, Devendra 82
Shanebeck, Kyle 115
Shapiro, Hannah 83
Shapiro, Karen 15
Sharma, Prisha 29
Shaw, David 29
Shea, Stephanie 56
Shearn-Bochsler, Valerie 182, 195
Sheldon, Julie 161
Sheley, Wesley 117, 120, 167, 188
Shender, Lisa 16, 73, 88, 187
Sherrill-Mix, Scott 215
Shetty, Dharma 228
Shirkey, Nicholas J. 49
Shoemaker, Rachel 153
Shriner, Susan 85, 184
Sigafus, Brent 64
Silas, Kirk 40
Silva Seixas, Julia 16
Sobreira, Elisângela 100
Sondgeroth, Kerry 109
Sondgeroth, Kerry 119
Spraker, Terry 13
Springer, Matthew T. 12
Sreyem, Sours 62
Stajich, Jason 91
Stalknecht, Dave 54
Stallknecht, David 19, 66, 69, 79, 80
Steinfeldt, Stephanie 72
Stelzer, Erin 140
Stengle, Anne 91
Stepanov, Sergey 194
Stephen, Craig 41
Stewart, Kimberly 206
STEWART, HOLLIS 55
Stillings, Bruce 79
Stone, Christopher 35
Stone, Suzanne 153
Storm, Dan J. 9
Storm, Daniel 50
Storm, Daniel 70
Stout, Virginia 179
Strand, Olav 94
Strelau, Katherine 215
Strickland, Bronson K. 51
Stroh, Geoff 170
Strom, Sean 135
Stukenbrock, Eva H. 61
Sugimoto, Taro 157
Sullins, D. S. 176
Sullivan, Kelsey 23, 56
Sumners, Jason 39
Sun, Zhengxin 124
Suriyamongkol, Thanchira 216
Suse, Phillip 130
Sutton, William 167
Suwanpakdee, Sarin 99
Swanson, William F. 10
Swarts, Hilary M. 10
Sykes, Chelsea 137

Sine, Sarah 41

T

Taetzsch, Sara 88
Takagi, Shun 157
Takahashi, Fumika 174
Talledo Albujar, Michael 7
Tatz, Matthew 97
Taylor, Kyle 82
Taylor, Matthew D. 141, 142
Teager, Kim 177
Tell, Rachel 85
Them, Cara 76
Theppayna, Watthana 62
Thiel A, 98
Thompson, Alec 29
Thompson, Lesa 228
Thomson, Gavin R. 37
Thurber, Mary 182
Tillitt, Donald 196
Tizzani, Paolo 228
Toledo, Felipe 198
Tolliver, E. Morgan 176
Tonie, Rocke 3
Torchetti, Mia 85
Torhorst, Carson 14
Torres, Steve G. 49
Towe, Anastasia 117, 120, 188
Towner, Jonathan 88
Tranulis, Michael A. 93
Triana, Nicolas 176
Trimble, Rebecca 209
Troiano, Alexandro 187
Tschritter, Christina 124
Tseng, Chi-yen 134
Tum, Sothyra 62
Tunseth, Devin 183
Turner, Wendy 50
Turner, Wendy C. 9, 70
Tuten, Holly 35
Twarowski, Magdalena 72

U

UC Davis PREEMPT consortium, 217
Ufer, Danielle 95
Uhart, Marcela 57
Utaaker, Kjersti Selstad 94
Uzal A, 98

V

Valencia, Carolina 155
Valituto, Marc 27
Valle, Rosa 127
Van Hemert, Caroline 30, 212
Van Rompay, Koen 27
Van Why, Kyle 211
Van Wick, Peach 173
Vanstreels, Ralph E. T. 57
VanWormer, Elizabeth 15
Varela, Kate 88
Venugopalan, Nagarajan 194
Vera, Frank 155
Verant, Michelle 88, 183
Verasay, Juan 155
VerCauteren, Kurt C. 51
Verissimo, Diogo 144
Verlander, Sarah 42
Vicencio, Rocio 155
Vigil, Stacey 29
Vilchez Delgado, Fernando Javier 7

Vashon, Jennifer 113
Veitch, Jasmine S.M. 17
Velázquez-Román, Jorge 163
Vendl, Catharina 141, 142
Venkateswaran, Kodumudi 27
Venkateswaran, Neeraja 27
Villaverde, Silvia 210
Vo, Thanh 62
Vogt, Adam 159
Vogt, Nadine 159
Vucak, Matej 217

V

van Deventer, Michelle 187
von Hugo, Tonia 59

W

Waddle, J Hardin 64
Walden, Heather 73
Waller, Diane 107
Walls, Susan C 64
Walsh, Dan P. 9
Walsh, Daniel 50, 58, 70, 92, 166
Walter, W. David 65, 67, 153
Walter, W. David 52
Walter, W David 186
Walters, Tyler 177
Walzer, Chris 77, 200
Wannous, Chadia 228
Warren, Robin 4
Weary, Taylor 6
Webb, Shevenell 113
Weese, J. Scott 128
Weger-Lucarelli, James 21
Wegmann, Alex 48
Weinstein, Philip 169
Welch, Anna Grace 51
Wellehan, James 106
Weston, Brent 79
Weyna, Alisia 16, 19, 187
Whalen, Connor 181
White, C. LeAnn 59, 78
White, Seth 29
White, Zoe 14
Wiig, Jørgen Ree 172
Wikle, Christopher K. 68
Wilcox, Alana 41
Wild, Margaret 82
Wilkinson, Vicky 126
Wille, Holger 173
Williams, Allison 105
Williams, David 112
Williams, Kathleen E. 12
Williams, Lisa 65
Williams, Lisa 20
Willis, Craig K. R. 40
Wilson-Welder, Jennifer 25
Wilson-Welder, Jenny 192
Winzeler, Megan 72
Winzeler, Megan E 64
Wiratsudakul, Anuwat 99
Wise, Benjamin 179
Wisely, Samantha M. 14
Wolf, Tiffany 123, 130, 150
Wolf, Tiffany 60
Wolf, Tiffany M. 153, 154, 177
Wolking, David 217
Wong, Talia 27
Woods, Alaina 116
Woosnam, Kyle 145
Work, Thierry 48
Wyneken, Jeanette 122

X

Xu, Qingping 194
Xu, Shenglan 194

Y

Yabsley, Michael 16, 28, 29, 113, 114, 145, 210
Yabsley, Michael 211
Yee, JoAnn 27
Yeung, Norine 168
Yim, Winfield 128
Yip, Lily 128
Yokoyama, Mayumi 157
Yoo, Myungsoo 68
Ytrehus, Bjørnar 93, 172
Ytrehus, Bjørnar 94
Yuan, Qi 149, 154

Z

Zachariah, Trevor 54
Zamudio, Kelly 198
Zavala Peña, Xiomara 7
Zavala-Félix, Kevin 163
Zavala-Norzagaray, Alan A 163
Zedrosser A, 98
Zeliff, Haley 215
Zhang, Michael 152
Zhang, Shuping 152
Zhou, Lijuan 54
Zhou, Weidong 162
Zhu, Jun 58
Zhu, Sophie 15
Ziccardi, Michael H. 49
Zimmer, Marnie 59
Zimmer, Patrick 59
Zyskowski, Justin 32

CONTINUING EDUCATION CERTIFICATE
70th International Wildlife Disease Association
July 23-29, 2022
Madison, WI

This is to certify that _____
has attended the 2022 International Wildlife Disease Association Conference and is eligible to receive the following continuing education credits:

WORKSHOPS

		Attended
Sunday, July 24th, 2022		
ACZM Workshop	6.0 credit hours	_____
Writing for Scientific Publications Workshop	1.5 credit hours	_____
Science Communications Workshop	2.0 credit hours	_____
Total Possible Workshop hours	**9.5 credit hours**	_____

LECTURES

Monday, July 25th, 2022		
Keynote Speaker	1.0 credit hours	_____
WDA Cutting Edge Speaker	0.5 credit hours	_____
AAWV, Al Franzmann Speaker	0.5 credit hours	_____
Total Possible Hours	**2.0 credit hours**	_____
Tuesday, July 26th, 2022		
Keynote Speaker	0.5 credit hours	_____
Student Presentations: Session 1	0.5 credit hours	_____
Student Presentations: Session 2	1.25 credit hours	_____
Student Presentations: Session 3	1.5 credit hours	_____
Student Presentations: Session 4	1.25 credit hours	_____
Total Possible Hours	**5.0 credit hours**	_____
Wednesday, July 27th, 2022		
Can We Create Transformative Change in Wildlife Health?	1.5 credit hours	_____
Wildlife and Environmental Zoonoses	1.5 credit hours	_____
Emerging and Legacy Contaminant and One Health	1.5 credit hours	_____
Systems Thinking and Approaches to One Health	1.5 credit hours	_____
What's Happening with Wildlife at the WOAH?	1.5 credit hours	_____
Total Possible Hours	**7.5 credit hours**	_____

Thursday, July 28th, 2022

The Power of Collaboration for One Health Outcomes	1.5 credit hours	____
AAWV Special Session on Wildlife Disease: Part 1	1.25 credit hours	_____
Disease Outbreaks and Investigations: Part 1	1.25 credit hours	_____
AAWV Special Session on Innovation: Part 1	1.25 credit hours	_____
The Future of Training Wildlife Health Professionals	1.5 credit hours	_____
AAWV Special Session on Wildlife Disease: Part 2	1.25 credit hours	_____
Disease Outbreaks and Investigations: Part 2	1.25 credit hours	_____
AAWV Special Session on Innovation: Part 2	1.25 credit hours	_____
Total Possible Hours	**10.5 credit hours**	_____

Friday, July 29th, 2022

AAWV Special Session on Wildlife Disease	1.5 credit hours	_____
Lessons Learned from COVID-19	1.5 credit hours	_____
Human Dimensions and Wildlife Health	1.5 credit hours	_____
Total Possible Hours	**4.5 credit hours**	_____

Maximum lecture credit hours attainable: 29.5
Total lecture hours attended: ____

Maximum laboratory and workshop credit hours attainable: 9.5
Total laboratory and workshop hours attended: _____

Continuing Education hours are sponsored by the American College of Zoological Medicine, a statutorily approved CE provider.

Disclaimer: The ACZM is a registered veterinary specialty college of the American Veterinary Medical Association for sponsoring of continuing education credits. Individual States or Provinces may have different laws or policies on acceptability of conferences, meetings or courses to qualify for continuing education (CE) credit. You are advised to check with the State(s) or Provinces in which you are licensed to ensure that the CE credits provided are acceptable.

Anne Justice-Allen, DVM, MS

Anne Justice-Allen, DVM, MS, HonDACZM
President, American Association of Wildlife Veterinarians

Jennifer D'Agostino

Jennifer D'Agostino, DVM, Dipl. ACZM
Secretary, American College of Zoological Medicine