



74TH ANNUAL INTERNATIONAL CONFERENCE OF THE WILDLIFE DISEASE ASSOCIATION

Thriving Together: Urban One Health and Ecosystem Resiliency

July 26-31, 2026
Chicago, Illinois, USA
www.wda2026.com



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WELCOME FROM THE LOCAL ORGANIZING COMMITTEE

Dear attendees,

Welcome to Chicago, Illinois, United States for the 74th annual International Conference of the Wildlife Disease Association! This conference is being hosted by the Wildlife Epidemiology Lab and Zoological Pathology Program at the University of Illinois, Brookfield Zoo Chicago, and the Forest Preserves of Cook County. In addition, key contributions from colleagues at Shedd Aquarium and Lincoln Park Zoo were included in our host organizing committee.

The WDA and attendees acknowledge the traditional custodians of the land where we are holding this meeting, the Council of Three Fires (Ojibwa, Ottawa, and Potawatomi), as well as the Miami, Peoria, Ho-Chunk, Menominee, Sauk, and Meskwaki peoples, and pay respect to their elders, past and present. We acknowledge and respect the ongoing care that they and other Indigenous peoples give to the lands, water, skies, and animals.

The theme for this year's conference is "Thriving Together: Urban One Health and Ecosystem Resiliency". As you can see from our venue location, we have embraced the urban interface with an Ice Breaker and Picnic on Forest Preserve Property where many native wildlife species call home. Take time to enjoy the over 70,000 acres of natural space set aside in Cook County while you are here. The space represents the largest forest preserve system in the United States!

You will see common components of this conference, such as workshops, social events, and all are networking opportunities. In addition to traditional general and student sessions we have one large poster session spread throughout the week during breaks. The Thursday evening break provides off-site activities or time on your own to explore more of the local environment, community and what Chicago has to offer.

Please see our Thanks to Our Sponsors section in this book for a complete list. The organizing committee (see below for a full list) is so grateful to them, but also for our student workers (donated by WEL) who you will see throughout the week.

This conference would not be possible for the numerous volunteer hours made by many members. This includes over 20 reviewers for posters and abstracts, WDA Council members for input and guidance, Brookfield Zoo Chicago staff, Forest Preserves of Cook County staff and biologists, WDA student committee, and the WDA auction committee. And finally, the Crowne Plaza venue, their staffs and caterers have provided us with all our requests. We know that you will appreciate their efforts to keep each and everyone of you fed, watered and cared for.

Enjoy the conference and have a wonderful time in Chicago!

Your Organizing Committee is Matt Allender (chair), Karen Terio (Scientific Program chair) Peri Wolff, Cat Vendl (Global Voice chair), Martha Delaney (Workshop co-chair), Laura Adamovicz (Workshop co-chair), Chris Anchor, Megan Strobel, Michael Becker and Henry Adams.

WELCOME FROM THE PRESIDENT



Welcome to the 74th Annual International Conference of the Wildlife Disease Association, in our 75th year of existence! From 28 founders from the USA and Canada in 1951, the organisation has expanded to over 1900 members representing over 90 countries on six continents, a community uniquely focused on the health of free-ranging wildlife. This event marks the start of a celebration of our past which will continue right up to our 75th conference, in Mérida, México in 2027. A new ad hoc History Taskforce, chaired by Ted Leighton is forming and Vice President, Heather Fenton has put together a programme acknowledging long-term members and celebrating achievements, a visual archive on display at the conference.

This longevity and growth have ensured our resilience and is allowing us to change, to extend our reach beyond a past focused solely on disease and into a future where wildlife health is an urgent priority. But right now, any emphasis on “health” is lost in our name, which currently suggests only disease expertise, and we have felt the need to address this disparity over recent years. So, guided by our strategic plan, WDA leadership has undertaken internal and external consultation over a number of years on the future WDA brand. A referendum, currently ongoing, will inform our future path.

Why are we doing this? Simply put, we are not an isolated community, we have global reach in a world where ecosystem biodiversity is under huge pressure. The conference theme of ***Thriving Together: Urban One Health and Ecosystem Resiliency*** highlights the way the expanding human world has infiltrated the natural one particularly via infrastructure and agriculture. This stress on wildlife is increasingly evidenced by decline. Our work is no longer just a great thing to do, or a side event of interest to human and veterinary medicine, it is vital to the future recovery and conservation of many populations of wild animals, added to which loss of biodiversity is an existential threat to humanity.

While our members, a diverse community of professionals, practitioners, conservationists and scientists, address wildlife health issues across all taxa, terrestrial and marine, WDA's main job is to bring you together. We provide platforms to share your discoveries with the world, inform you of current issues, hear your voices and extend friendship and support as we all work to generate knowledge for outreach and impact.

The international conference is our global platform. If new to WDA, you will learn about us and hear from our members about cutting-edge science in wildlife health in Chicago and via [GlobalVoice](#) broadcasting to our diverse membership around the world. This year two of our Geographic Sections will also hold conferences; The [European section in Serbia](#) and [Australasia in New Zealand](#).

I wish you all a great time in Chicago and at the conference! I would like to extend my sincere thanks to the conference team; Karen Terio, Matt Allender, Laura Adamovicz, Martha Delaney, Cat Vendl, Stuart Patterson, Leigh Combrink, Laurie Baeten, Peri Wolff and Lyndell Whyte, our other WDA officers who have supported this process, WDA council, our conference partners, Brookfield Zoo Chicago and Forest Preserves of Cook County and our many sponsors. They are all remarkable people, uncomplaining about a huge job, and leaders in our association. If you want to help WDA in action, as a committee or council member, in our sections, or as an officer, you are welcome to come to the council meeting on July 26 at 1pm or the scheduled Business Meeting and lunches to find out more.

I have 46 years of professional commitment to wildlife behind me, wildlife defines me, this community is my home. Thank you for committing to our mission by attending and contributing to this meeting, especially in very difficult international conditions for travel and finance and thank you to those who attend Global Voice, we are listening.

Sincerely,

Richard Kock,
President, Wildlife Disease Association

MEET OUR GENEROUS SPONSORS

Without their amazing support, this conference would not be possible

PARTNERS



Brookfield Zoo Chicago is a recognized leader in influencing people's actions to conserve wildlife and value nature. Since the Zoo opened in 1934, it has been known worldwide for its leading work in animal care and wildlife conservation. Today, strong conservation leaders are needed more than ever to inspire people to protect threatened animals and ecosystems. Beyond supporting conservationists, the Zoo also motivates children, students, teachers, and the wider community to make a positive difference for the natural world. Their mission is to inspire conservation leadership by connecting people to wildlife and nature.



The Forest Preserves of Cook County boast nearly 70,000 acres of protected land, home to thousands of species of plants and animals. Their diverse natural systems including savannas, prairies, woodlands and wetlands, are biological field stations for important scientific research at the forefront of the study of urban wildlife. Since 1988, its Wildlife Management Division has collected wildlife blood samples, making FFPC one of the oldest and largest contributors of data on zoonotic diseases to the US Centers for Disease Control. Since 2022, they have been partners in the nation's first ever ACZM compliant free-ranging wildlife health management residency.

GOLD



The USDA provides leadership on food, agriculture, natural resources, rural development, nutrition, and related issues based on public policy, the best available science, and effective management. With 29 agencies and offices and more than 4,500 locations across the country and abroad, its vision is to provide economic opportunity through innovation; to promote agriculture production that better nourishes Americans while also helping feed others throughout the world; and to preserve the nation's natural resources through conservation, restored forests, improved watersheds, and healthy private working lands.

SILVER



The American Association of Wildlife Veterinarians is committed to promoting the health and welfare of wildlife through research, education, and outreach and advancing wildlife medicine, management, and conservation. With the rise of conservation biology and a better societal appreciation for what veterinarians bring to wildlife health and conservation, current members work at academic institutions, in domestic animal private practice, at zoos and aquaria, in wildlife rehabilitation facilities, and with state/federal/provincial/tribal agencies.



Wildlife is central to global health and while good science exists, support to translate it into impact is often lacking. Ceva Wildlife Research Fund addresses this gap by; Supporting the development of field-applicable health solutions for wildlife populations facing disease-driven survival threats; Funding epidemiological research and tools to anticipate and limit pathogen transmission across populations; Supporting evidence-based strategies to restore ecological balance and reduce human-wildlife conflict under increasing anthropogenic pressure. Ceva is currently funding 16 projects across 13 countries.



One Health Concepts – Moving One Health to Policy and Practice



Created by an act of Congress in 1879, the USGS provides *science for a changing world*, which reflects and responds to society's continuously evolving needs. As the science arm of the Department of the Interior, the USGS brings an array of earth, water, biological, and mapping data and expertise to bear in support of decision-making on environmental, resource, and public safety issues.

MEET OUR GENEROUS SPONSORS

Without their amazing support, this conference would not be possible

BRONZE



The American College of Zoological Medicine (ACZM) is a recognized veterinary specialty organization dedicated to advancing the health and welfare of wild animals through excellence in clinical care, research, education, and public service. ACZM certifies veterinarians who demonstrate extensive knowledge, experience, and expertise in the field of zoological medicine, including the care of wildlife, zoo, aquatic, and zoological companion animals. It is committed to fostering the next generation of specialists.



The Cornell K. Lisa Yang Center for Wildlife Health strives to sustain a healthier world by developing and implementing proactive, science-based solutions to challenges at the interface of wildlife health, domestic animal health, human health and livelihoods, and the environment. With an emphasis on interdisciplinary collaboration, we work to promote environmental stewardship, build capacity for sustainable change through training and education, and undertake research and discovery that leads to real-world conservation outcomes.



Shedd Aquarium is a recognized leader in animal care, education, conservation and science whose mission is to spark compassion, curiosity and conservation for the aquatic animal world. Every year, Shedd serves as a portal for millions of guests a year, bringing them eye-to-eye with belugas and bluegills, stingrays, sturgeons and countless other aquatic species. Shedd is an accredited member of the Association of Zoos & Aquariums (AZA) and a nonprofit organization, supported by the Chicago Park District, philanthropic leaders and guests from all around the world.



Disney's Animals, Science and Environment (ASE) is comprised of nearly 1,000 Cast Members including professionals in the fields of science, conservation, education, nutrition, animal husbandry and animal health. As an accredited member of the Association of Zoos and Aquariums (AZA), ASE Cast have collaborated with renowned experts to help increase populations of endangered and threatened species.

ADDITIONAL SPONSORS



THE UNIVERSITY of EDINBURGH
The Royal (Dick) School
of Veterinary Studies

CURRENT WDA OFFICERS



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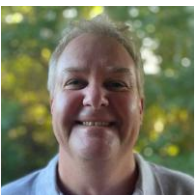
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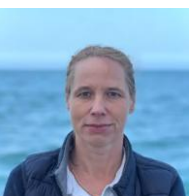
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MISSION STATEMENT

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

In August 2021 the Council voted to adopt a Charter of values. These eight statements represent the basic, common goals and values that WDA members hold 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;



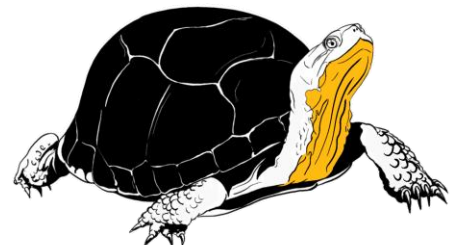
That communicating the science of our members and values of our Association through advocacy and outreach is integral to achieving our mission;



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.



What is WDA REBRANDING all about?

WHY REBRAND?

Rebranding will:

***Celebrate* our growth and expansion of purpose:** We have moved on from a singular focus on diseases, and we need a name which embraces that journey

***Showcase* our broad expertise to effect global change:** At a time when nature, and wildlife particularly, is under attack from all sides, our global expertise can contribute to meaningful wildlife conversations, helping shift agendas back in wildlife's favor. Our extensive leadership capacity in wildlife health should be clearly reflected in our identity—for our members, allied and external organizations, donors and the public

***Expand* our opportunities and donor base:** A name that embodies a holistic view of wildlife health and its importance will help us achieve our goals. The right name says: "We are part of the solution" and this proactive approach will resonate strongly with donors

***Reflect* our global profile:** The current name does not capture WDA's international reach

HOW DID WE GET HERE?



WDA's **Charter of Values and Strategic Plan** highlight that WDA members view wildlife health as a critical component in preserving biodiversity and One Health, providing the impetus for a brand that clearly expresses that connection



The Committee and Focus Groups involved in drafting the Strategic Plan comprised a large group representing the WDA Sections



We shared information about rebranding in the Transmission, held Town Halls to consult the membership and met individually with WDA Section Chairs



A survey of outside agencies and potential donors on the current name and logo also reinforced the need for rebranding



What's Next? A membership-wide vote is currently taking place

WHAT WILL REBRANDING MEAN?



A name and logo change will be incorporated into all materials (e.g., website)



An extensive promotional campaign will take place to inform all stakeholders

What is WDA REBRANDING all about?

WHAT COULD THE NEW BRAND BE?

The new name and logo should capture the diversity of our members' work, evoke positive feelings towards wildlife and wildlife health, represent our international membership, and attract donors

Potential names include:



International Association for Wildlife Health

International Wildlife Health Association



World Wildlife Health Alliance

World Wildlife Health Association



Global Wildlife Health Alliance

Global Wildlife Health Association



QUESTIONS???



Learn more and share your thoughts on the process...



Ask one of the WDA leadership team

Send the WDA leadership an email

[Watch the rebranding video with WDA president Richard Kock](#)



WILDLIFE DISEASE ASSOCIATION CODE OF CONDUCT

The mission of the Wildlife Disease Association (WDA) is to promote healthy wildlife and ecosystems, biodiversity conservation, and environmentally sustainable solutions to One Health challenges. Through our Charter of Values, we recognize that we are most effective in advancing our mission when there is respectful and equitable treatment of all those engaged in our community. In this context, respectful means being polite with due regard for another's rights, abilities, achievements, life experiences, and traditions; equitable means being fair, reasonable, honest, and impartial.

We value your, and everyone's, participation in the WDA community and at WDA events. Your support will keep our community and our events a safe, welcoming and friendly space for all fellow participants.

Therefore, all members across our international Association must agree upon application, or renewal, of membership to uphold and conduct their professional and membership-related activities in accordance with the Code of Conduct as prescribed by the Association and set forth in the sections below.

Our Association is committed to providing a safe, positive, and professional environment that is free of prejudice in our meetings, functions, and online forums, and that is free of harassment and fosters active, equal participation. Harassment is defined as speech or behavior that is not welcome, is personally offensive, or causes distress, whether it is based on national origin, ethnicity, race, geographic, socioeconomic, and educational backgrounds, gender identity and expression, intersex status, sexual orientation, religion, age, physical appearance, disability, military or veteran status, political beliefs or affiliation, career stage, marital status, carer responsibilities or pregnancy status. Harassment expressed in a joking manner still constitutes harassment and is unacceptable. Behavior that is acceptable to one person may not be acceptable to others. As such, one must use words and actions that clearly communicate respect for others.

This Code of Conduct is intended to establish the expectation for respectful and equitable speech and behavior for all those engaged in our community, as well as a process for reporting and responding to harassment. Retaliation for reporting harassment and making false reports are a violation of this Code of Conduct. The failure to uphold these expectations harms the well-being of individuals and the broader community, our scientific credibility, our respective professions, and our mission.

Reporting a harassment allegation

It is the responsibility of the WDA community to promote an inclusive and positive environment for our scholarly activities. If you are being harassed or notice that someone else is being harassed, and this has not been resolved immediately, e.g. through an appropriate apology or explanation acceptable to the injured party, please take action by making either an informal or formal report.

An informal report can be made verbally (via phone or in-person) to a Diversity Champion at the annual meeting (recognizable by name tag badge), the Chair of the Ethics Committee or the designated ombudsman for the event. An informal report is appropriate if the reporter does not want an investigation, but simply wants to report an incident. It may also be appropriate if they would prefer to explore resolution options before filing a formal report and identifying the accused. A formal report is, however, needed for the Association to investigate an incident.

WILDLIFE DISEASE ASSOCIATION CODE OF CONDUCT cont'd

A formal written report should be sent to the Chair of the Ethics Committee or the designated ombudsman for the event, detailing the allegation, including all of those involved and any supporting documentation as well as clearly stating that they have read the “Wildlife Disease Association Code of Conduct” and that “The statements made are truthful and factual to the best of my knowledge” and the complaint should be signed and dated.

Anonymous reports may be submitted, however, more information is required for a formal report. Anonymity may limit the extent to which the Committee can and/or will respond to the concern. The shorter the period between an incident and report, the greater the committee’s ability to investigate and respond effectively.

At any point, if an individual is in immediate danger, venue security (if applicable) and/or the local emergency authority (for example, call 911 in the United States) should be contacted.

Committee response to a harassment allegation

Once a complaint is received, the Chair of the Ethics Committee will ensure that the complaint has been properly filled out and will record the date received and confirm receipt with the sender within 24 hours (or the next business day). If no response from the Chair is received in that period, the report should also be sent to the Association President and Executive Manager. Reports will be reviewed by the Ethics Committee within seven (7) calendar days from the receipt of the complaint.

The WDA is committed to confidentiality when addressing harassment allegation reports. However, the Association also acknowledges that full confidentiality is not always possible when investigating a complaint, and disclosure may in some cases be legally required.

Ethics Committee members named in a report, or with a close working or personal relationship with anyone named in the report, will be required to recuse themselves from the review, investigation, and determination process.

If there is not sufficient evidence or documentation to support a Code of Conduct violation, the chair of the Ethics Committee will notify in writing, the individual filing the report, indicating that the complaint has been dismissed and the rationale for the decision.

1. Notification that a complaint has been filed and that there is adequate information in the complaint to justify it be processed.
2. A copy of the complaint, as received by the Ethics Committee
3. A copy of the WDA Code of Conduct
4. A request for a written response to be received in 14 days.

Once a written response by the offender(s) has been received, the Ethics Committee may choose to investigate further before any decisions on the outcome of the investigation are made. Any requests for further information should be in writing, and only written responses from these individuals will be accepted. Such investigations should not exceed four (4) weeks.

Once a written response by the offender(s) has been received, the Ethics Committee may choose to investigate further before any decisions on the outcome of the investigation are made. Any requests for further information should be in writing, and only written responses from these individuals will be accepted. Such investigations should not exceed four (4) weeks.

If the Ethics Committee determines that a Code of Conduct violation occurred, then an appropriate, formal response(s) will be determined. The Ethics Committee will provide a recommendation to the Council at the next scheduled council meeting. The Council may accept the recommendation of the Committee or elect another response. All responses from the Ethics Committee must be in writing. Depending on the severity of the violation, an appropriate, formal response may include, but are not limited to, the following:

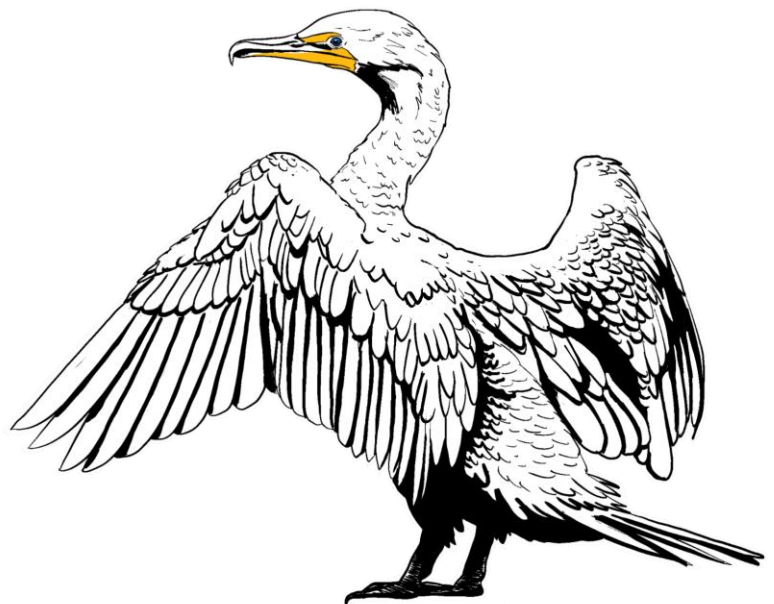
1. Requesting a formal apology or mediation process
2. Encouraging the offender(s) to participate in relevant training or counselling
3. Removing the offender(s) from a WDA meeting, function, sponsored activity, or online forum without refund of any expenses
4. Reporting the actions of the offender(s) to their home institution
5. Suspending the offender(s) from WDA for a specified period. During this suspension, individuals may not receive any awards/honors or serve in leadership positions
6. Banning the offender(s) from WDA and revocation of past and future awards/honors

All records regarding the incident shall be kept in a confidential file for seven (7) years from the date of the complaint having been lodged. Repeated offenses by the same individual within a calendar year may result in increased action on the part of the Executive Council.

Constitution of the Ethics Committee

The WDA Ethics Committee shall consist of at least one member from each section, including one Council member-at-Large, and at least one, but no more than two, student members. Members of the committee are nominated based on a demonstrated interest in promoting diversity and equity and are selected by Council. Each member including the chair is selected for a 36-month term and may be re-selected for one additional term. The Committee Chair shall act as the primary contact for complaints and convene the committee when a complaint is received and shall be the primary contact with Council.

The Code of Conduct shall be reviewed by the Membership Committee in consultation with the Ethics Committee and re-approved by the Council at least every 36 months.



SUSTAINABILITY

Welcome to Chicago, Illinois, USA!

We ask that all attendees of the 74th Annual International Conference help uphold our 8th Charter of Values ethic which states that: **we should conduct our business according to principles of environmental sustainability**. The conference planning committee has reviewed all our activities to ensure that we are considering sustainability whenever possible throughout the event.

Everyone registered for the conference should bring their own reusable mug for refreshments, better yet, bring your mug from another meeting or buy a WDA mug! Wherever possible we have sourced locally or from the US, including many of the WDA-branded items, catering services and use of local businesses to help reduce shipping costs and keep WDA's economic impact within the community.

WDA branded materials and some auction items were specifically chosen for their eco-friendly materials and durability.

The event information will be available in electronic format on screens to minimize printed materials. Name tags, plastic badge holders, lanyards, and badge ribbons are made of recycled and recyclable or compostable materials. We will provide collection bins 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.

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, exec.manager@wildlifedisease.org.



PHOTO CONTEST

The Annual Conference student photo contest is run by the Student Activities Committee (SAC) and all proceeds support student activities. For details, contact SAC chair Fernando Vilchez-Delgado at student.activities@wildlifedisease.org with the subject line "WDA Photo Contest 2026."

REGISTRATION

Anyone attending the in-person conference or the Global Voice virtual event can participate in the photo contest. A maximum of 3 photos per individual can be submitted. Photos must be submitted via the official [WDA Photo Contest website by July 29](#) in one or all the following categories.

Wildlife – free ranging

Wildlife – captive or at the urban interface

Landscapes/Flora – can either contain animals or not

Entrants must have taken the photo(s) and have all rights to its distribution and use.

In-person attendees can register for the photo contest, pay your participation fee, and send in your photos when you arrive at the meeting **OR** Register and pay ahead of time via the WDA 2026 Ex Ordo website.

Global Voice participants can also register and pay ahead of time via the WDA 2026 Ex Ordo website. If you have already registered for either event but would like to enter, you can edit your registration and add the contest to your activities (under Social Events list).

SUGGESTED SUBMISSION GUIDELINES

- Accepted formats: JPEG or PNG
- Minimum resolution: 3000 pixels on the longest side
- Maximum file size: 10 MB
- Basic adjustments (contrast, brightness, and cropping) are allowed
- Excessive alterations (composites, AI-generated elements, or heavy retouching) are not permitted
- Watermarks, signatures, or borders should not be added
- Must be submitted via the [official WDA Photo Contest website by July 29](#)

DISPLAY

All photos will be showcased virtually on the official website.

Each photo must be accompanied by the following information:

- Photographer's name
- Contact information (email, and cell number)
- The category in which your photo is to be judged.
- Photo title
- A concise description of the photo (location, purpose, species in the photo, etc.) – 25 words max
- Whether you are willing to have the photo included in the silent auction

PHOTO EXHIBITION

The photos will be set up from Sunday afternoon and will remain on display until judging is complete on Thursday. If you want your photo(s) included in the silent auction, then it/they will be transferred to the auction location by the auction committee and then returned. If it is purchased, then it will be collected by the buyer after judging is complete. Those not sold at the silent auction must be collected by their owners.

Copyright and Usage

Participants retain full copyright over their images. By submitting, you grant the contest organizers (WDA Student Activities Committee) permission to use the images for promotional purposes with full credit to the photographers and prior authorization from them.

Photo Evaluation

Photos will be judged by a group of WDA members. There is also a "popular vote" by conference attendees. Judges will base their decisions on image clarity, color, lighting, contrast, composition, and "wow factor."

Winners will be announced during the annual banquet. If the winner is not present at the banquet, he/she/they will be contacted via email (or phone) after the conference.

WDA2026 CONFERENCE SCHEDULE - JULY 25-31, 2026

At a glance

Saturday, 25 July

8am **Davis-Thompson Pathology Workshop**
Kitty Hawk

8am **ACZM Short Course**
Midway Auditorium

Sunday, 26 July

7:30am **Wildlife Capture Techniques: Anesthesia and Tagging**
Off Site

7:30am **Outbreak Mitigation, Disease Investigation, Necropsy and Sampling**
Off Site

8am **Call of the Wild: WDA Wildlife Rehabilitation Medicine Workshop**
Midway Auditorium

8am **Effective Communication Workshop**
Dulles

Monday, 27 July

7am **Registration**

8am **Conference Welcome and Land Acknowledgement**
O'Hare 1-2

8:30am **Urban Wildlife Keynote 1**
O'Hare 1-2

The Urban Coyote Research Project: 25 years of monitoring human-coyote coexistence within the Chicago Metropolitan Area
» Stanley Gehrt, PhD

9:15am **Urban Wildlife Keynote 2**
O'Hare 1-2

One Health for All: Social inequality helps us understand the drivers of wildlife health and consequences for human well-being
» Maureen Murray, PhD

10am **Morning Break and Poster Session**
O'Hare 5

10:30am **Urban Wildlife**
O'Hare 1-2

Continued from Monday, 27 July

- 10:30am **Uninvited Guests: Shared Cat Food Stations and the Unexpected Transmission of Canine Distemper Virus Among Domestic Cats and Wild Urban Species in New York City**
» [Ximena A. Olarte-Castillo](#), Laura Plimpton, Shayna Orens, Abigail Schlecht, Maria Diuk-Wasser, Gary Whittaker, Laura Goodman
- 10:45am **Bats as bio-sentinels of environmental contaminants in Tucson, Arizona**
» [Ana Sanchez Zapata](#), Leigh Combrink
- 11am **Bird feeders are a source of multiple and novel pathogen exposure for backyard birds**
» [Sonia Hernandez](#), Kimberly Perez, Kayla Garrett, Raquel Francisco, Jomari Rivera Reyes, Carter Coleman, Sarah Dean, Nikole Castleberry, Liam Amman, Valor Lekas, Erin Lipp, Michael J. Yabsley
- 11:15am **The impact of anticoagulant rodenticides in non-target wildlife in Washington, DC**
» [Sarah Sirica](#), Dan Rauch
- 11:30am **Intercity Collaborations to Survey Brown Rat (*Rattus norvegicus*) Pathology across Canada, United States, and Hong Kong**
» [Lisa Lee](#), Theethawat Uea-Anuwong, Ioannis Magouras, Jonathan Richardson, Jacqueline Buckley, Maureen Murray, Sarah J. Robinson, Claire M. Jardine, Marieke H. Rosenbaum, Kim Waggle, Chelsea G. Himsworth, Bruce Wobeser
- 11:45am **Quantifying Ecosystem Resiliency: A Spatial Artificial Intelligence Approach to Managing the Human-Wildlife Interface**
» [Jared George](#)
- 10:30am **Cervid Virology and Prion Disease**
O'Hare 4

- 10:30am **Reduced nutritional reserves and antler size associated with SARS-CoV-2 exposure in free-ranging white-tailed deer (*Odocoileus virginianus*) of South Texas**
» [Joseph Hediger](#), Gabriel Hamer, Kendall Bancroft, Tyler Campbell, Walter Cook, Randy DeYoung, David Hewitt, Miranda Hopper, Francisco Ferreira, Aaron Foley, Kevin Lovasik, Allyn Martin, J. Alfonso Ortega-Santos, Landon Schofield, Ashley Tanner, Logan Thomas, Michael Cherry, Sarah Hamer
- 10:45am **Ecological Variables Influencing Epizootic Hemorrhagic Disease Outbreaks in Kentucky**
» [Kristen Hirst](#), Mark G. Ruder, Joe McDermott, Iga Stasiak, Sonja Christensen
- 11am **Exploring how movement patterns and human encounters influence SARS-CoV-2 seropositivity in deer**
» [Tyler Garwood](#), Jeremy Alder, Sara Hathaway, George Wittemyer, Guillaume Bastille-Rousseau, Tadao Kishimoto, Michael Egan, Travis Gallo, Jennifer M. Mullinax, Amira Roess, Taylor Anderson, Tiffany Wolf, James Forester, Jennifer Malmberg, Marnee Roundtree, Georgia Titcomb, Rebecca Windell, Maria Diuk-Wasser, Kim Pepin, Meggan Craft
- 11:15am **Blink and You'll Detect It: Comparing the Efficacy of Prion Diagnostic Assays for Chronic Wasting Disease Detection in The Nictitating Membrane**
» [Madison Davis](#), Jack C. Davis, John Armstrong, Janet E. Yacabucci, Jennifer Høy-Peterson, Andrea Korman, Roderick B. Gagne, Michelle Gibson
- 11:30am **Decay of chronic wasting disease prion detection at infectious deer carcass sites**
» [Marie Gilbertson](#), Heather Inzalaco, Hannah Sykes, Aaron Groves, Daniel Storm, Allen Herbst, Wendy Turner
- 11:45am **Indiana's First Case of Chronic Wasting Disease: A Partner Incentive Program success story**
» [Janetta Kelly](#)
- 12pm **WDA Business Lunch**
O'Hare 3

Continued from Monday, 27 July

- 1:30pm **Human-Wildlife Interface**
O'Hare 1-2
- 1:30pm **Optimizing chronic wasting disease surveillance and management on Tribal lands for the preservation of culture and food sovereignty**
» [Tiffany Wolf](#), Anirrhuda Belsare, Kristin Bondo, Lauren Wakefield, Tanya Roerick, Dustin Roy, Jason Clark
- 1:45pm **Potentially fatal human interactions in stranded southern right whales (*Eubalaena australis*) at Península Valdés, Argentina, 2003–2024**
» [Marcela Uhart](#), Adrianna Rotondi, Ralph E. T. Vanstreels, Matias Di Martino, Agustina Donini, Andrea Chirife, Santiago Fernandez, Marcos Ricciardi, Lucas Beltramo, Virginia Rago, nadia mohamed, Luciana Pozzi, Luciana Musmeci, Luciano La Sala, Victoria Rowntree, Denise McAloose, Carina Maron, Mariano Sironi
- 2pm **Texas ranches: a nidus for *Trypanosoma cruzi* transmission among wildlife, dogs, and triatomines**
» [Rachel Busselman](#), Juan Pablo Fimbres Macias, Jordan Salomon, Italo Zecca, Edward Davila, Carolyn Hodo, Ashley Saunders, Gabriel Hamer, Sarah Hamer
- 2:15pm **A qualitative study of human-deer interactions with implications for pathogen spillover**
» [Kyle Smith](#), Meggan Craft, Maria Diuk-Wasser, Pilar Fernandez, David Fulton, Heather Kopsco, Celine Miller, Brody Mynatt, Logan Park, Kim Pepin, Neelam Poudyal, Amira Roess, Arun Regmi, Carrera Romanini, Elias Rosenblatt, Keith Carlisle
- 2:30pm **A transdisciplinary One Health approach to human-wildlife coexistence**
» [A A Aguirre](#), Jon Salerno, Ray Gonzalez, Kevin Crooks

- 2:45pm **Toad Health is One Health: Detection of a novel *Salmonella enterica* subspecies from a localized mortality event involving wild gulf coast toads (*Incilius nebulifer*) within a residential neighborhood**
» [Sara Wyckoff](#), Marcos Isidoro Ayza, Jeffrey M. Lorch, Samantha Spencer, Kenneth Davis, Brent Jenkins, Blake Dinsmore, Charlotte Lane, Paul Crump, Benjamin Olsen
- 1:30pm **Parasitology**
O'Hare 4
- 1:30pm **Molecular detection of *Plasmodium floridense* in a rescued Iguana iguana (Squamata: Iguanidae) from Northeastern Brazil**
» [Lilian Catenacci](#), Clara Vanessa Azevedo Oliveira, Gabriela Ferreira de Oliveira, Amanda Maria Barbosa de Sousa, Osmakon Lobato, Vinicius Soares Esteves, Kathleen Apakupakul, Fabiano Barbosa Pessoa, Sharon Deem, Lucilene dos Santos Silva, Ana Carolina Ewbank, Carlos Sacristán
- 1:45pm **Spatiotemporal hotspots of invasive Longhorned tick (*Haemaphysalis longicornis*) infestations in the eastern United States**
» [Zulma Rojas-Sereno](#), Denise Bonilla, Matthew Bickerton, Gillian Eastwood, Goudarz Molaei, Ashley C. Kennedy, Christian Boyer, Michael J. Yabsley, Danielle M. Tufts, Erika T. Machtinger, Jennifer M. Mullinax, Andreas Eleftheriou
- 2pm **Multi-organ transcriptomic signatures reveal systemic inflammatory and metabolic disruption in wombats with severe sarcoptic mange**
» [Christina Naesborg-Nielsen](#), Tamieka Fraser, Kate Mounsey, Scott Carver
- 2:15pm **Spotted, Infested, and Studied: A Survey of Ectoparasites on Ocelots (*Leopardus pardalis*) and Bobcats (*Lynx rufus*) of the Southern United States**
» [Tiffany Pope](#), Allyn Martin, Michael Tewes, Richard Gerhold, Ashley Reeves

Continued from Monday, 27 July	
2:30pm	Tick-borne pathogen surveillance: a collaborative, multiagency approach » <u>Marnee Roundtree</u> , Jeff Hamik, Halie Smith, Alexandria Welch, Shaun Cross
2:45pm	Characterization of larval Taeniid cestode infections in muskrat (<i>Ondatra zibethicus</i>) populations of the eastern United States. » <u>Nicholas Friedeman</u> , Mary Lacey, Christine Casey, Ellen Haynes, Mark G. Ruder, Michael J. Yabsley, Chris Cleveland
3pm	Afternoon Break and Poster Session <i>O'Hare 5</i>
3:45pm	One Health <i>O'Hare 1-2</i>
3:45pm	Gastrointestinal Community Dynamics of Mountain Gorillas (<i>Gorilla beringei beringei</i>) Across a Shared Landscape » <u>Kathryn Harper</u> , Natalie Payne, Karla Vargas, Melanie Culver, Jennifer L. Verdolin, Leigh Combrink
4pm	Protecting Wildlife Protects Children: A One Health Case Against Lead Ammunition » <u>Marcela Uhart</u> , Andrea Caselli, Valentina Fernández, Ayelen Andrea Muchiutti, Ralph E. T. Vanstreels, Martin Santiago
4:15pm	Investigations into social and ecological aspects of lead ammunition for big game hunting with a focus on New York, USA » <u>Andreas Eleftheriou</u> , Krysten Schuler
4:30pm	Respawn, Reconnect, Collaborate: Teaching One Health Through Video Game Worlds » <u>Justin D. Brown</u> , Zachary Zidik, Andrew Kennedy, Amy Kuntz, Jennifer Wright, Sarah Zipf

3:45pm	Toxicology <i>O'Hare 4</i>
3:45pm	Neonicotinoid insecticide exposure is associated with later migration in a neotropical songbird, the Gray Catbird (<i>Dumetella carolinensis</i>) » <u>Meredith Anderson</u> , Brett Blackwell, Sofia Horn, Nina Johnson, Kes Luchini, Christina Farrell, Amy Janik, Emily Cohen, Jeanne Fair, Sarah Hamer
4pm	Neonicotinoid insecticide exposure and immune function in native free-ranging Texas lizards » <u>Mycha Van Allen</u> , Kira Gangbin, Nathan Rains, Diane Barber, John Buchweitz, Lori NeumanLee, Sarah Hamer
4:15pm	Widespread exposure to neonicotinoid insecticide in bobcats (<i>Lynx rufus</i>), fishers (<i>Pekania pennanti</i>), and river otters (<i>Lontra canadensis</i>) in North Dakota, USA » <u>Charlie Bahnson</u> , Eric Michel, William Jensen, Stephanie Tucker, Samantha Courtney, Jonathan Jenks, Jonathan Lundgren, Justin Zyskowski
4:30pm	Creating a Biomarker for Antemortem Detection of Anticoagulant Toxicity in Raptors » <u>Jennifer Bloodgood</u> , Yao Zhu, Cynthia Hopf-Dennis, Krysten Schuler, Nichole Maughan, Melissa Fadden, Marjory Brooks
4:45pm	Investigating the Connection Between Heavy Metal Water Pollution and Avian Influenza in Indiana's Waterfowl » <u>Erin Gleason</u> , Emily McCallen, Adam Phelps, Michelle Benavidez Westrich
3:45pm	Science Cafe: Animal Welfare and Urban Wildlife Health <i>Love Field (Love A/B)</i> Chaired by: M. Camille Hopkins
5pm	Student-Mentor Mixer <i>O'Hare 3</i>

Tuesday, 28 July	
7am	AAWV Meeting <i>O'Hare 3</i>
8am	Keynote Student Speaker <i>O'Hare 1-2</i>
8am	From Cryptic to Contextualized: Understanding <i>Trichinella chanchalensis</i> Through Metabarcoding » <u>Cody Malone</u> , Jane Harms, Naima Jutha, Kimberlee Beckmen, Raphaela Stimmelmayer, Malik Awan, Vladislav Lobanov, Emily Jenkins
8:30am	Student Presentations - Mammals and Birds <i>O'Hare 1-2</i>
8:30am	Drivers of Multipathogen Exposure in White-Tailed Deer (<i>Odocoileus virginianus</i>) in Southern Wisconsin » <u>Md Nurul Islam</u> , Marie Gilbertson, Aaron Groves, Daniel Storm, Wendy Turner
8:45am	Green lung syndrome in white-tailed deer: Evidence towards <i>Conidiobolus</i> sp. fungal disease » <u>Victoria A. Andreasen</u> , Alisia A.W. Weyna, Jeffrey M. Lorch, Melanie R. Kunkel, Kevin D. Niedringhaus, Chloe C. Goodwin, Xuan Hui Teo, C. Robert Stitz, Heather Fenton, Justin D. Brown, Mark G. Ruder, Bambi C. Ferree Clemons, Mark W. Cunningham, Amy S. McKinney, Michael J. Yabsley, Nicole M. Nemeth
9am	Continued surveillance for influenza A antibodies in wild raptors of the upper Midwest (2023-2025) following the arrival of highly pathogenic influenza A virus in the flyway (2022) » <u>Kelsey Rayment</u> , Victoria Hall, Kristelle Mendoza, Carol Cardona, Rebecca Poulson, Elizabeth Kurimo-Beechuk, David Stalknecht, Dana Framzen-Klein

9:15am	Baseline Parasitological Survey and Detection of Ocular Helminths (<i>Oxyspirura</i> spp.) in Hunter-Harvested Grey Partridge (<i>Perdix perdix</i>) and Sharp-tailed Grouse (<i>Tympanuchus phasianellus</i>) from Montana » <u>Henry Valencia</u> , Ronald Kendall
9:30am	From penguin (<i>Spheniscus magellanicus</i>) fatalities to a broader ecological understanding: avian malaria in captive zoo birds, local wild birds, and mosquitoes in Texas » <u>Amanda Waugh</u> , Francisco Ferreira, Claire Nevins, Victoria Milne, Misty Garcia, Gabriel Hamer, Sarah Hamer
9:45am	Reproductive site and season impact the milk proteome of South American fur seals (<i>Arctocephalus australis</i>) » <u>Serena Zhang</u> , Susana Cardenas-Alaya, Matthew Allender, Michael Adkesson, Jason McAllister, Jennifer Geddes-McAllister, Mauricio Seguel
10am	AM Break & Poster Session <i>O'Hare 5</i>
10:45am	Student Presentations - Reptiles & Aquatics <i>O'Hare 1-2</i>
10:45am	Determining Comprehensive Health Parameters and Pathogen Presence in Wild Spotted Turtles (<i>Clemmys guttata</i>) of Northern Illinois » <u>Madison Kasbaum</u> , Laura Adamovicz, Kaitlin Moorhead, Rose Arnold, Joey Cannizzaro, Chitra Basyal, John Winter, Matthew Allender
11am	Epidemiology of Tortoise Intranuclear Coccidiosis in free-ranging aquatic turtles in Illinois » <u>Grace Minge</u> , Laura Adamovicz, Carly Etter, Gary Glowacki, Dan Thompson, William Graser, Chris Anchor, Matthew Allender

Continued from Tuesday, 28 July

- 11:15am **Hematological Analysis in Free-Ranging Native Snakes Associated with One or More Potential Pathogens in the Southeastern United States**
» [Corinna Hazelrig](#), Terence Farrell, Jenna Palmisano, Ellen Haynes, John Maerz, Kristina Meichner, Jian Zhang, Kayla Garrett, Michael J. Yabsley, Jason Ortega, Chris Cleveland, Nicole M. Nemeth
- 11:30am **Hemolymph analysis and antemortem assessments in three species of unionid mussels in northern Cook County, Illinois**
» [Eliza Baker](#), John Winter, Michael Neri, Charles Rizzo, Chris Anchor, Matthew Allender
- 11:45am **Cerebral Microsporidiosis in Cold-stressed Threadfin Shad (*Dorosoma petenense*) in Eastern Tennessee**
» [Isabel Correia](#), Michelle Dennis, Sophie Hall, Jan Lovy, Richard Gerhold
- 12pm **Analyzing broadscale environmental risk factors for initiation of historical botulism events in the Great Salt Lake marshes, 1910-2024**
» [Jaclyn C. Plasterer](#), Virginia Stout, John Neill, Jonathan D. Lautenbach, Jessica N. Sanchez
- 12:15pm **WDA Business Meeting Luncheon**
O'Hare 3
- 1:30pm **Student Presentations - Urban Wildlife & Wildlife Interfaces**
O'Hare 1-2

- 1:30pm **Viral surveillance in wild mammals in an urban center in Brazil**
» [Bruna Hermine de Campos](#), Daniel Oliveira dos Santos, Janaina Ribeiro Duarte, Vinicius Henrique Barbosa Amaral, Nadja Simbera Hemetrio, André Duarte Vieira, Leticia Neves Ribeiro, Sara Cândida Ferreira dos Santos, Talita Emile Ribeiro Adelino, Maurício Teixeira Lima, Carlyle Mendes Coelho, Herlandes Penha Tinoco, Luiz Carlos Junior Alcantara, Felipe Campos de Melo Iani, Erica Azevedo Costa, Renato Lima Santos, Marcelo Pires Nogueira de Carvalho
- 1:45pm **Urban Adaptation and Emerging Disease: Molecular Characterization of Burrowing Owl Diet Illuminates Rat Lungworm Transmission Ecology**
» [Håkon Jones](#), Nikole Castleberry, Brittany Piersma, Michael J. Yabsley
- 2pm **Where Worlds Collide: Spatial patterns of disease risk in African buffalo at the human-wildlife interface of Kruger National Park**
» [Eberle Yarborough](#), Hendrik Combrink, Robert Spaan, Peter Buss, Lin Mari de Klerk-Lorist, Cambrey Knapp, Lauren Schreck, Intimate Shongwe, Michele Miller, Govert van Dam, Paul L.A.M. Corstjens, Petunia Msuthwana, Khethiwe Mtshali, Marché Duarte, Nicola Collins, Brianna Beechler, Anna Jolles
- 2:15pm **INTRA-URBAN STRUCTURING OF HEAVY METAL EXPOSURE AND MORPHOLOGY IN MUSCOVY DUCKS (*CAIRINA MOSCHATA*)**
» [Matt Tat](#), Sonia Hernandez, Stacey Lance
- 2:30pm **How social behavior shapes viral transmission: A phylodynamic study of foot-and-mouth disease in African buffalo**
» [Cambrey Knapp](#), Ranjitha Bommana, Richard Orton, Simon Gubbins, Eva Perez-Martin, Brianna Beechler, Anna Jolles, Roman Biek
- 2:45pm **A calibrated metapopulation framework for evaluating chronic wasting disease management scenarios in white-tailed deer (*Odocoileus virginianus*)**
» [Maris Daleo](#), Jameson Mori, Nohra Mateus-Pinilla

Continued from Tuesday, 28 July

- 3pm **Afternoon Break & Poster Session**
O'Hare 5
- 3:45pm **Student Presentations - Analyses, Detection and Treatment**
O'Hare 1-2
- 3:45pm **Medgene Lab's rabbit hemorrhagic disease virus 2 vaccine efficacy and potential use in cottontail conservation**
» [Cole Wzientek](#), Hannah Shapiro, Dana Karelus, Angela Bosco-Lauth, Alyn Martin
- 4pm **Development and Validation of a Quantitative PCR Assay for Detection of Two Novel Adenoviruses in Ornate Box Turtles (*Terrapene ornata ornata*)**
» [Erika R. Suniga](#), Stephanie Brien, Crystal Moreno-Garcia, Amber Simmons, Matthew Allender, Laura Adamovicz
- 4:15pm **VISUALIZATION AND DETECTION OF SIN NOMBRE HANTAVIRUS IN MULTIPLE TISSUES OF WILD DEER MICE, INCLUDING THE REPRODUCTIVE TRACT**
» [Rebecca Radisic](#), Alexandra Stone, Ernesto Rojas-Sanchez, Reena Grewal, Erin Howell, Tracy Drazenovich, Alexandre Tremeau-Bravard, Jalika Joyner, Olivia Cords, Ken Jackson, Patricia Pesavento, Brian Bird
- 4:30pm **Development and Pathophysiology of Chimeric Invasive Gastrovascular Multicellular Structures (IGMS) in Montipora White Syndrome**
» [Chutimon McGuire](#)

- 4:45pm **Treatment trial of terbinafine submersion and increased water salinity in the treatment of *Emydomyces testavorans* in chronically infected captive Blanding's turtles (*Emydoidea blandingii*) and alligator snapping turtles (*Macrochelys temminckii*)**
» [Marguerite Bednarek](#), Madeline Brookings, Laura Adamovicz, Kaitlin Moorhead, Carly Etter, Kamila Grochowski-Grum, Surina K. Birk, Katelyn Deppe, Madison Kasbaum, Erika R. Suniga, Ryland Darling, Jaime R. Lyke, Javelis Marin Castro, Becca Chenoweth, Grace Minge, Jenna Camargo, London Wimberly, Amber Simmons, Crystal Moreno-Garcia, Matthew Allender
- 5pm **Biodiversity linkages with wildlife host prevalence and human spillover**
» [Shariful Islam](#), Gideon Wasserberg, Luis Escobar
- 5:15pm **The Structure of Wildlife Health Collaboration Networks in California**
» [Hannah Shapiro](#), Mark Lubell, Deana Clifford, Alex Heeren, Brandon Munk
- 6:30pm **WDA Auction and Reception**
Crust Brewing

Wednesday, 29 July

- 7am **WDA Wildlife Veterinary Section Annual Member Meeting**
O'Hare 4
- 8:30am **Welcome - Global Voice**
O'Hare 1-2
- 8:45am **Global Voice - Invited Presentation**
O'Hare 1-2

Continued from **Wednesday, 29 July**

Monitoring wildlife health in peridomestic habitats – the power of participatory science

» [Becki Lawson](#)

9:25am Global Voice Oral Abstract Presentations

O'Hare 1-2

9:25am Urban Wildlife Incident Reporting as a One Health Surveillance Tool: Monitoring Morbidity and Mortality in Cape Town

» [Dorothy Breed](#), Jonathan Bell, Kashiefa Amos

9:40am Breaking the Rescue Bottleneck: A Dual-Hub Strategy to Disrupt the Illegal Lemur Trade and Restore Madagascar's Most Endangered Primates

» [Justerien RAMBELONIAINA](#), Jhoanny Rasojivola, Abigail Ross

10am AM Break & Posters

O'Hare 5

10:30am Global Voice Announcements

O'Hare 1-2

10:35am Global Voice Oral Abstract Presentations

O'Hare 1-2

10:35am Death Tells a Story: Necropsy as a Tool Against Wildlife Crime in Europe

» [Andreia Garcês](#), Andreia Garcês

10:50am

Mitogenomic insights into *Sarcoptes scabiei* in American black bears (*Ursus americanus*): COI utility for regional surveillance and cross-species transmission

» [Michael J. Yabsley](#), Raquel Francisco, Ryan Grunert, Jomari Rivera Reyes, Jillian Broadhurst, Amanda Sullivan, Megan Beaudry, Julia Frederick, Marissa Howard, Troy Kieran, Travis Glenn, Justin D. Brown, John Wares, Colin Carpenter, Ethan Barton, Jennifer Bloodgood, Therese McNamee, John Tracey, Carl Tugend, Amanda Riggs

11:05am Global Voice Invited Presentation

O'Hare 1-2

Amphibians in the union of the Americas: study models for the conservation challenges in Mesoamerica

» [Abel Batista](#), PhD

12pm WDA Business Lunch

O'Hare 3

1:30pm WDA Business Meeting

O'Hare 3

2:30pm Brookfield Zoo Chicago and BBQ/Picnic

Off Site

Thursday, 30 July

8:15am Announcements

O'Hare 1-2

8:30am Al Franzmann Memorial Speaker

O'Hare 1-2

11:15am Tularemia Exposure and Ectoparasite Dynamics in Black-Footed Ferrets in South Dakota from 2002-2024

» [Madisen Hartlaub](#), Shelli Dubay, Travis Livieri, Zach Wilson, Rachel Santymire

11:30am Emergence of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) in the Western United States: A Threat to the Vulnerable Davis Mountain Cottontail

» [Hannah Shapiro](#), Cole Wzientek, Dana Karelus, John McLaughlin, Alynn Martin

11:45am Sin Nombre hantavirus interacts with helminth parasite co-infections in Montana deer mice (*Peromyscus maniculatus*)

» [Madeline Rowland](#), Amy Kuenzi, Mike Kinsella, Angela Luis

10:30am World Organization of Animal Health

O'Hare 1-2

11am Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses I

O'Hare 1-2

11am The role of host identity in transmission dynamics of a multi-host infectious disease

» Hendrina Joel, Yen-Hua Huang, Zoe Barandongo, Amelie Dolfi, Kimberlie Vera, John Mfune, [Wendy Turner](#)

11:15am Epidemiological factors and causes of pneumonia in white-tailed deer (*Odocoileus virginianus*) in Pennsylvania, USA from 2022-2025

» [Taylor C. Chan](#), Kevin D. Niedringhaus, Perry Habecker, Andrew R. Di Salvo, Johannes Nelson, Xinye Kou, Sabrina S. Greening

11:30am From Pathogens to Pathways: Using Genomics to Predict Disease Spread Across Landscapes

» [Sarah Tomke](#), Noelle Thompson, A. S. Apostolopoulos, Matthew Springer, Steven Price, John Cox, Emily Boyd, Roderick B. Gagne

Continued from **Thursday, 30 July**

» Heather Barron, DVM

9:15am Carlton Herman Speaker

O'Hare 1-2

» Eyal Frank

10am AM Break & Poster Session

O'Hare 5

10:30am Wildlife Health: Infectious Disease Surveillance

O'Hare 4

10:30am Serial *Brucella suis* biovar 4 serology reveals insights into pathogen transmission dynamics and health of a free-ranging caribou (*Rangifer tarandus granti*) herd in decline

» [Kimberlee Beckmen](#), Camilla Lieske, Kristin Denryter

10:45am Historical Trends of *Leptospira* exposure in White-tailed Deer Health across the Southeastern United States

» [Ania Majewska](#), Sathwik Katkam, Kira Buford-Rucker, Ellen Haynes, Michael J. Yabsley, Elizabeth Kurimo-Beechuk, Chris Cleveland, Marcelo Jorge, Gino D'Angelo, Mark G. Ruder

11am *Salmonella* serovars and antimicrobial resistance profiles in wild European hedgehogs (*Erinaceus europaeus*): over 13 years of surveillance in the Ferrara Province, Italy

» [Elisa Massella](#), Martina Munari, Simone Russo, Letizia Cirasella, Roberta Taddel, Andrea Luppi, Silva Rubini

Continued from Thursday, 30 July

11:45am **Filling in the gaps: Leveraging passive surveillance to better understand the distribution of a bat fungal pathogen in Iowa**
» [Rachel Ruden](#), Stephanie Shepherd, Kelly Poole, Riggs Wilson, Faith Hansen, Laura Bradner, Phillip Gauger

12pm **WDA Banquet Luncheon**
O'Hare 3

2:30pm **Science Cafe - New World Screwworm**
Love Field (Love A/B)

2:30pm **Wildlife Health: Infectious Disease Surveillance**
O'Hare 4

2:30pm **Regional assessment of canine distemper virus prevalence in wild carnivores submitted to public health laboratories in the eastern United States for rabies virus testing**
» [Seth Lattner](#), Ellen Haynes, Michael J. Yabsley, Chris Cleveland

2:45pm **Serologic evidence of canine distemper virus and protoparvovirus exposure in a multi-host carnivore community supporting endangered ocelots in southern Texas**
» [MAURICIO Rued](#), Alyn Martin, Christopher Kozakiewicz, Lisanne Petracca, Michael Tewes, Ashley Reeves

3pm **Unprecedented wildlife impacts of HPAI H5N1 viruses in the Neotropics: how was it different from the northern hemisphere?**
» [Marcela Uhart](#), Ralph E. T. Vanstreels

3:15pm **Wild Coypu as a Sentinel Species to monitor Waterborne Antimicrobial Resistance using *Pseudomonas* spp. as bacterial indicator**

» [Elisa Massella](#), Simone Russo, Stefano Bussolari, Fabrizio Mezzetti, Tommaso Fulgaro, Stefano Martini, Alessandro Morabito, Tommaso Mazzini, Pier Francesco Fontana, Giacomo Gallerani, Manuel Gamberini, Roberta Artioli, Martina Munari, Mario D'Incau, Silva Rubini, Virginia Carfora, Letizia Cirasella, Maria Sampieri, Andrea Luppi

2:30pm **Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses II**
O'Hare 1-2

2:30pm **Impacts of Predator Calls on Eastern Bluebird Embryogenesis and Offspring Phenotype**
» [Raena McCown](#), Andrew Benson, Kristen Navara, Sonia Hernandez

2:45pm **Gobblers in Good Shape? Assessing Wild Turkey Health in Minnesota**
» [Elizabeth Baker](#), Michelle Carstensen, Mary Wood, Erik Hildebrand, Arno Wuenschmann, Nicole M. Nemeth

3pm **Quantifying Chronic Stress in Free-Ranging Mule Deer: Development and Validation of a Multi-System Allostatic Load Index**
» [Sara Hathaway](#), Barbara Wolfe, George Wittemyer

3:15pm **Investigating the potential for bovine tuberculosis to persist in Indiana wildlife**
» [Jonathan Brooks](#), Joe Caudell, Sonja Christensen, Patrick Zollner, Wendy Beauvais

3:30pm **PM Break and Poster Session**
O'Hare 5

4pm **Science Cafe: WDA-WOAH Collaborations**
Love Field (Love A/B)

Continued from Thursday, 30 July

4pm **Wildlife Medicine**
O'Hare 4

4pm **Inflammatory Biomarkers as Early Screening Tools for Unknown Pathogen Exposure in Wild Carnivores in Taiwan**
» [Wanyi Lu](#), Hao Fen Chuang, Hui-Wen Chen, Kun-Hsien Tsai, Amy Ho, Hui-Yun Tseng, Pin-huan Yu

4:15pm **Sampling at 14,000 feet: Lessons learned in field sampling procedures and processing of high Andean flamingos at Laguna Colorada, Bolivia**
» [John Griffioen](#), Emily Freeman, Erin McNally, Brad Hazelton, Rene Serafino, Sol Aguilar, Omar Rocha

4:30pm **Evaluation of butorphanol-azaperone-medetomidine-ketamine to immobilize free-ranging wild Rocky Mountain elk (*Cervus canadensis nelsoni*), American black bear (*Ursus americanus*), and white-tailed deer (*Odocoileus virginianus*)**
» [Andrew R. Di Salvo](#), Jeremiah E. Banfield, Brandon M. Snavely, Carson W. Torhorst

4:45pm **Safety and Immunogenicity of an inactivated H5N2 Avian Influenza Vaccine in Stranded Pinnipeds – a Possible Tool for Protecting the Endangered Hawaiian Monk Seal (*Neomonachus schauinslandi*)**
» [Sophie Whoriskey](#), Cara Field, Emily Whitmer, Gregory Nitzel, Suman Mahan, David White, Darrell Kapczynski, David Suarez, Chang-Won Lee, Michelle Barbieri

5pm **Regional limb perfusion as an adjunct therapy for osteomyelitis in sea turtles**
» [Emily McDermott](#), Heather Barron

5:15pm **Investigation of dental and periodontal conditions in wild Formosan black bear (*Ursus thibetanus formosanus*)**
» [Guan-Ru Wang](#), Yun-Chieh Tuan, Izzie Yi-Chin Tsai, Pin-huan Yu

4pm **Wildlife Health**
O'Hare 1-2

4pm **Eastern Oyster (*Crassostrea virginica*) Health and Reproductive Assessments in the Indian River Lagoon**
» [Kyle Donnelly](#), Bryce Miller, Nicole Stacy, Ashley Rearden, Hope Leonard

4:15pm **Bleeding eyes and darkened skies: Histopathology summary of a large mortality event of green sea turtles (*Chelonia mydas*) on the coast of New South Wales (NSW), Australia**
» [Heather Fenton](#), Adelaide Dedden, Jane Hall, Edward Holmes, Lauren Limm, Duane March, Ryan Pereira, Melissa Tan, Tom Tran, Karrie Rose

4:30pm **Hidden Fungal hazards: *Fusarium* dynamics in leatherback sea turtle nest sand**
» Elizabeth Schultheis, [Samantha Kuschke](#), Tiffany Briggs, Jeanette Wyneken

4:45pm **Integration of plasma metabolomics into the comprehensive health assessment of wild ornate box turtles (*Terrapene ornata ornata*) in Illinois**
» [Laura Adamovicz](#), Madeline Brookings, Erika R. Suniga, Eliza Baker, John Winter, Matthew Allender

5pm **Epidemiology of *Ophidiomyces ophidiicola*, *Paranannizziopsis* spp., and *Nannizziopsis* spp. in wild snakes across North America**
» [Maya Iyer](#), Laura Adamovicz, Amber Simmons, Crystal Moreno-Garcia, Ellen Haynes, Christopher Petersen, Robert Lovich, Matthew Allender

5:15pm **From blotchy bass syndrome to malignant cancer: neoplastic transformation associated with adenovirus infection in black bass (*Micropterus* spp.)**
» [Mandy Womble](#), Clayton Raines, Heather Walsh, Mike Stafford, Frances Mackie, R. Kent Passingham, Esteban Soto, Susan Fogelson, Amanda Curry, Gregory Lewbart, Luke Iwanowicz, Abigail Armwood

Friday, 31 July

8:15am **Announcements**
O'Hare 1-2

8:30am **Wildlife Health - Avian I**
O'Hare 1-2

8:30am **Detection of *Rickettsia hoogstraalii* and *Rickettsia lusitaniae* in *Argas (Persicargas) ricei* ticks infesting California Condors (*Gymnogyps californianus*)**
» [Sarah Hamer](#), Julia Gonzalez, Lisa Auckland, Sara Neumann, Arianna Punzalan, Jennifer Kennedy, Julie Barnes, Jordan Davis-Powell

8:45am **Avian blood parasites in waterfowl from managed wetlands in Central Wisconsin**
» [Sarah Orlofske](#), Jeffrey Bell, Roxanne Gasperetti, Craig Ziolkowski, Vasyi Tkach, Robert Jadin

9am **Eastern Equine Encephalitis Virus in New York Raptors**
» [Jill Western](#), Elizabeth Buckles, Cynthia Hopf-Dennis, Sara Childs-Sanford

9:15am **Wild Birds Pathogen Surveillance in the Brazilian unique caatinga biome**
» [Lilian Catenacci](#), Bruno Rodrigues Oliveira, Clara Vanessa Azevedo Oliveira, Gabriela Ferreira de Oliveira, Amanda Maria Barbosa de Sousa, Osmakon Lobato, Alessandro Domingos Araújo Filho, Fabiano Barbosa Pessoa, Kathleen Apakupakul, Sharon Deem, Lucilene dos Santos Silva

9:30am **Trait-based assessment of West Nile virus impacts in Pennsylvania wild bird populations**
» [Brock Geary](#), Sean Murphy, Lisa Williams, Roderick B. Gagne

9:45am **AM Break**

10:15am **Wildlife Health - Avian II**
O'Hare 1-2

10:15am **Parasitism in quail: drivers of spatial patterns in Texas**
» [Alynn Martin](#), Maedean Cardenas, Liza Soliz, Alejandro Bazaldua, Andrea Esqueda, Fidel Hernández

10:30am **Climate change and extreme weather events to intensify West Nile virus activity**
» [Desiree Bliss](#), Gracie Fischer, Leigh Combrink

10:45am **Surveillance for influenza A virus H5-specific antibodies in Canada Geese (*Branta canadensis*) in Pennsylvania**
» [Justin D. Brown](#), David Stalknecht, Jeremy Stempka, Andrew R. Di Salvo, Amanda Hoyt, Kyle Van Why, Kevin D. Niedringhaus, Lane Potts, Erica Miller, Emma Grunwald, Madison Stevens, Luke Scherer, Whitney Kistler, Nate Brown, Rebecca Poulson

11am **Predicting Wildlife Disease Risk from Space: Avian Tick Parasitism and Land-Use Change Across the Colombian Andes**
» [Sreeja Puthumana](#), Gustavo A. Londoño, Julie M. Allen, [Mohamed Sallam](#)

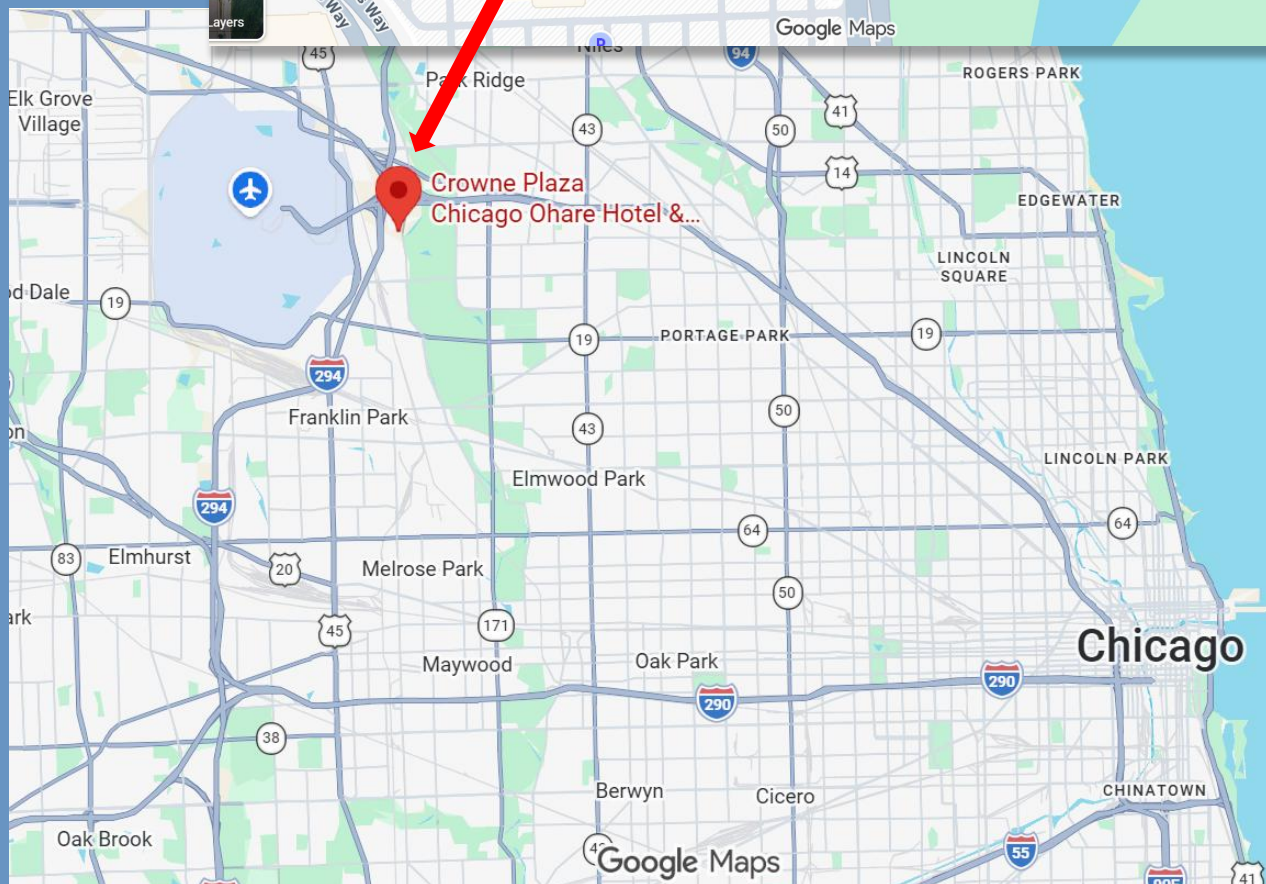
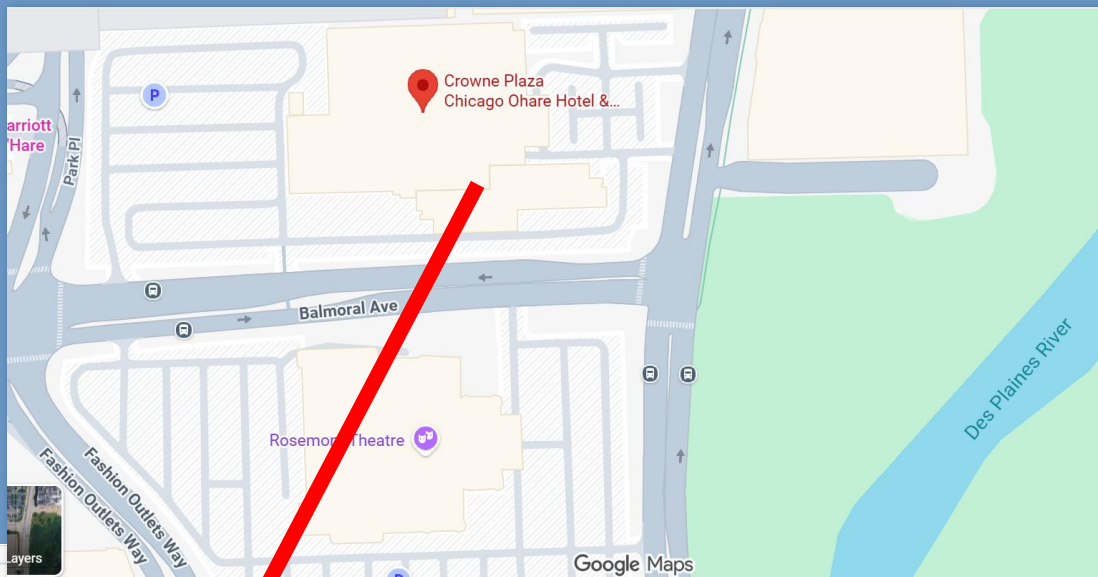
11:30am **Conference Closing**
O'Hare 1-2

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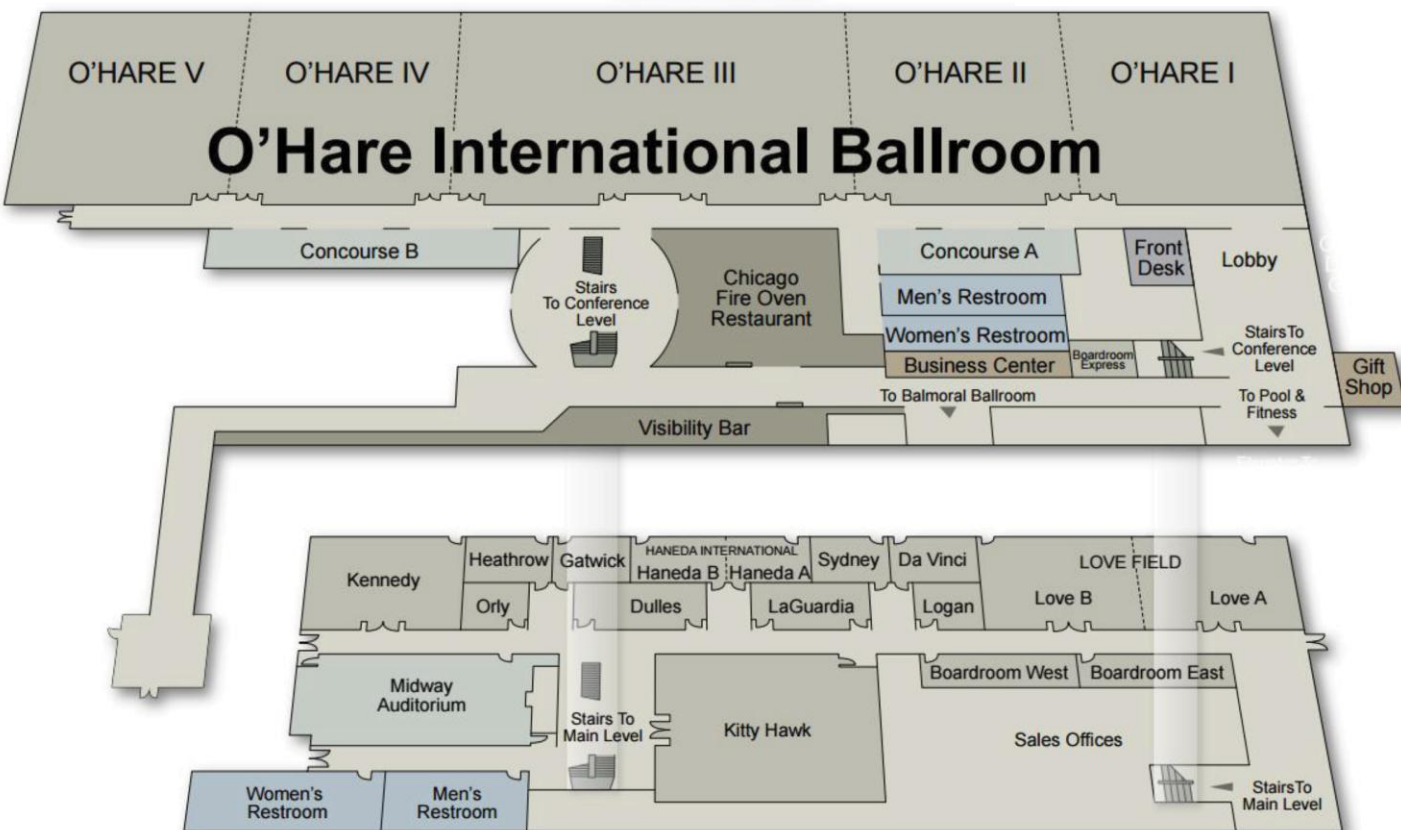
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Our goal is to maintain a safe and healthy environment during the conference. To prevent infection and to slow transmission of illnesses like COVID-19, we recommend the following:

- Please stay home if you do not feel well. We will offer a virtual platform for our attendees – Global Voice – which is accessible to all in-person attendees.
- While at the meeting, wash your hands regularly with soap and water, or clean them with alcohol-based hand rub.
- Masks are not mandatory, but please consider wearing a mask when in public settings or around others.
- Maintain at least six feet distance between you and people coughing or sneezing.
- Avoid touching your face.
- Cover your mouth and nose with your elbow when coughing or sneezing.
- Consider testing yourself for COVID-19 before traveling to the conference and at the conference if you feel unwell.

Thank you!

KEY CONTACTS FOR WDA 2026

If you need local assistance:

Overall concerns and program enquiries contact:

- Matt Allender +1 (217) 621-7121
- WDA Exec Manager Peri Wolff +1 (805) 857-5809

Scientific program enquiries contact:

Karen Terio +1 (708) 228-6489

Ombuds enquiries contact:

- Tiffany Wolf +1 352 638-3292
- Amanda Fine +1 352 638-3292

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Ombuds at WDA 2026

ombuds [ˈäm-, budz] (noun, plural also ombuds)

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Tiffany Wolf and Amanda Fine

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ABSTRACTS

Thriving Together: Urban One Health and Ecosystem Resiliency



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Oral

European Bat Lyssavirus Type 2 (EBLV-2) in a Daubenton's Bat (*Myotis daubentonii*) in Central Germany – Detection and Response: An Example of Interdisciplinary Collaboration

Monday, 27th July - 09:55: Global Voice Short Presentations (Virtual/Online) - Oral

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In July 2025, a Daubenton's bat (*Myotis daubentonii*) tested positive for European bat lyssavirus type 2 (EBLV-2) as part of a bat health project in central Germany. EBLV-2 is one of six *Lyssavirus* species identified in European bats. Although bat-associated lyssaviruses are rarely detected in Germany, with a prevalence of 1.2% among tested dead bats, they pose a relevant zoonotic risk. Transmission to humans may occur through e.g. bites, and untreated infections are fatal. In this case, potential contact with children at a daycare center could not be excluded. Therefore, the local public health authority recommended post-exposure prophylaxis, and 45 children received vaccination. Following a report from the daycare center, the responsible authority submitted the bat for routine examination, including necropsy, histopathology, and immunohistochemistry. Findings revealed mild, subacute, oligofocal lymphocytic polioencephalitis with Negri bodies. Rabies diagnostics were performed on brain tissue using the fluorescent antibody test and RT-PCR. Confirmation and virus isolation were carried out at the National Reference Laboratory for Rabies.

This case underscores the importance of close trans- and interdisciplinary collaboration in line with the One Health approach. Strong media attention and parental reactions further highlighted the need for effective risk and crisis communication that conveys potential risks without causing panic, while emphasizing the ecological importance of bats. To provide context and perspective, we organized an informational event and recorded a podcast to raise awareness among the public, experts, and decision-makers about the challenges of managing zoonotic risks at the interface of species conservation and public health.

Integrated Approaches to Bat Health: Parasites, Vectors, and Fungal Interactions

Monday, 27th July - 10:15: Global Voice Short Presentations (Virtual/Online) - Oral

**Aneira Williams¹, Pamela Medina-van Berkum², Melissa de Waal³, Océane Fogliani⁴, Milan Jirku⁵,
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1. University of South Bohemia, Biology Centre of the Czech Academy of Sciences, Institute of Entomology, and Operation Wallacea,
2. Operation Wallacea and Kiel University, 3. Fairleigh Dickinson University, 4. University of South Bohemia and Biology Center of
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6. University of Ghent and Biology Centre of the Czech Academy of Sciences, Institute of Entomology

Bats play a vital role in ecosystems but also host diverse pathogens and parasites that influence wildlife health and One Health dynamics. Emerging fungal diseases such as white-nose syndrome, caused by *Pseudogymnoascus destructans*, may alter host immunity and increase susceptibility to co-infections. However, these interactions remain poorly understood in wildlife, particularly in Central and South America.

Our lab investigates health and parasite dynamics in free-ranging bat populations in Cusuco National Park, Honduras, and the adjacent community of Buenos Aires. This protected-area–community interface is characterised by increasing ecotourism and ongoing deforestation, creating conditions that may alter host–pathogen interactions. Sampled species include *Desmodus rotundus*, the common vampire bat, and *Bauerus dubequercus*, a Near Threatened species, underscoring both public health and conservation relevance.

Captured bats are examined for ectoparasites and screened for hemoparasites and fungal pathogens, including *P. destructans* and bat fly-associated microfungi in the order Laboulbeniales. The objectives of this study are to: (1) assess the impact of *P. destructans* on bat populations and host physiological condition; (2) determine whether cutaneous fungal infections are associated with altered susceptibility to blood parasites, and vice versa; (3) evaluate the potential use of ectoparasites as diagnostic tools for hemoparasites; and (4) examine whether Laboulbeniales infections are associated with reduced hemoparasite prevalence, suggesting a role in limiting pathogen transmission by insect vectors.

By characterising parasite assemblages in a human-impacted protected area, this work contributes to wildlife health surveillance and supports a One Health framework for understanding disease risk in increasingly anthropogenic landscapes.

Uninvited Guests: Shared Cat Food Stations and the Unexpected Transmission of Canine Distemper Virus Among Domestic Cats and Wild Urban Species in New York City

Monday, 27th July - 10:30: Urban Wildlife (O'Hare 1-2) - Oral

Ximena A. Olarte-Castillo¹, Laura Plimpton², Shayna Orens³, Abigail Schlecht³, Maria Diuk-Wasser², Gary Whittaker³, Laura Goodman⁴

1. Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, **2.** Columbia University, **3.** Cornell University College of Veterinary Medicine, **4.** Department of Public and Ecosystem Health, College of Veterinary Medicine, Cornell University; James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University

The five boroughs of New York City (NYC) are home to a large population of raccoons (*Procyon lotor*) and free-ranging domestic cats (*Felis catus*). Free-ranging cats often live in large groups (or cat colonies), promoted by feeding stations set up by “colony caretakers”. These stations also attract urban wildlife, such as raccoons, which fosters inter-species contact and the transmission of pathogens. Canine distemper virus (CDV) is a highly contagious virus that can cause lethal systemic disease in a wide range of domestic and wild carnivores. Although serological studies indicate that domestic cats can be exposed to and survive infection by CDV, there is a lack of genetic evidence showing naturally occurring CDV infections in cats. Since 2022, we have monitored the spread of CDV in urban wildlife in NYC. We conducted genetic screening of brain tissue, saliva, and rectal swabs, along with whole-genome sequencing, and identified the co-circulation of two distinct CDV genotypes. Interestingly, both genotypes were also detected in free-ranging domestic cats. Serum neutralization assays of serum collected from free-ranging domestic cats in 2021 and 2022 also indicated previous exposure to CDV. We hypothesize that the increased interspecific contact facilitated by the cat food stations leads to free-ranging cats becoming exposed to the CDV circulating in raccoons. Understanding the dynamics of CDV in urban landscapes is essential to assessing whether peri-domestic animal populations serve as pathogen reservoirs for wildlife species, especially domestic cats, which are not regarded as typical hosts of CDV.

Bats as bio-sentinels of environmental contaminants in Tucson, Arizona

Monday, 27th July - 10:45: Urban Wildlife (O'Hare 1-2) - Oral

*Ana Sanchez Zapata*¹, *Leigh Combrink*²

1. The University of Arizona, School of Natural Resources and the Environment, 2. University of Arizona

Urbanization alters landscapes and often increases wildlife exposure to environmental contaminants such as heavy metals. These contaminants can affect animal health by disrupting physiological processes and increasing disease susceptibility. As key insect predators and pollinators, bats are especially vulnerable to these emerging environmental stressors. This study examines the presence of environmental contaminants that could impact bat health across an urban-rural gradient in Tucson, Arizona, using bat fur as a non-invasive monitoring method.

Bats are sampled at sites representing urban, suburban, and rural conditions. Individuals are captured using mist nets and fur samples are obtained from small clippings collected during the insertion of passive integrated transponder (PIT) tags between the shoulder blades. The fur is used for laboratory analysis of environmental contaminants at the University of Arizona, including heavy metals commonly associated with urban development. Bat fur provides a record of contaminant exposure over time, allowing assessment of chronic environmental stress.

By comparing contaminant concentrations across different levels of urbanization, this project evaluates how land-use intensity influences exposure to environmental pollutants in bats, supporting their use as bio-sentinels of environmental quality and providing a framework applicable to other wildlife species exposed to similar contaminants. This research will inform bat conservation strategies and enhance understanding of how pollution influences wildlife health in human-modified landscapes.

Bird feeders are a source of multiple and novel pathogen exposure for backyard birds

Monday, 27th July - 11:00: Urban Wildlife (O'Hare 1-2) - Oral

***Sonia Hernandez*¹, *Kimberly Perez*², *Kayla Garrett*³, *Raquel Francisco*², *Jomari Rivera Reyes*², *Carter Coleman*², *Sarah Dean*², *Nikole Castleberry*², *Liam Amman*², *Valor Lekas*², *Erin Lipp*², *Michael J. Yabsley*⁴**

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1. *djdkkd*, 2. *University of Georgia*, 3. *Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA*, 4. *Southeastern Cooperative Wildlife Disease Study*

Wildlife feeding is typically discouraged because of concerns about health and/or pathogen transmission with downstream effects to wildlife, livestock and public health. Yet bird feeding is overlooked because it is touted as an important way for people to connect with nature, particularly in urban settings. However, artificial aggregation, increased density, contaminated surfaces and inappropriate food can alter pathogen dynamics. Traditional wildlife health studies have traditionally focused on single host-pathogen relationships (e.g. house finches and *Mycoplasma*) particularly for species that develop clinical disease, but co-infections, spillover into novel hosts, sublethal impacts and the overall “community” of pathogens at the bird feeder are important. We captured and collected morphological data, body condition, ectoparasite load and biological samples from backyard birds from 2024-2025 at nine sites across an urbanization gradient in Georgia, USA to describe the prevalence of common pathogens. We found that 1) *Salmonella* spp. prevalence was low (1-3%, n=1,379), but environmental persistence at the feeder is likely to predict future outbreaks, 2) *Knemidokoptes* spp. infested 4% of 87 birds in 2024, some of which were new hosts, 3) *Trichomonas* spp. was found in 2.7%, of 148 birds including new hosts and is the first detection of *T. gypaetini* in a passerine. Furthermore, we analyzed the community composition and seasonal species turnover at bird feeders, which allowed us to make predictions about risk of multiple pathogen exposure for common backyard birds. In concert, our results indicate that the “bird feeder” community requires simultaneous multi-pathogen surveillance to truly untangle impacts on fitness.

The impact of anticoagulant rodenticides in non-target wildlife in Washington, DC

Monday, 27th July - 11:15: Urban Wildlife (O'Hare 1-2) - Oral

Sarah Sirica¹, Dan Rauch²

1. City Wildlife, 2. DC Department of Energy and Environment Fish and Wildlife Division

Anticoagulant rodenticides (AR) have well-documented adverse effects across a wide variety of wildlife species. However surveillance data is lacking in some regions and further research is needed to characterize non-target exposure, particularly in urban environments. City Wildlife, Washington DC's only wildlife rehabilitation center, collaborated with the DC Department of Energy and Environment (DOEE) to conduct a prospective surveillance study assessing AR exposure in non-target species. The target sample size was 100 individuals, and non-target species were defined as free-ranging wild animals that may obtain primary access to ARs or secondary exposure from consuming contaminated prey items. This presentation will summarize study outcomes. Of the 101 individuals sampled, 85 percent tested positive for the presence of ARs, including 12 with evidence of single agent exposure, and 74 with multi-agent exposure. The high rate of exposure is leading to unnecessary death of non-target species and may play a role in disease ecology of wildlife and zoonotic diseases prevalent in the region, such as West Nile Virus. To address the unintended outcomes of ARs, City Wildlife has formed a conservation-focused working group with other local stakeholders to address these impacts, potential public health risks, and minimize use of these toxins and other harmful rat management compounds.. This presentation will outline the findings of the study and the subsequent conservation efforts being taken at this urban wildlife rehabilitation center.

Intercity Collaborations to Survey Brown Rat (*Rattus norvegicus*) Pathology across Canada, United States, and Hong Kong

Monday, 27th July - 11:30: Urban Wildlife (O'Hare 1-2) - Oral

***Lisa Lee*¹, *Theethawat Uea-Anuwong*², *Ioannis Magouras*², *Jonathan Richardson*³, *Jacqueline Buckley*⁴,
*Maureen Murray*⁴, *Sarah J. Robinson*⁵, *Claire M. Jardine*⁶, *Marieke H. Rosenbaum*⁷, *Kim Waggie*⁸,
*Chelsea G. Himsworth*⁹, *Bruce Wobeser*¹**

1. University of Saskatchewan, 2. City University of Hong Kong, 3. University of Richmond, 4. Lincoln Park Zoo, 5. Faculty of Health Sciences, Simon Fraser University, 6. University of Guelph, 7. Tufts University, 8. University of Washington, 9. University of British Columbia

Brown rats (*Rattus norvegicus*) are ubiquitous pests capable of infrastructure damage, economic loss, and zoonotic pathogen carriage. Identifying disease presence/drivers in urban rat populations may contribute to understanding pathogen spread and inform public health measures. However, wild brown rat pathology studies are limited globally. The objective was therefore to survey histopathologic lesions in free-ranging brown rats across multiple geographic regions. Rats were trapped in urban centres in Canada (Vancouver, n=22; Greater Toronto Area, n=138), USA (Seattle, n=35; Richmond, n=123; Chicago, n=101; Boston, n=9), and Hong Kong (urban: n=60; semi-rural: n=84). Lung, liver, heart, kidney, and/or other organs were examined histologically. Lesions causing significant morbidity were uncommon (19/491; 4%), including bronchopneumonia, bacterial granulomas, and chronic progressive nephropathy. Cardiomyopathy was common across cities (60/293; 20%). Mineralized blood vessels were most frequent in Seattle rats (12/35; 34%) compared to 3-7% from other cities. *Capillaria hepatica*, a liver nematode, was widely distributed across cities (9-56%). Liver protozoal cysts (presumed *Toxoplasma gondii*; 27/251, 11%) were observed in rats except for from Vancouver and Seattle. Hong Kong rats had presumed hepatic *Cysticercus fasciolaris* (10/144; 7%) and intramuscular *Sarcocystis* sp. (5/142; 4%). Hong Kong (13/144; 9%) and Richmond rats (8/123; 7%) had rare pulmonary larval nematodes (suspected *Angiostrongylus cantonensis*) associated with granulomatous pneumonia and hemorrhage. Additional work will examine lesion risk factors. Overall, significant disease was infrequent, while degenerative changes like cardiomyopathy were common. Parasite diversity varied geographically. Future work is needed to examine how cumulative disease burden affects social interactions and pathogen spread across rat populations.

Quantifying Ecosystem Resiliency: A Spatial Artificial Intelligence Approach to Managing the Human-Wildlife Interface

Monday, 27th July - 11:45: Urban Wildlife (O'Hare 1-2) - Oral

Jared George¹

1. Masai Mara University

Anthropogenic encroachment into natural habitats is rapidly expanding the human-wildlife interface (HWI), accelerating habitat fragmentation, ecological degradation, and the risk of zoonotic spillover. Traditional spatial planning often relies on static geospatial models that lack the temporal resolution required to address these complex “One Health” challenges in dynamic urbanizing landscapes. This study aims to quantify ecosystem resiliency by developing a Spatial Artificial Intelligence (Spatial AI) framework to dynamically monitor and manage ecological vulnerability at the HWI. Utilizing spatio-temporal modeling, the system ingests high-resolution satellite telemetry specifically Sentinel-1 (SAR) and Sentinel-2 multispectral datasets alongside local Geographic Information Systems (GIS) data. Machine learning algorithms are applied to classify land-use/land-cover (LULC) changes, detect spatial anomalies, and compute ecological stress indices in real time. Spatial simulations indicate that this AI-driven approach quantifies degradation vectors with high precision, demonstrating a 35% improvement in predicting anthropogenic encroachment and spatial stress zones compared to conventional static mapping techniques. By providing a highly predictive, data-driven tool for continuous landscape monitoring, this framework operationalizes Urban One Health principles. It equips physical planners and wildlife ecologists with the empirical metrics necessary to transition from reactive conservation to proactive, resilient human-wildlife coexistence.

Reduced nutritional reserves and antler size associated with SARS-CoV-2 exposure in free-ranging white-tailed deer (*Odocoileus virginianus*) of South Texas

Monday, 27th July - 10:30: Cervid Virology and Prion Disease (O'Hare 4) - Oral

***Joseph Hediger*¹, *Gabriel Hamer*², *Kendall Bancroft*¹, *Tyler Campbell*³, *Walter Cook*⁴, *Randy DeYoung*¹, *David Hewitt*¹, *Miranda Hopper*¹, *Francisco Ferreira*², *Aaron Foley*¹, *Kevin Lovasik*¹, *Alynn Martin*⁵, *J. Alfonso Ortega-Santos*¹, *Landon Schofield*³, *Ashley Tanner*¹, *Logan Thomas*⁴, *Michael Cherry*¹, *Sarah Hamer*⁶**

1. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, **2.** Department of Entomology, Texas A&M University, College Station, TX, **3.** East Foundation, **4.** Department of Veterinary Integrative Biosciences, Texas A&M University, **5.** Department of Biology, Grand Valley State University, **6.** Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX

Wild animals play a key role in the epidemiology of SARS-CoV-2 (SC2). Yet little is known about the host-related factors leading to infection and the consequences on free-ranging wildlife. Our objectives were to identify 1) host-related predictors for previous SC2 exposure in white-tailed deer (*Odocoileus virginianus*); and 2) consequences associated with exposure. We captured 750 white-tailed deer via aerial net-gunning during 2023-2024 across five populations in South Texas, USA to assess serostatus and nutritional condition. We quantified neutralizing antibodies to SC2 using a Plaque Reduction Neutralization Test. The average SC2 seroprevalence across sites was 18.5% (range = 11.5–60.9%). Males were twice as likely to be exposed to SC2 than females in all age classes and mature deer (≥ 2 years-old) were five times more likely to be exposed than fawns. The probability of depleting rump fat reserves was 8.6% more likely in SC2-exposed individuals, regardless of sex. We found exposure may mediate the relationship between body mass on antler size, such that antler size was 11% smaller than expected in SC2-exposed males. However, we did not observe an effect of SC2 exposure on lactation status, which served as an index of recruitment. Given the associations of viral exposure on nutritional reserves and antler size, the latter serving as an important secondary sexual characteristic tied to mate selection, deer viral infections may have important consequences. Our findings suggest SC2 may be an additive stressor that may influence population performance through its effects on nutritional condition.

Ecological Variables Influencing Epizootic Hemorrhagic Disease Outbreaks in Kentucky

Monday, 27th July - 10:45: Cervid Virology and Prion Disease (O'Hare 4) - Oral

***Kristen Hirst*¹, *Mark G. Ruder*², *Joe McDermott*³, *Iga Stasiak*⁴, *Sonja Christensen*¹**

1. Michigan State University, 2. Southeastern Cooperative Wildlife Disease Study, University of Georgia, 3. Kentucky Department of Fish and Wildlife Resources, 4. Saskatchewan Ministry of Environment

Epizootic hemorrhagic disease (EHD) is a vector borne virus transmitted by *Culicoides* midges and primarily infects domestic and wild ruminants. In 2017, a substantial EHD outbreak occurred in the eastern United States, resulting in mortalities of numerous white-tailed deer (WTD). Of the states impacted by this outbreak, Kentucky experienced an exceptional number of EHD cases and caused concern broadly from hunters and non-hunters alike. The Kentucky Department of Fisheries and Wildlife Resources (KDFWR) took advantage of this event and solicited members of the public to report any WTD morbidity and mortality they observed during the duration of the outbreak. In total, 1812 reports were received, comprising 4581 suspected EHD cases. The detailed recordings of the condition of sick and dead deer and spatial resolution of point locations of the reports during the outbreak provide a unique opportunity to evaluate drivers of this epizootic in wildlife. Biotic and abiotic factors have been connected to EHD outbreaks, particularly factors relating to climate and landscape, but these studies typically focus on seroprevalence or domestic animals rather than wildlife outbreaks. In this study, we modeled the distribution of the disease, and identified the predominant variables associated with disease outbreaks at a broad and fine scale. In addition, separate models were applied for morbid deer and mortalities to compare variables associated with disease state. We found wetlands, forest landscapes, and cattle density play an important role at broader scales, and shrub landscapes, distance to water and edge influence EHD prevalence at finer scales.

Exploring how movement patterns and human encounters influence SARS-CoV-2 seropositivity in deer

Monday, 27th July - 11:00: Cervid Virology and Prion Disease (O'Hare 4) - Oral

Tyler Garwood¹, ***Jeremy Alder***², ***Sara Hathaway***², ***George Wittemyer***², ***Guillaume Bastille-Rousseau***³, ***Tadao Kishimoto***³, ***Michael Egan***³, ***Travis Gallo***⁴, ***Jennifer M. Mullinax***⁴, ***Amira Roess***⁵, ***Taylor Anderson***⁵, ***Tiffany Wolf***¹, ***James Forester***¹, ***Jennifer Malmberg***⁶, ***Marnee Roundtree***⁷, ***Georgia Titcomb***², ***Rebecca Windell***², ***Maria Diuk-Wasser***⁸, ***Kim Pepin***⁶, ***Meggan Craft***¹

1. University of Minnesota, 2. Colorado State University, 3. Southern Illinois University, 4. University of Maryland, 5. George Mason University, 6. USDA, 7. Nebraska Game and Parks Commission, 8. Columbia University

Deer can transmit severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to humans and harbor human-extinct variants. Despite this public health threat, ecological mechanisms driving exposure patterns in deer populations remain poorly understood. Our objective was to identify behavioral risk factors by linking serostatus of individual deer to their space use and movement behavior using multilevel logistic regression. We examined serosurveillance data of white-tailed (*Odocoileus virginianus*) and mule deer (*O. hemionus*) equipped with global positioning system devices across an urban-rural gradient in the United States (1305 individuals, 19 sites, eight states). Average human footprint index was positively associated with seropositivity, indicating that human-to-deer transmission is a primary driver of the spatial patterns of deer SARS-CoV-2 exposure. Deer that moved more quickly and spent more time in high-density deer habitat were more likely to be exposed to SARS-CoV-2, suggesting that deer movement behaviors within different habitats influence exposure risk. Integrating human and environmental indices with space use and movement behaviors can thus clarify pathways that maintain zoonotic pathogens in wildlife.

Blink and You'll Detect It: Comparing the Efficacy of Prion Diagnostic Assays for Chronic Wasting Disease Detection in The Nictitating Membrane

Monday, 27th July - 11:15: Cervid Virology and Prion Disease (O'Hare 4) - Oral

***Madison Davis*¹, *Jack C. Davis*¹, *John Armstrong*¹, *Janet E. Yacabucci*¹, *Jennifer Høy-Peterson*¹, *Andrea Korman*², *Roderick B. Gagne*¹, *Michelle Gibison*¹**

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The continued spread of chronic wasting disease (CWD), a fatal neurodegenerative prion disease, has significant implications for free-ranging cervid populations globally. As CWD prevalence increases across North America, the need for sensitive and reliable diagnostic tests is greater than ever. Current USDA-approved assays rely on the use of retropharyngeal lymph nodes (RPLNs) or obex samples to be tested using enzyme-linked immunosorbent assay (ELISA) or immunohistochemistry (IHC). Although these tissues contain high concentrations of prions, their extraction from deceased cervids can be challenging for novice biologists and hunters. The nictitating membrane, better known as third eyelids, may serve as an alternative sample type, as prions can accumulate in the lymphoid follicles while also being a more accessible post-mortem tissue. In this study, we compared the performance of ELISA and the ultra-sensitive prion amplification assay known as real-time quaking induced conversion (RT-QuIC) for CWD detection in third eyelid tissue. Paired RPLNs and third eyelids were collected from CWD-positive (N=30) and negative (N=30) white-tailed deer. Despite intense optimization efforts, including adjusting sample volumes and lymphoid area of third eyelid, and the use of two different CWD-approved ELISA kits (BioRad and IDEXX), CWD detection remained low. ELISA results produced a sensitivity of 23% and a specificity of 100%. In contrast, RT-QuIC drastically outperformed ELISA, achieving 90% sensitivity and 100% specificity in third eyelid samples. Our results demonstrate that RT-QuIC and third eyelid tissues can provide a highly effective alternative to ELISA, offering easier, more reliable diagnostics to support CWD management efforts.

Decay of chronic wasting disease prion detection at infectious deer carcass sites

Monday, 27th July - 11:30: Cervid Virology and Prion Disease (O'Hare 4) - Oral

***Marie Gilbertson*¹, *Heather Inzalaco*², *Hannah Sykes*³, *Aaron Groves*¹, *Daniel Storm*⁴, *Allen Herbst*⁵,
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Chronic wasting disease (CWD) is a fatal prion disease of cervids with significant animal health and economic consequences. CWD is transmitted both directly and through the environment, but prion persistence and transmission risk in soils in the natural environment remains uncertain. We aimed to determine the risk of detecting CWD prion activity in soils at carcass sites of CWD-infected white-tailed deer over space and time in southwest Wisconsin. We identified three fresh CWD mortalities and collected soil samples zero to nine feet from the carcass at death, and then longitudinally for up to two years. We also collected soil at two marked CWD-positive carcass sites from previous research, which were up to four years old. CWD prion seeding activity was detected in soils using real-time quaking-induced conversion (RT-QuIC). Generalized linear mixed effect models showed that detection of CWD prions in soils was uncommon (12% of replicates from positive sites), but higher at CWD-positive sites than at eight control carcass sites (odds ratio = 2.7; $P = 0.001$). Immediately under carcasses, prion detections appeared to begin waning after about two years, but the exact timing remains uncertain due to small sample sizes. Our results indicate that CWD-positive deer carcasses can be a source of prion contamination in soil, so ongoing carcass management is merited. The limited seeding activity detected over space and time, however, suggests individual carcasses may not create large, high-risk sites of contaminated soil, though additional long-term studies and bioassays would clarify the actual magnitude and duration of risk.

Indiana's First Case of Chronic Wasting Disease: A Partner Incentive Program success story

Monday, 27th July - 11:45: Cervid Virology and Prion Disease (O'Hare 4) - Oral

Janetta Kelly¹

1. Indiana Department of Natural Resources

Routine surveillance for chronic wasting disease (CWD), a fatal prion disease in white-tailed deer, has been conducted in Indiana since 2002 following detections in nearby states. Historically, Indiana Department of Natural Resources (IDNR) operated state agency staffed check stations in a single area of the state each year to collect the samples. This type of surveillance is costly in staff time, materials, and travel. In addition to cost, this method is not efficient for covering statewide sampling and areas of the state often go un-sampled for many years.

IDNR piloted a taxidermist sampling program in 2020 of less than 20 taxidermists across the state that yielded around 200 samples a year. In 2023, IN DNR expanded that program to cover CWD testing across the state and moved away from multiple DNR staffed check stations. This expansion included adding approximately 40 taxidermists to the program from multiple areas across the state. That same year, 1,500 CWD samples were collected from taxidermists, CWD was detected for the first time in Indiana from a taxidermist sample, samples were collected from 91 of the 92 counties, and an estimated \$206,000 were saved in costs during a single season. In 2024, we renamed the program to the "Partner Incentive Program" with the intent of making it more inclusive and beginning to explore partnerships with multiple deer stakeholders, such as meat processors. States without incentive programs should explore the feasibility, especially in areas that are commonly missed by routine sampling.

Conservation Medicine Meets Invasion Science: A Veterinary Approach to Wildlife Health

Monday, 27th July - 13:10: Global Voice Short Presentations (Virtual/Online) - Oral

***João Rato**¹, **Rita Rocha**², **Pedro Anastácio**¹*

1. MARE - Marine and environmental science centre, 2. Hospital Veterinário da Universidade de Évora

Biological invasions are not only ecological disturbances, they are also epidemiological events. By transporting pathogens, reshaping host communities, and altering transmission networks, invasive species can influence disease risk across wildlife, domestic animals, and humans. While invasions are widely recognized as drivers of biodiversity loss, their health-related consequences often remain overlooked. Non-native species may modify pathogen dynamics through co-introduction, spillover to native hosts, or changes in host density and diversity. These processes frequently go unnoticed when invaders act as asymptomatic reservoirs or when disease impacts are sublethal and do not immediately translate into population declines.

Understanding these hidden effects requires integration between ecology and veterinary science. Ecological approaches help identify invasion pathways, establishment mechanisms, and ecosystem-level consequences, but interpreting health outcomes demands complementary expertise. Veterinary science provides essential tools for pathogen detection, clinical and pathological assessment, and evaluation of host responses. Such contributions strengthen surveillance programs, inform biosecurity strategies, and support risk assessments that consider consequences for wildlife, domestic animals, and human health.

Veterinary involvement is also critical during management interventions. Control or eradication programs often require animal handling, sedation, euthanasia, and post-mortem examination, all of which benefit from clinical oversight to ensure scientific rigor and ethical standards.

Single-discipline approaches are no longer sufficient to address invasion-related disease risks. Integrating ecological and veterinary perspectives enhances early detection, clarifies transmission pathways, and supports more effective conservation decisions. As biological invasions accelerate globally, interdisciplinary collaboration is essential for safeguarding biodiversity and understanding the health consequences of environmental change.

Biodiversity as a natural health shield: invasive mammals, ecosystem degradation and pathogen dynamics in Uruguay

Monday, 27th July - 13:25: Global Voice Short Presentations (Virtual/Online) - Oral

*Alexandra Cravino*¹, *Belén Crampet*², *Romina Icasuriaga*², *Andrés Cabrera*³, *Florencia Cancela*²,
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Biodiversity is essential for regulating pathogen transmission among wildlife, livestock, and humans. However, changes in land use and the introduction of invasive species are increasingly affecting mammal communities and changing disease dynamics. In South America, particularly in Uruguay, expanding populations of invasive meso-mammals are altering ecological networks and providing new pathways for pathogen spread.

This study combines methods from community ecology, disease ecology, and the One Health approach to assess how the structure of mammal assemblages affects pathogen prevalence.

Field surveys were conducted at four locations with varying levels of human impact, including forest plantations, livestock systems, and less disturbed habitats. Over 11,000 camera-trap nights, along with fecal and blood sampling, were used to characterize mammal communities and test for significant pathogens such as Hepatitis E virus (HEV), *Neospora caninum*, and *Toxoplasma gondii*. Community diversity was measured using Hill numbers, and species co-occurrence networks were constructed to analyze species interactions.

Mammal assemblages ranged from 9 to 15 species, with invasive species such as axis deer and wild boar often found in central positions within interaction networks. Sites dominated by invasive species and characterized by degraded habitats exhibited lower effective diversity, as well as higher pathogen prevalence (up to 60%). Conversely, more diverse communities exhibited patterns similar to the dilution effect, indicating reduced simultaneous exposure to multiple pathogens.

These findings underscore the protective role of biodiversity as a natural barrier against disease. Incorporating wildlife ecology into One Health frameworks is crucial for predicting disease emergence and informing conservation and management practices.

Infectious and Zoonotic Agents in Stranded South American Sea Lions at the Human-Wildlife Interface in Central Patagonia

Monday, 27th July - 13:40: Global Voice Short Presentations (Virtual/Online) - Oral

***Carla Daniela Fiorito*¹, *Lucas Arce*¹, *Marcelo Bertellotti*¹, *Daniel Lombardo*²**

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Marine mammal strandings provide an opportunity to investigate pathogen circulation at the human-wildlife interface, serving as indicators of ecosystem and public health risks. In Chubut, Argentina, the South American sea lion (*Otaria flavescens*; SASL) is a key sentinel species whose coastal habitat increasingly overlaps with human recreational and occupational activities.

This study summarizes findings on infectious and zoonotic agents in stranded SASLs along the Chubut coast as part of a long-term research effort on marine mammal health.

Between 2013 and 2026, necropsies were performed on 31 stranded SASLs. A multidisciplinary approach integrated gross pathology, histopathology, microbiological cultures, and PCR-based screening to identify primary and contributing causes of disease and mortality.

Twenty-one animals met preservation and sampling criteria for comprehensive diagnostic analyses. Lesions compatible with infectious disease were identified in 12 animals (57%) and in eight individuals, infectious agents were directly associated with the cause of death. Detected agents include *Klebsiella* spp., beta-hemolytic *Streptococcus*, *Staphylococcus aureus*, *Edwardsiella tarda*, *Pseudomonas* spp., and *Mycoplasma* sp. Notably, some bacterial isolates demonstrated antimicrobial resistance. Among pathogens with high zoonotic potential, we detected *Mycobacterium tuberculosis* complex members and HPAI H5N1 virus, which was the driver of a massive mortality event in the region.

These results demonstrate that infectious diseases are significant drivers of morbidity and mortality in SASLs in Central Patagonia. The detection of zoonotic agents and antimicrobial-resistant bacteria underscores the importance of marine mammal health surveillance as a One Health tool for understanding pathogen circulation at human-wildlife interfaces.

Optimizing chronic wasting disease surveillance and management on Tribal lands for the preservation of culture and food sovereignty

Monday, 27th July - 13:30: Human-Wildlife Interface (O'Hare 1-2) - Oral

***Tiffany Wolf*¹, *Anirrhuda Belsare*², *Kristin Bondo*¹, *Lauren Wakefield*², *Tanya Roerick*³, *Dustin Roy*⁴,
*Jason Clark*⁴**

1. University of Minnesota, 2. Auburn University, 3. Leech Lake Division of Resource Management, 4. White Earth Department of Natural Resources

CWD threatens the food sovereignty and cultural heritage of Tribal nations. Yet, Tribal nations are often left out of decisions related to CWD management and control. In recognizing the need for community-informed and science-based CWD response plans, the management agencies of White Earth Nation and Leech Lake Band of Ojibwe, located within 15 mi of recent CWD detections in white-tailed deer (*Odocoileus virginianus*), embarked on an effort to evaluate specific actions for their effectiveness in CWD detection and control. This university-Tribal partnership adapted and calibrated an agent-based, OvCWD, to simulate CWD introductions on reservation lands and determine 1) the probability of early CWD detection using different surveillance schemes and 2) the effectiveness of control under different management scenarios. Early findings indicate that landscape and population dynamics on these two reservations may contribute to different probabilities of outbreak development. However, because adult male deer tend to have higher prevalence levels, surveillance efforts that target adult males resulted in higher detection probabilities. Management scenarios under exploration include management zone size and harvest strategies within those zones to effectively reduce CWD transmission. Results of the scenarios will be introduced to Tribal members through community events where additional questions and scenarios might be explored directly with the community. Model outcomes and community responses will be used to finalize CWD response plans that will guide the management of CWD on Tribal lands.

Potentially fatal human interactions in stranded southern right whales (*Eubalaena australis*) at Península Valdés, Argentina, 2003–2024

Monday, 27th July - 13:45: Human-Wildlife Interface (O'Hare 1-2) - Oral

Marcela Uhart¹, Adrianna Rotondi¹, Ralph E. T. Vanstreels¹, Matias Di Martino², Agustina Donini², Andrea Chirife², Santiago Fernandez², Marcos Ricciardi², Lucas Beltramino², Virginia Rago², nadia mohamed², Luciana Pozzi², Luciana Musmeci², Luciano La Sala², Victoria Rowntree³, Denise McAloose⁴, Carina Maron⁵, Mariano Sironi⁵

1. University of California, Davis, 2. Southern Right Whale Health Monitoring Program, 3. University of Utah, 4. Wildlife Conservation Society, 5. Instituto de Conservacion de Ballenas

Southern right whales (*Eubalaena australis*, SRW) are recovering from commercial whaling, yet ongoing threats affect their conservation and welfare. At the Península Valdés (PV), Argentina, breeding ground, SRW overlap with whale watching and commercial vessel traffic during the calving and nursing season, raising concerns about potentially fatal human interactions (PFHI).

We reviewed SRW stranding records from PV between 2003 and 2024 (excluding 2020), assessing 873 carcasses, an average of 41.6 ± 28.4 per year (range 5–105). Most were calves (n = 763; 311 males, 341 females, 111 unknown), followed by 84 adults (7, 73, 4) and 26 juveniles (3, 16, 7). Evidence of PFHI was identified in 22 carcasses (2.5%), representing an annual mean of $3.3\% \pm 3.2\%$ of strandings (range 0–10%). PFHI evidence (not mutually exclusive) included ship-strike trauma (55%), internal bruising (55%), internal hemorrhage (36%), penetrating wounds (23%), mutilation (9%), bone fractures (5%), and other lesions (9%). PFHI prevalence differed significantly among age classes ($P < 0.001$), being higher in juveniles (26.9%) compared to adults (4.8%) and calves (1.4%). Fresh carcasses (decomposition code 2) showed marginally higher PFHI prevalence than more decomposed carcasses (6.1% vs. 2.2%; $P = 0.056$). No significant sex differences were detected ($P = 0.142$). Although PFHI occur at PV, they do not appear to be a primary driver of mortality in newborn calves, a sensitive age category representing over 87% of SRW deaths at this site. Strengthening and enforcing vessel-related regulations remains important to maintain PV as a safe breeding habitat for this population.

Texas ranches: a nidus for *Trypanosoma cruzi* transmission among wildlife, dogs, and triatomines

Monday, 27th July - 14:00: Human-Wildlife Interface (O'Hare 1-2) - Oral

***Rachel Busselman*¹, *Juan Pablo Fimbres Macias*², *Jordan Salomon*³, *Italo Zecca*¹, *Edward Davila*¹,
*Carolyn Hodo*⁴, *Ashley Saunders*⁵, *Gabriel Hamer*³, *Sarah Hamer*¹**

1. Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, 2. Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Nuevo León, General Escobedo, 3. Department of Entomology, Texas A&M University, College Station, TX, 4. The University of Texas MD Anderson Cancer Center, Michale E. Keeling Center for Comparative Medicine and Research, Bastrop, Texas, 5. Department of Small Animal Clinical Sciences, Texas A&M University, College Station, TX

Chagas disease is a zoonotic neglected tropical disease caused by the protozoan parasite *Trypanosoma cruzi* and transmitted by triatomine insects ('kissing bugs'). Our prior work identified hunting dogs in group kennel environments across Texas ranches as a high-risk group for *T. cruzi* infections and associated Chagas disease. We initiated an epidemiological investigation to compare *T. cruzi* infections in wildlife to those in resident hunting dogs and triatomines to improve our understanding of *T. cruzi* transmission in this ecological context. Working with a ranch in south Texas, we collected blood, cardiac tissue, and esophageal tissue samples from wild mammals- including raccoon (*Procyon lotor*), coyote (*Canis latrans*), javelina (*Pecari tajacu*), wild hog (*Sus scrofa*), and bobcat (*Lynx rufus*)- during nuisance predator control efforts. Using PCR methods, one bobcat (50%), one hog (17%), 7 coyotes (35%), and 15 raccoons (83%) were positive for *T. cruzi*. While samples from most infected animals showed either the TcI or TcIV *T. cruzi* discrete typing unit (DTU) in blood or tissue, four raccoons showed evidence of mixed-DTU infections with TcI versus TcIV found in different tissue types. Additionally, histopathological analysis of wildlife tissues will be interpreted in relation to the genetic variant and anatomic location of the parasite. Among the resident hunting dogs, 23% were PCR-positive (n=54), and 53% of local triatomines (n=19) were PCR-positive. Considering the high infection prevalence among raccoons in the southern US, we suggest this species be prioritized in the development of future host-targeted vector control interventions.

A qualitative study of human-deer interactions with implications for pathogen spillover

Monday, 27th July - 14:15: Human-Wildlife Interface (O'Hare 1-2) - Oral

***Kyle Smith*¹, *Meggan Craft*¹, *Maria Diuk-Wasser*², *Pilar Fernandez*³, *David Fulton*¹, *Heather Kopsco*², *Celine Miller*⁴, *Brody Mynatt*⁵, *Logan Park*⁵, *Kim Pepin*⁶, *Neelam Poudyal*⁷, *Amira Roess*⁸, *Arun Regmi*⁹, *Carrera Romanini*⁷, *Elias Rosenblatt*¹, *Keith Carlisle*⁶**

1. University of Minnesota, 2. Columbia University, 3. Washington State University, 4. George Mason University, 5. Southern Illinois University, 6. USDA, 7. University of Tennessee Knoxville, 8. George Mason University, 9. The Pennsylvania State University

SARS-CoV-2 infection in white-tailed deer across much of the U.S. suggests repeated spillover from humans, though the activities driving transmission remain unclear. Understanding human-deer interactions and the behavioral drivers behind them is a key step toward mitigating both spillover and spillback of pathogens. To explore this, we conducted community workshops and interviews at six sites (Minnesota, Tennessee, New York, Illinois, Pennsylvania, and Washington, D.C.). Using qualitative methods, we examined participants' perceptions of deer interactions, including frequency, type, and location. Analysis revealed three central themes: (1) behaviors potentially relevant to pathogen transmission, (2) variability of transmission risks among participant groups, and (3) perceived knowledge and awareness of risks. These insights highlight how community perspectives shape exposure dynamics and can guide future research and surveillance. Ultimately, the findings emphasize the importance of addressing human behavior at the wildlife interface to reduce the emergence and spread of zoonotic pathogens.

A transdisciplinary One Health approach to human-wildlife coexistence

Monday, 27th July - 14:30: Human-Wildlife Interface (O'Hare 1-2) - Oral

A A Aguirre¹, Jon Salerno², Ray Gonzalez³, Kevin Crooks¹

1. Colorado State University, Department of Fish, Wildlife and Co, 2. Colorado State University Department of Human Dimensions of Natural Resources, 3. Colorado State University Center for Human Carnivore Coexistence

Coexistence between people and wildlife is a defining challenge of the Anthropocene, spanning terrestrial, freshwater, and marine systems. As human populations expand and land-use change accelerates, interactions between people and wildlife intensify, affecting livelihoods, public health, biodiversity, and ecosystem stability. Human-wildlife conflict includes crop and property damage, disease transmission, safety risks, and broader social conflict among stakeholders with differing values about wildlife. Successful coexistence requires the sustained co-occurrence of thriving wildlife populations and secure human communities, with minimized ecological and social conflict. We integrate coexistence science with a One Health framework to better understand the interconnected relationships among human, domestic animal, wildlife, and ecosystem health. We conceptualize coexistence at the convergence of these domains, recognizing ecosystem health as the foundation for shared resilience and well-being. One Health extends beyond infectious disease to include conflict reduction, cross-sectoral collaboration, and integrated surveillance at human-animal interfaces. Because coexistence outcomes are shaped by both ecological dynamics and human behavior, we incorporate a social-ecological systems perspective to examine drivers and solutions across scales, land-use gradients, and governance contexts. We propose transdisciplinary research priorities including disease transmission; impacts of wildlife on livelihoods and food systems; benefits of biodiversity for human and animal health; climate-driven changes in human-wildlife interactions; coexistence in urbanizing landscapes; and strategies to reduce social conflict, strengthen trust, and inform evidence-based policy. Together, these themes advance a comprehensive One Health approach to wildlife coexistence that links science, policy, and community engagement to support resilient human and ecological systems.

Toad Health is One Health: Detection of a novel *Salmonella enterica* subspecies from a localized mortality event involving wild gulf coast toads (*Incilius nebulifer*) within a residential neighborhood

Monday, 27th July - 14:45: Human-Wildlife Interface (O'Hare 1-2) - Oral

***Sara Wyckoff*¹, *Marcos Isidoro Ayza*², *Jeffrey M. Lorch*², *Samantha Spencer*³, *Kenneth Davis*³, *Brent Jenkins*⁴, *Blake Dinsmore*⁴, *Charlotte Lane*⁴, *Paul Crump*¹, *Benjamin Olsen*¹**

1. Texas Parks and Wildlife Department, 2. U.S. Geological Survey, National Wildlife Health Center, 3. Texas Department of State Health Services, 4. US Centers for Disease Control and Prevention

In June 2025, Texas Parks and Wildlife Department (TPWD) investigated a morbidity and mortality event in gulf coast toads (*Incilius nebulifer*) within a neighborhood located in the Dallas-Fort Worth metroplex area. Over a period of two to three weeks, five gulf coast toads were found dead in a privately owned backyard, and four additional toads were noted to be lethargic, emaciated and discolored. Three carcasses were sent to the National Wildlife Health Center (NWHC) where necropsy findings included bacterial splenitis, pleuroperitonitis and myositis with isolation of *Salmonella enterica*. Additional analysis from the Texas Department of State Health Services (DSHS) and the Center of Disease Control (CDC) determined this isolated strain as a novel *Salmonella enterica* subsp. with the closest relative being *Salmonella enterica* subspecies *diarizonae* (IIIb).

This discovery of a novel subspecies strain of *Salmonella enterica*, a known zoonosis, within a residential neighborhood emphasizes the ongoing issues of wildlife and human encroachment in expanding suburban areas. In addition, this outbreak represents the first reported mortality event due to salmonellosis in a wild amphibian population in the United States. This discovery brings additional questions of the role this novel subspecies has within wild amphibian population health, including risk to threatened and endangered species.

Molecular detection of *Plasmodium floridense* in a rescued *Iguana iguana* (Squamata: Iguanidae) from Northeastern Brazil

Monday, 27th July - 13:30: Parasitology (O'Hare 4) - Oral

***Lilian Catenacci*¹, *Clara Vanessa Azevedo Oliveira*², *Gabriela Ferreira de Oliveira*¹, *Amanda Maria Barbosa de Sousa*¹, *Osmakon Lobato*¹, *Vinicius Soares Esteves*³, *Kathleen Apakupakul*², *Fabiano Barbosa Pessoa*⁴, *Sharon Deem*², *Lucilene dos Santos Silva*³, *Ana Carolina Ewbank*⁵, *Carlos Sacristán*⁶**
 1. Universidade Federal do Piauí, Programa de Pós-Graduação em Tecnologias Aplicadas a Animais de Interesse Regional, 2. Saint Louis Zoo Institute for Conservation Medicine, 3. Hospital Veterinário Universitário, Universidade Federal do Piauí, 4. Instituto Brasileiro do Meio Ambiente dos Recursos Naturais e dos Recursos Naturais e, 5. Animal Health Research Center, INIA-CSIC,, 6. Animal Health Research Center, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA-CSIC),

The genus *Plasmodium* comprises one of the major arthropod-borne hemoparasites, and previous studies have demonstrated the negative consequences of parasitic infection in lizard malaria parasite-host associations. In Brazil, however, reports of *Plasmodium* infection in reptiles remain scarce. This study investigated the occurrence of *Plasmodium* spp. by PCR in a green iguana (*Iguana iguana*). The specimen was rescued from an urban area and admitted to the Veterinary Hospital of the Federal University of Piauí, Brazil. The animal was in critical condition, and a WBC differential indicated marked leukocytosis and macrocytic anemia. After clinical exam, we extracted DNA from blood samples, and a nested PCR protocol targeting the *Plasmodium* genus was performed. Amplicons were visualized by agarose gel electrophoresis, and Sanger sequencing of positive bands identified *Plasmodium floridense*, showing 100% query coverage and 95.82% sequence identity. To our knowledge, this is the first report of *P. floridense* infecting *I. iguana* in Brazil. Previous studies involving iguanids of the genera *Sceloporus*, *Anolis*, and *Crotaphytus* have associated malarial infections with anemia, immature erythrocytes, and reduced hemoglobin concentrations, findings consistent with the hematological alterations observed in the present case. Urban environments have also been identified as predictors of hemoparasite occurrence in reptile hosts, suggesting ecological influences on transmission dynamics. These findings emphasize the relevance of molecular pathogen screening in rescued wildlife, given the potential impact of infectious agents on species conservation, while also supporting clinical management, epidemiological surveillance, and conservation strategies prior to repatriation.

Spatiotemporal hotspots of invasive Longhorned tick (*Haemaphysalis longicornis*) infestations in the eastern United States

Monday, 27th July - 13:45: Parasitology (O'Hare 4) - Oral

***Zulma Rojas-Sereno*¹, *Denise Bonilla*², *Matthew Bickerton*³, *Gillian Eastwood*⁴, *Goudarz Molaei*⁵, *Ashley C. Kennedy*⁶, *Christian Boyer*⁷, *Michael J. Yabsley*⁸, *Danielle M. Tufts*⁹, *Erika T. Machtinger*¹⁰, *Jennifer M. Mullinax*¹¹, *Andreas Eleftheriou*¹**

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The Longhorned tick (LHT, *Haemaphysalis longicornis*) has recently invaded and expanded mostly in the eastern United States. Because it can lead to severe infestations and is known to transmit numerous important veterinary and medical pathogens in its native and invasive ranges, it is of veterinary and public health concern. To characterize how LHTs expanded across space and time, we collected county-level data on LHT abundances between 2017 and 2024 from 10 states and Washington, D.C. The northernmost states were New York and Connecticut, and the southernmost, Virginia and North Carolina. We conducted two cluster analyses (host-seeking versus host-derived LHTs) using Getis-Ord (Gi*) statistics to identify statistically significant hotspots of infestation per year. Using aggregated host-seeking tick data, which indicate environmental detections, we identified two significant infestation hotspots in New Jersey and New York. We also identified one New Jersey hotspot using aggregated data of host-derived ticks, indicative of host burdens. Although there was an annual shift in significant hotspots from northern to southern states, suggesting active regional spread, northern hotspots persisted, suggesting active local spread. Additionally, a preliminary analysis suggests that major interstate highways pass through or near significant hotspots, which may indicate human-mediated transport as a mechanism of regional spread. While we acknowledge inherent limitations of detection and reporting biases, our descriptive analysis may be useful for risk factor assessments and highlights the importance of surveillance conducted collaboratively by academic, state, and federal partners, particularly at human–livestock–wildlife interfaces.

Multi-organ transcriptomic signatures reveal systemic inflammatory and metabolic disruption in wombats with severe sarcoptic mange

Monday, 27th July - 14:00: Parasitology (O'Hare 4) - Oral

***Christina Naesborg-Nielsen*¹, *Tamieka Fraser*², *Kate Mounsey*³, *Scott Carver*⁴**

1. University of Georgia, 2. University of Tasmania, 3. University of the Sunshine Coast, 4. Odum School of Ecology, University of Georgia, Athens

Sarcoptic mange is a globally disease affecting wildlife, domestic animals, and humans, and is recognized as a neglected tropical disease in humans ("scabies"). Although mange is typically considered a skin-limited disease, advanced crusted mange in many species is associated with severe debilitation and high mortality, suggesting broader systemic involvement. However, the extent to which mange reshapes host immunity and physiology across multiple organs remains poorly understood.

We used multi-tissue RNA sequencing to test whether severe sarcoptic mange induces coordinated systemic transcriptional changes in a free-living wildlife host. Six tissues (skin, liver, lung, lymph node, skeletal muscle, and thyroid) were collected from 10 adult bare-nosed wombats (*Vombatus ursinus*), including five clinically healthy individuals and five with advanced crusted mange. Diseased animals exhibited widespread transcriptional remodeling with 5667-6178 DEGs per tissue and clear separation of healthy and diseased individuals.

Severe mange was associated with consistent activation of Th17/IL-23-related immune pathways and chemokine signaling across tissues, indicating coordinated inflammatory responses beyond the skin. The myeloid alarmin S100A8 was upregulated across all tissues (log2FC ~5.5), alongside enrichment of neutrophil- and macrophage-associated pathways. Diseased animals also exhibited activation of innate pattern-recognition modules, including LPS/TLR signaling, complement activation, and platelet-associated pathways, forming a transcriptional profile reminiscent of sepsis-like inflammatory states. Concurrently, we detected metabolic and neuroendocrine alterations consistent with systemic catabolism, oxidative stress, and physiological exhaustion.

Together, these findings demonstrate that severe sarcoptic mange represents a multi-organ inflammatory and metabolic syndrome rather than a skin-restricted disease, underscoring the importance of early intervention in wildlife management.

Spotted, Infested, and Studied: A Survey of Ectoparasites on Ocelots (*Leopardus pardalis*) and Bobcats (*Lynx rufus*) of the Southern United States

Monday, 27th July - 14:15: Parasitology (O'Hare 4) - Oral

Tiffany Pope¹, **Alynn Martin**², **Michael Tewes**³, **Richard Gerhold**⁴, **Ashley Reeves**⁵

1. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, 2. Department of Biology, Grand Valley State University, Allendale, MI, 49401, USA; Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, 78363, USA, 3. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, 78363, USA, 4. Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, 2407 River Drive, University of Tennessee, Knoxville, TN, 37996, USA, 5. East Foundation, San Antonio, TX, 78216, USA

The risk of vector-borne diseases in wildlife depends on several factors, including the presence and abundance of hosts, the susceptibility and immunity of hosts, the distribution and diversity of pathogens, and the environmental and climatic conditions that influence the interactions among these variables. With climate change, landscape changes and other biotic and abiotic factors, vector species are both expanding in geographic range and experiencing less seasonality, which increases the risk of vector-host encounters. In the United States, the last remaining populations of the nationally endangered ocelot (*Leopardus pardalis*) persist in southern Texas. These populations exhibit low genetic diversity and are susceptible to stochastic events (e.g., drought), but no baseline understanding of health risks from disease and parasitism exists. Other sympatric species exist in this landscape, including bobcats (*Lynx rufus*), which may harbor and share parasites with ocelots. Our objectives for this ongoing study are to determine ectoparasite prevalence and host preference for these two wild felid species which will then be used to inform vector-borne disease surveillance. Specimen review was conducted for 38 ectoparasite collections (ocelots, n=14; bobcats, n=24) spanning four years (2019-2022) with additional collections through 2026 under review. The most common species observed belong to the genus *Dermacentor* (tick) and *Pulex* (flea). In this preliminary assessment, there were three unique tick species observed on bobcats compared to ocelots, indicating some host specificity, although, these observations are not yet statistically assessed and may change as more specimens are reviewed.

Tick-borne pathogen surveillance: a collaborative, multiagency approach

Monday, 27th July - 14:30: Parasitology (O'Hare 4) - Oral

***Marnee Roundtree*¹, *Jeff Hamik*², *Halie Smith*², *Alexandrea Welch*³, *Shaun Cross*³**

1. Nebraska Game and Parks Commission, 2. Nebraska Department of Health and Human Services, 3. University of Nebraska Medical Center

Background: Tick-borne pathogens (TBPs) represent a growing global health concern for human and animal populations. Increased urbanization and subsequent human and wildlife overlap provide ideal environments for vector-facilitated transmission to occur. In recent years, Nebraska has documented increased TBP infections in humans, and in 2025, confirmed *Francisella tularensis* infections in a cluster of human cases. Every individual reported favorable tick habitat exposure. In response, Nebraska Department of Health and Human Services (DHHS), Nebraska Game and Parks Commission (NGPC), and the University of Nebraska Medical Center (UNMC) developed a multiagency rapid response plan for tick surveillance and pathogen testing.

Methods/Results: During July 2025, NGPC field biologists surveilled three recreational sites spanning three counties; DHHS provided training, tick collection materials, and entomological expertise; UNMC Nebraska Tick Testing Laboratory provided all qPCR pathogen testing. A minimum of 750 m² was surveyed by tick flagging and collected ticks were stored in 95% ethanol prior to morphological identification and pathogen testing.

Efforts yielded 323 *Dermacentor variabilis* ticks. qPCR testing detected *F. tularensis* in 5.6% (n = 18), *Rickettsia* spp. in 13.0% (n = 42), and *Rickettsia rickettsii* in 0.6% (n = 2) of ticks. Coinfection of *F. tularensis* and *Rickettsia* spp. was found in 1.8% (n = 6).

Conclusions & Wildlife Health Impact: Through multiagency collaboration, environmental investigations confirmed increased TBPs – *F. tularensis* prevalence increasing approximately ten-fold comparative to historic levels. These findings highlight the value of collaborative response efforts to gather essential health data using ticks as environmental sentinels for emerging infectious diseases.

Characterization of larval Taeniid cestode infections in muskrat (*Ondatra zibethicus*) populations of the eastern United States.

Monday, 27th July - 14:45: Parasitology (O'Hare 4) - Oral

Nicholas Friedeman¹, Mary Lacey², Christine Casey³, Ellen Haynes⁴, Mark G. Ruder², Michael J. Yabsley⁴, Chris Cleveland⁴

1. University of Georgia, 2. Southeastern Cooperative Wildlife Disease Study, University of Georgia, 3. Kentucky Department of Fish and Wildlife Resources, 4. Southeastern Cooperative Wildlife Disease Study

Cestodes of the family Taeniidae have been documented in muskrats (*Ondatra zibethicus*) with species like *Hydatigera* spp., *Echinococcus multilocularis*, and *Versteria* spp. reported as common or able to cause disease. However, there has been limited contemporary studies of larval cestode infections in muskrat populations across the eastern United States, despite muskrat population declines. The objective of this study was to identify and quantify cestodes from trapper harvested muskrats across 13 eastern US states. Observable hepatic cysts were excised, and parasites were identified via morphological and molecular analyses. Of the 483 muskrats collected, 58 (12%) had at least one liver cyst. A total of 96 cyst structures were removed from these muskrats. To date, 64 (66.7%) are members of the *Hydatigera taeniaeformis* s.l. species complex. Of these, 34 metacestodes belonged to *H. kamiyai* (clade B) and 30 belonged to the currently unresolved clade referred to as *Hydatigera* sp. (clade C). Morphological comparisons between 21 metacestodes were completed by measuring and counting large and small hooks located on scolices. There were no significant morphological differences between the two clades except in the guard length of small hooks and total length for large hooks, suggesting that hook morphology alone is not enough to distinguish metacestodes of the two clades. Two muskrats (2%) from Missouri and Kansas displayed hepatic multilocular cysts molecularly confirmed as *E. multilocularis* (European lineage). Our findings contribute to understanding the ecology and distribution of the *Hydatigera taeniaeformis* s.l. species complex and *E. multilocularis* among muskrats in the eastern United States.

Impacts of an HPAI H5N1 outbreak in a seabird community in northern Patagonia, Argentina

Monday, 27th July - 14:15: Global Voice (Virtual/Online) - Oral

***Ralph Vanstreels*¹, *Flavio R. Quintana*², *Martin I. Brogger*², *Luciana Gallo*³, *Valeria S. Oliveira*⁴,
*Agustina Rimondi*⁴, *Marcela Uhart*¹**

1. University of California, Davis, 2. Instituto de Biología de Organismos Marinos, 3. Servicio Nacional de Sanidad y Calidad Agroalimentaria, 4. Instituto Nacional de Tecnología Agropecuaria

Since 2020 the world has experienced an unprecedented panzootic of high pathogenicity avian influenza (HPAI) viruses. From August 2023 to February 2024, the marine wildlife community of northern Patagonia, Argentina, experienced widespread HPAI outbreaks in pinnipeds and seabirds. We investigated the manifestations, spatiotemporal dynamics, and population-level impacts of HPAI at Punta León, a mixed-species seabird colony. Over 50 days, an estimated 2,125 birds died at Punta León (1,500 cayenne terns, 486 royal terns, 126 South American terns, 86 kelp gulls, and 17 imperial cormorants). The impact was far greater for cayenne/royal terns (919.8 carcasses per 1,000 nests) than for kelp gulls (14.8) or imperial cormorants (2.9). Long-term monitoring reveals that between 2022 and 2024 cayenne/royal tern and imperial cormorant nests at Punta León decreased by 72.1% and 14.5%, respectively, possibly attributed to HPAI, although other ecological factors may have contributed this decline. While terns exhibited severe neurological signs, kelp gulls generally showed milder neurological signs accompanied by ocular discharge and diarrhea. Viral genomic and epidemiological data suggest HPAI dissemination was initially driven by pinniped-pinniped transmission, followed by pinniped-bird spillback and subsequent bird-bird transmission, with kelp gulls potentially acting as “bridge” hosts from pinnipeds to terns. Spatial analysis reveals most unmonitored tern colonies in northern Patagonia were near suspected/confirmed HPAI cases and may have been likewise affected. Understanding how HPAI outbreaks manifest in different wildlife communities is critical to inform surveillance, risk mitigation, and conservation strategies as the virus continues to expand into new regions and ecosystems.

Gastrointestinal Community Dynamics of Mountain Gorillas (*Gorilla beringei beringei*) Across a Shared Landscape

Monday, 27th July - 15:45: One Health (O'Hare 1-2) - Oral

Kathryn Harper*¹, *Natalie Payne*¹, *Karla Vargas*¹, *Melanie Culver*¹, *Jennifer L. Verdolin*², *Leigh Combrink

¹

1. University of Arizona, 2. Empire State University

The mountain gorillas (*Gorilla beringei beringei*) of Bwindi Impenetrable National Park exist in a dynamic ecosystem where forest boundaries meet community lands. Because gastrointestinal health is a critical bioindicator of overall physiological status, understanding how this shared landscape influences gorilla physiology is key to integrated conservation management. To support evolving management strategies, this study evaluated fecal microbiome and parasite genetic sequencing as a non-invasive health monitoring tool. We analyzed fecal samples ($n = 29$) across four gorilla groups to identify how varying levels of human proximity influence gastrointestinal community signatures. We found that groups with higher overlap in community areas exhibited significantly reduced bacterial richness, but increased parasitic richness compared to groups ranging exclusively within the park. These findings add significant value to existing research regarding gorilla health concerns, deepening our understanding of gastrointestinal disease and the dynamics of co-infections. These distinctive signatures, along with positive correlations observed between specific bacterial and parasitic taxa, can serve as sensitive, non-invasive biomarkers for early detection of physiological changes. By understanding these complex ecological interactions, managers can better monitor gorilla groups to provide proactive veterinary care and implement integrated strategies, such as improved community sanitation, to ensure the mutual well-being of local communities and wildlife.

Protecting Wildlife Protects Children: A One Health Case Against Lead Ammunition

Monday, 27th July - 16:00: One Health (O'Hare 1-2) - Oral

***Marcela Uhart*¹, *Andrea Caselli*², *Valentina Fernández*³, *Ayelen Andrea Muchiutti*², *Ralph E. T. Vanstreels*¹, *Martin Santiago*²**

1. University of California, Davis, 2. Universidad Nacional del Centro de la Provincia de Buenos Aires, 3. Universidad Nacional de San Martín

Lead (Pb) from hunting ammunition is a pervasive but preventable pollutant affecting both wildlife and human health. Bird scavengers and predators frequently suffer Pb poisoning from ingesting ammunition fragments in carcasses. Waterfowl ingest spent Pb pellets in wetlands, leading to Pb accumulation in their tissues. These same exposure pathways can affect people who rely on wild meat for subsistence. We investigated the interface between wildlife exposure and human health by examining blood lead levels (BLL) in children from rural northern Argentina, where hunting is common, and game meat is a major protein source for impoverished families. Blood samples were collected from 101 children (1–12 years old) and tested for Pb, and caregivers of 276 children completed dietary surveys. Over half (51.5%) of tested children had BLL above the current reference level (≥ 3.5 $\mu\text{g/dL}$). Elevated BLL were strongly associated with game meat consumption, particularly whole-carcass use, stewing, and consumption of ducks and capybaras. Removing visibly damaged tissue offered only limited protection, consistent with evidence that undetectable Pb fragments disperse through meat or Pb is retained in animal tissues. This study highlights a shared exposure pathway linking wildlife contamination to pediatric Pb exposure in vulnerable populations. Children in subsistence-hunting communities may face neurodevelopmental and cognitive risks from the same Pb sources known to harm wildlife. Transitioning to non-Pb ammunition, stronger regulation, improved risk communication, and community engagement are critical One Health interventions that protect biodiversity while reducing toxic exposure in families dependent on wild meat.

Investigations into social and ecological aspects of lead ammunition for big game hunting with a focus on New York, USA

Monday, 27th July - 16:15: One Health (O'Hare 1-2) - Oral

Andreas Eleftheriou¹, Krysten Schuler²

1. Washington State University, 2. Cornell University

Lead is a heavy metal that is toxic to wildlife and humans. Consequently, lead has been banned from several consumer products. However, it is not regulated in ammunition for big game hunting in most of the US. Wildlife scavengers and humans can be exposed to lead fragments through consumption of contaminated game meat. As part of the New York Lead ammunition Working Group, our team conducted two studies to better define the associated risks and potential management practices. First, to characterize exposure risk in wildlife, we collected game camera images from deer hunters in New York through an online survey and identified what species actively scavenge on deer remains. Second, to help inform voluntary programs that promote use of non-lead ammunition, we leveraged results from an online survey on knowledge, attitudes, and practices by New York deer hunters to identify why they may use non-lead ammunition (versus lead). In the wildlife study, we identified avian (n =17) and mammalian (n =14) scavengers that ranged from small passerines to large obligate carnivores. In the human dimensions study, we identified that concern for human health and ammunition availability were the most significant predictors of non-lead ammunition use. Additionally, we found that hunters who were more aware of lead health impacts and were more concerned about human and wildlife health, had greater odds of using non-lead ammunition. We hope our findings that reflect social and ecological aspects of lead ammunition use in big game hunting can help to inform voluntary programs.

Respawn, Reconnect, Collaborate: Teaching One Health Through Video Game Worlds

Monday, 27th July - 16:30: One Health (O'Hare 1-2) - Oral

Justin D. Brown¹, Zachary Zidik¹, Andrew Kennedy¹, Amy Kuntz¹, Jennifer Wright¹, Sarah Zipf¹

1. Pennsylvania State University

There is an increasing need to introduce the One Health concept to younger learners, including middle school, high school, and early undergraduate students, in ways that are accessible and engaging. Historically, education in agricultural and wildlife sciences has relied heavily on in-person instruction and static materials, which can make complex, interdisciplinary ideas difficult to grasp for inexperienced audiences. In response, our team has explored how immersive technologies can support early exposure to One Health thinking while expanding access and engagement. Early phases of this work incorporated 360° video and 3D scanning to bring farms, laboratories, field sites, and biological specimens into classrooms, allowing younger learners to observe real-world systems that are often inaccessible in person. Building on this foundation, the most recent phase of our work extends immersive learning into educational gaming through *One Health Agency*, a Roblox-based role-playing game (RPG) designed specifically to introduce One Health concepts to novice learners. *One Health Agency* places students at the intersection of human, animal, and environmental health through narrative-driven cases. What begins as a simple illness shared between an owner and their pet unfolds into interconnected quests involving disease vectors, toxic exposures, and interdisciplinary collaboration. Acting as investigators-in-training, students question non-player characters, gather evidence, and persuade skeptical experts to work together. Through gameplay, students practice systems thinking, collaboration, and reflection at an introductory level appropriate for younger audiences. This session will describe the game's development, classroom implementation, student responses, and future directions, including broader middle and high school outreach and interdisciplinary use.

Neonicotinoid insecticide exposure is associated with later migration in a neotropical songbird, the Gray Catbird (*Dumetella carolinensis*)

Monday, 27th July - 15:45: Toxicology (O'Hare 4) - Oral

***Meredith Anderson*¹, *Brett Blackwell*², *Sofia Horn*², *Nina Johnson*², *Kes Luchini*², *Christina Farrell*³, *Amy Janik*⁴, *Emily Cohen*⁵, *Jeanne Fair*⁶, *Sarah Hamer*⁷**

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Neonicotinoids are the most used insecticides globally and are frequently detected throughout water, soil, insects, and seeds, making them an important threat to migrating birds. Experimental studies show neonicotinoids affect migrating birds through severe mass loss, impaired orientation, and delayed departure timing. At a high-volume spring migratory stopover site along the Texas Gulf coast, we tested associations between avian neonicotinoid exposure/concentration and factors that impact the success of migration and subsequent reproductive fitness: arrival timing and body condition. Across spring migrations in 2022 and 2023 we collected 484 blood samples from 46 bird species and 127 fecal samples predominantly from the focal species- the Gray Catbird (*Dumetella carolinensis*), determining the concentration of ten neonicotinoids, six neonicotinoid metabolites, and six diamide insecticides in each sample. The probability of acetamiprid exposure ($p=5.45e-5$, $\beta=0.15729$), and concentrations of both imidacloprid ($p=0.000127$, $\beta=0.13135$) and acetamiprid ($p=0.00396$, $\beta=0.13820$) in feces increased significantly with arrival day. These findings suggest that neonicotinoid exposure risk may (i) be greater in the later part of the spring migratory season; or (ii) occur throughout the season, causing exposed individuals to migrate later. Fat ($p=0.04171$, $\beta=0.3836$) and muscle scores ($p=0.003785$, $\beta=1.0211$) had significant positive relationships to fecal acetamiprid, suggesting that exposed birds may compensate for lost time by arriving to the stopover site in better condition than unexposed conspecifics in order to spend less time refueling. As later arriving migrants are associated with worse reproductive outcomes, neonicotinoid impacts must be an avian conservation priority.

Neonicotinoid insecticide exposure and immune function in native free-ranging Texas lizards

Monday, 27th July - 16:00: Toxicology (O'Hare 4) - Oral

***Mycha Van Allen*¹, *Kira Gangbin*², *Nathan Rains*³, *Diane Barber*⁴, *John Buchweitz*⁵, *Lori NeumanLee*⁶,
*Sarah Hamer*¹**

1. Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, 2. Department of Biology, Texas Christian University, Fort Worth, TX, 3. Texas Parks and Wildlife Department, Brownwood, TX, 4. Fort Worth Zoo, Fort Worth, TX, 5. Departments of Pharmacology, Toxicology and Animal Science, Michigan State University, East Lansing, MI, 6. Department of Biological Sciences, Arkansas State University, Jonesboro, AR

Neonicotinoid insecticides provide important pest control with wide application in agricultural, domestic, and veterinary settings. However, they persist in the environment, including in pollen, soil, and water. Adverse effects are increasingly documented in non-target taxa, especially pollinators and other invertebrates. Reptiles remain largely understudied in environmental toxicity assessments. Currently, mammals, birds, and fish are used as proxies to interpret safety for reptiles. However, reptile biology is distinct from endotherms and other ectothermic vertebrates. Further, reptile numbers are declining with 21% of all squamate species at risk of extinction. We hypothesize that sub-lethal exposure to neonicotinoids in the environment may contribute to the suppression of immune function, decreasing fecundity and survivability among wild reptiles, and increasing their susceptibility to disease. Using a cross-sectional design, we sampled diverse lizard species, including the state-threatened Texas horned lizard (*Phrynosoma cornutum*) at 8 sites across 4 ecoregions of Texas, with 98 lizards sampled through 2025. We are analyzing plasma samples for 7 neonicotinoid compounds and metabolites using high-performance liquid chromatography-tandem mass spectrometry. We will use microbicidal assays and heterophil:leukocyte counts to quantify immune function. We will use generalized linear mixed models to assess associations between neonicotinoid exposure and immune response while controlling for confounding variables. Our study fills an important knowledge gap in reptilian ecoimmunotoxicology, providing data to inform conservation efforts, pesticide regulation, and infectious disease management.

Widespread exposure to neonicotinoid insecticide in bobcats (*Lynx rufus*), fishers (*Pekania pennanti*), and river otters (*Lontra canadensis*) in North Dakota, USA

Monday, 27th July - 16:15: Toxicology (O'Hare 4) - Oral

***Charlie Bahnson*¹, *Eric Michel*², *William Jensen*³, *Stephanie Tucker*³, *Samantha Courtney*⁴, *Jonathan Jenks*⁵, *Jonathan Lundgren*⁶, *Justin Zyskowski*⁷**

1. Wyoming Game and Fish Department, 2. Department of Wildlife, Fisheries and Aquaculture, Mississippi State University, 3. North Dakota Game and Fish, 4. Michigan Department of Natural Resources, 5. Department of Natural Resource Management, South Dakota State University, 6. Ecdysis Foundation, 7. Veterinary Diagnostic Laboratory, Michigan State University

Neonicotinoids are the most widely used class of insecticides and are marketed as being safe for wildlife because of their specificity to the nervous system of invertebrates. However, recent work has found widespread environmental exposure to neonicotinoids for several vertebrate species, as well as an adverse effect on behavior and survival of non-target species, including captive white-tailed deer (*Odocoileus virginianus*). Our objective was to measure levels of imidacloprid, a commonly used agricultural neonicotinoid, in the spleens of three wild mesocarnivore species in North Dakota: bobcats (*Lynx rufus*), fishers (*Pekania pennanti*) and river otters (*Lontra canadensis*). Using direct competitive ELISAs, we detected imidacloprid in 13% (n = 112), 15% (n = 100), and 35% (n = 100) respectively with mean concentrations of 3.25, 4.07, and 3.33 ng/g. For otters, the probability of detecting imidacloprid was related to Julian date, peaking around 18 July, and varied by minor watershed. Detection probability and imidacloprid concentration was not related to age, sex, Julian date, distance to water, or year for bobcats or fishers. Our findings confirm the presence of imidacloprid in vertebrate species unlikely to have direct contact with treated grain crops. This suggests that the perpetuation or maintenance of imidacloprid within food webs potentially extends well beyond the seasonal agricultural influx. Further research is needed to understand these dynamics, and their impact to animal and environmental health.

Creating a Biomarker for Antemortem Detection of Anticoagulant Toxicity in Raptors

Monday, 27th July - 16:30: Toxicology (O'Hare 4) - Oral

***Jennifer Bloodgood*¹, *Yao Zhu*², *Cynthia Hopf-Dennis*³, *Krysten Schuler*¹, *Nichole Maughan*⁴, *Melissa Fadden*⁵, *Marjory Brooks*²**

1. Cornell Wildlife Health Lab, Cornell University College of Veterinary Medicine, Cornell K. Lisa Yang Center for Wildlife Health, 2. Department of Population Medicine and Diagnostic Sciences, Cornell University College of Veterinary Medicine, 3. Department of Clinical Sciences, Cornell University College of Veterinary Medicine, Cornell K. Lisa Yang Center for Wildlife Health, 4. Animal Health Diagnostic Center, Cornell University College of Veterinary Medicine, 5. Cornell Wildlife Health Lab, Animal Health Diagnostic Center, Cornell University College of Veterinary Medicine

Anticoagulant rodenticides (ARs) are widely deployed in urban and rural environments to control rodent populations, yet their impacts extend far beyond target species. Raptors are at high risk of AR toxicosis from consumption of AR-poisoned rodents. Global surveys show that more than half of tested birds of prey carry AR residues, with some documenting 100% exposure. However, detecting and understanding the clinical effects of AR exposure in wildlife is complicated. Currently, detection involves analyzing postmortem liver tissue for individual compounds; the antemortem coagulation testing developed for domestic animals is unreliable for birds. Furthermore, the thresholds of exposure associated with clinical signs of toxicosis are unknown for raptors. This limits our ability to diagnose and provide effective treatment for individual birds and predict population risks. To address these problems, we are developing a novel biomarker assay to detect a dysfunctional coagulation protein indicative of vitamin K deficiency – the mechanism by which ARs cause hemorrhage and death. Our initial experiments confirm the feasibility of this approach using the small volume blood samples collected routinely in wildlife practice. We are now optimizing assay protocols to relate biomarker results with liver AR concentrations to better clarify the harmful effects of AR residues in samples collected from deceased birds. Ultimately, this assay could be used patient-side to screen for AR toxicosis from any AR compound in any raptor species. These results will improve treatment of exposed wildlife and inform policy decisions surrounding AR use.

Investigating the Connection Between Heavy Metal Water Pollution and Avian Influenza in Indiana's Waterfowl

Monday, 27th July - 16:45: Toxicology (O'Hare 4) - Oral

Erin Gleason¹, Emily McCallen¹, Adam Phelps¹, Michelle Benavidez Westrich¹

1. Indiana DNR Division of Fish, Wildlife, & Nature Preserves

Indiana's rich history of industrial and agricultural production has led to polluted waterways throughout the state. Substances such as pesticides, agricultural runoff, pharmaceuticals, and heavy metals found in Indiana's waters are known endocrine disruptors, which have cascading physiological effects that can lead to lower immune system function, potentially making wildlife more susceptible to diseases like highly pathogenic avian influenza (HPAI). The purpose of this study is to understand the relationship between heavy metals and avian influenza exposure in wild waterfowl in Indiana. To identify waterfowl sampling sites, we created a statewide pollution gradient using existing water quality data from 2019-2023. During goose banding events in 2024 and 2025, we collected blood and cloacal samples from 411 Canada geese and 23 mallards to test for avian influenza antibodies, active avian influenza infection, and heavy metal levels. Preliminary results show that 29% of the sampled Canada geese tested positive for avian influenza antibodies, but no active infection was detected. Of the 23 mallards tested, 65% had avian influenza antibodies, and 91% tested non-negative for active infection, although no highly pathogenic strains have yet been detected. Heavy metal testing and analyses are currently pending. A series of generalized linear models and mixed models will be used to explore the relationship between heavy metal levels and avian influenza viral loads as waterfowl cope with this novel H5N1 strain on the landscape. Through this effort, we hope to gain a better understanding of how environmental pressures can affect waterfowl health, thereby informing future management actions.

Active Disease Surveillance in the Little Penguin (*Eudyptula minor*)

Monday, 27th July - 18:00: Global Voice Student Session 1 (Virtual/Online) - Oral

***Catherine Binns*¹, *Lee Skerratt*¹, *Jasmin Hufschmid*¹, *Leanne Renwick*²**

1. Melbourne Veterinary School, The University of Melbourne, 2. Phillip Island Nature Parks

Phillip Island (“Milawul”) supports the world’s largest colony of little penguins (*Eudyptula minor*), a population of ecological, cultural, and economic significance. Despite decades of research and targeted conservation by Phillip Island Nature Parks stabilising population numbers, information on current colony health and emerging disease risks remain limited.

Following an interdisciplinary Disease Risk Analysis (Vaughan-Higgins et al., 2024), an active disease surveillance program was implemented in 2025 to address critical knowledge gaps in pathogen presence and prevalence, complemented by ongoing passive surveillance.

The health of 400 wild penguins is being assessed in a cross-sectional study over a two-year period, representing 1% of the population. Physical examinations, clinical pathology and targeted screening for high-risk and emerging pathogens are being undertaken to evaluate current colony health and disease risks. Sampling aligns with critical physiologic timepoints in the little penguin annual cycle, investigating the influence of seasonality and energy demand on both individual disease susceptibility and potential colony-level impacts. The first 18 months of findings will be presented, with detected pathogens and their corresponding impact reported.

The insights from this study will guide future biosecurity planning, risk mitigation strategies and outbreak preparedness supporting the long-term resilience of this globally significant population.

References:

Vaughan-Higgins, R., Skerratt, L., & Hufschmid, J. (2024). *Disease Risk Analysis: Little Penguins for Phillip Island (Millowl)*. University of Melbourne, PINP, The Penguin Foundation. https://www.penguins.org.au/assets/Research/Phillip-Island-Little-Penguin-DRA-_Final-Report-_May_2024.pdf

Establishment of Hematologic and Clinical Chemistry Reference Intervals (RIs) and RI-Based Prognostic Models for Sarcoptic Mange in Raccoon Dogs (*Nyctereutes procyonoides*)

Monday, 27th July - 18:15: Global Voice Student Session 1 (Virtual/Online) - Oral

Kangyeon Yu¹, Minjae Jo¹, Sohwon Bae¹, Woojin Shin², Youngbin Kim¹, Sumin Kim³, Son-Il Pak¹, Sangjin Ahn¹

1. College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, 2. Gangwon Wildlife Medical Rescue Center, 3. College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, Chuncheon 24341, Republic of Korea

Hematologic and clinical chemistry reference intervals (RIs) are essential for health assessment, clinical decision-making, and population-level health monitoring in wildlife medicine; however, species-specific RIs remain limited for many wild carnivores. The raccoon dog (*Nyctereutes procyonoides*) is frequently admitted to wildlife medical rescue centers (WMRCs) in Korea, with sarcoptic mange representing a major cause of admission. This study aimed to establish species-specific hematologic and chemistry RIs for raccoon dogs and to develop RI-based prognostic models to predict survival in raccoon dogs presenting with sarcoptic mange at admission. Blood samples were collected from clinically stable raccoon dogs admitted to the Gangwon WMRC. Hematologic and chemistry analyses were performed, and RIs were established in accordance with American Society for Veterinary Clinical Pathology guidelines. Using the established RIs as biological reference standards, prognostic analyses were conducted in raccoon dogs with sarcoptic mange at initial presentation. A multivariable logistic regression model including blood urea nitrogen, platelet count, albumin, white blood cell count, and alkaline phosphatase demonstrated good discrimination (area under the receiver operating characteristic curve [AUC] = 0.78) and acceptable calibration. A simplified 0–10 point scoring system based on RI deviations using a 1.5×RI threshold showed comparable discrimination (AUC = 0.74), with no significant difference from the continuous model. These RI-based prognostic models may support risk stratification, treatment prioritization, and triage decision-making in raccoon dogs with sarcoptic mange. This work was supported by the National Institute of Wildlife Disease Control and Prevention through the “Specialized Graduate School Support Project for Wildlife Disease Specialists”.

Behavioral characteristics of the endangered Korean long-tailed goral based on global positioning system data

Monday, 27th July - 18:30: Global Voice Student Session 1 (Virtual/Online) - Oral

Minjae Jo¹, Gyu-Cheol Kim², Kangyeon Yu³, Youngbin Kim¹, Sumin Kim⁴, Chae-un Cho⁵, Sangjin Ahn¹

1. College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, **2.** Department of Biological Science (Ecology and Taxonomy), Daegu University, Gyeonsan 38453, Republic of Korea, **3.** College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, Chuncheon 24341, Republic of Korea Gangwon Wildlife Medical Rescue center, Chuncheon 24341, Republic of Korea, **4.** College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University, Chuncheon 24341, Republic of Korea, **5.** Yanggu Goral and Musk Deer Conservation Center, Yanggu, Republic of Korea

An understanding of the basic ecology and behavior of the endangered long-tailed goral (*Naemorhedus caudatus*, LTG) constitutes a logical starting point for successful conservation and restoration of the species. To reveal the ecological and behavioral characteristics of LTGs, a study was undertaken between 2006 and 2019 for 57 LTGs (21 males, 36 females) in 7 regions of Korea. We used 48,741 location coordinates to analyze home-ranges and habitat use characteristics. The overall annual home range of males in 95% minimum convex polygon (MCP) was greater than that of females. Monthly home ranges of adult LTGs were the widest in June and October at the 95% MCP, while sub-adult LTGs had the widest home range in April and Oct. The adult LTGs had the smallest home range in February, while the sub-adults had the smallest home range in September. As a result of analyzing the characteristics of habitat use, we identified the aspect (211.96 ± 101.79 , Southwest), altitude (527.99 ± 199.2), slope (37.80 ± 16.14), distance from the road (515.01 ± 531.57), and distance from the water (146.99 ± 125.54). Our results provide a novel insight into the behavioral ecology and habitat use of LTGs to be used for habitat management policy. Furthermore, the results can be used to evaluate LTG restoration projects and supplement conservation plans. This work was supported by the National Institute of Wildlife Disease Control and Prevention under the “Specialized Graduate School Support Project for Wildlife Disease Specialists.

Host community traits driving Crimean-Congo hemorrhagic fever virus maintenance in Iberian ecosystems

Tuesday, 28th July - 07:50: Global Voice (Virtual/Online) - Oral

Patricia Xavier ¹

1. Health & Biotechnology (SaBio) group, Instituto de Investigación en Recursos Cinegéticos (IREC), CSIC-UCLM-JCCM, Ciudad Real, Spain

Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne zoonosis of significant public health concern, maintained in complex multi-host systems shaped by ecological, climatic, and anthropogenic drivers. In the Iberian Peninsula, changing land-use patterns and biodiversity loss may be reshaping host communities in ways that alter local transmission dynamics. We conducted a landscape-scale study across 18 sites, integrating serological surveillance of wild ungulates (n = 1461; 69.4% wild boar, 30.6% red deer) with camera-trap monitoring of mammalian communities, land-cover analysis, and climatic data. To capture ecological drivers at different scales, we fitted two GLMM: one including all sites to identify broad landscape-level predictors of exposure, and another restricted to endemic sites to evaluate fine-scale dynamics within established transmission foci. Overall, 44.5% of sampled individuals tested positive for CCHFV antibodies, with site-level seroprevalence ranging from 1.5% to 81.4%. Across all sites, seroprevalence was positively associated with red deer abundance, underscoring the potential role of red deer as key amplifying host, forest cover, and precipitation seasonality, while small ruminant presence was linked to reduced exposure risk. Within endemic areas, higher mammalian diversity and greater lagomorph abundance were negatively associated with exposure, whereas warmer temperatures promoted circulation. This pattern suggests that more balanced host communities can reduce pathogen transmission. This study highlights how community structure and environmental change jointly shape CCHFV ecology. The context-dependent nature of ecological drivers supports integrated One Health strategies that conserve biodiversity, promote mixed grazing systems, and regulate wild ungulate populations to reduce CCHFV circulation in Iberian ecosystems undergoing socio-ecological transformation.

From Cryptic to Contextualized: Understanding *Trichinella chanchalensis* Through Metabarcoding

Tuesday, 28th July - 08:00: Keynote Student Speaker (O'Hare 1-2) - Oral

***Cody Malone*¹, *Jane Harms*², *Naima Jutha*³, *Kimberlee Beckmen*⁴, *Raphaela Stimmelmayer*⁵, *Malik Awan*⁶,
*Vladislav Lobanov*⁷, *Emily Jenkins*¹**

1. University of Saskatchewan, 2. Government of Yukon - Department of Environment, 3. Government of the Northwest Territories - Department of Environment and Climate Change, 4. Alaska Department of Fish and Game, 5. Department of Wildlife Management, North Slope Borough, 6. Government of Nunavut, Department of Environment, 7. Canadian Food Inspection Agency, Centre for Foodborne and Animal Parasitology

Trichinella chanchalensis (T13) is a recently discovered zoonotic nematode originally identified in wolverines and an American marten from the Northwest Territories and Yukon. Because traditional diagnostics cannot distinguish T13 from *T. nativa*, its host associations, distribution, and evolutionary context have remained unclear. Phylogenetic work indicates that T13 is deeply divergent from *T. nativa* and T6 and more closely related to the South American *T. patagoniensis*, suggesting an ancient lineage and potentially earlier entry into the Americas than other northern *Trichinella* spp.

We assessed the ecology of T13 by examining host use, geographic distribution, and infection composition in carnivores from Alaska and three Canadian territories. Larvae were recovered using the double separatory funnel method and genotyped using deep amplicon next-generation sequencing. *Trichinella* spp. were detected in wildlife from the Yukon (74%), Alaska (33.8%), Nunavut (82%), and Northwest Territories (70%). Mixed infections with *T. nativa* and T6 dominated (60%). T13 was detected in the Yukon (19%), Nunavut (18%), NWT (4%), and Alaska (0.6%), almost exclusively in co-infections. Expanded testing revealed T13 in lynx, wolves, and a coyote, and in two new geographic areas, Nunavut and Alaska.

A lower prevalence in Alaska and NWT and higher in the Yukon and Nunavut are consistent with a post-glacial dispersal history involving persistence in refugia, early colonization of the Yukon via the Ice-Free Corridor, and later expansion into Nunavut. The broad host range of T13, suggests non-specialist ecology and suggests that the geographic distribution of T13 may be more extensive than currently recognized.

Drivers of Multipathogen Exposure in White-Tailed Deer (*Odocoileus virginianus*) in Southern Wisconsin

Tuesday, 28th July - 08:30: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

***Md Nurul Islam*¹, *Marie Gilbertson*², *Aaron Groves*², *Daniel Storm*³, *Wendy Turner*⁴**

1. Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, UW-Madison, **2.** Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin–Madison, **3.** Wisconsin Department of Natural Resources, **4.** U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology University of Wisconsin, Madison

White tailed deer (*Odocoileus virginianus*) may act as potential reservoirs for pathogens affecting wildlife, livestock, and human health. Understanding patterns in disease prevalence and how these are modified by landscape features for different infectious diseases may inform wildlife management, particularly in endemic regions of chronic wasting disease (CWD). We conducted a cross-sectional serosurvey of 314 deer in southwestern Wisconsin (2017–2020) to evaluate prevalence and environmental drivers of pathogen exposure. As part of a long-term CWD monitoring project, deer were captured, fitted with GPS collars, and sampled for serology and CWD status (ante-mortem and post-mortem). Serum samples were screened for bovine parainfluenza virus 3 (BPIV-3), *Leptospira* spp., *Coxiella burnetii*, epizootic hemorrhagic disease virus (EHDV), and bluetongue virus (BTV). We used logistic regression to assess the role of demographic and environmental factors (e.g., habitat composition, proximity to livestock operations) in predicting exposure to or infection with our pathogens of interest. CWD prevalence was 34.7% of the monitored population. Among other pathogens detected, seroprevalence was highest for BPIV-3 (17.8%), followed by *Leptospira* spp. (16.9%) and *C. burnetii* (2.4%). Predominant *Leptospira* serovars included *L. icterohaemorrhagiae* (11.5%) and *L. pomona* (3.5%). There was no evidence of exposure to EHDV or BTV. Co-exposure to multiple pathogens was detected in 8.9% of sampled deer, based on serology. Sex and age class did not explain exposure or infection patterns for any of our pathogens. Understanding environmental risk factors will provide essential baseline data on the wildlife-livestock interface and inform management strategies for multi-pathogen systems in high-density deer herds

Green lung syndrome in white-tailed deer: Evidence towards *Conidiobolus* sp. fungal disease

Tuesday, 28th July - 08:45: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

Victoria A. Andreasen¹, **Alisia A.W. Weyna**², **Jeffrey M. Lorch**³, **Melanie R. Kunkel**⁴, **Kevin D. Niedringhaus**⁵, **Chloe C. Goodwin**⁶, **Xuan Hui Teo**⁶, **C. Robert Stiltz**¹, **Heather Fenton**⁷, **Justin D. Brown**⁸, **Mark G. Ruder**¹, **Bambi C. Ferree Clemons**⁹, **Mark W. Cunningham**⁹, **Amy S. McKinney**¹⁰, **Michael J. Yabsley**¹, **Nicole M. Nemeth**¹

1. Southeastern Cooperative Wildlife Disease Study, University of Georgia, 2. Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin-Madison, 3. U.S. Geological Survey, National Wildlife Health Center, 4. Northeast Association of Fish and Wildlife Agencies, 5. Wildlife Futures Program, University of Pennsylvania, 6. Department of Pathology, University of Georgia, 7. Taronga Conservation Society, Australian Registry of Wildlife Health, 8. Department of Veterinary and Biomedical Sciences, Penn State University, 9. Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, 10. Athens Veterinary Diagnostic Laboratory, University of Georgia

Green lung syndrome (GLS) has been an increasingly frequent diagnosis in white-tailed deer (*Odocoileus virginianus*) evaluated at the Southeastern Cooperative Wildlife Disease Study in recent years. Since 2003, 81 hunter-harvested, sick, or dead deer were submitted as targeted tissue samples or carcasses and diagnosed with GLS. Our objectives were to characterize the pathology, identify etiology(ies), and evaluate for spatiotemporal and demographic data trends in GLS-affected deer. Grossly, deer had focal to multifocal, often large, nodular pulmonary masses that were bright green on cut surfaces. Histologically, eosinophilic and granulomatous inflammation with variable necrosis and fibrosis obscured pulmonary architecture and contained negatively-staining hyphae. The gastrointestinal tract (e.g., dental pad, rumen, abomasum, colon) had similar lesions in nine deer, but was often not submitted for evaluation. Cases originated from 16 states across the southeastern, midwestern and northeastern U.S., with highest numbers from Florida (20.9%), Pennsylvania (17.3%) and North Carolina (11.1%). Most cases were submitted in fall (56.8%), suggesting that seasonal conditions (e.g., temperature, precipitation) could impact epidemiology. 66.3% were female (n=80) and 93.4% were >1-year old (n=76). A subset of lung samples (frozen or paraffin-embedded) underwent molecular testing; *Conidiobolus* sp. was identified in 35/40 (87.5%) samples. Less commonly, oomycete (*Pythium* spp.) or other fungal species were detected. Consistent pulmonary lesions suggest exposure via inhalation, while gastrointestinal involvement may derive from ingestion of fungal-contaminated vegetation or water. Continued GLS surveillance and full carcass postmortem evaluations in wild deer are critical to understanding this potentially emerging disease threat, including ecoepidemiologic patterns and disease risk factors.

Continued surveillance for influenza A antibodies in wild raptors of the upper Midwest (2023-2025) following the arrival of highly pathogenic influenza A virus in the flyway (2022)

Tuesday, 28th July - 09:00: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

***Kelsey Rayment*¹, *Victoria Hall*², *Kristelle Mendoza*³, *Carol Cardona*³, *Rebecca Poulson*⁴, *Elizabeth Kurimo-Beechuk*⁴, *David Stallknecht*⁵, *Dana Framzen-Klein*⁶**

1. Utah State University, 2. Oiled Wildlife Care Network, UC Davis, 3. College of Veterinary Medicine - University of Minnesota, 4. Southeastern Cooperative Wildlife Disease Study, University of Georgia, 5. Southeastern Cooperative Wildlife Disease Study, 6. The Raptor Center, University of Minnesota

The global outbreak of 2.3.4.4b Gs/GD highly pathogenic (HP) influenza A virus (IAV) H5N1 has had unprecedented effects on wild birds, including North American raptors. In the face of a disease outbreak, sampling animals admitted to wildlife rehabilitation facilities can augment free-ranging outbreak data with enhanced surveillance and sampling especially at the human-wildlife interface. The Raptor Center (TRC) at the University of Minnesota is the largest raptor rehabilitation center in the United States, admitting over 1,000 wild raptors annually. A serosurveillance project was initiated at TRC during the fall of 2022, 6 months after HP H5N1 was detected in the state, to screen admitted raptors for evidence of exposure to HP H5N1 IAV. Since 2023, 2,201 individual raptors representing 27 species have been tested for IAV antibodies. 385 individual raptors had detectable IAV antibodies. Bald eagles (*Haliaeetus leucocephalus*, BAEA) were the species with the highest IAV seroprevalence detected with 54.49% (91/176) positive in 2023 and 61.66% (119/193) testing positive in 2024, with preliminarily 73.02% (46/73) positive in 2025. All species who had IAV antibodies were screened for antibodies specific to H5 and N1. Subtyping of BAEAs with IAV antibodies found 63.7% (58/91) in 2023 and 68.06% (81/119) in 2024 had antibodies specific to H5 and N1. This rate of exposure and survival to HP H5N1 is higher than had been documented in raptors and seroprevalence in BAEAs has maintained since 2022. This collaborative project highlights how wildlife rehabilitation can be used to supplement our understanding of disease exposure in wildlife.

Baseline Parasitological Survey and Detection of Ocular Helminths (*Oxyspirura* spp.) in Hunter-Harvested Grey Partridge (*Perdix perdix*) and Sharp-tailed Grouse (*Tympanuchus phasianellus*) from Montana

Tuesday, 28th July - 09:15: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

Henry Valencia¹, Ronald Kendall¹

1. Texas Tech University

Grey partridge (*Perdix perdix*) and Sharp-tailed grouse (*Tympanuchus phasianellus*) are ecologically and culturally important upland game birds in Montana, yet parasitic infections affecting these species remain poorly characterized in northern prairie ecosystems. Ocular nematodes of the genus *Oxyspirura* have been associated with impaired vision, ocular pathology, and reduced fitness in galliform birds, but surveillance has largely focused on southern populations. This study provides baseline parasitological data for Montana upland game birds using hunter-harvested surveillance. During the 2024 upland game season, twelve legally harvested birds (Grey partridge n = 5; Sharp-tailed Grouse n = 7) from north-central Montana were examined via necropsy. Ocular and gastrointestinal tissues were evaluated for helminths, and recovered parasites were identified morphologically. Ocular nematodes consistent with *Oxyspirura* spp. were detected in both species, while no gastrointestinal helminths were observed. Grey partridge exhibited higher infection prevalence (80%) and mean intensity (3.8) compared to Sharp-tailed grouse (28.5% prevalence; mean intensity = 0.4). Eyeworms were recovered beneath the nictitating membrane and within associated ocular ducts and glands. These findings represent the first recent documentation of *Oxyspirura* spp. in Grey partridge and Sharp-tailed grouse from Montana and extend the known geographic occurrence of ocular helminths into northern upland systems. Detection of *Oxyspirura* spp. within both species indicates parasitism as an underrecognized factor in northern ecosystems further informing wildlife disease monitoring and management. Expanded sampling, molecular confirmation, and integration of parasitological assessments into monitoring programs are warranted to better understand the role of helminths as potential stressors in upland avian populations.

From penguin (*Spheniscus magellanicus*) fatalities to a broader ecological understanding: avian malaria in captive zoo birds, local wild birds, and mosquitoes in Texas

Tuesday, 28th July - 09:30: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

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Avian malaria blood parasites (Haemosporida) of birds can cause a spectrum of health consequences, but severe pathology is often caused by generalist lineages of *Plasmodium*, when they infect individuals from species that did not co-evolve with mosquitoes. This is a well-established challenge for zoos housing penguins outside of their native range. Despite being on prophylactic treatment, multiple Magellanic penguins (*Spheniscus magellanicus*) died from avian malaria in the summers of 2024 and 2025; these birds were in a zoological collection in far west Texas as part of a national conservation program. We conducted an ecological study of the parasite community in vectors and avian hosts around the zoo. Using mist nets on zoo grounds, we trapped 7 wild birds and found 3 (42.8%) to be infected based on PCR methods. We curated a collection of 10 blood samples from living zoo birds and 14 tissues from deceased zoo birds, and found 11 (35.5%) to be infected, including multiple Swainson's hawks (*Buteo swainsoni*) and Inca terns (*Larosterna inca*). Notably the lineage found in two of the deceased penguins was the same as that found in one Swainson's hawk. Finally, we salvaged mosquitoes that are regularly trapped around the penguin enclosure. Efforts are underway to identify and pool mosquitoes for Haemosporida testing; blood-fed females will undergo a molecular bloodmeal analysis to identify the host species upon which they have previously fed. The parasite transmission networks created through this ecological investigation are useful in source tracking lethal variants and in future protective measures.

Reproductive site and season impact the milk proteome of South American fur seals (*Arctocephalus australis*)

Tuesday, 28th July - 09:45: Student Presentations - Mammals and Birds (O'Hare 1-2) - Oral

***Serena Zhang*¹, *Susana Cardenas-Alayza*², *Matthew Allender*³, *Michael Adkesson*⁴, *Jason McAlister*⁵,
*Jennifer Geddes-McAlister*⁵, *Mauricio Seguel*⁶**

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Milk is a critical determinant of neonatal survival, transferring ecological context, nutrition, and immunity from mother to offspring. Capital breeders such as otariids (sealions and fur seals) are particularly dependent on milk delivery and composition as the pups are subject to a unique feast-and-famine cycle and have a prolonged lactation period. Little is known, however, about otariid milk composition and the spatiotemporal factors that shape it. Here, we characterized the milk proteome of South American fur seals (*Arctocephalus australis*) and investigated for proteome differences between reproductive sites and breeding seasons. Between 2022 to 2024, milk samples were collected from 72 females from Guafo Island, Chile (n=50) and Punta San Juan, Peru (n=22). Using mass spectrometry, we identified over 700 proteins from the milk samples and evaluated for drivers of proteome variation using generalized linear latent variable models (GLLVM). Immune proteins—including lactotransferrin, immunoglobulin G (IgG), and clusterin—were higher during the 2023-2024 breeding season, suggesting that animals were under a higher disease burden during the 2023-2024 El Niño event. Similarly, at Guafo Island—a colony where infectious disease is the predominant driver of pup mortality—IgG was more abundant. In contrast, proteins indicative of cellular stress and catabolism were higher at Punta San Juan, where the leading cause of mortality is trauma and malnutrition. Altogether, our results not only provide the first proteomic data of milk from this species, but also demonstrate how otariid milk composition is influenced by the environment and reflects the health status of the mother.

Determining Comprehensive Health Parameters and Pathogen Presence in Wild Spotted Turtles (*Clemmys guttata*) of Northern Illinois

Tuesday, 28th July - 10:45: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

***Madison Kasbaum*¹, *Laura Adamovicz*², *Kaitlin Moorhead*³, *Rose Arnold*⁴, *Joey Cannizzaro*⁵, *Chitra Basyal*⁵, *John Winter*³, *Matthew Allender*⁶**

1. University of Illinois College of Veterinary Medicine, 2. University of Illinois College of Veterinary Medicine, Veterinary Diagnostic Laboratories, Wildlife Epidemiology Laboratory, Urbana-Champaign IL, 3. University of Illinois College of Veterinary Medicine, Urbana-Champaign IL, 4. University of Illinois, Illinois Natural History Survey - Prairie Research Institute, Champaign IL, 5. University of Illinois, Illinois Natural History Survey - Prairie Research Institute, Champaign IL, 6. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section; Brookfield Zoo Chicago, Brookfield IL

Spotted turtles (*Clemmys guttata*) are endangered in Illinois due to multiple anthropogenic factors. However, the role of health in this species' decline is poorly understood. This study aimed to characterize the health status of the last two populations of wild spotted turtles in Illinois using physical examination, molecular surveillance for 28 pathogens, and hematology. Spotted turtles (n = 124) were evaluated from April - June 2024 and 2025. Common examination abnormalities included shell lesions (61.29%), asymmetrical nares (18.55%), cutaneous injuries (15.32%), eyelid lesions (8.06%), and appendage abnormalities (7.26%). Hematology parameters varied significantly by month, sex, study site, and the presence of physical examination abnormalities, largely following expected patterns for chelonians. Detected pathogens included Chlamydiaceae family bacteria (12.9%), *Emydoidea* herpesvirus 1 (EBHV1; 12.9%), Emydid herpesvirus 2 (3.25%) and *Leptospira* spp. (1.61%). EBHV1 detection was more prevalent in April compared to later months (p = 0.004) and was associated with the presence of eyelid lesions (p = 0.02) and lower lymphocyte counts (p = 0.002). Other pathogens were not associated with clinical signs or hematology changes. Turtles from the smaller population had more eyelid lesions (p = 0.048), developmental shell abnormalities (p = 0.005), and active shell lesions (p = 0.003). They also had higher eosinophil counts (p = 0.045) and lower total solids concentrations (p = 0.01), consistent with a poorer overall plane of health. This is the largest and most comprehensive study on the health of wild spotted turtles, and our findings provide a useful baseline for future studies.

Epidemiology of Tortoise Intranuclear Coccidiosis in free-ranging aquatic turtles in Illinois

Tuesday, 28th July - 11:00: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

***Grace Minge*¹, *Laura Adamovicz*², *Carly Etter*¹, *Gary Glowacki*³, *Dan Thompson*⁴, *William Graser*⁵,
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Tortoise intranuclear coccidiosis (TINC) is a systemic infectious disease of chelonians spread via fecal-oral route and is poorly understood in free-ranging populations. This study aims to investigate the epidemiology of intranuclear coccidiosis in free-ranging aquatic chelonian species in northern Illinois. TINC quantitative PCR was performed on combined oral/cloacal/shell swabs from 3,278 turtles representing eight species, six counties, and three years (2023 – 2025). Painted turtles (*Chrysemys picta*) were the only species that tested positive, with an overall prevalence of 3.16% (23/728) and a mean qPCR quantity of 193 target copies/reaction (range = 3.45 – 1,918). TINC detection was not associated with year, season, sex, age class, presence of physical examination abnormalities, or hematology parameters, but prevalence did differ by county ($p = 0.0003$). Specifically, TINC prevalence was significantly greater in turtles from DuPage County (10.94%, 7/64) compared to Cook (1.29%, 4/310, OR = 9.39, $p = 0.005$) and Kane Counties (0.62%, 1/161, OR = 19.65, $p = 0.046$). TINC prevalence in McHenry (5.88%, 1/17) and Lake Counties (5.68%, 10/176) were intermediate between DuPage and Kane Counties. One adult male painted turtle from Lake County that presented with poor body condition, severe blepharodema, and nasal discharge tested positive (148 copies/reaction), but did not have histologically-apparent TINC organisms in any tissue. Overall, this investigation indicates that TINC is present in free-ranging painted turtle populations and implicates the need for further studies to better understand the impact of this disease on non-native hosts.

Hematological Analysis in Free-Ranging Native Snakes Associated with One or More Potential Pathogens in the Southeastern United States

Tuesday, 28th July - 11:15: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

Corinna Hazelrig¹, Terence Farrell², Jenna Palmisano³, Ellen Haynes¹, John Maerz⁴, Kristina Meichner⁵, Jian Zhang⁵, Kayla Garrett¹, Michael J. Yabsley¹, Jason Ortega⁶, Chris Cleveland¹, Nicole M. Nemeth¹

1. Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, **2.** Department of Biology, Stetson University, DeLand, FL, **3.** Department of Biology, University of Central Florida, Orlando, FL, **4.** Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, **5.** Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, **6.** Department of Biological Sciences, University of Arkansas – Fort Smith, Fort Smith, AR

Infectious diseases are of increasing concern in free-ranging snakes. Hematology offers valuable insights into the physiological impacts of disease. Our study evaluated the health of free-ranging snake populations in the southeastern United States by describing associations between hematological parameters and detection of seven infectious agents. We sampled 319 snakes (plus 42 recaptures) representing 20 species from Athens-Clarke County, Georgia (n = 17, 2 recaptures), Jasper County, South Carolina (n = 102, 16 recaptures), and Volusia County, Florida (n = 200, 24 recaptures). Samples (swabs, feces, and blood) were tested via PCR for *Cryptosporidium* spp., *Hepatozoon* spp., *Mycoplasma* spp., *Ophidiomyces ophidiicola* (*Oo*), *Raillietiella orientalis* (*Ro*), *Salmonella enterica*, and serpentoviruses. We conducted physical examinations to assess skin lesions, nutritional condition, and measured leukocyte counts, packed cell volume, and total solids. We found relative azurophilia, heterophilia, and leukopenia associated with *Oo* detection; relative azuropenia associated with *Ro* detection; and relative monocytosis and elevated total solids associated with *Hepatozoon* spp. detection. Further, relative azurophilia, heterophilia, monocytosis, lymphopenia, and decreased total solids were associated with diminished nutritional condition. Together, low nutritional condition and hematologic changes suggest the possibility of infection response resulting in a negative energy balance. Severity scores of gross skin lesions were positively associated with relative heterophilia, azurophilia, and leukopenia, consistent with a stress response. These results suggest a systemic inflammatory response to *Oo* and *Hepatozoon* spp. infections, and immunosuppression associated with *Ro*. Our study provides a hematological evaluation across multiple snake species highlighting circulating pathogens and host responses essential to snake conservation.

Hemolymph analysis and antemortem assessments in three species of unionid mussels in northern Cook County, Illinois

Tuesday, 28th July - 11:30: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

***Eliza Baker*¹, *John Winter*², *Michael Neri*³, *Charles Rizzo*³, *Chris Anchor*³, *Matthew Allender*⁴**

1. Wildlife Epidemiology Lab, College of Veterinary Medicine, University of Illinois Urbana-Champaign, **2.** University of Illinois, **3.** Forest Preserve District of Cook County, **4.** Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign

Freshwater mussels are one of the most imperiled taxonomic groups in the world, with over one third of North American species threatened or extinct. Additionally, though enigmatic mass mortality events have been occurring for decades, there is no consensus on the underlying cause of many of these events. This study's objective was to improve antemortem diagnostic capabilities in local unionid mussels by determining baseline health parameters. We performed examinations and hemolymph cytology on 62 giant floater (*Pyganodon grandis*), 30 ellipse (*Venustaconcha ellipsiformis*), and 21 plain pocketbook mussels (*Lampsilis cardium*). Unlike many other assessed species, agranulocytes were the predominant cell type in all three species, with granulocyte percentage significantly increasing over time from July through September ($p=0.01$). Plain pocketbook mussels had higher granulocytes counts than ellipse and giant floaters ($p<0.001$). Numerous nematodes were present in the hemolymph of one giant floater, and suspected protozoan parasites were present within hemocytes of a second giant floater. Repeat assessment of that mussel two weeks later revealed a significant decline in parasite density. Physical examination abnormalities were present in 38 mussels (34%) and included erosions of the periostracum, valve asymmetry, gill inclusions, and mantle edema. Fourteen mussels (12%) were suspected to be gravid based on gill examination. These findings provide a baseline of mussel physical examination and hemolymph characteristics that can be used to assess health during future outbreaks or mortality events. Further work determining hemocyte counts, identifying suspect parasites, and determining the impact on health of the documented physical examination abnormalities is ongoing.

Cerebral Microsporidiosis in Cold-stressed Threadfin Shad (*Dorosoma petenense*) in Eastern Tennessee

Tuesday, 28th July - 11:45: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

***Isabel Correia*¹, *Michelle Dennis*¹, *Sophie Hall*², *Jan Lovy*², *Richard Gerhold*³**

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In February 2025, there was an unusual mortality event of threadfin shad (*Dorosoma petenense*) in Knoxville, Tennessee following a period of unusually cold weather, consistent with cold stress syndrome. Several moribund fish were observed swimming abnormally on site, and 23 deceased individuals were sampled for diagnostic investigation. Comprehensive postmortem examination with histology was done on 8 fish, and wet-mounted squash preparation of brain tissue stained with diff-quick on 13 fish. Histologically, 4/8 fish had cerebral microsporidiosis; 1 of these had associated granulomatous encephalitis, and 1 had granulomatous peritonitis. Additionally, 1 fish had lamellar ichthyophthiriasis, 5 had cutaneous or lamellar oomycetosis ("saprolegniosis"), and 1 had visceral granulomas with nematode larvae. On wet mount, 8/13 fish had mature microsporidial spores present. Genetic sequencing using a PCR product of the small subunit (SSU) 16S rDNA, internal transcribed spacer (ITS) and partial large subunit (LSU) revealed a 99.3% similarity to an undescribed Microsporidia species that was isolated from a wild swamp guppy (*Micropoecilia picta*) in Grenada, West Indies. To our knowledge, this is the first report of cerebral microsporidiosis in threadfin shad. It is unclear if cerebral microsporidiosis is associated with cold stress syndrome historically impacting threadfin shad populations in the region. Further investigation is needed to know if microsporidiosis is a direct cause of observed clinical signs (erratic swimming) and mortality, or an incidental finding (i.e. subclinical infection normally present in the population to some level).

Analyzing broadscale environmental risk factors for initiation of historical botulism events in the Great Salt Lake marshes, 1910-2024

Tuesday, 28th July - 12:00: Student Presentations - Reptiles & Aquatics (O'Hare 1-2) - Oral

***Jaclyn C. Plasterer*¹, *Virginia Stout*², *John Neill*², *Jonathan D. Lautenbach*³, *Jessica N. Sanchez*¹**

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Avian botulism is a fatal paralytic disease that causes large-scale mortality events in waterfowl populations across North America. These outbreaks are caused by ingestion of a botulinum neurotoxin (BoNT, Type C) produced by an endospore forming, anaerobic bacterium known as *Clostridium botulinum*. In Utah, specifically wetlands in and around the Great Salt Lake, outbreaks have been recorded with some regularity since 1910. We consolidated 60 avian botulism mortality records from the USGS National Wildlife Health Center's WHISPers database spanning 1910–2024 for the five counties comprising Great Salt Lake wetlands. Estimates of affected birds ranged from 2 to over 500,000 with a median of 2,300 bird affected. The start date of these outbreaks ranged from February–November, with 88% of incidents beginning in June–September. We gathered historical precipitation, temperature, and wind data from the National Oceanic and Atmospheric Administration's Local Climatological Data tool and estimates of water depth and bird abundance provided by collaborators at Utah State University. We utilized a generalized linear model to assess climatological risk factors and waterbird abundance associated with the initiation of botulism outbreaks. Our research provides a broadscale risk assessment across the Great Salt Lake marshes, an essential wetland in the Pacific and Central Flyways that provides nesting and feeding grounds for millions of waterfowl during their annual migration. Findings will support wildlife managers in their efforts to support waterfowl conservation and provide a framework for future botulism investigations in wetlands across the globe.

Leptospira seroprevalence and serovar distribution in urban and rural wildlife in Ontario, Canada.

Tuesday, 28th July - 11:00: Global Voice Student Session 2 (Virtual/Online) - Oral

***Kellie Libera*¹, *Larissa Nutich*², *David L. Pearl*³, *Davor Ojkic*⁴, *Alexandra Reid*⁵, *J. Scott Weese*⁶, *Katie M. Clow*³, *Lauren E. Grant*³, *E. Jane Parmley*³, *Claire M. Jardine*⁶**

1. Department of Pathobiology, University of Guelph, 2. Ontario Ministry of Natural Resources, 3. Department of Population Medicine, University of Guelph, 4. Animal Health Laboratory, University of Guelph, 5. Ontario Ministry of Agriculture, Food and Agribusiness, 6. Department of Pathobiology, University of Guelph

Leptospirosis is a widespread and neglected zoonosis maintained in wildlife reservoirs, which may serve as sentinel populations for detecting transmission changes. In North America, limited routine surveillance has resulted in knowledge gaps regarding *Leptospira* prevalence and serovar distribution.

Our objectives were to (1) describe seroprevalence and serovar distribution and (2) assess temporal and habitat-related patterns of *Leptospira* antibodies in raccoons (*Procyon lotor*) and skunks (*Mephitis mephitis*) in southern Ontario, Canada.

Serum samples (raccoons, n=520; skunks, n=235) collected between 2016 and 2020 underwent microscopic agglutination testing against seven *Leptospira* serovars. Species-specific multivariable logistic regression models were fitted to assess associations between year and habitat type (urban vs rural) with seroprevalence.

Overall seroprevalence was 46% (95% CI: 42–50%) in raccoons and 34% (95% CI: 29–40%) in skunks. Multivariable models showed seroprevalence varied significantly by year, but habitat type was not significantly associated with seropositivity in either species.

Antibodies to serovars Canicola and Hardjo in raccoons and Autumnalis, Bratislava, and Grippotyphosa in skunks were detected at similar frequencies between years, whereas other detected serovars varied significantly. Across both wildlife host species, detected antibodies to serovars that are not included in Canadian canine vaccines increased over time. Temporal variation in seroprevalence and serovar distribution suggests dynamic wildlife exposure patterns that may reflect broader transmission and environmental fluctuations, supporting the potential of wildlife as sentinel populations for monitoring emerging leptospirosis trends.

Temporal dynamics of mosquito blood-feeding networks in an Urban Park of Mérida, Mexico

Tuesday, 28th July - 11:20: Global Voice Student Session 2 (Virtual/Online) - Oral

Elizabeth Linares Alcantara¹, Roger Arana Guardia¹, Omar Garcia Suarez¹, Gerardo Suzan¹, Maria Jose Tolsa Garcia¹

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Urban parks provide an interface between human society and nature. Their diversity allows us to study a wide variety of interactions that are important for public health. Mosquitoes are vectors for arboviral diseases, and urban landscapes provide unique habitats for interactions between mosquitoes and vertebrates that sustain cycles and facilitate disease transmission. This study aims to survey the changes in mosquito blood-feeding networks in a public park in Merida, Yucatán, Mexico, assessing mosquito abundance, interaction diversity and identifying vertebrate hosts and mosquito vectors that could be potentially important in arbovirus transmission. Mosquito collection was carried out weekly in Parque Arqueo-Ecológico del Poniente Xoclán, one of the largest public parks in Merida, from August 2023 to August 2024. Collection was performed in natural and artificial resting sites along 4 non-linear transects of 150 m each, using Prokopack aspirators. Molecular blood meal analysis targeted vertebrate mitochondrial 12S and 16S DNA. Mosquito abundance peaked during the rainy season, in June and July, while mosquito and interaction diversity were greater in November and December 2023 and January 2024, characterized by being colder months. Network analysis revealed that key species with high betweenness centrality, such as *Homo sapiens*, *Canis lupus familiaris* and *Aedes taeniorhynchus*, were consistent across time intervals, they are important for facilitating network connectivity and, consequently, for maintaining potential disease transmission cycles. By integrating fine-scale blood-feeding data with ecological network analysis this research contributes to a better understanding of urban ecological interactions and their implications for public health.

Extended-spectrum β -lactamase-producing *Escherichia coli* in stranded marine mammals from the northern Atlantic coast of Argentina

Tuesday, 28th July - 11:35: Global Voice Student Session 2 (Virtual/Online) - Oral

Walter Ezequiel Condorí¹, Agostina Tammone Santos¹, Marília Salgado-Caxito², Juliana Cantón¹, Claudio Santiago Cacciato¹, María Laura Chiapparrone¹, Cecilia Karina Alvarez³, Sergio Rodriguez-Heredia³, Juan Pablo Loureiro³, Alejandra Corso⁴, Diego Faccone⁴, Sylvain Godreuil², Marcela Uhart⁵, Silvia Marcela Estein¹, Julio Andre Benavides Tala²

1. Centro de Investigación Veterinaria de Tandil (CIVETAN/UNCPBA-CICPBA-CONICET), Tandil, 2. MIVEGEC, University of Montpellier, IRD, CNRS, Montpellier, 3. Fundación Mundo Marino, San Clemente del Tuyú, 4. Instituto Nacional de Enfermedades Infecciosas (INEI)-ANLIS "Dr. C. Malbrán", Buenos Aires, 5. University of California, Davis

Extended-spectrum β -lactamase-producing *Escherichia coli* (ESBL-*E. coli*) are antimicrobial-resistant bacteria of global concern at human–animal–environment interfaces, yet data from South American marine ecosystems remain scarce. This study assessed the occurrence and genomic characteristics of ESBL-*E. coli* in stranded marine mammals along the northern Atlantic coast of Argentina. Between 2021 and 2023, fecal samples (n=128) were collected from pinnipeds (n=93) and cetaceans (n=35) along ~600 km of the Buenos Aires Province coastline, a populated coastal region influenced by agriculture runoff and other anthropogenic inputs. Isolates obtained by selective culture were phenotypically confirmed as ESBL producers and characterized by whole-genome sequencing and core-genome SNP analysis against South American reference genomes. ESBL-*E. coli* was detected in two samples (1.6%) from a South American fur seal (*Arctocephalus australis*) and a humpback whale (*Megaptera novaeangliae*). Both isolates were multidrug resistant, carried *bla*_{CTX-M-14} with additional resistance determinants, and belonged to sequence type ST1049. Despite originating from a resident pinniped and a migratory cetacean, the genomes differed by only six core SNPs, suggesting exposure to closely related environmental strains. Conversely, both isolates showed large genetic distances (≥ 724 SNPs) from human-derived ST1049 genomes from Argentina and Brazil. These findings provide the first evidence of ESBL-*E. coli* in marine mammals from Argentina and support coastal ecosystems as sites of antibiotic resistance dissemination. The detection of closely related resistant strains in ecologically distinct marine mammal species highlights environmental contamination pathways and underscores the need for integrative One Health approaches to understand AMR dynamics at the land-sea interface.

Prevalence of *Plasmodium* sp. in *Larus dominicanus* along the coast of Santa Catarina between 2020 and 2021

Tuesday, 28th July - 11:50: Global Voice Student Session 2 (Virtual/Online) - Oral

***Luiz Filipe Moreira Pereira*¹, *Vitória Loiola Batista*¹, *Lis Marques de Carvalho e Vieira*¹, *Luiz Gustavo Magalhães Alves*¹, *Regiane da Silva Rodrigues*², *Thais Marcelino Silva*³, *Amanda Maria Picelli*¹, *Joaquim Olinto Branco*⁴, *Érika Martins Braga*¹**

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Haemosporidians are heteroxenous protozoa transmitted by hematophagous dipterans. These parasites are widely studied in birds, have a global distribution, and can be highly pathogenic in seabirds. Despite this, the prevalence of haemosporidian infections in seabirds is generally described as low or even absent. This study aimed to report the prevalence of *Plasmodium* sp. in *Larus dominicanus* along the coast of Santa Catarina, Brazil. Blood samples from 87 individuals found stranded and monitored by the Beach Monitoring Program of the Bay of Santos, SC/PR Area (PMP-BS), between 2020 and 2021 were analyzed. Duplicate blood smears were prepared, stained with 10% Giemsa, and examined by light microscopy at 100× magnification. Microscopy identified blood forms compatible with *Plasmodium* sp. in 6 individuals, corresponding to a prevalence of 6.4%. Cases occurred in all seasons except winter, reinforcing the seasonality and the low-prevalence pattern observed in other seabird groups. *Plasmodium* is a cosmopolitan parasite with pathogenic potential reported especially in penguins and procellariiforms kept in captivity. Thus, the epidemiological data presented here contribute to understanding haemosporidian infections in seabirds in Brazil and suggest a possible role of *L. dominicanus* as a wild reservoir of this potentially pathogenic parasite, whose investigation should be prioritized in future studies.

Wildlife Considerations in Disaster Risk Reduction and Resilience Planning: A Biodiversity Gap Analysis in Coastal, South Carolina

Tuesday, 28th July - 12:05: Global Voice Student Session 2 (Virtual/Online) - Oral

***Michelle Dzurenda**¹, **Pamela Martin**²*

1. Coastal Carolina University, 2. Coastal Carolina University

Disaster risk reduction and resilience planning efforts along coastal communities of South Carolina have historically focused on mitigating the impacts of hurricanes and flooding. Other climate-related hazards have intensified in recent years such as fluctuating weather patterns, increasing temperatures, and wildfires. Climate change is not solely responsible; human impact including an increase in urban expansion, coastal development, and habitat fragmentation has further contributed to biodiversity loss and ecosystem disruption. Although disasters threaten both human and ecological communities, resilience planning frameworks remain largely anthropocentric. Existing preparedness and mitigation strategies often prioritize human infrastructure, economic recovery, and public health, while insufficiently considering wildlife populations. This interdisciplinary gap analysis examines biodiversity inclusion within resilience planning efforts along coastal South Carolina. The disaster-vulnerable area continues to rapidly develop, increasing the need for biodiversity conservation and ecosystem interdependence. This analysis explores how wildlife considerations are often overlooked, insufficiently integrated, or excluded in disaster risk preparedness plans, causing negative impacts across environmental, social, and economic sustainability outcomes. This work further examines opportunities to strengthen mitigation plans using a collective impact of related disaster preparedness strategies and a One Health perspective. This topic aligns with the United Nations Sustainable Development Goals (SDGs) including SDG 13 Climate Action, SDG 14 Life Below Water, and SDG 15 Life on land, and emphasizes the need for interdisciplinary resilience planning models in disaster prone regions.

Predicting Wildlife Disease Risk from Space: Avian Tick Parasitism and Land-Use Change Across the Colombian Andes

Tuesday, 28th July - 12:45: Global Voice Short Presentations (Virtual/Online) - Oral

***Sreeja Puthumana*¹, *Gustavo A. Londoño*², *Julie M. Allen*³, *Mohamed Sallam*¹**

1. Global Public Health Diseases Ecology Lab, Preventive Medicine and Biostatistics Department, Uniformed Services University of the Health Sciences, Bethesda, 2. Departamento de Ciencias Biológicas, Facultad de Ciencias Naturales, Universidad Icesi, 3.

Department of Biological Sciences, Virginia Tech

Wild birds disperse immature ixodid ticks and their pathogens across landscapes, making avian–tick infestation a critical but underused indicator of wildlife disease risk in fragmented tropical ecosystems. Yet the environmental and host drivers structuring these interactions across changing Neotropical landscapes, and their implications for avian conservation and pathogen surveillance, remain poorly resolved. Across 12 years (2008–2019), we screened 1,164 birds (12 orders, 204 species) for ixodid ticks at 15 Colombian Andean localities spanning ~500–3,121 m a.s.l. across Eastern, Western, and Middle slopes. Macrohabitat predictors, seven Sentinel-2 land-use/land-cover (LULC) classes (10-m resolution, Google Earth Engine), elevation, and climate, were extracted within 10-km buffers, with decadal LULC change quantified in ArcGIS Pro. Three Random Forest models (host-trait, macrohabitat, integrated) partitioned drivers of tick prevalence across ecological scales. Infestation peaked in the Eastern Andes (up to 46.5% of birds at 3,120 m) and was lowest in mid-elevation valleys, spatially overlapping known regional foci of spotted-fever group rickettsiae. LULC trajectories diverged: Evergreen Broadleaf Forest expanded across Western sites while grasslands encroached on the Eastern slope (net shift -1.530 km²), reshaping habitat suitability for off-host tick survival in opposite directions. The integrated model achieved near-ceiling discrimination (AUC = 0.98); elevation and vegetation structure dominated, with host traits (mixed-flock participation, bill morphology, foraging stratum) acting as secondary modulators. These findings identify Andean elevational and LULC-change hotspots where avian ectoparasite burdens and the tick-borne pathogens they mediate concentrate, offering a satellite-based One Health framework to prioritize wildlife disease surveillance and conservation of vulnerable montane avifauna.

Queering Urban Ecology and Conservation

Tuesday, 28th July - 13:20: Global Voice Short Presentation (Virtual/Online) - Oral

*Genevieve Barnett*¹

1. Night Flight Rehabilitation

The use of the word “queer” is not limited to sex and gender, but includes those concepts, and they should not be left out of the larger ecological picture. It is impossible to see our world and its needs by constantly looking through a pinhole. We leave out vast swaths of knowledge when we try to sterilize our discussions. We are never free of bias; who we are and what we do shapes the kinds of questions we ask and the solutions we may find. Language matters, and so does inclusion. To be seen is to be understood is to be cared for. How can we protect wildlife and ecosystems that we do not know or acknowledge. Persistence and tenacity, especially in making large-scale change, is not only found in othered groups of people, but it is a commonality linking those of us who are Queer. As problem-solvers, we must resort to the many ways of knowing our world. What has been presented does not work, and so we make our own solutions.

Awareness of queer biology and wildlife encourages more queer rehabilitators to enter the field. This in turn helps reverse declining population of rehabbers, and directly benefits our local wildlife populations, many of which are dealing with severe health and conservation issues. Queer(ing) ecology is vital to preservation, conservation, and implementing One Health concepts for the sake of life and wildlife.

Viral surveillance in wild mammals in an urban center in Brazil

Tuesday, 28th July - 13:30: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

***Bruna Hermine de Campos*¹, *Daniel Oliveira dos Santos*¹, *Janaina Ribeiro Duarte*¹, *Vinicius Henrique Barbosa Amaral*¹, *Nadja Simbera Hemetrio*², *André Duarte Vieira*¹, *Letícia Neves Ribeiro*¹, *Sara Cândida Ferreira dos Santos*¹, *Talita Emile Ribeiro Adelino*³, *Maurício Teixeira Lima*¹, *Carlyle Mendes Coelho*², *Herlandes Penha Tinoco*², *Luiz Carlos Junior Alcantara*⁴, *Felipe Campos de Melo Iani*³, *Erica Azevedo Costa*¹, *Renato Lima Santos*¹, *Marcelo Pires Nogueira de Carvalho*¹**

1. Universidade Federal de Minas Gerais, **2.** Fundação de Parques Municipais e Zoobotânica de Belo Horizonte, **3.** Fundação Ezequiel Dias, **4.** René Rachou Institute, Oswaldo Cruz Foundation

Environmental challenges from anthropogenic pressures in urban ecosystems favor generalist species with high ecological plasticity, which can serve as strategic sentinels for pathogen surveillance. Belo Horizonte, in southeastern Brazil, has reported circulation of Influenza A and SARS-CoV-2, detected in asymptomatic coatis. Following this finding, this study monitored 28 viral agents over three years in generalist mammals from six urban parks. Specimens were captured using traps, restrained, anesthetized, clinically examined, and subjected to non-lethal biological sampling (whole blood, oral, and rectal swabs), following protocols approved by the required ethical and environmental licenses. Samples underwent DNA and RNA extraction and purification using magnetic beads. Molecular and serological analyses were conducted to detect viral agents. A total of 390 animals from the genera *Nasua*, *Callithrix*, *Didelphis*, and *Cerdocyon* were captured, in addition to carcasses collected within the study areas. Molecular analyses detected canine distemper virus in *Callithrix* (n = 7) and *Cerdocyon* (n = 2), and herpesvirus in *Nasua* (n = 34), *Callithrix* (n = 34), and *Didelphis* (n = 15). Next-generation sequencing (NGS) revealed a distinct clade of canine distemper virus and the presence of *Human alphaherpesvirus 1* in primates. Serological analyses showed exposure over the three-year period to three subtypes of *Alphainfluenzavirus influenzae*, rabies virus, and canine parvovirus across the three species, while SARS-CoV-2 exposure was detected only in coatis (*Nasua nasua*), indicating prior viral contact. These findings highlight the importance of integrated epidemiological surveillance, the impacts of urbanization on wildlife populations, and potential implications for the One Health approach.

Urban Adaptation and Emerging Disease: Molecular Characterization of Burrowing Owl Diet Illuminates Rat Lungworm Transmission Ecology

Tuesday, 28th July - 13:45: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

Håkon Jones¹, Nikole Castleberry¹, Brittany Piersma¹, Michael J. Yabsley²

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

The Florida burrowing owl (*Athene cunicularia floridana*) is a state-threatened subspecies increasingly restricted to urban landscapes where novel health threats emerge. A population on Marco Island, Florida was recently documented with fatal neuroangiostrongyliasis caused by *Angiostrongylus cantonensis*, a zoonotic nematode cycling through rodent definitive hosts, mollusk intermediate hosts, and diverse paratenic hosts. Understanding transmission pathways requires detailed knowledge of owl foraging ecology, yet traditional diet studies using morphological identification of pellet contents underestimate dietary breadth. We employed next-generation sequencing (NGS) of pellets and fecal samples collected from nest sites during the 2024 breeding season to comprehensively characterize diet and identify potential parasite transmission sources. Using three primer sets targeting arthropods, universal metazoans, and vertebrates, we documented exceptional taxonomic breadth encompassing 60 families, 80 genera, and 74 species. Owls consumed numerous confirmed and suspected *A. cantonensis* hosts, including veronicellid slugs, centipedes, decapod crustaceans, and multiple amphibian and reptile species. Strikingly, non-native species comprised approximately 71% of species-level dietary reads, reflecting the highly altered fauna of southern Florida and demonstrating remarkable dietary plasticity. The diversity of potential transmission pathways precludes identification of a single dominant infection source, suggesting risk mitigation in this population will require broad-based approaches. This study illustrates how urban wildlife species serve as sentinels for One Health concerns, with owl infections signaling *A. cantonensis* establishment in prey communities shared with human environments. NGS dietary analysis offers a powerful tool for simultaneously characterizing wildlife foraging ecology and surveilling zoonotic parasite distribution in urban ecosystems.

Where Worlds Collide: Spatial patterns of disease risk in African buffalo at the human-wildlife interface of Kruger National Park

Tuesday, 28th July - 14:00: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

***Eberle Yarborough*¹, *Hendrik Combrink*², *Robert Spaan*¹, *Peter Buss*³, *Lin Mari de Klerk-Lorist*⁴, *Cambrey Knapp*¹, *Lauren Schreck*⁵, *Intimate Shongwe*⁶, *Michele Miller*⁷, *Govert van Dam*⁸, *Paul L.A.M. Corstjens*⁹, *Petunia Msuthwana*¹⁰, *Khethiwe Mtshali*¹⁰, *Marché Duarte*¹¹, *Nicola Collins*¹¹, *Brianna Beechler*¹, *Anna Jolles*⁵**

1. Oregon State University, Carlson College of Veterinary Medicine, Department of Biomedical Sciences, **2.** The University of Arizona, School of Natural Resources and the Environment, **3.** South African National Parks (SANParks), Veterinary Wildlife Services, **4.** Republic of South Africa, National Department of Agriculture, State Veterinary Services, **5.** Oregon State University, Department of Integrative Biology, **6.** University of Mpumalanga, School of Biology and Environmental Sciences, **7.** Stellenbosch University, SAMRC Centre for TB Research, Faculty of Medicine and Health Sciences, **8.** Leiden University Medical Center, Leiden University Center for Infectious Diseases, **9.** Leiden University Medical Center, Department of Cell and Chemical Biology, **10.** Tshwane University of Technology, Department of Biomedical Sciences, **11.** University of Pretoria, Department of Veterinary Tropical Diseases

Diseases threaten wildlife conservation both directly, through reductions in wildlife population health, and indirectly, by putting human and domestic animal health at risk. Increased disease transmission risk along these wildlife-livestock-human interfaces frequently leads to conflict, and in sub-Saharan Africa, buffalo are often portrayed as the villain in these narratives. From a management and policy perspective, understanding the spatial distribution of potential disease spillover risks is essential for conflict mitigation and safeguarding the long-term viability of key conservation areas. Here, we used a novel analytical tool, Integrated Nested Laplace Approximation - Stochastic Partial Differential Equations (INLA-SPDE), to identify disease hotspots for three important pathogens in one of Africa's most important conservation areas, Kruger National Park (KNP). We tested buffalo samples across KNP for bovine tuberculosis (zoonotic TB), schistosomiasis, and anaplasmosis, representing directly transmitted, environmentally transmitted, and tick-borne pathogens, respectively. Annually, zoonotic TB and schistosomiasis affect around 140-250 million people each, while anaplasmosis is considered to be one of the most important tick-borne pathogens of cattle in South Africa. We uncovered striking spatial heterogeneity in disease prevalence for these pathogens and elucidated key landscape features associated with risk hotspots. Our results will guide park management in engaging with targeted surveillance and resource distribution efforts and enhance understanding of landscape features that drive these patterns, which may be modified to mitigate transmission risk. Thus, this study exemplifies how to determine locally specific priorities for disease control and prevention, ensuring healthy populations - both human and animal, domestic and wild.

INTRA-URBAN STRUCTURING OF HEAVY METAL EXPOSURE AND MORPHOLOGY IN MUSCOVY DUCKS (*CAIRINA MOSCHATA*)

Tuesday, 28th July - 14:15: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

***Matt Tatz*¹, *Sonia Hernandez*², *Stacey Lance*³**

1. Odum School of Ecology, University of Georgia, **2.** Warnell School of Forestry and Natural Resources, University of Georgia, **3.** Savannah River Ecology Laboratory, University of Georgia

Urban environments are often treated as homogeneous systems, with many wildlife health studies comparing urban and non-urban sites rather than examining fine-scale variation within cities. Orange County, Florida represents a heterogeneous urban landscape characterized by dense development, artificial water bodies, and variable environmental exposure conditions, making it well suited for examining intra-urban structuring of wildlife health. We evaluated relationships between multivariate heavy metal exposure and morphometric residuals in adult Muscovy ducks (*Cairina moschata*) across Orange County.

Feathers were analyzed for mercury, and livers were analyzed for eight metals: chromium, nickel, copper, zinc, selenium, strontium, lead, and cadmium. Multivariate contaminant profiles were assessed using non-metric multidimensional scaling and permutational multivariate analysis of variance (PERMANOVA) and were compared with site and morphometric residuals. Heavy metal composition differed significantly among sites ($R^2 = 0.176$, $p = 0.001$), indicating strong fine-scale spatial structuring of contaminant exposure despite close geographic proximity. Individual bird morphometric structure also differed significantly among sites ($R^2 = 0.16$, $p = 0.003$), suggesting localized developmental or environmental influences on body morphology. A cross-comparison revealed that multivariate metal exposure was significantly associated with morphometric structure independent of site clustering ($R^2 = 0.325$, $p = 0.044$).

Collectively, these findings indicate that contaminant exposure and morphology are strongly structured at fine spatial scales within urban landscapes. The observed coupling between heavy metal exposure and morphometric structure suggests that localized contaminant exposure profiles may align closely with developmental or structural processes. Overall, these patterns highlight the importance of examining intra-urban heterogeneity when evaluating wildlife health.

How social behavior shapes viral transmission: A phylodynamic study of foot-and-mouth disease in African buffalo

Tuesday, 28th July - 14:30: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

***Cambrey Knapp*¹, *Ranjitha Bommanna*², *Richard Orton*³, *Simon Gubbins*², *Eva Perez-Martin*², *Brianna Beechler*¹, *Anna Jolles*⁴, *Roman Biek*⁵**

1. Oregon State University, Carlson College of Veterinary Medicine, Department of Biomedical Sciences, 2. The Pirbright Institute, 3. Center for Viral Research, 4. Oregon State University, Department of Integrative Biology, 5. University of Glasgow

Recent pandemics driven by rapidly-evolving pathogens such as foot-and-mouth disease virus (FMDV), SARS-CoV-2 and avian influenza have underscored the importance of combining phylodynamic inference and behavioral data to understand and predict transmission. This is particularly important for diseases circulating at human, wildlife, and domestic animal interfaces. However, the opportunity to link longitudinal pathogen genetics and high-resolution behavioral data necessary for epidemiologic inference within wildlife populations is rare, leaving major gaps in our understanding of transmission patterns in free-ranging hosts. FMDV, the most infectious livestock pathogen globally, remains difficult to control in sub-Saharan Africa in part because African buffalo serve as a wildlife reservoir. This study follows an isolated population of wild African buffalo in Kruger National Park, South Africa, where we captured and sampled 108 collared individuals for FMDV every two months during a 15-month study period. By using a Structured Coalescent Transmission Tree Inference framework implemented in BEAST2, we reconstructed how FMDV lineages moved through the population. By integrating this network with host traits and continuous association data from proximity collars, we demonstrate how social connectivity within a population has a measurable effect on transmissibility. This study provides both new insight into the ecological drivers of FMDV transmission and also demonstrates a generalizable framework for linking host social structure with infectious disease dynamics in wildlife.

A calibrated metapopulation framework for evaluating chronic wasting disease management scenarios in white-tailed deer (*Odocoileus virginianus*)

Tuesday, 28th July - 14:45: Student Presentations - Urban Wildlife & Wildlife Interfaces (O'Hare 1-2) - Oral

***Maris Daleo*¹, *Jameson Mori*¹, *Nohra Mateus-Pinilla*¹**

1. Wildlife Veterinary Epidemiology Laboratory, Illinois Natural History Survey-Prairie Research Institute, University of Illinois Urbana-Champaign

The ongoing spread of chronic wasting disease (CWD) in white-tailed deer (*Odocoileus virginianus*) across the United States underscores the need for robust modeling tools to evaluate disease spread and management strategies. We present a stochastic, spatially aggregated, age-structured metapopulation model designed to assess CWD invasion risk and management scenarios. The model integrates four parameter classes to balance foundation parameters with projected estimates: 1) empirically fixed parameters derived from demographic and harvest data, 2) latent transmission and environmental parameters estimated via time-series calibration, 3) scenario parameters representing management actions, and 4) structural parameters defining model form. This hierarchical parameter structure allows the model to be constrained by available data while maintaining the flexibility to explore management alternatives and test competing hypotheses about disease dynamics. We demonstrate a calibration approach that fits simulated apparent prevalence to observed zone-specific prevalence time series across multiple harvest intensities, allowing the model to capture real-world disease dynamics. The model achieved strong validation performance, demonstrating its capacity to project future scenarios. To demonstrate the model's utility, we are evaluating the relationship between harvest intensity and CWD invasion risk in Illinois. This modeling framework will provide a quantitative tool to evaluate management scenarios—including a “do nothing approach” after CWD has been identified at different apparent prevalence estimates— to test mechanistic hypotheses, and inform ongoing discussions about long-term CWD control strategies. The modular structure allows adaptation to different regions, deer populations, and management contexts, making it a valuable addition to the growing toolkit for CWD management.

Medgene Lab's rabbit hemorrhagic disease virus 2 vaccine efficacy and potential use in cottontail conservation

Tuesday, 28th July - 15:45: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

***Cole Wzientek*¹, *Hannah Shapiro*¹, *Dana Karelus*², *Angela Bosco-Lauth*³, *Alynn Martin*⁴**

1. Caesar Kleberg Wildlife Research Institute, **2.** Texas Parks and Wildlife Department, **3.** Department of Biomedical Sciences, Colorado State University, **4.** Department of Biology, Grand Valley State University

Rabbit hemorrhagic disease virus 2 (RHDV2) is a highly transmissible pathogen that causes rapid death (~2 days) in lagomorphs via internal hemorrhaging, with up to 80% mortality. Since its first documentation in wild lagomorphs in the United States (U.S.; New Mexico, March 2020), RHDV2 has spread throughout the western U.S. and is now considered endemic. With vulnerable species like the Davis Mountains cottontail (DMC; *Sylvilagus holzneri robustus*) occupying the region, a vaccination strategy is crucial for effective wildlife management. While the Medgene® RHDV2 vaccine has proven successful in mitigating disease in domestic rabbits, its efficacy in DMCs is unknown. Our objective was to measure antibody production in eastern cottontails (*S. floridianus*) as a DMC surrogate. Rabbits (n=19) were divided into three vaccine treatment group: two dosages (days 0 and 21, recommended posology; group₁), a single dosage (day 0; group₂), or control (group_c). Serum was obtained weekly to quantify antibody development via enzyme-linked immunosorbent assays. No difference in baseline antibody concentrations was observed (mean ± standard error, group₁= 0.0503±0.0206, group₂= 0.1006±0.0435, group_c= 0.0307±0.0149). By week 5, antibody concentrations were significantly different across all three treatment groups ($p < 0.05$; mean ± standard error, group₁= 1.1656±0.324, group₂= 0.3996±0.113, group_c= 0.0351±0.0118). At week 29 (April 2026), individuals will be challenged with RHDV2 to determine the Medgene® vaccine's long-term efficacy. This study demonstrates that a reduced dosage may still provide partial protection against RHDV2, an important finding given the logistical challenges of vaccine administration in wildlife, where completing the full posology may not be feasible.

Development and Validation of a Quantitative PCR Assay for Detection of Two Novel Adenoviruses in Ornate Box Turtles (*Terrapene ornata ornata*)

Tuesday, 28th July - 16:00: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

***Erika R. Suniga*¹, *Stephanie Brien*¹, *Crystal Moreno-Garcia*², *Amber Simmons*², *Matthew Allender*³,
*Laura Adamovicz*²**

1. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign, 2. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign, 3. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Chicago Zoological Society, Brookfield Zoo, Brookfield, IL

Ornate box turtles (*Terrapene ornata ornata*) are endangered in Illinois, but disease threats are poorly understood in this species. Novel adenoviruses, including Ornate Box Turtle Adenoviruses 2 and 3 (OBTAdv-2; OBTAdv-3) have recently been identified in this species, but characterization of the epidemiology and clinical impacts of these viruses requires sensitive and specific diagnostic tests. The purpose of this study was to develop and validate two quantitative PCR (qPCR) assays for detection of OBTAdv-2 and OBTAdv-3 in ornate box turtles. TaqMan primer-probes were developed targeting the DNA polymerase gene and evaluated using plasmid-derived standard curves and clinical samples. Inter- and intra-assay variability, dynamic range, limit of detection, and analytical specificity were assessed. Both assays were highly specific for OBTAdv-2 and OBTAdv-3, failing to amplify eighteen closely related reptile adenoviruses. The assays were also highly repeatable both within (OBTAdv-2 coefficients of variation [CV] = 0.13-0.51%, OBTAdv-3 CV = 0.26-1.41%) and between runs (OBTAdv-2 CV = 0.72-3.29%, OBTAdv-3 CV = 0.13-1.26%). Assay performance fell within acceptable parameters (OBTAdv-2 slope = -3.46, R-squared = 0.998, efficiency = 94.56%; OBTAdv-3 slope = -3.255, R-squared = 1, efficiency = 102.86%) and was not impacted by the presence of sample matrix. Both assays had a dynamic range of 10 – 10,000,000 target copies and a limit of detection of 10 copies. Overall, both assays meet established criteria for acceptable qPCR assays and will be a valuable diagnostic tool for future surveillance and characterization of OBTAdv-2 and OBTAdv-3 epidemiology in ornate box turtles.

VISUALIZATION AND DETECTION OF SIN NOMBRE HANTAVIRUS IN MULTIPLE TISSUES OF WILD DEER MICE, INCLUDING THE REPRODUCTIVE TRACT

Tuesday, 28th July - 16:15: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

***Rebecca Radisic*¹, *Alexandra Stone*¹, *Ernesto Rojas-Sanchez*¹, *Reena Grewal*¹, *Erin Howell*¹, *Tracy Drazenovich*¹, *Alexandre Tremeau-Bravard*¹, *Jalika Joyner*¹, *Olivia Cords*¹, *Ken Jackson*², *Patricia Pesavento*², *Brian Bird*¹**

1. University of California, Davis, Weill School of Veterinary Medicine, One Health Institute, 2. University of California, Davis, Weill School of Veterinary Medicine, Department of Pathobiology, Microbiology, and Immunology

The North American deer mouse (*Peromyscus maniculatus*) is a natural reservoir of Sin Nombre hantavirus (SNV), which can cause fatal disease in humans via inhalation of aerosolized rodent excreta. While rodent-to-rodent transmission occurs through saliva during fighting and mating, the role of reproductive tissues in maintaining or transmitting SNV is unclear. We collected tissues from 169 deer mice in an SNV-endemic area of northern California, including oral and urogenital swabs, kidney, spleen, liver, lung, and ovary or testis. Samples were evaluated by RT-qPCR and in situ hybridization (ISH); electron microscopy and genomic sequencing are pending. Overall, 48.5% (82/169) of animals were RT-qPCR positive in at least one tissue. ISH was performed on a selection of eight animals (four RT-qPCR negative, four positive). No probe hybridization was detected in PCR negative animals. In PCR positive animals, ISH detected virus in the lung, spleen, and kidney, consistent with known tissue distribution in naturally infected deer mice and supporting routes of exposure relevant to spillover. Notably, 32.0% (54/169) of animals had RT-qPCR-positive reproductive tissues (32 males, 22 females); however, no ISH signal was observed in the reproductive tract segments analyzed. These findings confirm SNV localization in multiple tissues of naturally infected deer mice, verified by RT-qPCR and ISH, complementing prior experimental and immunohistochemistry studies. They also underscore the need for further investigation of reproductive tissues and transmission dynamics among deer mice.

Development and Pathophysiology of Chimeric Invasive Gastrovascular Multicellular Structures (IGMS) in Montipora White Syndrome

Tuesday, 28th July - 16:30: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

Chutimon McGuire¹

1. University of Hawaii at Manoa

Montipora white syndrome (MWS) or tissue loss is a major cause of mortality in *Montipora capitata* in Hawai'i and has the potential to degrade Hawai'i's coral reefs over time. The causes of Montipora white syndrome in corals are multiple and complex including invasive gastrovascular multicellular structure (IGMS), ciliates, helminths, fungi, cyanobacteria, and bacteria. Substantial knowledge exists about the role of *Vibrio coralliilyticus* in causing Montipora white syndrome, little is known about the role of IGMS in MWS. IGMS has been found in up to 34% of MWS cases using histology and remains a recurring issue in both wild and nursery corals. IGMS are hypothesized cell-lineage parasites that are a result of chimeric fusion between *M. capitata* and *M. flabellata* larvae. A deeper understanding of how IGMS develop, function, and survive is essential to elucidating their role in the pathophysiology of MWS.

Through viability assays, we determined that IGMS can survive in raw seawater for up to five days. Microscopic analysis revealed that IGMS possess an ostium connected to a central cavity containing cellular debris, along with specialized cells capable of mucus secretion. TEM and SEM ultrastructural analysis confirmed the presence of motile cilia, which facilitate movement and potentially mediate interactions with bacteria on the external surface of the IGMS. We used proteomics to identify potential pathological pathways and characterize the molecular interactions between IGMS and the coral host. Our findings provide a foundational understanding of how these unique chimeric structures contribute to tissue loss in *M. capitata*.

Treatment trial of terbinafine submersion and increased water salinity in the treatment of *Emydomyces testavorans* in chronically infected captive Blanding's turtles (*Emydoidea blandingii*) and alligator snapping turtles (*Macrochelys temminckii*)

Tuesday, 28th July - 16:45: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

Marguerite Bednarek¹, Madeline Brookings¹, Laura Adamovicz², Kaitlin Moorhead¹, Carly Etter¹, Kamila Grochowski-Grum¹, Surina K. Birk¹, Katelyn Deppe¹, Madison Kasbaum¹, Erika R. Suniga¹, Ryland Darling¹, Jaime R. Lyke¹, Javelis Marín Castro¹, Rebecca Chenoweth¹, Grace Minge¹, Jenna Camargo¹, London Wimberly¹, Amber Simmons³, Crystal Moreno-Garcia³, Matthew Allender³

1. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign, 2. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Lab, College of Veterinary Medicine, University of Illinois Urbana-Champaign, 3. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign

Emydomyces testavorans (ET) is an emerging fungal pathogen in the order *Onygenales* associated with shell lesions of conservation concern in multiple chelonian species. A treatment protocol consisting of thrice-weekly terbinafine baths (1mg/mL x 30 min) combined with continuous immersion in 3ppt salt water has resulted in clinical and molecular resolution of ET infection in acutely-infected headstarted Blanding's turtles (*Emydoidea blandingii*), however, successful treatments are not yet described for turtles with chronic ET infection and those of different age classes. The purpose of this study was to assess the efficacy of the terbinafine bath protocol for treatment of chronic (at least three years duration) ET infections in adult Blanding's turtles (N = 5), sub-adult Blanding's turtles (N = 5), and alligator snapping turtles (*Macrochelys temminckii*, N = 5). Turtles were individually housed and treated as described above. Physical examinations and cloacal/oral/shell swabs were collected monthly for ET qPCR testing. Adult Blanding's turtles achieved their first negative result for ET after 4 months (N = 2) or 6 months (N = 2) of treatment, however, all turtles subsequently tested positive 9 – 11 months after discontinuing treatment. All other turtles remain qPCR positive after 18 months of treatment. This study demonstrates that the terbinafine bath protocol is less efficacious for treatment of chronic ET infections and indicates that additional work is needed to identify effective treatment options.

Biodiversity linkages with wildlife host prevalence and human spillover

Tuesday, 28th July - 17:00: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

***Shariful Islam*¹, *Gideon Wasserberg*², *Luis Escobar*³**

1. Department of Fish and Wildlife Conservation, Virginia Tech, Blacksburg, VA, **2.** Biology Department, University of North Carolina at Greensboro, Greensboro, NC, **3.** Department of Fish and Wildlife Conservation, Virginia Tech, Blacksburg, VA, United States, **2**GlobalChange Center, Virginia Tech, Blacksburg, VA

Lyme disease, caused by *Borrelia* spp. and transmitted by *Ixodes scapularis*, continues to rise across the United States. Although the “dilution effect” hypothesis suggests that higher host diversity reduces pathogen infection, mechanisms linking *Borrelia* circulation in wildlife to human spillover remain elusive. We examined *Borrelia* prevalence in rodents and ticks, their interrelationship, and associations with human Lyme disease incidence.

We utilized NEON rodent and tick data alongside CDC Lyme surveillance data from 2020–2023. Polymerase chain reaction testing was conducted on 12,762 rodent blood samples from 20 species across 35 sites and 1,211 *I. scapularis* ticks from eight sites. Linear regression model evaluated the association among rodent prevalence, tick prevalence, rodent diversity, and county-level human Lyme incidence (per 1,000 people).

Rodent species richness ranged from five species in Konza, Kansas to one in Moab, Utah. *Peromyscus leucopus* (34.2%, n=4370) and *P. maniculatus* (32.8%, n=4191) were most abundant. Seven rodent species tested positive for *Borrelia*, with an overall prevalence of 0.52% (n=66); Treehaven, Wisconsin had the highest site-level prevalence (2.04%). *Onychomys torridus* showed the highest species-level prevalence (2.56%). Among ticks, 246 (20.28%) were positive, with the highest prevalence in Maryland (29.20%). Rodent and tick prevalence were positively but not significantly associated. Human Lyme incidence was best explained by rodent prevalence and the first diversity PCA ($P=0.001$); rodent prevalence alone was strongly associated with human incidence ($P=0.0004$).

We found no evidence supporting the dilution effect. Rodent infection prevalence was the strongest predictor of human Lyme incidence, highlighting rodents as key sentinels of Lyme disease risk.

The Structure of Wildlife Health Collaboration Networks in California

Tuesday, 28th July - 17:15: Student Presentations - Analyses, Detection and Treatment (O'Hare 1-2) - Oral

***Hannah Shapiro*¹, *Mark Lubell*¹, *Deana Clifford*², *Alex Heeren*², *Brandon Munk*²**

1. UC Davis, 2. California Department of Fish and Wildlife

Wildlife health cannot be managed by wildlife agencies alone, as the health of free-ranging wildlife populations is intertwined with the health of domestic animals, humans, and ecosystems. Collaborative networks emerge to address jurisdictional and resource challenges related to the management of wildlife health in these complex systems. We created a two-mode network from interviews with animal, human, and ecosystem health experts to map the collaborative wildlife health networks in California and identify key brokerage institutions that connect distant parts of the network. Two-mode networks consist of two different sets of nodes (organizations and collaboratives), where the ties only connect nodes of different sets. We identified over 70 collaborative forums and 550 organizations. We found that organizations were often clustered based on One Health sector (animal, ecosystem, human health). This result indicates there are limited cross-disciplinary collaborations despite growing calls for a more integrated approach to wildlife and zoonotic disease management. The wildlife health collaborative forming in California will likely be an important brokerage collaborative, as its current membership has animal and human health expertise with connections to diverse collaborative forums across the network, including disease-specific forums, species recovery teams, professional societies, and stakeholder interest groups. Our research design and analysis demonstrate how networks can be used to identify gaps in collaborative networks and opportunities for further collaboration.

Integrating communities, science, and conservation: the experience of a participatory wildlife health surveillance network in Argentina

Tuesday, 28th July - 17:30: Global Voice (Virtual/Online) - Oral

Marcela Orozco¹

1. CONICET- Universidad de Buenos Aires

Wildlife health surveillance faces significant challenges in regions with limited infrastructure, extensive natural areas, and multiple interfaces between wildlife, domestic animals, and human populations. In Latin America, these limitations hinder the early detection of health events and sustained epidemiological monitoring. In this context, participatory approaches have emerged as valuable tools. This work describes the development and implementation of a wildlife health surveillance network in Argentina, within the framework of an integrated multispecies system that combined participatory, passive, and active surveillance modalities under the One Health approach. Participatory surveillance functioned as a cross-cutting component of the system, integrating stakeholders with different levels of territorial presence, including park rangers, local residents, researchers, veterinarians, and government agencies. The network comprised 110 participants and was strengthened through training, standardized protocols, communication channels, and joint field activities. Coordination with concurrent research projects was promoted, fostering joint campaigns and the shared use of resources and data. The incorporation of rescue centres and a diagnostic network made up of academic institutions, laboratories, and national agencies made it possible to expand the coordinated processing of samples for multiple pathogens. Operational differences between territories were associated mainly with the degree of institutional presence, continuity of activities, and consolidation of local relationships. Nevertheless, the integration between the parts strengthened the operational sustainability of the system and optimized resources. The results highlight the value of participatory networks as structural components of wildlife surveillance systems and their potential to strengthen conservation, public health, and environmental management strategies.

Urban Wildlife Incident Reporting as a One Health Surveillance Tool: Monitoring Morbidity and Mortality in Cape Town

Wednesday, 29th July - 09:25: Global Voice Oral Abstract Presentations (O'Hare 1-2) - Oral

***Dorothy Breed**¹, **Jonathan Bell**¹, **Kashiefa Amos**¹*

1. Environmental Management Department, City of Cape Town

Objective

To describe the development and early implementation of a municipal Wildlife Incident Reporting system designed to monitor wildlife morbidity and mortality and support One Health decision-making in an urban environment.

Context

The City of Cape Town manages 26 nature reserves and 16 Biodiversity Agreement Conservation Areas forming part of the City's Biodiversity Network (BioNet), spanning more than 20 000 hectares within a rapidly urbanising coastal city. Wildlife and human activities frequently intersect across this landscape, creating a need for structured monitoring of wildlife health events.

Methods

Launched in July 2025, the reporting system provides a standardized digital framework to document wildlife incidents including injury, disease, poisoning, vehicle collisions, snaring and mortality events. Both live morbidity cases and mortality investigations are recorded. Where indicated, diagnostic samples are submitted to the Provincial Veterinary Laboratory to support passive disease surveillance. Incident records are being integrated with the City's GIS platform to support spatial analysis and identification of incident hotspots.

Preliminary Findings

Early implementation has improved documentation and coordination of wildlife incident responses and provides a structured mechanism for detecting abnormal wildlife health events.

Conclusion

This municipal reporting system provides a practical framework for monitoring wildlife health in an urban landscape and strengthens early detection of emerging wildlife health risks within a One Health context. The approach may provide a useful model for other cities seeking to establish wildlife health surveillance at the urban-wildlife interface.

Breaking the Rescue Bottleneck: A Dual-Hub Strategy to Disrupt the Illegal Lemur Trade and Restore Madagascar's Most Endangered Primates

Wednesday, 29th July - 09:40: Global Voice Oral Abstract Presentations (O'Hare 1-2) - Oral

Justorien RAMBELONIAINA¹, Jhoanny Rasojivola¹, Abigail Ross¹

1. The Dr. Abigail Ross Foundation for Applied Conservation

Despite increasing conservation awareness, northern Madagascar—particularly the DIANA region—remains a critical hotspot for the illegal lemur pet trade, driven by a persistent “tourist magnet” effect in which an estimated 15% of hospitality establishments have historically displayed lemurs as illicit attractions. Although visible exploitation declined following enforcement operations in 2025, covert “backroom” captivity persists, sustaining demand and exacerbating pressures on critically endangered species such as the Northern Sportive Lemur, whose wild population is estimated at fewer than 50 individuals. This domestic challenge is compounded by resilient international trafficking networks, exemplified by the May 2024 Thailand seizure of 48 individuals, and by a severe regional rescue bottleneck as existing facilities have reached capacity. To address this enforcement–rehabilitation deadlock, we propose a dual-hub conservation framework integrating a Rescue, Rehabilitation, and Release Center in Nosy Kisimany - Nosy Be with a diagnostic and research hub in Ivato. The approach combines coordinated confiscation operations with environmental authorities (DREDD); standardized veterinary triage including pathogen screening and nutritional stabilization; behavioral rehabilitation protocols to reduce human habituation and restore survival competencies; and genomic analyses to assign geographic origin, inform reintroduction, and map trafficking networks. Post-rehabilitation individuals will undergo pre-release fitness assessments, soft-release strategies, and longitudinal monitoring. Capacity-building components include Malagasy veterinary training and data integration platforms. We hypothesize this integrated system will resolve capacity constraints, enable rehabilitation and reintroduction of ≥ 50 individuals annually, improve post-release survival, and convert confiscated lemurs into agents of population recovery, while strengthening enforcement and disrupting trafficking networks nationally and internationally.

Death Tells a Story: Necropsy as a Tool Against Wildlife Crime in Europe

Wednesday, 29th July - 10:35: Global Voice Oral Abstract Presentations (O'Hare 1-2) - Oral

Andreia Garces ¹, Andreia Garcês ²

1. Wildlife Rehabilitation Center University Tras-os-Montes and Alto Douro, 2. University of Tras-os-Montes and Alto Douro

Wildlife welfare and conservation are increasingly recognized as critical components of biodiversity preservation and ecosystem integrity. Nevertheless, anthropogenic pressures on wildlife are intensifying, leading to a growing incidence of wildlife-related crimes. Illegal trade in animals and animal derivatives (e.g., skins, bones, ivory), illegal hunting for bushmeat, poisoning, and environmental contamination represent major threats to wildlife populations across Europe. Annually, numerous wild animals in Europe die due to human-mediated causes, both accidental and intentional. These impacts include excessive hunting, habitat degradation and fragmentation, introduction of invasive species, dissemination of pathogens, pollution, and climate change. Acting individually or synergistically, these drivers contribute to population declines and increased extinction risk for several taxa. This presentation explores the application of necropsy in the investigation of wildlife crime in Europe and its importance for conservation strategies. Through forensic examination, necropsy can reveal trauma, toxic substances, infectious diseases, and other pathological indicators that help distinguish natural mortality from anthropogenic causes. The integration of pathology, toxicology, and forensic science enables authorities and researchers to reconstruct events leading to animal deaths and to prosecute illegal activities more effectively. Wildlife pathology and forensic veterinary medicine are rapidly evolving disciplines that provide essential tools for detecting illegal activities, supporting legal proceedings, and informing conservation strategies. The identification of non-natural causes of mortality is critical for early intervention and mitigation of anthropogenic threats. Strengthening collaboration among veterinarians, conservation biologists, and law enforcement agencies is fundamental to improving detection, reporting, and prevention of wildlife crimes and to safeguarding Europe's wildlife heritage.

Mitogenomic insights into *Sarcoptes scabiei* in American black bears (*Ursus americanus*): COI utility for regional surveillance and cross-species transmission

Wednesday, 29th July - 10:50: Global Voice Oral Abstract Presentations (O'Hare 1-2) - Oral

***Michael J. Yabsley*¹, *Raquel Francisco*², *Ryan Grunert*², *Jomari Rivera Reyes*², *Jillian Broadhurst*², *Amanda Sullivan*², *Megan Beaudry*², *Julia Frederick*², *Marissa Howard*², *Troy Kieran*², *Travis Glenn*², *Justin D. Brown*³, *John Wares*², *Colin Carpenter*⁴, *Ethan Barton*⁴, *Jennifer Bloodgood*⁵, *Therese McNamee*⁶, *John Tracey*⁷, *Carl Tugend*⁷, *Amanda Riggs*⁸**

1. Southeastern Cooperative Wildlife Disease Study, **2.** University of Georgia, **3.** Pennsylvania State University, **4.** West Virginia Division of Natural Resources, **5.** Department of Public and Ecosystem Health, Cornell University College of Veterinary Medicine, Cornell Wildlife Health Lab, Cornell K. Lisa Yang Center for Wildlife Health, **6.** New York State Department of Environmental Conservation, **7.** Virginia Department of Wildlife Resources, **8.** Arkansas Game and Fish Commission

Sarcoptic mange is a skin disease caused by the mite *Sarcoptes scabiei* that affects humans and >150 species of domestic animals and wildlife worldwide. For the American black bear (*Ursus americanus*), sarcoptic mange is considered a significant emerging disease and case numbers have increased dramatically over the past four decades. While molecular techniques, such as DNA sequencing, are commonly used for diagnosis, they remain underutilized for studying cross-species transmission and regional mite variation. We captured complete mitochondrial genomes from *S. scabiei* mites (n = 17) collected from infested black bears in the Eastern United States (U.S.) using custom-designed oligonucleotide baits. These full mitogenomes were then used to refine primers targeting the cytochrome c oxidase subunit I (COI) gene. We then amplified and analyzed 281 *S. scabiei* COI sequences collected across multiple North American wildlife hosts to assess their utility in inferring regional diversity and host specificity. Full mitogenome comparisons with sequences from the U.S., Japan, and Australia revealed three major global *S. scabiei* clades, with two circulating among North American black bears. The COI haplotype networks showed regional clustering rather than host-specific patterns, suggesting that ecological or geographic factors influence transmission dynamics. Our findings confirm the presence of multiple *S. scabiei* lineages in American black bears and other U.S. wildlife and support the use of the COI gene for large-scale, cost-effective screening of genetic variation and potential cross-species transmission. The integration of mitogenome and COI data offers a scalable model for investigating *S. scabiei* diversity in wildlife and domestic hosts.

Record of a Congenital Facial Anomaly in the South American Sea Lion (*Otaria flavescens*)

Wednesday, 29th July - 16:40: Global Voice (Virtual/Online) - Oral

***Ailin Sosa Drouville*¹, *Camila Merodio*¹, *Paula Olivera*¹, *Florencia Soto*¹, *Soledad Barandiaran*², *María Soledad Leonardi*¹**

1. Instituto de Biología de Organismos Marinos (IBIOMAR), Centro Nacional Patagónico (CENPAT - CONICET), 2. Instituto de Investigaciones en Producción Animal (INPA-CONICET-UBA)

In this study, the first case of cleft lip in a South American sea lion (*Otaria flavescens*) pup from Punta Buenos Aires, Península Valdés, Chubut, Argentina was reported. During sampling, morphometric, hematological, and biochemical parameters were recorded and evaluated using inferential statistical analyses (one-sample t-tests). The affected pup showed significantly lower hematocrit (19%; group mean = 53.83%; $t = 19.143$; $df = 5$; $p = 7.17 \times 10^{-6}$) and total protein levels (52 g/L; mean = 78.17 g/L; $t = 8.319$; $df = 5$; $p = 0.0004$) than the rest of the pups. It also exhibited the lowest standard length (69 cm; mean = 79.75 cm; $t = 5.48$; $df = 7$; $p = 0.0009$) and the lowest body mass (12.38 kg; mean = 16.05 kg; $t = 2.603$; $df = 7$; $p = 0.0353$) among the pups evaluated. Although the individual was active and showed no evident behavioral alterations during the observation period, the results suggest a possible impairment of nutritional status, potentially associated with suckling difficulties during lactation. This finding highlights the importance of systematic health monitoring to detect and document rare congenital anomalies in wild pinniped populations.

Risks at the domestic–wildlife interface: a case report of canine distemper in a maned wolf (*Chrysocyon brachyurus*) from Córdoba, central Argentina

Wednesday, 29th July - 16:47: Global Voice (Virtual/Online) - Oral

***Maria del Rosario Ahumada*¹, *Fernando Bettolli*¹, *Javier Edgardo Alvarez*², *Maria Pia Belluzo*³, *Alberto Ighina*⁴**

1. Universidad Católica de Córdoba, 2. Centro de rescate Tatu Carreta, 3. Laboratorio LACE, 4. Veterinaria Giardino

Canine distemper virus (CDV) is a morbillivirus that affects a wide range of wild carnivore species and represents a significant threat, particularly in domestic–wildlife interface areas. The maned wolf (*Chrysocyon brachyurus*) is the largest canid in South America and is considered critically endangered in Córdoba Province, Argentina. Local population status remains poorly known, and recent rescue events associated with injuries have increasingly occurred near populated areas with agricultural activity, reflecting a domestic–wildlife interface scenario. We describe a severe clinical case of CDV infection in an adult female maned wolf found in a comatose state and referred for medical care to the Tatú Carreta Wildlife Rescue Center, a regional reference center for the species. At admission, the animal showed severe neurologic signs compatible with canine distemper, cachexia, hypothermia, and a critical general condition. Medical treatment included intravenous fluid therapy, immunostimulant support, broad-spectrum antibiotic therapy, and vitamin and mineral supplementation. Blood and urine samples were collected for clinical analyses. The diagnosis of canine distemper was confirmed by RT-PCR from blood samples. Despite intensive supportive treatment, the animal died within 48 hours of admission. This case provides relevant information on the role of domestic–wildlife interfaces in viral transmission to wild carnivores, particularly in landscapes affected by deforestation and agricultural expansion. It also highlights the importance of wildlife rescue centers as key components of epidemiological surveillance and the urgent need for domestic dog population control and vaccination programs in rural areas within the distribution range of the species.

Viral spillover and the ecology of emerging infectious diseases

Wednesday, 29th July - 17:00: Global Voice (Virtual/Online) - Oral

David Hayman ¹

1. Massey University

Emerging infectious diseases often arise when ecological, environmental, and social changes create new opportunities for pathogens to move between wildlife, domestic animals, and people. This presentation will explore how wildlife disease ecology can help us understand and anticipate viral spillover, with a focus on host–pathogen–environment interactions, land-use change, wildlife movement, and the interfaces where transmission risk is generated. Drawing on examples from bat-borne viruses and other zoonotic systems, I will discuss how field studies, surveillance, ecological data, and mathematical models can be combined to identify where and how spillover risk emerges. The talk will also consider the importance of One Health approaches that connect wildlife health, ecosystem change, livestock systems, and public health, and how these perspectives can support more targeted prevention. Rather than viewing emerging infections as isolated events, I will highlight the value of understanding the ecological processes that make spillover more or less likely, and the opportunities this creates for earlier, more practical intervention.

Wildlife Disease Surveillance at an Australian Veterinary School since 2008.

Wednesday, 29th July - 18:00: Global Voice Short Presentations (Virtual/Online) - Oral

Pam Whiteley¹

1. Melbourne Veterinary School, The University of Melbourne

Wildlife Health Victoria: Surveillance was established in 2008 at the Melbourne Veterinary School modelled on the Canadian Wildlife Health Cooperative (1990) and Wildlife Health Australia (WHA 2002) for disease surveillance in endemic mammals, birds, reptiles and frogs. Veterinary schools have expertise including pathology, microbiology, parasitology, virology, toxicology, epidemiology and students can be involved. Regional networks including Indigenous and community groups, land managers, zoos, veterinary practices and governmental agencies detect, report, collect and transport dead wildlife for examination and WHA's database is used. Objectives are to understand normal disease patterns and identify changes due to infections, environmental contaminants, climate, host genetic, and human factors. Understanding zoonoses may use samples from live wildlife.

We contributed evidence about spillover of infections from introduced animals (domestic and feral) during colonization to wildlife populations for *Chlamydia pecorum* in koalas, Sarcoptic mange in koalas, and *Pasteurella multocida* in waterbirds. Introduced Phalaris grass causes toxicity in Eastern Grey Kangaroos and endemic *Globocephaloides tridospicularis* nematodes cause mortalities in juveniles. Powerful Owls are exposed to second generation anticoagulant rodenticides and Platypus are exposed to a wide range of environmental contaminants while freshwater systems are impacted by droughts fragmenting populations.

Wildlife disease surveillance requires expertise and partnerships between First Peoples, universities, CSIRO, state and national agencies in agriculture, environment, zoos, EPA, parks and health: One Health. Ongoing education is important. WDA has contributed to informing us of international best practice as does Wildlife Health Australia. Wildlife disease surveillance is collaborative, and I wish to acknowledge and thank them all.

Surveillance of *Mycobacterium ulcerans* in Urban Possums of Geelong, Australia

Wednesday, 29th July - 18:15: Global Voice Short Presentations (Virtual/Online) - Oral

***Pranab Paul*¹, *Kim Blasdell*², *Meaghan Heyward*², *Marcel Klaassen*², *Alyssa E. Barry*¹, *Andy Flies*³,
*Daniel O'Brien*⁴, *Bridgette Mcnamara*⁴, *Eugene Athan*¹**

1. School of Medicine, Deakin University, Geelong, Australia, **2.** Health and Biosecurity, Commonwealth Scientific and Industrial Organisation, Geelong, Australia, **3.** Menzies Institute for Medical Research, University of Tasmania, Hobart, Australia, **4.** Departments of Public Health and Infectious Disease, Barwon Health, Geelong, Australia

Buruli ulcer (BU), a neglected tropical disease caused by *Mycobacterium ulcerans* (MU), is emerging in Geelong, a regional city in Victoria, Australia. Common ringtail possums (*Pseudocheirus peregrinus*) and common brushtail possums (*Trichosurus vulpecula*) are recognised hosts for MU, but little is known about environmental characteristics and urban infrastructure influencing possum distribution and environmental contamination with MU. This longitudinal One Health study investigates the distribution of possums and MU-positive faeces across urban Geelong and associated environmental characteristics. From 2024 to 2026, four serial cross-sectional surveys of possum faecal deposits were conducted every six months at >1,000 systematically spaced locations aligned with a previous 2020 survey. At each site, possum species, estimated faecal pellet number, faecal freshness, vegetation type, drainage, and proximity to urban infrastructure were recorded using Epicollect5. Faecal samples were tested for MU DNA using IS2404 qPCR.

Over 3,400 faecal samples were collected, with ~90% from ringtail possums and ~10% from brushtail possums. Possum faeces were detected at 68%, 78%, and 73% of surveyed locations in the first three surveys compared with 62% in 2020, suggesting expansion into northern and southern suburbs. MU positivity rates were 5.64%, 3.96%, and 7.96%, higher than the 3.07% reported in 2020. Spatial analyses identified clusters of MU-positive possum faeces in residential suburbs reporting human BU cases. These findings demonstrate continued geographic spread of possums and MU in an urban BU endemic area. Future work will develop a field-deployable CRISPR-SHERLOCK assay and integrate wildlife, environmental, and human health data to support predictive risk modelling.

Immune system changes during torpor and winter hibernation in southern hemisphere bent-winged bats: implications for White-nose Syndrome sensitivity

Wednesday, 29th July - 18:30: Global Voice Short Presentations (Virtual/Online) - Oral

***Anna Langguth*¹, *Lindy Lumsden*², *Christopher Turbill*³, *Tomás Villada-Cadavid*³, *Nicholas Wu*⁴, *Nicola Bail*⁵, *Laura Brannelly*¹, *Jasmin Hufschmid*¹**

***1.* Melbourne Veterinary School, The University of Melbourne, *2.* Arthur Rylah Institute for Environmental Research, Department of Energy, Environment and Climate Action Victoria, *3.* Hawkesbury Institute for the Environment, Western Sydney University, *4.* Centre for Terrestrial Ecosystem Science and Sustainability, Harry Butler Institute and *4* School of Environmental and Conservation Science, Murdoch University, *5.* School of Biological Sciences, The University of Adelaide; Southern Bent-wing Bat National Recovery Team; Zoos Victoria**

As reservoirs for zoonotic pathogens, and amid growing threats from habitat loss and diseases like White-nose Syndrome (WNS), it is increasingly urgent to understand how environmental cues like seasonality influence the biology of bats and, in turn, shape their immune function. However, little is known about how winter hibernation and torpor affect immunity in bats, particularly in southern hemisphere species.

We investigated how torpor and winter hibernation influence immune function in eastern and southern bent-winged bats (*Miniopterus orianae oceanensis* and *M. orianae bassanii*) in southeastern Australia. We seasonally sampled blood from over 500 individuals, detecting significant winter immunosuppression, modulated by climate and year. In 52 bats sampled before, during, and after torpor, we observed a profound yet rapidly reversible decline in total white blood cell counts during torpor. Finally, experimental pathogen challenge using the fungal antigen Zymosan showed that white blood cell counts, and bacterial inhibition ability of plasma were unaffected, but torpid bats exposed to Zymosan aroused more frequently - suggesting immune stimulation can alter their hibernation behaviour.

Our findings demonstrate that even brief/ shallow torpor, and relatively mild southern hemisphere winters, significantly influence immune function of bent-winged bats. These results support the hypothesis that Australian bats may be sensitive to *Pseudogymnoascus destructans* infection during hibernation, although the less extreme winters they experience compared to northern hemisphere species may reduce disease severity. Our work provides key data for disease risk assessments and highlights how energy conservation during winter trades off against immune function, shaping bats' sensitivity to emerging pathogens.

Urban Living and Dolphin Health: Insights from Indo-Pacific Bottlenose Dolphins (*Tursiops aduncus*) in South Australia

Wednesday, 29th July - 19:30: Global Voice Invited Talk and Q&A (Virtual/Online) - Oral

Rebecca Souter¹, Lucy Woolford¹

1. School of Animal and Veterinary Sciences, Adelaide University

Marine ecosystems are under increasing pressure from anthropogenic disturbance and modification. Long-lived, high trophic level species such as dolphins are considered important indicators of marine ecosystem health. An urbanised shipping port in Adelaide, South Australia, supports a resident population of approximately 20 Indo-Pacific bottlenose dolphins (*Tursiops aduncus*). In 2005, the region was declared the Adelaide Dolphin Sanctuary (ADS) to improve protection of this iconic population. In recent years, the population has gradually declined, with reduced calf survival identified as a contributing factor. In 2021, a mortality event involving five sexually immature males occurred over a six-month period. No consistent cause of death was identified. Anthropogenic influence is considered a potential contributor to the decline of the ADS dolphin population. This study used necropsy investigations to assess dolphin health, blubber hormone concentrations, and hepatic contaminant burdens (i.e., per- and polyfluorinated alkyl substances, metals, and metalloids). Health indices were developed to aid interpretation of this multi-parameter dataset, and variables were compared between dolphins from different regions, including ADS. Twenty-four dolphins were examined, including six ADS dolphins. ADS dolphins were more likely to exhibit opportunistic skin infections and display higher thyroid hormone concentrations. One ADS male exhibited the highest concentration of 17 β -estradiol among all dolphins tested, including adult females. Emaciation and cause of death by inflammatory disease was overrepresented within the ADS dolphin population. Although limited by small sample sizes, the findings of this study provide preliminary evidence that an urban lifestyle may be a risk factor for adverse health outcomes in dolphins.

Citizen science to mitigate impacts of linear infrastructure on biodiversity: The Northern Kenya Road Watch

Thursday, 30th July - 08:45: Global Voice (Virtual/Online) - Oral

*David Kimiti*¹

1. Grevy's Zebra Trust

Northern Kenya's rangelands support some of East Africa's most important wildlife populations and ecological connectivity corridors, sustaining seasonal movements of species such as elephant, giraffe, lion, and the endangered Grevy's zebra across vast multi-use landscapes. However, rapid expansion of infrastructure—including roads, electricity transmission lines, fencing, and urban development—is increasingly fragmenting habitats and disrupting wildlife movement. Poorly planned infrastructure can create barriers to migration, reduce access to critical resources such as water and grazing areas, increase wildlife mortality, and intensify human-wildlife conflict. Despite growing recognition of these impacts, infrastructure planning in arid and semi-arid ecosystems is often constrained by limited spatial information on wildlife movements and corridor use, particularly at landscape scales. The Northern Kenya Road Watch (NKRW), led by the Grevy's Zebra Trust and Ewaso Lions, provides an innovative community-based monitoring approach that addresses this information gap through citizen science and mobile technology. Road users traveling along the A2 highway collect geo-referenced observations on wildlife collisions and accidents. These datasets are being used in conjunction with collared animal data to identify critical wildlife corridors and movement bottlenecks that intersect with existing or proposed infrastructure developments.

Information generated through NKRW has directly led to implementation of mitigation measures aimed at reducing collisions and mortalities along the important Isiolo-Moyale highway. This presentation explores how crowd sourced monitoring systems can generate actionable spatial data to inform infrastructure planning, reduce fragmentation impacts, and strengthen landscape-scale conservation in northern Kenya's rapidly changing rangelands.

Electrocution risk in augur buzzards (*Buteo augur*) across a human-modified landscape in Kenya

Thursday, 30th July - 09:25: Global Voice (Virtual/Online) - Oral

Juliet Waiyaki¹

1. Kenya Birds of Prey Trust

Electrocution from powerlines is an emerging but underquantified source of mortality in raptors across sub-Saharan Africa. The study assesses electrocution risk in Augur Buzzards (*Buteo augur*) within the Naivasha-Soysambu landscape, a rapidly changing environment characterized by expanding electrical infrastructure and increasing human activity. Since September 2025, 19 Augur Buzzards have been fitted with GSM transmitters to monitor movement, habitat use and survival in near real-time. Mortality events were identified through transmitter signals, followed by rapid field response and postmortem examination to determine cause of death. To date, 5 of 19 tagged individuals (26.3%) have been confirmed dead due to electrocution. Diagnosis is supported by consistent field and necropsy findings, such as burn lesions on distal extremities and recovery beneath or adjacent to powerline structures.

The pattern of mortality over several months shows a persistent exposure risk instead of isolated cases. These findings suggest electrocution as a significant and ongoing threat to a common raptor species within a human-modified landscape. As Augur Buzzards play an important ecological role in regulating rodent populations, continued losses may have wider ecosystem implications. This study demonstrates the value of integrating telemetry and field diagnostics to quantify anthropogenic mortality and provides a foundation for targeted mitigation strategies. In landscapes where human expansion continues to reshape natural systems, addressing unintended impacts on wildlife is critical to maintaining ecological resilience.

Adenovirus Detection Following Juvenile Mortality in Rewilded Aldabra Giant Tortoises: Evaluation of Viral and Potential Toxicological Factors

Thursday, 30th July - 10:00: Global Voice (Virtual/Online) - Oral

*Herizoa Ionia Rasolofoniaina*¹

1. Anjajavy Protected Area

In 2025, a significant fatal event occurred at the unique nursery of the reintroduced *Aldabrachelys gigantea* population in Madagascar's Anjajavy Reserve. The event resulted in the deaths of 30 juvenile tortoises. Molecular diagnostics performed by the Mahaliana laboratory confirmed the presence of an active adenovirus within the population, suggesting viral infection as the primary cause. However, plant toxicity associated with dietary exposure remains under investigation as a potential contributing factor.

Immediate veterinary interventions and enhanced health surveillance have been implemented to minimize further losses. Thorough virological, pathological, and toxicological analyses are urgently needed to determine the cause of this event and ensure the long-term success of this pioneering megafauna reintroduction program.

Freshwater turtles as reservoirs and vectors of infectious pathogens in biological invasions

Thursday, 30th July - 10:15: Global Voice (Virtual/Online) - Oral

***João Rato*¹, *Rita Rocha*², *Pedro Brandão*³, *Filipe Banha*³, *Raquel Xavier*⁴, *D. James Harris*⁴, *Pedro Anastácio*³**

1. MARE, 2. Hospital Veterinário da Universidade de Évora, 3. MARE - Marine and environmental science centre, 4. CIBIO- Centro de Investigação em biodiversidade e recursos genéticos

Freshwater turtles are increasingly recognized as important agents of biological invasions, largely driven by the global pet trade and frequent releases into natural ecosystems. While their ecological impacts are well documented, their role in pathogen transmission remains comparatively understudied. To address this gap, we conducted a comprehensive synthesis of published records on bacterial, viral, and fungal pathogens reported in freshwater turtles. Drawing from 163 peer-reviewed studies, we compiled 815 pathogen occurrences spanning 188 genera. The most frequently documented host species were *Trachemys scripta*, *Pelodiscus sinensis*, and *Emys orbicularis*. Notably, *T. scripta*, one of the most widespread invasive turtles globally, showed strong associations with zoonotic pathogens, particularly *Salmonella*, highlighting its dual relevance as both an invasive species and a potential public health concern.

Our analysis revealed frequent pathogen sharing between native and introduced turtles, including across phylogenetically distant taxa, suggesting that shared environments and anthropogenic activities facilitate cross-species transmission. Although bacterial pathogens dominated available records, viral data indicated biogeographic links between Asia and North America, whereas fungal pathogens appeared more geographically restricted. Despite these findings, non-native turtle species remain underrepresented in disease surveillance and are rarely incorporated into invasion management or One Health frameworks.

Overall, these results emphasize the need to explicitly integrate disease risk into invasion biology, aquatic biosecurity, and conservation planning, recognizing freshwater turtles as potential drivers of pathogen dissemination with implications for biodiversity, wildlife health, and public health.

Anthropogenic pressure on reef marine fishes: a histopathological approach

Thursday, 30th July - 10:30: Global Voice (Virtual/Online) - Oral

Gabriela Novacovsky¹, Tamara Rubilar¹, María Gabriela Palacios¹, María Cruz Sueiro¹

1. Centro para el Estudio de Sistemas Marinos (CESIMAR), Centro Nacional Patagónico - (CENPAT), CONSEJO NACIONAL DE INVESTIGACIONES CIENTÍFICAS Y TÉCNICAS (CONICET)

Anthropogenic pollution is a major threat to coastal biodiversity, where industrial and domestic waste activities release complex mixtures of pollutants. Fishes inhabiting these polluted environments are exposed from early-life stages, which can impact their individual health and population viability. Understanding the effects of pollutants on aquatic fauna and developing reliable monitoring tools are essential for protecting these ecosystems. In this sense, histopathology is widely used as an indicator of organism health, as well as to investigate potential adverse effects of environmental pollutants. Nuevo Gulf (Chubut, Argentina) includes the city of Puerto Madryn, characterized by intense port activity, tourism, fisheries, and aluminum production, all representing anthropogenic sources of pollution. Previous studies have reported immunological, body condition, and parasitological alterations in fishes from impacted sites compared to reference areas. This study evaluated the effect of pollution exposure on two ecologically important marine fish species: the rockfish (*Sebastes oculatus*) and the sandperch (*Pinguipes brasiliensis*), through the histopathological analysis of gills, liver, and spleen. Histopathological indices based on the extension and severity of alterations were calculated for each organ to allow comparison of damage between individuals from impacted and reference sites. Individuals from impacted areas exhibited higher indices, with histological lesions ranging from mild to severe in all examined organs. These findings suggest that pollutant exposure alters organ structure and function, which in turn may compromise individual health and population stability.

Serial *Brucella suis* biovar 4 serology reveals insights into pathogen transmission dynamics and health of a free-ranging caribou (*Rangifer tarandus granti*) herd in decline

Thursday, 30th July - 10:30: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Kimberlee Beckmen*¹, *Camilla Lieske*¹, *Kristin Denryter*¹**

1. Alaska Department of Fish and Game

Alaska Department of Fish and Game researchers examined health factors in a caribou (*Rangifer tarandus granti*) population that had experienced a precipitous decline of >90% utilizing serial live-capture-release techniques. This provided a unique opportunity to monitor *Brucella* titers and potential reproductive effects over multiple years and seasons in 28 individual females from a population <10 years since first evidence of *Brucella suis* biovar 4.

Sera collected during spring and fall handlings was tested for *Brucella* spp. antibodies by BAPA, FPA and complement fixation (CF). New cases are defined as individuals found to have detectable *Brucella* titers by CF after previously testing negative, or the first positive sample when no previous sample was available (such as for 10-month-old caribou).

Analyses demonstrated false negative Brucellosis screening tests (BAPA) on sera with detectable titers on the gold standard CF. Intensity of titers decrease before a detectable change in titer. Titers can last greater than 5 years. Some caribou were aged 7-8 years before developing a titer. Waxing/waning titers were detected in several individuals where titers are higher in autumn than spring. Most titers decreased over time.

Although fewer new cases were detected in 2025 (N=3) compared to 2024 (N=7), newly detected cases indicated continued disease transmission at a rate greater than the enzootic equilibrium found in the arctic herds.

Pregnancy rates were high (>90%) and the serologic findings do not implicate *Brucella* having a direct population level impact on reproduction in this herd at this time.

Historical Trends of *Leptospira* exposure in White-tailed Deer Health across the Southeastern United States

Thursday, 30th July - 10:45: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Ania Majewska*¹, *Sathwik Katkam*², *Kira Buford-Rucker*², *Ellen Haynes*¹, *Michael J. Yabsley*¹, *Elizabeth Kurimo-Beechuk*², *Chris Cleveland*¹, *Marcelo Jorge*³, *Gino D'Angelo*³, *Mark G. Ruder*²**

1. Southeastern Cooperative Wildlife Disease Study, 2. Southeastern Cooperative Wildlife Disease Study, University of Georgia, 3. University of Georgia

White-tailed deer (*Odocoileus virginianus*) are an important game and keystone herbivore species with significant ecological influence across their range throughout North America. Given this significance, long-term monitoring of herd health is essential for informing evidence-based wildlife management decisions. Here, we provide a comprehensive temporal analysis of herd health data collected by the Southeastern Cooperative Wildlife Disease Study (SCWDS) and partner state wildlife agencies. We examined data originating from nine states (AL, AR, GA, KY, LA, NC, OK, TN, WV) between 1961 and 2024 (n= 5994 deer). We examined *Leptospira* spp. exposure, kidney fat index (KFI) and weight. Preliminary analysis of the temporal trends in *Leptospira* serovar antibody prevalence indicates that overall seroprevalence has increased over time: prior to 1990 about 5% of sampled deer were seropositive; post 1990, 19% were seropositive. The increase was significant in most states. Grippotyphosa was the most common serovar in AL, AR, GA, NC and TN, while Pomona was most common for KY, OK, and WV. In LA, the most common serovar was Icterohaemorrhagiae. In general, weight and KFI at each geographic location tended to increase over decades within each sex and age category. These findings enhance our understanding of how deer health has changed temporally and spatially. This work enhances our understanding of white-tailed deer population health over time and space in the southeastern US. Continued data collection on deer health metrics is needed to provide long-term monitoring of herd health and to inform management strategies across the region.

Salmonella serovars and antimicrobial resistance profiles in wild European hedgehogs (*Erinaceus europaeus*): over 13 years of surveillance in the Ferrara Province, Italy

Thursday, 30th July - 11:00: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Elisa Massella*¹, *Martina Munari*¹, *Simone Russo*¹, *Letizia Cirasella*¹, *Roberta Taddei*¹, *Andrea Luppi*¹, *Silva Rubini*¹**

1. Istituto Zooprofilattico della Lombardia e dell'Emilia Romagna, Brescia

European hedgehogs (*Erinaceus europaeus*) are broadly distributed wild mammals, hosting numerous pathogens of One Health importance, including *Salmonella*. This study investigates their role as reservoirs of different *Salmonella* serovars, the associated antimicrobial resistance (AMR) profiles and the potential risk of transmission to other animals and humans.

From January 2012 to December 2025, 667 hedgehog carcasses from the Ferrara Province, Italy, were analysed within the regional wildlife monitoring plan. *Salmonella* was isolated according to ISO 6579-1:2017/Amd.1:2020 and serovars identified using the White–Kauffmann–Le Minor scheme. AMR profiles were determined for 154 isolates by broth microdilution method.

Salmonella was detected in 217/667 hedgehog carcasses. Fifteen serovars were identified, most commonly *Salmonella* Enteritidis (141/667), *Salmonella* Veneziana (32/667) and *Salmonella* Typhimurium (15/667). Notably, *Salmonella* detection steadily increased from 2012 to 2025, reaching a prevalence of 40.82% samples in 2025. Seventeen/153 isolates were resistant to at least one antimicrobial, with 4 strains multidrug-resistant to 3–5 different antimicrobial classes. The highest resistance was observed to chloramphenicol (11/153), followed by ampicillin (6/153), ciprofloxacin (5/153), tetracycline (4/153), colistin (2/153) and tigecycline-ceftazidime-cefotaxime (1/153 each).

The increasing detection of *Salmonella* highlights hedgehogs as potential reservoirs, contributing to *Salmonella* environmental persistence and transmission to other animals. Several zoonotic serovars were detected, including *Salmonella* Enteritidis, *Salmonella* Typhimurium and its monophasic variant, even without alarming AMR profiles. These findings suggest hedgehogs may pose a risk for the spread of zoonotic *Salmonella* to humans due to their synanthropic behavior and the increasing trend in Italy of keeping wild hedgehogs as pets.

Tularemia Exposure and Ectoparasite Dynamics in Black-Footed Ferrets in South Dakota from 2002-2024

Thursday, 30th July - 11:15: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Madisen Hartlaub*¹, *Shelli Dubay*¹, *Travis Livieri*², *Zach Wilson*³, *Rachel Santymire*⁴**

1. University of Wisconsin-Stevens Point, 2. Prairie Wildlife Research, 3. USDA, 4. Georgia State Univeristy

The black-footed ferret (*Mustela nigripes*; ferret), one of North America's most endangered mammals, persists within prairie dog (*Cynomys* spp.) burrow systems where disease remains a major obstacle to their recovery. While plague (*Yersinia pestis*) is well recognized as a primary threat, tularemia, a bacterial disease caused by *Francisella tularensis* and vectored by ticks and other ectoparasites, also occurs in grassland ecosystems. Ferrets appear capable of surviving tularemia infection, although the ecological drivers, biological impact, and vector pathways involved remain unknown. Our objective was to determine variables that explain ferret exposure to tularemia over time, evaluate ectoparasites found on ferrets and their prey, and determine the role of ectoparasites in pathogen transmission to ferrets. Serological analyses indicated that 6.3% of ferret serum samples (81/1277) were seropositive for tularemia between 2002-2024. Juvenile males exhibited the highest likelihood of exposure, particularly in 2015–2016. Ferrets recaptured within 5-12 months showed changes in serostatus, indicating that antibodies do not persist long-term. From 2022–2025, 304 ferrets were sampled, and ticks were detected on 92% of individuals. Additionally, no ticks or fleas collected from seropositive ferrets tested positive for *F. tularensis* DNA by PCR, suggesting *Ixodes* spp. may not directly drive tularemia epizootics. These results provide the first long-term assessment of tularemia in black-footed ferrets. Tularemia is likely not a significant conservation concern for black-footed ferret populations, although continued research on immune response dynamics and vector ecology is warranted.

Emergence of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) in the Western United States: A Threat to the Vulnerable Davis Mountain Cottontail

Thursday, 30th July - 11:30: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Hannah Shapiro*¹, *Cole Wzientek*¹, *Dana Karelus*², *John McLaughlin*², *Alynn Martin*³**

1. Caesar Kleberg Wildlife Research Institute, 2. Texas Parks and Wildlife Department, 3. Department of Biology, Grand Valley State University

Rabbit hemorrhagic disease virus (RHDV) first emerged in Europe in the late 20th century, causing the deaths of over 250 million domestic and wild rabbits worldwide. In 2010, a novel strain, RHDV2, was identified in France and later detected in North America in 2016. Now endemic in the western United States, RHDV2 has caused outbreaks in wild rabbit populations across 14 states, including Texas. In western Texas, RHDV2 threatens four native lagomorph species, including the vulnerable Davis Mountain cottontail rabbit (DMCR). However, it remains unclear whether DMCR populations have been exposed to RHDV2 or how outbreaks may impact them. Using five years of RHDV2 case data from the Wildlife Health Information Sharing Partnership (WHISPer; United States Geological Survey), we analyzed spatiotemporal patterns of disease spread. First detected in wild lagomorphs in New Mexico in March 2020, RHDV2 has since spread into western Texas and neighboring states, with over 5,000 reported mortalities. Several counties have experienced multiple distinct outbreaks over time, suggesting that direct contact between rabbits is not the only means of disease spread. We also utilized 20 years of standardized roadside surveillance data collected by Texas Parks and Wildlife Department to assess lagomorph abundance trends across Texas in relation to spread of disease. Future research will focus on serosurveillance of DMCR populations to determine historical exposure to RHDV2 and assess potential risks to this vulnerable species.

Sin Nombre hantavirus interacts with helminth parasite co-infections in Montana deer mice (*Peromyscus maniculatus*)

Thursday, 30th July - 11:45: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Madeline Rowland*¹, *Amy Kuenzi*², *Mike Kinsella*³, *Angela Luis*¹**

1. University of Montana, 2. Montana Technological University, 3. Helm West Labs

Wildlife populations are exposed to diverse parasite communities, where co-infection is the rule rather than the exception. Understanding the mechanistic effects of co-infection on disease dynamics requires moving beyond the traditional focus on single pathogen - single host systems. We use Sin Nombre hantavirus (SNV) in wild deer mice (*Peromyscus maniculatus*) as a model system to identify potential mechanistic effects of co-infection on disease dynamics of SNV in its reservoir host. We trapped and removed wild deer mice (n = 1,065) from six sites across western Montana from 2023-2025 and tested individual SNV serostatus (n = 78 seropositive) and adult helminth infection via gastrointestinal dissection (n = 181 infected of 318 dissected to date). We used joint species occupancy models to estimate parameters of single infection (presence/absence) and of non-independent interactions of co-infecting parasites. We compared models to determine whether *Trichuris stansburyi*, *Calodium hepaticum* (tissue-invasive helminths), and SNV interact (are not independent of one another) in individual mice and to estimate effects of sex and body length on single infection and on interactions. The top model incorporated (1) non-independent interactions (co-infections) between parasite species, (2) a strong positive effect of body length on each infection and (3) a positive effect of sex (being male) on interactions. Predicted SNV infection probability was significantly higher in male mice that were co-infected with *C. hepaticum*. These results confirm that co-infections in this system are not independent and are impacted by host characteristics, emphasizing the importance of integrating co-infection into investigations disease dynamics.

The role of host identity in transmission dynamics of a multi-host infectious disease

Thursday, 30th July - 11:00: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses I (O'Hare 1-2) - Oral

**Hendrina Joel¹, Yen-Hua Huang², Zoe Barandongo², Amelie Dolfi², Kimberlie Vera², John Mfune¹,
Wendy Turner³**

1. Department of Biological Sciences, Faculty of Science, University of Namibia, **2.** Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology University of Wisconsin, Madison, **3.** U.S. Geological Survey, Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology University of Wisconsin, Madison

For multi-host infectious diseases, host species often contribute unequally to transmission dynamics. This study investigated the role of host species identity in the natural anthrax transmission cycle in Etosha National Park, Namibia. We compared infectivity and exposure risk at carcass sites of plains zebra (*Equus quagga*) and African savanna elephant (*Loxodonta africana*). We investigated *Bacillus anthracis* spore concentrations and persistence in soil, carcass effects on soil nutrients and vegetation cover, and host visitations and behaviors. Despite significantly larger body size, elephant carcass sites did not contain higher spore concentrations than zebra carcass sites, and spore concentrations started low and remained low regardless of site age or season of death. In contrast, zebra mortalities during wet seasons had higher spore counts and spore concentrations decreased over time. The biggest changes to soil nutrients and vegetation cover occurred near death, however soil phosphorus remained elevated after more than a decade. A greater diversity of potential host species visited elephant sites than zebra sites and exhibited a wider range of behaviors. Of behaviors considered a risk for pathogen exposure, foraging was the predominant risky behavior at zebra sites, while at elephant sites more species interacted with the carcass remains and engaged in osteophagia. While zebras are the main host species in Etosha and most cases in the system are detected in grazing herbivores, elephants use different habitats than grazing hosts and could serve as a bridge host, transporting the pathogen into different habitats and potentially exposing a wider variety of host species.

Epidemiological factors and causes of pneumonia in white-tailed deer (*Odocoileus virginianus*) in Pennsylvania, USA from 2022-2025

Thursday, 30th July - 11:15: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses I (O'Hare 1-2) - Oral

***Taylor C. Chan*¹, *Kevin D. Niedringhaus*¹, *Perry Habecker*¹, *Andrew R. Di Salvo*², *Johannes Nelson*¹, *Xinye Kou*³, *Sabrina S. Greening*⁴**

1. Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, 2. Pennsylvania Game Commission, Bureau of Wildlife Management, 3. Master of Environmental Studies, University of Pennsylvania College of Liberal and Professional Studies, 4. University of Pennsylvania School of Veterinary Medicine, Wildlife Futures Program

Pneumonia is one of the most commonly diagnosed causes of morbidity and mortality in free-ranging white-tailed deer (*Odocoileus virginianus*). While pneumonia is not always the direct cause of death, the inflammation can result in massive tissue destruction, leading to systemic disease, emaciation and carcass condemnation. Free-ranging ruminant populations in United States, including bison, bighorn sheep, and pronghorn antelope, are affected by fatal pneumonia caused by pathogens common in domestic livestock. Pneumonia as a respiratory disease complex is a significant animal health and economic issue, driving research to understand etiopathogeneses and risk factors in domestic livestock. This knowledge remains limited in wildlife.

We categorize and describe cases of pneumonia in free-ranging white-tailed deer submitted to the Pennsylvania Animal Disease Laboratory System for diagnostic testing from January 2022 to September 2025. Of 2756 case submissions, 332 carcasses (32 fawns, 111 juveniles, 236 adults) were diagnosed with pneumonia based on gross and/or microscopic examination. Infectious causes were most common (n = 222; 66.9%), with a bacterial etiology predominating (n = 119; 53.6%), followed by verminous (n = 94; 42.3%) and fungal etiologies (n = 9; 2.3%). Aspiration pneumonia was diagnosed in 11.1% (n = 37) of cases of pneumonia. Lungworms were detected in 8.2% (n = 227) of all cases submitted and 60% of cases diagnosed with pulmonary disease.

By describing trends in demographic risk factors, location, and seasonality, we can begin to understand the predisposing factors, pathogeneses, transmission pathways, epidemiology, and management implications for pneumonia in free-ranging white-tailed deer in Pennsylvania.

From Pathogens to Pathways: Using Genomics to Predict Disease Spread Across Landscapes

Thursday, 30th July - 11:30: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses I (O'Hare 1-2) - Oral

***Sarah Tomke*¹, *Noelle Thompson*², *A. S. Apostolopoulos*³, *Matthew Springer*⁴, *Steven Price*⁴, *John Cox*⁴,
*Emily Boyd*⁵, *Roderick B. Gagne*⁶**

1. University of Pennsylvania School of Veterinary Medicine, 2. Western Association of Fish and Wildlife Agencies, 3. Kentucky Department of Fish and Wildlife Resources, 4. University of Kentucky, 5. Pennsylvania Game Commission, Bureau of Wildlife Management, 6. University of Pennsylvania School of Veterinary Medicine, Wildlife Futures Program

Effective management of wildlife diseases is often constrained by our inability to predict how disease dynamics will respond to an ever-changing environment. Pathogen transmission, in particular, is heavily influenced by the movement of free-ranging individuals across the landscape, which are primarily driven by available habitat and its configuration over time and space. Here, we illustrate how integrating genetic tools can facilitate our understanding of how wild populations are structured and connected across the landscape, thus informing likely transmission pathways for communicable diseases in highly heterogeneous environments. We present two case studies in which we applied genomic analyses to identify likely pathways of disease spread: 1) chronic wasting disease (CWD) in white-tailed deer (*Odocoileus virginianus*) in western Kentucky and Tennessee, and 2) rabbit hemorrhagic disease virus 2 (RHDV2) in eastern cottontails (*Sylvilagus floridanus*) in Pennsylvania. In both studies, we used reduced representation sequencing to acquire genomic datasets. We then used population genomic analyses to determine how populations were structured across the study area, estimated the genetic differentiation among populations as a proxy for their connectedness, and identified landscape features that drove the observed population structure. We then applied landscape genetics, a tool that combines genomic data with landscape resistance modeling to map patterns of gene flow across the landscape, to infer disease transmission routes and identify populations at risk of infection. Our research demonstrates that genomics can be a powerful tool when studying disease dynamics at a landscape scale and inform effective management response plans in the wake of disease outbreaks.

Filling in the gaps: Leveraging passive surveillance to better understand the distribution of a bat fungal pathogen in Iowa

Thursday, 30th July - 11:45: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses I (O'Hare 1-2) - Oral

**Rachel Ruden¹, Stephanie Shepherd¹, Kelly Poole¹, Riggs Wilson¹, Faith Hansen², Laura Bradner²,
Phillip Gauger²**

1. Iowa Department of Natural Resources, 2. Iowa State University Veterinary Diagnostic Laboratory

White-nose syndrome is caused by a fungal pathogen, *Pseudogymnoascus destructans* (Pd), that has caused population declines in some North American bat species in excess of 90%. In Iowa, surveillance efforts have historically been limited, with Pd first detected along the eastern edge of Iowa in 2011 and symptomatic bats found during winter surveys in 2014 and 2015. However, as the disease front expanded westward, in-state surveillance efforts waned. In 2021, the Iowa Department of Natural Resources (DNR) began developing the framework for a guano surveillance project using field collection and diagnostic protocols developed by the U.S. Geological Survey and adapted by the Iowa State University Veterinary Diagnostic Laboratory. Since 2022, the Iowa DNR has worked with state park staff, county partners, and even private landowners to collect bat guano for four weeks following spring emergence. The guano is then processed and screened for Pd. With annual grant support from U.S. Fish and Wildlife Service, Iowa DNR has tested 240 samples from 19 counties, with 61 samples from four counties with no previous baseline data testing positive. Notably, samples from four counties known to have symptomatic bats in 2015 have, to date, tested negative. In 2026, Iowa DNR will add targeted surveillance of individual bats using two post-emergence roost sites that have consistently tested positive for Pd since 2022.

From wildlife to humans: design, data sources, and cross-sector integration in leptospirosis surveillance

Thursday, 30th July - 11:50: Global Voice Short Presentations (Virtual/Online) - Oral

***Kellie Libera*¹, *Sarah J. Robinson*², *Katie M. Clow*³, *Lauren E. Grant*³, *J. Scott Weese*⁴, *E. Jane Parmley*³,
*Claire M. Jardine*⁴**

1. University of Guelph, 2. Faculty of Health Sciences, Simon Fraser University, 3. Department of Population Medicine, University of Guelph, 4. Department of Pathobiology, University of Guelph

Leptospirosis is a globally important zoonotic disease maintained in wildlife reservoirs and transmitted to humans and domestic animals through direct contact or environmental exposure. Wildlife surveillance is central to understanding pathogen maintenance, spillover risk, and environment-mediated transmission; however, the incorporation of wildlife data into existing leptospirosis surveillance programs is poorly documented. This scoping review examined leptospirosis surveillance systems to characterize wildlife involvement, data sources, design approaches, and cross-sector data integration.

A systematic literature search identified leptospirosis surveillance studies published between 2013 and 2023. In total, 158 articles were included for full data extraction. Animals were the exclusive focus of one-third of studies, encompassing more than 100 wildlife species across multiple taxa. Wildlife surveillance primarily relied on biological sampling, particularly blood or kidney tissue, to assess infection or pathogen exposure.

Despite the recognized reservoir role of wildlife for *Leptospira*, surveillance activities were frequently initiated in response to human disease outbreaks. Wildlife data were most often generated through short-term research projects or outbreak investigations rather than sustained programs. Active environmental sampling to contextualize wildlife infection risk was rarely described (4/158), and cross-sector integration of wildlife data into human or environmental surveillance activities was infrequent (18/158).

The predominance of reactive, short-term wildlife investigations and limited cross-sector integration observed in this review suggest missed opportunities for sustained wildlife-based surveillance. Strengthening ongoing and systematic wildlife surveillance and integrating these data with environmental monitoring and human disease data may improve leptospirosis detection and enhance understanding of zoonotic transmission dynamics.

Integrating Pet Trade Outreach and Engagement across Disciplinary Boundaries: Disease and Invasive Species Mitigation

Thursday, 30th July - 13:50: Global Voice (Virtual/Online) - Oral

*Alexa Warwick*¹, *Paige Filice*¹

1. Michigan State University

The global movement of animals and plants through the pet trade spans hundreds of countries and constitutes a multibillion-dollar industry. Unfortunately, this trade also facilitates disease and invasive species spread, leading to biodiversity loss, economic damage, and potential risks to human health. These issues are often addressed separately by different organizations and agency divisions. For instance, conference presentations are siloed into one or the other, despite overlapping goals. However, the target audiences of outreach programs—and many best practices—are the same for both issues. Delivering inconsistent yet similar messages to these shared audiences can cause confusion and frustration among industry, ultimately hindering effective action.

To enhance communication between aquatic invasive species and wildlife disease experts on a global scale, we are conducting semi-structured interviews with leading experts across disciplines. Our objectives are to (1) identify international organizations and leaders involved in managing the movement of exotic pets, specifically amphibians, reptiles, and fish; (2) develop evidence-based best practices to reduce the spread of invasive species and diseases in the pet trade; and (3) promote adoption of these practices among pet wholesalers and retailers by creating adaptable outreach materials

Our preliminary findings show that organizations tend to be focused on a particular species or group of species but often have overlapping best practices for businesses and pet owners. The organizations also vary as to how much of their efforts are shared publicly, making it difficult for these groups to connect. Illegal trade is an additional challenge for some species in outreach efforts.

Making the connections: feral pigs, crocodiles, and a dingo

Thursday, 30th July - 14:25: Global Voice (Virtual/Online) - Oral

Michael Ward¹

1. Sydney School of Veterinary Science, The University of Sydney

The wildlife–domestic animal interface is critical for the risk of disease emergence. Whilst pathogen characteristics influence this risk, it is the nature of contacts between wild and domestic animals that drives such risk. In 2025 the Disease Ecology Lab at the University of Sydney was created with the purpose of understanding the wildlife–domestic animal interface and its relevance to disease spillover risk. What conditions create a strong interface to such the extent that diseases can be transmitted across this interface? To answer this question several case studies have been commenced in which contacts are being measured and characterised, allowing extraction and extrapolation to answer our key question.

In this presentation one such study will be presented, to provide insights into research approaches and applications. In a high biosecurity risk region of northern Australia, experiments using feral pig carcasses have been undertaken during pre- and post-monsoonal seasons. We have generated preliminary data to show who-contacts-who, sometimes with unexpected and extreme results. For example, feral pigs, dingoes and dogs promote and re-enforce the wildlife–domestic interface, whereas crocodiles are the ultimate dead-end host. Ongoing focus is on the extraction of explanatory data and development of models of this interface and the consequences for disease spillover risk.

Regional assessment of canine distemper virus prevalence in wild carnivores submitted to public health laboratories in the eastern United States for rabies virus testing

Thursday, 30th July - 14:30: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

Seth Lattner¹, Ellen Haynes¹, Michael J. Yabsley¹, Chris Cleveland¹

1. Southeastern Cooperative Wildlife Disease Study

Wild carnivores globally experience outbreaks of canine distemper virus (CDV), a highly infectious morbillivirus (Family Paramyxoviridae). Infection with CDV can result in neurological disease closely resembling rabies virus (RABV). Often, animals presenting with neurological signs are submitted to state public health agencies for RABV testing, without testing for CDV or other pathogens. We investigated the CDV prevalence in wild carnivores previously submitted to seven US state public health agencies for RABV testing. From 2022-2025, we tested brain samples from RABV-negative carnivores for CDV using real-time RT-PCR. Additionally, hemagglutinin (H) gene amplification was performed on positive samples to conduct phylogenetic analyses. Overall, CDV was detected in 32% (296/920) of brain samples tested. By species, CDV was detected in 38% of raccoons (*Procyon lotor*, 271/715), 9% of foxes (unspecified; 8/92), 16% of striped skunks (*Mephitis mephitis*, 14/90), 20% of coyotes (*Canis latrans*, 2/10), and one American mink (*Neogale vison*, 1/1). No detections have been recorded in other species (13 samples). Prevalence was higher in 2024 (37%, n=128) and 2025 (37%, n=559) compared to 2022 (16%, n=102) and 2023 (16%, n=114). Prevalence was higher in New Jersey (65%, n=80), Kentucky (44%, n=70), and Missouri (40%, n=204) and lower in Tennessee (34%, n=53), Maryland (25%, n=168), and Pennsylvania (6%, n=174). Currently, complete H gene sequences have been obtained from six raccoons, three skunks, and one fox from Kentucky and Missouri, all of which grouped within the America-5 lineage of CDV. These results suggest that testing public health samples improves CDV surveillance efforts.

Serologic evidence of canine distemper virus and protoparvovirus exposure in a multi-host carnivore community supporting endangered ocelots in southern Texas

Thursday, 30th July - 14:45: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

MAURICIO Rued¹, Alynn Martin², Christopher Kozakiewicz³, Lisanne Petracca¹, Michael Tewes⁴, Ashley Reeves⁵

1. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, **2.** Department of Biology, Grand Valley State University, **3.** Kellogg Biological Station in the College of Natural Science, Michigan State University, Hickory Corners, MI, 49060, USA, **4.** Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, 78363, USA, **5.** East Foundation, San Antonio, TX, 78216, USA

Habitat loss and fragmentation can increase interspecific contact and facilitate pathogen transmission in multi-host wildlife communities, creating conservation concerns when endangered species are present. In southern Texas, endangered ocelots (*Leopardus pardalis*) persist in small isolated populations that coexist with abundant mesocarnivores, including bobcats (*Lynx rufus*) and coyotes (*Canis latrans*). We evaluated serological exposure to canine distemper virus (CDV) and carnivore protoparvovirus (CPPV-1) in free-ranging carnivores sampled from 2020–2025 at two sites in the Lower Rio Grande Valley. Serum samples from 44 ocelots, 61 bobcats, and 17 coyotes were analyzed using indirect immunofluorescence and hemagglutination inhibition assays. Seroprevalence was estimated using Bayesian bernoulli generalized linear mixed models with a logit link, including demographic covariates and year as a random intercept. Antibodies to both viruses were detected in all species, indicating community circulation, and no animals showed overt clinical signs at capture. For CDV, estimated seroprevalence at El Sauz Ranch was 25% (95% HDI: 10–42%) in ocelots, 23% (9–38%) in bobcats, and 31% (12–52%) in coyotes. CPPV-1 exposure was higher overall (about 40% in ocelots and coyotes) but lower in bobcats (about 10%). Species identity and study site showed detectable differences in predicted seroprevalence, whereas demographic traits (sex, age class, body condition) showed no clear associations. Interannual variation was small and consistent with endemic circulation rather than sporadic outbreaks. These findings indicate that CDV and CPPV-1 are maintained within a sympatric carnivore community and suggest that abundant mesocarnivores may contribute to sustained pathogen exposure risk for endangered ocelots in fragmented landscapes.

Unprecedented wildlife impacts of HPAI H5N1 viruses in the Neotropics: how was it different from the northern hemisphere?

Thursday, 30th July - 15:00: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

Marcela Uhart¹, Ralph E. T. Vanstreels¹

1. University of California, Davis

High pathogenicity avian influenza H5N1 (HPAIV) are renowned for their impact on poultry, wildlife, and human health. Previously confined to Eurasia, these viruses begun spreading globally in 2021 and reached Central and South America for the first time in late 2022. Wildlife outbreaks in Central America were limited and primarily affected pelicans. In contrast, South America experienced catastrophic losses in colonial seabirds and marine mammals, with over 610,000 wild birds and 60,000 mammals reported dead, including endangered and endemic species. Colony-breeding seabirds such as cormorants, boobies, pelicans, terns, gulls, and penguins were most impacted, with greatest mortality in Peru and northern Chile. Additional localized mortalities involved waterfowl (especially swans), albatrosses, flamingos, and frigatebirds, along with sporadic cases in shorebirds and terrestrial wild birds. Mammal mortality affected mostly sea lions, elephant seals, and fur seals in Argentina and Chile, with occasional detections in cetaceans, otters, and terrestrial carnivores. Genomic analyses revealed that most mammal outbreaks were caused by an evolutionarily-distinct viral subclade carrying mammal-adaptive mutations and capable of mammal-mammal transmission. Although outbreaks declined by mid-2024, novel reassortant HPAIV containing South American low pathogenicity avian influenza gene segments re-emerged in 2025, indicating ongoing, largely undetected circulation and evolution. Wildlife surveillance across the region remains uneven, predominantly passive, and under-resourced, with limited genomic sequencing relative to outbreak scale. Strengthening integrated One Health surveillance across wildlife, environmental, and agricultural sectors, alongside expanded genomic monitoring, is essential to track viral evolution, protect biodiversity, and reduce emerging zoonotic risks in the Neotropics.

Wild Coypu as a Sentinel Species to monitor Waterborne Antimicrobial Resistance using *Pseudomonas* spp. as bacterial indicator

Thursday, 30th July - 15:15: Wildlife Health: Infectious Disease Surveillance (O'Hare 4) - Oral

***Elisa Massella*¹, *Simone Russo*¹, *Stefano Bussolari*², *Fabrizio Mezzetti*², *Tommaso Fulgaro*², *Stefano Martini*², *Alessandro Morabito*², *Tommaso Mazzini*², *Pier Francesco Fontana*², *Giacomo Gallerani*², *Manuel Gamberini*², *Roberta Artioli*³, *Martina Munari*¹, *Mario D'Incau*¹, *Silva Rubini*¹, *Virginia Carfora*⁴, *Letizia Cirasella*¹, *Maria Sampieri*¹, *Andrea Luppi*¹**

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Pseudomonas spp. are ubiquitous in aquatic environments and may represent important indicators and reservoirs of waterborne antimicrobial resistance (AMR). This study aims to monitor AMR spread in surface waters using *Pseudomonas* spp. isolated from wild coypu (*Myocastor coypu*), a sedentary, long-lived semiaquatic species. This project was funded by the Italian Ministry of Health (IZSLER-13/23-RC).

Ninety-five wild coypu faeces/carcasses were collected along the Reno River, Italy, between December 2024 and April 2025. *Pseudomonas* spp. were isolated using standard microbiological procedures and identified by MALDI-TOF. Minimal Inhibitory Concentrations were evaluated for 6 molecules and interpreted according to the EUCAST epidemiological cut-off or, when not available, to CLSI clinical breakpoints.

Pseudomonas spp. were isolated from 25/90 (27.78%) animal samples. Three species were identified: *Pseudomonas putida* (20/25), *Pseudomonas aeruginosa* (3/25) and *Pseudomonas fluorescens* (1/25), while one isolate could not be classified at the species level. Six strains showed resistance to at least one antimicrobial, predominantly *Pseudomonas putida* (5/6). Notably, resistance was most frequently observed to meropenem (4/6 isolates) and ceftazidime (3/6 isolates), both representing critical antimicrobials for humans. Resistance to amikacin, gentamicin and colistin was identified in a single isolate each. No resistance to ciprofloxacin was observed. Multidrug-resistance was detected in only one strain, which was resistant to ceftazidime, colistin, amikacin and gentamicin. These preliminary results suggest *Pseudomonas* spp. as a reliable indicator of waterborne AMR and the wild coypu as a practical and effective bioindicator, also suitable for future surveillance programs in aquatic environments.

Impacts of Predator Calls on Eastern Bluebird Embryogenesis and Offspring Phenotype

Thursday, 30th July - 14:30: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses II (O'Hare 1-2) - Oral

Raena McCown¹, Andrew Benson¹, Kristen Navara², Sonia Hernandez¹

1. University of Georgia, 2. Kennesaw State University

Embryonic development in hard-shelled eggs has long been viewed as an isolated and independent experience. However, growing evidence suggests that avian embryos can perceive and respond to acoustic cues, producing lasting behavioral, physiological, and morphological changes after hatch. To test the impact of predator-associated acoustic signals, we investigated the developmental programming of Eastern Bluebirds in a field study spanning 120 nest boxes across three sites in Athens, Georgia. Experimental clutches were exposed to predator calls during days 10–12 of incubation, while controls were subjected to the same variables, excluding the acoustic treatment. Offspring were measured for growth (length of tarsi and wings, and mass), at key developmental stages (1, 5, 10, and 14 days). On day 5, begging rates were recorded and on day 10 stress responsiveness was evaluated through blood plasma corticosterone. Offspring were exposed to the same predator-playbacks on day 14 to assess fear responsiveness.

Preliminary results reveal significant differences in hatch success and skeletal morphology: experimental broods exhibited reduced hatch success and altered tarsus diaphysis symmetry compared to controls. These findings demonstrate that acoustic cues during embryonic development can influence not only survival, but early skeletal growth. Our work highlights the potential for acoustic programming to shape avian fitness, adding to a recognition that the environment during embryogenesis influences phenotypes and contributes to adaptive responses in wild populations. This research also contributes to the growing literature on how the health of birds that thrive in anthropogenic environments, like Eastern bluebirds, may be influenced by changing landscapes.

Gobblers in Good Shape? Assessing Wild Turkey Health in Minnesota

Thursday, 30th July - 14:45: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses II (O'Hare 1-2) - Oral

***Elizabeth Baker*¹, *Michelle Carstensen*¹, *Mary Wood*¹, *Erik Hildebrand*¹, *Arno Wuenschmann*², *Nicole M. Nemeth*³**

1. Minnesota DNR, 2. University of Minnesota, 3. University of Georgia

In 2025, the Minnesota Department of Natural Resources conducted a pilot project to assess the health of wild turkeys in central Minnesota. This effort followed increased reports in fall 2024 of turkeys with lesions suggestive of avian pox, which led to the first detection of lymphoproliferative disease virus (LPDV), a pathogen not previously known to occur in wild turkeys in the state. This new detection, combined with the ongoing threat of highly pathogenic avian influenza (HPAI) and increased cases of avian metapneumovirus in domestic turkey flocks, heightened concerns about disease transmission at the wildlife-domestic interface. The pilot project focused on assessing wild turkey health in one turkey hunting unit in central Minnesota with substantial spatial overlap between domestic turkey production facilities.

Community science sampling was used to estimate the prevalence of six avian pathogens that may affect both wild and domestic turkey populations: LPDV, Reticuloendotheliosis virus (REV), HPAI, *Mycoplasma synoviae*, *Mycoplasma gallisepticum*, and avian metapneumovirus. Sampling kits from 320 successful hunters were received between April 16 and July 31, 2025. Oropharyngeal swabs were collected from turkey heads for HPAI, Mycoplasma, and avian metapneumovirus testing, and tarsus bones were submitted for LPDV and REV testing.

Approximately 62% of turkeys tested positive for LPDV, 37% for REV, and 13 individuals for *Mycoplasma synoviae*. Collectively, these findings demonstrate widespread exposure of wild turkeys in central Minnesota to multiple avian pathogens and highlight the value of targeted, hunter-based surveillance for detecting emerging diseases at the wildlife-domestic poultry interface.

Quantifying Chronic Stress in Free-Ranging Mule Deer: Development and Validation of a Multi-System Allostatic Load Index

Thursday, 30th July - 15:00: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses II (O'Hare 1-2) - Oral

Sara Hathaway¹, Barbara Wolfe², George Wittemyer³

1. Colorado State University, Department of Fish, Wildlife and Co, 2. Colorado State University, Department of Clinical Sciences, Fort Collins, CO USA, 3. Colorado State University

Wildlife health and ecosystem resilience in the Anthropocene are increasingly constrained by repeated and persistent human-induced stressors that disrupt physiological recovery and lead to allostatic overload—the physiologic “wear and tear” that accrues with adaptation to stress. In humans and other vertebrates, high allostatic load has been associated with immune compromise, increased risk of disease, and early mortality. At the human–wildlife interface, wild ungulates experience persistent disturbance long before overt disease becomes detectable. Yet wildlife stress monitoring remains poorly understood, relying on single-system biomarkers such as glucocorticoids, which capture isolated signaling pathways rather than cumulative physiological burden.

Here, we present the development and validation of a multi-system Allostatic Load Index (ALI) to estimate chronic stress and identify its causes and health impacts in free-ranging mule deer (*Odocoileus hemionus*). We integrate neuroendocrine, immune, and metabolic biomarkers of organ dysfunction known to be associated with chronic stress into a single measure using novel statistical models. We correlate the outcome with known stressors and with high-resolution heart rate variability (HRV), a mechanistic benchmark of autonomic balance, recorded using long-term surgically-implanted biologgers.

By aligning blood-based indicators with continuous autonomic monitoring, we provide a methodological framework for detecting subclinical stress in wildlife populations. This proactive approach advances One Health surveillance by identifying physiological dysfunction before disease emergence, informing adaptive management in urban and interface environments. Quantifying chronic stress in wild deer offers a scalable model for integrating physiological resilience metrics into conservation strategies aimed at sustaining ecosystem function in increasingly human-dominated systems.

Investigating the potential for bovine tuberculosis to persist in Indiana wildlife

Thursday, 30th July - 15:15: Wildlife Health: Epidemiology, Retrospectives and Meta-Analyses II (O'Hare 1-2) - Oral

***Jonathan Brooks**¹, **Joe Caudell**², **Sonja Christensen**³, **Patrick Zollner**¹, **Wendy Beauvais**¹*

1. Purdue University, 2. Indiana DNR Division of Fish, Wildlife, & Nature Preserves, 3. Michigan State University

Bovine tuberculosis (bTB) is a bacterial disease that affects livestock, wildlife, and humans. The presence of bTB in cattle can result in economic losses for producers. Furthermore, bTB can spill over into wildlife which become a persistent reservoir. Since 2008, sporadic case of bTB have been detected in two Indiana counties. These cases occurred in cattle, raccoons, captive cervids, and free-ranging white-tailed deer. The history bTB cases in these two counties raises questions about the potential for wildlife to become a persistent reservoir for bTB. Our objective was to develop a compartmental model to estimate the probability of white-tailed deer becoming a persistent reservoir for bTB. Our model simulated a deer population surrounding two farms. We incorporated realistic processes into the model including annual birth pulses, annual harvest morality pulses, non-harvest mortality, and social contact structure. We assumed that bTB was introduced into the deer population by a single infected deer. We conducted stochastic simulations to estimate the probability of bTB persisting for at least five years. Our results demonstrated the effect that increasing contact structure complexity has on disease dynamics in a small population. These results will provide guidance to future modeling efforts which incorporate additional host species. They also provide managers with data that can be used to guide bTB surveillance efforts.

Sanitary Management Protocols in the Reintroduction of the Spix's Macaw: An Analysis from a Conservation Medicine Perspective

Thursday, 30th July - 15:30: Global Voice (Virtual/Online) - Oral

Letycia Mendes¹, Mari Quintão¹

1. Universidade Metodista de São Paulo

The reintroduction of the Spix's Macaw (*Cyanopsitta spixii*) into the Caatinga ecosystem, while celebrated as a triumph of conservation biology, currently faces an ethico-sanitary impasse that challenges the project's governance. This study examines the implications of the Psittacine Circovirus (PBFD) through the lens of Conservation Medicine and Institutional Bioethics, discussing the moral responsibilities of managers toward national biological heritage. Based on evidence of epidemiological reporting omissions and systemic quarantine failures, we demonstrate non-compliance with IUCN technical standards (Guidelines for Reintroductions and Other Conservation Translocations), which prioritize absolute biosecurity over institutional schedules. The analysis points to the urgent need for independent and transparent state oversight, grounded in the One Health concept, where the biological viability of the species cannot be decoupled from the ethical and sanitary integrity of the receiving biome.

Keywords: *Cyanopsitta spixii*; Biosecurity; Bioethics; IUCN Guidelines; One Health.

An unintentional experiment in PBFD Or how a confiscation in North America can inform Extinct-in-the-wild management

Thursday, 30th July - 15:45: Global Voice (Virtual/Online) - Oral

***Patricia Latas*¹, *Brooke Durham*²**

1. Southern California International Avian Confiscation Center, 2. SoCal Parrot and Southern California International Avian Confiscation Center

Lessons from Kalaupapa to California to Brazil

A shameful but inspiring story of disease and sanctuary and redeeming hope: Kalaupapa.

Hawaii's former leper colony is located on Molokai, established in 1866 for forced quarantine of people with Hansen's disease (leprosy), a tragic place of exile for over 8,000 people. We share here a story from our own small world of parrot rescue, rehabilitation, and sanctuary that has borrowed strength and hope from the people of Kalaupapa and wisdom from their history.

In January 2025, while devastating fires ripped through LA, another tragedy was unfolding. Law enforcement confiscated approximately 300 birds, half derived from trafficking, and other animals from a severe hoarding situation. Many dozens were dead, sick or dying. In summary: 200 live, critically-ill birds entered quarantine and care. Nearly 300 tests include PCRs for Psittacine Circovirus and multiple zoonotic pathogens. We share here the challenges of managing PBFD and concurrent diseases in a large flock; our experiences informing confiscation planning; and real-life on-going suggestions for critically endangered parrots in re-introduction programs.

Psittacine Beak and Feather Disease can be considered a parallel to human leprosy. Although there are successful treatments and care for victims of leprosy, we have not quite reached that level for PBFD. We share lessons from a real-life tragedy of PBFD, and the ultimate lessons of disease, rescue networks, sanctuary and official support of hundreds of undeserving victims of irresponsible trade—and the practical application of our findings to life and death situations in wild parrot conservation.

Inflammatory Biomarkers as Early Screening Tools for Unknown Pathogen Exposure in Wild Carnivores in Taiwan

Thursday, 30th July - 16:00: Wildlife Medicine (O'Hare 4) - Oral

Wanyi Lu¹, **Hao Fen Chuang**², **Hui-Wen Chen**³, **Kun-Hsien Tsai**⁴, **Amy Ho**⁴, **Hui-Yun Tseng**⁵, **Pin-huan Yu**¹

1. Institute of Veterinary Clinical Sciences, National Taiwan University, 2. Bright Exotic Animal Hospital, 3. Department of Veterinary Medicine, National Taiwan University, 4. Institute of Environmental and Occupational Health Sciences, National Taiwan University, 5. Department of Entomology, National Taiwan University

In Taiwan, humans, stray animals, and wildlife are sympatric in suburban hills. From a One Health perspective, early screening of unknown pathogen transmission is crucial at these active interfaces. Acute-phase proteins (APPs) and Erythrocyte sedimentation rate (ESR) are hematological tests that can detect inflammatory activity within the body. While not specific to any particular disease, these tests are more sensitive than routine blood work. However, data on wildlife remain limited. This study aimed to determine whether APPs and ESR can function as sensitive indicators for health monitoring in 66 Formosan gem-faced civets (*Paguma larvata taiwana*) and 70 Formosan ferret-badgers (*Melogale moschata subaurantiaca*). Blood samples were analyzed for complete blood counts, ESR, micro-ESR (a capillary method), serum biochemistry, protein electrophoresis, and specific APPs: haptoglobin (Hp) and serum amyloid A (SAA). The established reference values are as follows: for civets, Hp 1.05 ± 0.72 mg/mL and SAA 1.33 ± 1.17 µg/mL; and for ferret-badgers, Hp 0.78 ± 0.44 mg/mL and SAA 24.98 ± 27.87 ng/mL. Correlation analyses revealed that parvovirus infection in civets was significantly associated with elevated Hp levels. Conversely, no clear correlation was observed between vector-borne diseases and inflammatory indices across these species. This study represents the first report of reference intervals for APPs in wild carnivores in Taiwan, providing a foundational framework for future wildlife health and infectious disease surveillance.

Sampling at 14,000 feet: Lessons learned in field sampling procedures and processing of high Andean flamingos at Laguna Colorada, Bolivia

Thursday, 30th July - 16:15: Wildlife Medicine (O'Hare 4) - Oral

John Griffioen¹, Emily Freeman¹, Erin McNally², Brad Hazelton¹, Rene Serafino¹, Sol Aguilar³, Omar Rocha³

1. Fort Worth Zoo, 2. Wildlife Aquatic Zoo Relief Network, 3. Centro de Estudios en Biología Teórica y Aplicada – BIOTA

High Andean flamingos, including Chilean (*Phoenicopaterus chilensis*), Andean (*Phoenicoparrus andinus*), and Puna Flamingos (*Phoenicoparrus jamesi*), inhabit some of the most challenging environments on the planet. Laguna Colorada, situated at 14,100' in Southwestern Bolivia is the primary breeding location for the near-threatened Puna flamingo and is critical habitat for this species. Andean and Chilean flamingos also utilize this lake for breeding and raising young, creating a unique opportunity for research. Given the remoteness of this location, fieldwork with biological sampling must be innovative and adaptable to produce consistent and quality results. The investigators report lessons learned over repeated seasons of health assessments on juvenile flamingos at Laguna Colorada. Beyond typical challenges associated with transportation of equipment via commercial air, additional restrictions for laboratory chemicals may complicate the ability to perform basic diagnostics. Use of drinking ethanol (vodka) obtained in Bolivia proves effective as an alternative slide fixative for Romanowsky staining of blood smears, without the need to arrange international shipping of commercial fixative. The altitude of the field location may impact efficiency and capacity without sufficient acclimation, and appears to also affect some aspects of sample processing such as time of hemocytometer preparation. Remote location field work also requires significant pre-travel planning in case of human and animal health emergencies. Creative thinking can lead to improved outcomes, such as use of a reusable grocery bag to provide sling support to a flamingo experiencing exertional myopathy. Flexibility, ingenuity, and preparedness are core elements of successful field sampling in extreme environments.

Evaluation of butorphanol-azaperone-medetomidine-ketamine to immobilize free-ranging wild Rocky Mountain elk (*Cervus canadensis nelsoni*), American black bear (*Ursus americanus*), and white-tailed deer (*Odocoileus virginianus*)

Thursday, 30th July - 16:30: Wildlife Medicine (O'Hare 4) - Oral

***Andrew R. Di Salvo*¹, *Jeremiah E. Banfield*¹, *Brandon M. Snavely*¹, *Carson W. Torhorst*¹**

1. Pennsylvania Game Commission, Bureau of Wildlife Management

Chemical immobilizations provide a safe and humane means of capturing free-ranging wild mammals to conduct research, monitor population health, resolve human-wildlife conflict, and perform additional conservation or management activities. Due to evolving legislation and compounded veterinary pharmaceutical availability, access to traditional immobilization protocols may be limited. In early 2026, we evaluated a novel chemical immobilization compound, CAP-K (butorphanol 60 mg/mL, azaperone 24 mg/mL, medetomidine 24 mg/mL, ketamine 100 mg/mL) with varying reversal protocols (atipamezole 60 mg/mL, naltrexone 50 mg/mL administered separately; atipamezole 60 mg/mL, naltrexone 60 mg/mL administered as all-in-one; atipamezole 60 mg/mL, naltrexone 30 mg/mL administered as all-in-one), in free-ranging wild Rocky Mountain elk (*Cervus canadensis nelsoni*), American black bear (*Ursus americanus*), and white-tailed deer (*Odocoileus virginianus*) across Pennsylvania, USA. Wildlife were administered CAP-K via remote drug delivery devices on the open landscape or via hand syringes following capture by Clover trap, barrel or culvert trap, or rocket net. Results indicate that CAP-K provides rapid induction and effective anesthesia across all species, but refinements to species-specific dose recommendations, particularly for wildlife in reduced or otherwise altered physiological states, should be considered. No significant side effects were observed with the separate or all-in-one reversal protocols and recoveries were generally smooth. These findings suggest that CAP-K with an all-in-one reversal may be a simple and suitable chemical immobilization protocol for North American wild mammals.

Safety and Immunogenicity of an inactivated H5N2 Avian Influenza Vaccine in Stranded Pinnipeds – a Possible Tool for Protecting the Endangered Hawaiian Monk Seal (*Neomonachus schauinslandi*).

Thursday, 30th July - 16:45: Wildlife Medicine (O'Hare 4) - Oral

***Sophie Whoriskey*¹, *Cara Field*¹, *Emily Whitmer*¹, *Gregory Nitzel*², *Suman Mahan*², *David White*³,
*Darrell Kapczynski*⁴, *David Suarez*⁴, *Chang-Won Lee*⁴, *Michelle Barbieri*⁵**

1. *The Marine Mammal Center*, **2.** *Zoetis Inc.*, **3.** *United States Department of Agriculture, Center for Veterinary Biologics*, **4.** *United States Department of Agriculture, Agricultural Research Service*, **5.** *National Oceanic and Atmospheric Administration*

Infections with the highly pathogenic avian influenza (HPAI) H5 clade 2.3.4.4b virus have resulted in the death of millions of domestic and wild birds in the U.S. since 2021 and spillovers of the virus to different mammalian species, including marine mammals have been documented. In November of 2024, H5 HPAI virus was detected in birds in the Hawaiian Islands for the first time. Hawaiian monk seals (HMS; *Neomonachus schauinslandi*) have no known natural immunity to influenza viruses and an outbreak from HPAI could pose a major threat to this endangered species. Vaccines are a well-established tool in reducing the severity and spread of infectious diseases. Established vaccination programs provided a roadmap for an HPAI vaccine program for HMS. A surrogate species trial was initiated at The Marine Mammal Center to assess the safety and immunogenicity of a reverse genetics-derived H5N2 inactivated vaccine for cattle (Zoetis Inc.). In July 2025, six Northern elephant seal (NES; *Mirounga angustirostris*) pups received two doses intramuscularly, 21 days apart (n=3 vaccinated, n=3 placebo). Serial examination on days 0, 21, and 44 included physical exam, venipuncture, and nasal and rectal swabs. Serum was tested for antibodies using multiple methods. Vaccinated seals were seropositive after second vaccination (day 44), and placebo seals were seronegative. All swab samples tested negative for influenza A virus by RT-PCR. No significant adverse reactions were observed. Trials in additional species are ongoing. These initial results provide encouraging data that the vaccine may be a useful tool in protecting HMS against HPAI.

Regional limb perfusion as an adjunct therapy for osteomyelitis in sea turtles

Thursday, 30th July - 17:00: Wildlife Medicine (O'Hare 4) - Oral

Emily McDermott¹, Heather Barron¹

1. Loggerhead Marinelife Center

Regional limb perfusion (RLP) is the concentrating of antimicrobials or other medications in a limb by injection distal to a tourniquet. This achieves high drug concentrations and reduces systemic absorption. It has been used in numerous taxa to treat bone and soft tissue infections. RLP was used to treat osteomyelitis in two wild juvenile green sea turtles (*Chelonia mydas*) at Loggerhead Marinelife Center in Juno Beach, Florida in 2025, which is the first report of its use in sea turtles. The first turtle presented with fore flipper entanglement, the second turtle with fibropapillomatosis (FP), the tumor disorder associated with chelonid herpesvirus-5. Neither turtle had boney changes on intake radiographs. The first turtle developed boney lysis at the entanglement site which progressed despite systemic antimicrobial therapy. RLP was initiated as follows: a tourniquet was placed on the proximal brachium, an antimicrobial was injected distal to the tourniquet into the brachial vein, and the tourniquet left in place for ten minutes. Antimicrobial choice was guided by culture and sensitivity. The second turtle underwent standard surgical FP tumor removal. A surgical site on a front flipper abscessed and developed boney lysis. RLP was initiated as above with an empirically chosen antimicrobial. After several RLP treatments, both turtles resolved their soft tissue lesions, showed radiographic improvement, and regained full function of the affected limb. The procedure was well tolerated by both turtles and no complications were encountered. We conclude that RLP should be considered as an adjunct therapy for osteolytic lesions in sea turtles.

Investigation of dental and periodontal conditions in wild Formosan black bear (*Ursus thibetanus formosanus*)

Thursday, 30th July - 17:15: Wildlife Medicine (O'Hare 4) - Oral

Guan-Ru Wang¹, Yun-Chieh Tuan¹, Izzie Yi-Chin Tsai², Pin-huan Yu¹

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Dental diseases are commonly seen in captive bears, whereas records in wild black bears are relatively limited. The Formosan black bear (*Ursus thibetanus formosanus*), as one of the subspecies of Asiatic black bear, is an endangered species and the focus of conservation efforts in Taiwan. With increasing cases of human-bear conflict, dental problems are commonly observed by frontline veterinarians. It seemed to be a crucial factor of repeat nuisance behavior and may negatively affect the outcome of rehabilitation and release. This concern prompted us to initiate further investigation. From 2023 to 2026, dental evaluations were conducted on rescued individuals under general anesthesia and on deceased individuals during necropsy. A total of 29 wild Formosan black bears underwent dental evaluation, with dental X-ray performed in 18 individuals and cementum annuli evaluation for age estimation in 16 bears. Incisors and canine teeth were found to be have worn earlier than other teeth, while the premolars were less frequently to wear. However, premolars are more frequently absent than other teeth. In addition, some bears show tooth root pathology under dental X-ray that were not obvious upon visual inspection. We also found 2 individuals with repeated nuisance behavior showing rapid deterioration in tooth wear. These findings provide preliminary epidemiology of dental diseases in wild Formosan black bears and highlighted the need for complete dental evaluation in rescue and rehabilitation situation. The possible association between dental problems and habitat quality, as well as frontline decision-making regarding human-conflict management, are further discussed in the report.

Eastern Oyster (*Crassostrea virginica*) Health and Reproductive Assessments in the Indian River Lagoon

Thursday, 30th July - 16:00: Wildlife Health (O'Hare 1-2) - Oral

***Kyle Donnelly*¹, *Bryce Miller*², *Nicole Stacy*³, *Ashley Rearden*⁴, *Hope Leonard*⁴**

1. Disney's Animals Science and Environment, 2. Zoo and Exotic Animal Pathology Service, University of Georgia, 3. Department of Large Animal Clinical Sciences, University of Florida, College of Veterinary Medicine, 4. Brevard Zoo

The Indian River Lagoon (IRL) is a highly diverse estuary in North America, and spans over 150 miles along Florida's east coast. Decades of pollution, eutrophic conditions, poor water quality, and overharvesting have contributed to widespread habitat loss for much of the historical biodiversity, including oysters. Eastern oysters (*Crassostrea virginica*) boast critical ecosystem functions including providing habitat structure, sequestering carbon, improving water quality, offering storm protection, as well as serving as excellent sentinels for ecosystem health. To better guide restoration efforts and understand the health threats and stressors facing this population, 15 sites within the IRL were monitored monthly for one year. Spat monitoring to assess the level of natural oyster larval settlement, water depth, salinity, pH, dissolved oxygen at the lagoon sediment's surface, water temperature, and air temperature were measured monthly. At four of the 15 oyster monitoring sites, 10 oysters were sampled monthly for one year for hemolymph and histologic analysis (n = 480). An additional 10 oysters were processed monthly for condition index (n = 480). Preliminary findings include non-specific hemocytic inflammation, lipofuscinosis, digestive gland atrophy, gonadal atrophy, gonadal neoplasia, trematode infection, *Nematopsis* sp., and rare *Perkinsus* sp infection. Seasonal gametogenesis was documented. Improved understanding of health trends in this population will drive restoration efforts and ultimately strengthen IRL recovery.

Bleeding eyes and darkened skies: Histopathology summary of a large mortality event of green sea turtles (*Chelonia mydas*) on the coast of New South Wales (NSW), Australia

Thursday, 30th July - 16:15: Wildlife Health (O'Hare 1-2) - Oral

***Heather Fenton*¹, *Adelaide Dedden*², *Jane Hall*¹, *Edward Holmes*³, *Lauren Limm*³, *Duane March*², *Ryan Pereira*⁴, *Melissa Tan*², *Tom Tran*⁴, *Karrie Rose*¹**

1. Australian Registry of Wildlife Health, 2. NSW National Parks and Wildlife Service, 3. the university of sydney, 4. Irukanji Shark and Ray Encounters

The green sea turtle (*Chelonia mydas*) is considered a key ecological indicator reflective of the overall health of the marine environment. The species is currently listed as vulnerable in Australia and the state of New South Wales (NSW). Between June and November 2025, at least 79 sick and dead juvenile and subadult green turtles were reported in the vicinity of the urban municipality of Port Stephens, NSW [32.7685° S, 151.8409° E]. Large storms with heavy rainfall were recorded in the region in the months preceding and at the beginning of the event, resulting in a cool surface layer of freshwater. Gross lesions were evaluated from necropsy images (when available) and included sloughing of the skin of the neck and extremities (15/29), blepharitis, conjunctivitis (14/29), and non-specific observations of enlarged gall bladders (7/29), large intestinal obstipation (9/29) and poor nutritional condition (12/29). Fixed tissues from 29 turtles, including six full carcasses, were examined by the Australian Registry of Wildlife Health. Notable microscopic lesions included severe, fibrinonecrotizing blepharitis, conjunctivitis and dermatitis in 6/6 eyes examined, muscular necrosis (6/7 skeletal muscle sections examined), fibrinonecrotizing meningoencephalitis with intralesional fungal hyphae (6/25 brain sections examined), and bacteria (3/25 brain sections examined). Toxicological analyses did not reveal significant contributions of any specific compounds to the overall event. The cause of the mortality event is interpreted to be associated with physiological imbalance and physical disturbance of the skin barrier subsequent to severe environmental conditions and concurrent immunosuppression resulting in mortality from sepsis due to opportunistic marine organisms.

Hidden Fungal hazards: *Fusarium* dynamics in leatherback sea turtle nest sand

Thursday, 30th July - 16:30: Wildlife Health (O'Hare 1-2) - Oral

*Elizabeth Schultheis*¹, *Samantha Kuschke*¹, *Tiffany Briggs*¹, *Jeanette Wyneken*¹

1. Florida Atlantic University

In recent years, the prevalence of fungal infections in marine ecosystems has risen significantly, and reports of fungal infections in sea turtle nests have increased worldwide. *Fusarium* spp. overgrowth in sea turtle clutches causes sea turtle egg fusariosis (STEF) and leads to embryo mortality. STEF is associated with decreased hatching success across all seven species of sea turtles. The leatherback turtle (*Dermochelys coriacea*), which has the lowest average hatching success globally, is at high risk of suffering negative impacts from STEF. While existing studies highlight the urgent need for research on the prevalence of *Fusarium* spp. in nest sand, we are not aware of any published research on this topic in southeastern Florida, USA, a leatherback nesting hotspot. To address this knowledge gap, we obtained sand samples from leatherback sea turtle nests at oviposition and excavation in Boca Raton, Juno Beach, and Jupiter, Florida. Using real-time polymerase chain reaction (qPCR), we detected and quantified *Fusarium* spp. present in nest sand at both timepoints. These data were used to determine if the presence, quantity, and growth of *Fusarium* spp. in leatherback nests covary with nest success, location, and key environmental factors. The results of this work can illuminate key factors contributing to the occurrence and abundance of *Fusarium* spp. in leatherback nests and their relationship to low hatching success. Additionally, the knowledge gained from this research enhances our understanding of STEF and may help regulators plan mitigation strategies to improve nest success.

Integration of plasma metabolomics into the comprehensive health assessment of wild ornate box turtles (*Terrapene ornata ornata*) in Illinois

Thursday, 30th July - 16:45: Wildlife Health (O'Hare 1-2) - Oral

***Laura Adamovicz*¹, *Madeline Brookings*², *Erika R. Suniga*³, *Eliza Baker*⁴, *John Winter*⁵, *Matthew Allender*¹**

1. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign, 2. Wildlife Epidemiology Laboratory, College of Veterinary Medicine, University of Illinois Urbana-Champaign, 3. Wildlife Epidemiology Lab, College of Veterinary Medicine, University of Illinois Urbana-Champaign, 4. Illinois Zoological and Wildlife Health Management Residency, Brookfield, IL USA, 5. University of Illinois

Ornate box turtles (*Terrapene ornata ornata*) are declining across their range and are state-threatened in Illinois. Health assessment is an important component of species recovery efforts, but characterizing health status in reptiles is challenging because most clinical pathology parameters have poor sensitivity and specificity in these species. Plasma metabolomics provides a comprehensive assessment of cellular metabolites (e.g. amino acids, lipids, sugars, hormones, etc.) which can be used to identify novel biomarkers for health assessment, though metabolomics studies are uncommon in wild reptiles. The purpose of this study was to incorporate untargeted plasma metabolomics into a state-wide ornate box turtle health assessment program including physical examination, hematology, plasma biochemistries, protein electrophoresis, and molecular surveillance for 20 pathogens. Data collection was performed in spring, summer, and fall 2024 using 57 serially-sampled wild turtles. Four hundred-forty-five metabolic compounds were successfully identified using existing databases, while 6,545 compounds of unknown identity were also recovered. Plasma metabolomic profiles were found to vary significantly between populations, sexes, and across the active season, correlating to shifts in other clinical data. Seven metabolites were significantly increased in turtles testing positive for novel adenoviruses, potentially consistent with subclinical pathogen impacts. Eight turtles died, and 24 metabolites were significantly different in these animals compared to survivors, indicating the possibility of novel health biomarkers within this dataset. This study reveals the potential utility of plasma metabolomics for evaluating health status in wild reptiles, particularly within the context of traditional health metrics.

Epidemiology of *Ophidiomyces ophidiicola*, *Paranannizziopsis* spp., and *Nannizziopsis* spp. in wild snakes across North America

Thursday, 30th July - 17:00: Wildlife Health (O'Hare 1-2) - Oral

***Maya Iyer*¹, *Laura Adamovicz*², *Amber Simmons*³, *Crystal Moreno-Garcia*³, *Ellen Haynes*⁴, *Christopher Petersen*⁵, *Robert Lovich*⁶, *Matthew Allender*³**

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The onygenalean fungi *Ophidiomyces ophidiicola*, *Paranannizziopsis* spp., and *Nannizziopsis* spp. are associated with cutaneous disease in snakes and produce overlapping clinical signs; however, epidemiologic investigations in North America have historically focused on *O. ophidiicola* alone. This study used a validated multiplex quantitative PCR assay to screen skin swabs from wild snakes for *O. ophidiicola*, *Paranannizziopsis* spp., and *Nannizziopsis* spp. to estimate pathogen-specific prevalence, describe geographic/host associations, and evaluate evidence of coinfection and alternative fungal etiologies for skin lesions. Samples were collected from 1,394 wild snakes on U.S. military installations, representing 79 species across 36 states and Puerto Rico. The prevalence of *O. ophidiicola* was 19.2% (95% CI: 12.2-21.4%). Results were consistent with prior surveys, although ophidiomycosis was detected in Nevada for the first time. *Paranannizziopsis* spp. were detected at low prevalence (0.5%; 95% CI: 0.2-1.0%) across seven states, including first detections in Georgia, Mississippi, Nevada, Oklahoma, Texas, Wisconsin, and in previously unreported host species (*Agkistrodon piscivorus*, *Phyllorhynchus decurtatus*). *Nannizziopsis* spp. were not detected. Skin lesions were observed in 20% of snakes. Coinfections were rare ($n = 1$). Snakes with skin lesions that previously tested negative for *O. ophidiicola* also lacked detectable *Paranannizziopsis* spp. and *Nannizziopsis* spp. DNA. Associations between *O. ophidiicola* detection and geographic, taxonomic, and demographic variables were consistent with prior studies, while no significant associations were identified for *Paranannizziopsis* spp. Overall, these findings reinforce *O. ophidiicola* as the predominant fungal pathogen affecting wild snakes in the U.S. and demonstrate the value of multiplex qPCR for wildlife pathogen surveillance.

From blotchy bass syndrome to malignant cancer: neoplastic transformation associated with adomavirus infection in black bass (*Micropterus* spp.)

Thursday, 30th July - 17:15: Wildlife Health (O'Hare 1-2) - Oral

Mandy Womble¹, Clayton Raines², Heather Walsh², Mike Stafford³, Frances Mackie³, R. Kent Passingham¹, Esteban Soto⁴, Susan Fogelson⁵, Amanda Curry⁶, Gregory Lewbart¹, Luke Iwanowicz⁷, Abigail Armwood¹

1. North Carolina State University College of Veterinary Medicine, 2. U.S. Geological Survey, Eastern Ecological Science Center, Leetown Research Laboratory, 3. Wonders of Wildlife National Museum and Aquarium, 4. University of California-Davis School of Veterinary Medicine, 5. Fishhead Labs, LLC., 6. Florida Fish and Wildlife Conservation Commission, Florida Bass Conservation Center, Richloam Fish Hatchery, 7. U.S. Department of Agriculture/Agriculture Research Service, National Center for Cool and Coldwater Aquaculture

Black bass (*Micropterus* spp.) are apex predators in North American freshwater ecosystems and are ecologically and economically important sportfish. Hyperpigmented melanistic skin lesions (HPMLs), colloquially termed “blotchy bass syndrome,” are increasingly reported in both free-ranging and aquarium-housed fish and are associated with a novel adomavirus. While adomaviruses are known to induce proliferative skin lesions, malignant transformation has not previously been documented.

We describe five cases of malignant neoplasia in aquarium-housed black bass with concurrent adomavirus infection. Two hybrid black bass (*Micropterus nigricans* x *M. salmoides*) housed in the same system, and one largemouth bass (*Micropterus nigricans*) and two Florida bass (*M. salmoides*) from separate locations developed plaque-like, variably pigmented, ulcerative cutaneous masses. Histopathologic diagnoses included malignant melanoma (n = 4) and soft tissue sarcoma (n = 1), with hepatic metastasis identified in two individuals. Molecular screening for three adomaviruses (*Micropterus salmoides* adomavirus [MsA]-1, MsA-2, and MsA-3) detected MsA-1 in affected fish. Fluorescent RNAscope™ in situ hybridization demonstrated viral signal within neoplastic cells.

Collectively, these findings support an association between adomavirus infection, HPMLs, and malignant transformation in black bass and represent the first report of malignant neoplasia associated with an adomavirus. The presence of putatively oncogenic viruses in both managed and free-ranging systems raises concerns for population health, fisheries sustainability, and urban-aquatic interfaces. Coordinated surveillance among researchers, wildlife managers, and citizen scientists will be critical to assess ecosystem-level impacts and inform resilient management strategies.

Sharing your story: writing and speaking about your work for diverse audiences

Thursday, 30th July - 17:30: Global Voice (Virtual/Online) - Oral

Jen Martin¹

1. The University of Melbourne

Your work in wildlife health and conservation matters, but does it reach the people you most want to influence? Whether you're speaking with a journalist, a funder, researchers or a community group, the way you frame your work shapes whether it resonates or gets overlooked.

In this session we'll explore how to capture attention from your opening line, make your work relevant to different audiences, and translate complexity into something genuinely engaging and accessible. You'll come away with practical strategies for shaping what you say and write to suit any audience.

SARS-CoV-2 Surveillance in Mammals Undergoing Rehabilitation in Central Illinois

Thursday, 30th July - 20:35: Global Voice (Virtual/Online) - Oral

***Riley Dunwoody*¹, *Stephany Lewis*¹, *Beth Nielsen*², *Katy Parise*², *Hayley Yaglom*², *Jeff Gruntmeir*³,
*Maureen Long*³**

1. Wildlife Medical Clinic, Department of Veterinary Clinical Medicine, College of Veterinary Medicine, University of Illinois at Urbana-Champaign, Urbana, IL, 2. Translational Genomics Research Institute, Flagstaff, AZ, 3. Emerging Pathogens Institute, University of Florida, Gainesville, FL

The role of wildlife in SARS-CoV-2 transmission and the potential for animal reservoirs remain incompletely understood. To better understand the risk of SARS-CoV-2 in a wildlife rehabilitation setting, the Wildlife Medical Clinic at the University of Illinois partnered with the University of Florida and T-Gen to screen oral and rectal swabs and serum samples from mammals undergoing rehabilitation for SARS-CoV-2 RNA and neutralizing antibodies. Between September 2024 and December 2025, 733 samples from 327 animals of 17 species were screened for SARS-CoV-2. One seropositive sample was detected in a white-tailed deer fawn (*Odocoileus virginianus*), and an oral swab from a meadow vole (*Microtus pennsylvanicus*) was positive for SARS-CoV-2 RNA via RT-qPCR. This work sheds light on the prevalence and susceptibility of SARS-CoV-2 in species presenting for rehabilitation, and can guide biosecurity practices.

Coffee Agroforestry and Wildlife Risk: Baseline Data on Javan Gibbon and Sunda Slow Loris Occurrence in Java

Thursday, 30th July - 20:55: Global Voice (Virtual/Online) - Oral

***Muhammad Ridwan Adyatama*¹, *Bryan Stephenson Wong*¹, *Steven Venaya*¹**

1. Kelompok Studi Satwa Liar, Faculty of Veterinary Medicine, Universitas Gadjah Mada, D.I. Yogyakarta 55281

Java is the most densely populated large island and is experiencing rapid forest loss and fragmentation driven by urbanization and agricultural expansion. Coffee agroforestry has been proposed as a land-use system that retains forest ecological functions while increasing land value, potentially slowing forest conversion. However, most Javan primates remain strongly dependent on intact old-growth forest. This preliminary study assesses populations of the Javan gibbon (*Hylobates moloch*) and Sunda slow loris (*Nycticebus coucang*) within coffee agroforestry landscapes in Petungkriyono and Kemuning, Central Java, Indonesia, to provide baseline data for conservation planning. Two field expeditions were conducted using vocal count and line transect methods, alongside observations of other primate species. Vocal count data, derived from triangulation of early-morning female gibbon vocalizations, yielded an estimated density of 1.13 groups/km². Line transect surveys across three transects produced gibbon density estimates of 1.7, 3.3, and 12 individuals/km² with the unusually high density near roads indicating an edge effect on gibbon foraging behavior. Overall, Javan gibbon density was estimated at approximately 5 individuals/km², representing a 29% decline from 2018 estimates prior to coffee agroforestry expansion. The presence of Sunda slow loris was confirmed through sightings and environmental marks, although density could not be estimated due to limited data. Javan lutung (*Trachypithecus aureus*), surili (*Presbytis comata*), and long-tailed macaque (*Macaca fascicularis*) were also recorded. These results suggest that coffee agroforestry may be tolerated by Javan primates to a limited extent, but adjacent intact forest remains essential to sustain viable populations and reduce human-wildlife interactions.

Conservation and Health at the Human–Wildlife Interface: Bacterial Risks to the Critically Endangered Bostami Turtle (*Nilssonia nigricans*) in Bangladesh

Thursday, 30th July - 21:10: Global Voice (Virtual/Online) - Oral

Sabrina Ferdous¹

1. Faculty of Veterinary and Animal Sciences, Gono University

The Bostami turtle (*Nilssonia nigricans*) is a Critically Endangered species that survives within a long-established shrine pond system in Bangladesh, where high animal density and close human contact raising concerns regarding zoonotic disease transmission. This ongoing study aims to investigate the bacteriological status of Bostami turtles and its shrine pond habitat, with a specific focus on zoonotic bacteria of public health importance using one health approach. So far, microbial analysis has been performed on turtle oral and cloacal swabs (6 samples) and pond water samples (8 samples from different location within the shrine pond). All samples were analyzed using selective and differential culture media for presumptive identification of enteric and aquatic bacteria. *Escherichia coli* and *Salmonella* spp. detected in all of pond water samples and turtle (oral) samples. This result suggests fecal contamination and environmental circulation of enteric bacteria. Additionally, *Pseudomonas* spp., and *Vibrio* spp. were isolated 100% and 80% of pond water respectively as well as from turtle rectal sample. Additionally, heavy bacterial growth (too numerous to count) was observed in 90% of water samples and 100% of turtle samples. Confirmatory biochemical and molecular identification of isolate, along with further characterization of zoonotic potential are ongoing. The high prevalence of enteric bacteria and opportunistic bacteria highlights potential health risks to *N. nigricans* and zoonotic risks within shrine pond environment. Integrating routine health surveillance and water quality management into conservation strategies is essential for the long-term protection of this unique and culturally significant turtle population.

Detection of *Rickettsia hoogstraalii* and *Rickettsia lusitaniae* in *Argas (Persicargas) ricei* ticks infesting California Condors (*Gymnogyps californianus*)

Friday, 31st July - 08:30: Wildlife Health - Avian I (O'Hare 1-2) - Oral

***Sarah Hamer*¹, *Julia Gonzalez*², *Lisa Auckland*³, *Sara Neumann*⁴, *Arianna Punzalan*⁵, *Jennifer Kennedy*⁴, *Julie Barnes*⁴, *Jordan Davis-Powell*⁶**

1. Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, 2. Schubot Center for Avian Health, Texas A&M University, 3. Department of Veterinary Integrative Biosciences, Texas A&M University, 4. Santa Barbara Zoo, California 93103, USA, 5. U.S. Fish and Wildlife Service, 6. Los Angeles Zoo, Los Angeles, CA

The California condor (*Gymnogyps californianus*) is the largest North American land bird and an endangered species. An international multi-entity recovery effort led by the US Fish and Wildlife Service is working to establish robust free-living populations of condors. In September 2024, a heavy soft tick infestation was reported on three pre-release juvenile condors at Bitter Creek National Wildlife Refuge. One was treated for tick paralysis, a neurotoxin-mediated paralytic syndrome. The remaining two condors had weight loss and extensive scabbing in the areas that had previous tick burdens. Eight ticks found on perches in the flight pen were collected and identified as *Argas (Persicargas) ricei*. Pathogen testing on those ticks resulted in four positives of *Rickettsia hoogstraalii*, a species previously detected in raptors and their soft ticks in the southwestern USA; and one tick was positive for *R. lusitaniae*, previously associated with soft ticks in bats worldwide. No ticks were positive for *Borrelia* species. Bloodmeal analysis confirmed California condor was the associated host for a subset of tested ticks. All birds improved clinically with ectoparasite treatment and supportive care. These findings confirm interaction between *A. (P.) ricei* ticks and condors. Managers can consider checking and removal of ticks from temporary bird housing and prophylactic or event-based treatments of translocated birds. Further, the presence of the detected *Rickettsia* species could be considered in future wildlife health investigations.

Avian blood parasites in waterfowl from managed wetlands in Central Wisconsin

Friday, 31st July - 08:45: Wildlife Health - Avian I (O'Hare 1-2) - Oral

***Sarah Orlofske*¹, *Jeffrey Bell*², *Roxanne Gasperetti*², *Craig Ziolkowski*³, *Vasyl Tkach*², *Robert Jadin*⁴**

1. University of Wisconsin-Stevens Point, 2. Department of Biology, University of North Dakota, 3. Wildlife Management Program-George W. Mead Wildlife Area, Wisconsin Department of Natural Resources, 4. Department of Biology, Lawrence University

Waterfowl can be divided into feeding guilds, dabblers and divers, based on morphological, behavioral, and dietary differences. Dabblers swim at the top of the water, skimming the surface for food such as seeds, plants, and insects, and can walk easily on land. In contrast, divers swim deeper in more open water, dive to feed on fish, snails, and other invertebrates, and walk with difficulty on land. Consequently, we expect that parasites and pathogens would also differ between dabblers and divers. Avian blood parasites (haemosporidians) use various blood feeding flies as vectors for transmission. Waterfowl are underrepresented in haemosporidian research, and most studies have focused on dabblers because they are more common than divers in many geographic areas. We collected 58 hunter-donated waterfowl carcasses of 5 species of dabblers and 3 species of divers co-occurring at George W. Mead State Wildlife Area. Using molecular screening techniques of bird liver samples, we identified 36 infected waterfowl. Prevalence of blood parasite infection was high and varied by species with the highest prevalence of 83% in Mallards (N=6) and 71% in Green Wing Teal (N=7). Wood ducks had the highest sample size and showed 13 of 21 hosts infected (62%). There was no statistical difference between blood parasite prevalence between dabblers (64%) and divers (54%) (p-value 0.68). Overall infection levels of blood parasites at Mead are high in all birds, but comparisons with other managed wetlands are needed to determine if infections are related to local habitat or typical of fall migrating waterfowl.

Eastern Equine Encephalitis Virus in New York Raptors

Friday, 31st July - 09:00: Wildlife Health - Avian I (O'Hare 1-2) - Oral

***Jill Western*¹, *Elizabeth Buckles*², *Cynthia Hopf-Dennis*¹, *Sara Childs-Sanford*¹**

1. Cornell University College of Veterinary Medicine, 2. Animal Health Diagnostic Center, Cornell University College of Veterinary Medicine

Eastern Equine Encephalitis virus (EEEV) is a zoonotic arbovirus that causes morbidity and mortality in humans and domestic horses, with birds as reservoir host. This case series describes infection with Eastern Equine Encephalitis virus in five raptors in New York State from 2019 to 2025. One Cooper's hawk (*Accipiter cooperii*), two red-tailed hawks (*Buteo jamaicensis*), and two bald eagles (*Haliaeetus leucocephalus*) tested positive for Eastern Equine Encephalitis virus on RT-PCR. Histopathology was only performed on three of these cases, but two cases had confirmation of encephalitis. Three of these cases demonstrated neurological clinical signs prior to death or euthanasia. Clinical progression of this disease has not been previously reported in raptors that have been naturally infected with EEEV.. This case series highlights the importance of thorough diagnostic screening for arboviruses in endemic regions, and Eastern Equine Encephalitis virus should be considered as a differential diagnosis for clinical neurologic disease in raptors in these areas. Additionally, detection in raptors could be an indicator for EEEV risk to horses and humans.

Wild Birds Pathogen Surveillance in the Brazilian unique caatinga biome

Friday, 31st July - 09:15: Wildlife Health - Avian I (O'Hare 1-2) - Oral

***Lilian Catenacci*¹, *Bruno Rodrigues Oliveira*², *Clara Vanessa Azevedo Oliveira*³, *Gabriela Ferreira de Oliveira*⁴, *Amanda Maria Barbosa de Sousa*⁴, *Osmaikon Lobato*⁴, *Alessandro Domingos Araújo Filho*⁵, *Fabiano Barbosa Pessoa*⁶, *Kathleen Apakupakul*³, *Sharon Deem*³, *Lucilene dos Santos Silva*⁵**

1. Institute for Conservation Medicine, Saint Louis Zoo, St Louis, Missouri, USA, 2. Universidade Federal do Piauí, 3. Saint Louis Zoo Institute for Conservation Medicine, 4. Universidade Federal do Piauí, Programa de Pós-Graduação em Tecnologias Aplicadas a Animais de Interesse Regional, 5. Hospital Veterinário Universitário, Universidade Federal do Piauí, 6. Instituto Brasileiro do Meio Ambiente dos Recursos Naturais e dos Recursos Naturais e

Anthropic pressures, including deforestation and wildlife trade, threaten Brazilian biodiversity. Despite this, pathogen surveillance in free-living birds from the Caatinga biome in northeastern Brazil remains scarce. This study investigated pathogen circulation in birds confiscated from illegal trade and admitted to the Federal Wildlife Rehabilitation Center (IBAMA), Piauí, Brazil. A total of 183 samples from birds received between 2023 and 2026 were analyzed during quarantine. Most individuals belonged to the family Psittacidae (91.8%), followed by Ramphastidae (3.28%). Genetic material was extracted from oral and cloacal swabs using a commercial kit, and PCR assays with specific primers were performed to detect amplicons of the family Herpesviridae and the genera *Mycoplasma* and *Chlamydia*. All samples tested negative for Herpesviridae and *Chlamydia* spp. Five birds were positive for *Mycoplasma* spp.: two Red-and-green macaws (*Ara chloropterus*), two Blue-and-yellow macaws (*Ara ararauna*), and one Cory's shearwater (*Calonectris borealis*). To our knowledge, this represents the first report of *Mycoplasma* spp. infection in *C. borealis* in Brazil. The genus *Mycoplasma* includes more than 100 species, ranging from commensals to opportunistic or pathogenic organisms associated with respiratory and reproductive disorders, conjunctivitis, arthritis, and skeletal abnormalities. None of the infected birds showed clinical signs. These findings help to reduce gaps and highlight the importance of continuous pathogen monitoring in wildlife rescue centers, especially in the Caatinga biome, which is globally unique and remains poorly studied.

Trait-based assessment of West Nile virus impacts in Pennsylvania wild bird populations

Friday, 31st July - 09:30: Wildlife Health - Avian I (O'Hare 1-2) - Oral

***Brock Geary*¹, *Sean Murphy*², *Lisa Williams*², *Roderick B. Gagne*³**

1. Wildlife Futures Program, University of Pennsylvania, 2. Pennsylvania Game Commission, Bureau of Wildlife Management, 3. University of Pennsylvania School of Veterinary Medicine, Wildlife Futures Program

Pathogens that infect multiple species may produce host-specific disease outcomes, leading to variable impacts at the community or landscape scale. This may occur as a result of interactions between hosts, vectors, and their environment, and long-term monitoring efforts are often required to accurately characterize these dynamics. Understanding how effects align with hosts' life histories or behaviors can inform direction of limited management resources toward more imperiled species and promote ecosystem health.

West Nile virus (WNV) has occurred throughout North America for 20+ years, and can threaten wild birds in environments that promote large, persistent mosquito populations. Following an analysis of how environmental conditions favorable to WNV occurrence influenced bird population trends in Pennsylvania, we evaluated the relationship between species-specific ecological traits and state-level measures of WNV impact. Using primary literature and databases such as AVONET and EltonTraits, we constructed phylogenetically-explicit models to assess how bird characteristics and behaviors potentially influence interspecific variation to measured WNV effects. Beyond detecting phylogenetic signal in patterns of WNV response, we found increased effects in ground-nesting birds, vertivores, and species that exhibit more gregarious behaviors during the nesting season. Additionally, we found that species nesting in cliffs and similar human-built structures showed reduced effects, possibly reflecting their relatively low mosquito exposure. Further analysis of community composition in areas where WNV effects are elevated, along with future field-based validation of model estimates, will benefit management strategies by adding to our understanding of how the virus shapes population trends relative to other threats such as habitat loss.

Parasitism in quail: drivers of spatial patterns in Texas

Friday, 31st July - 10:15: Wildlife Health - Avian II (O'Hare 1-2) - Oral

Alynn Martin¹, Maedean Cardenas², Liza Soliz², Alejandro Bazaldua², Andrea Esqueda², Fidel Hernández²

1. Department of Biology, Grand Valley State University, Allendale, MI, 49401, USA; Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, 78363, USA, 2. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, 78363

Quails in North America have been experiencing range-wide population declines. Although quail populations inhabiting semiarid environments are strongly influenced by precipitation, northern bobwhite (*Colinus virginianus*) populations have remained low despite above-average rainfall and ample habitat in some regions of Texas. Parasites (eyeworms [*Oxyspirura petrowi*] and cecal worms [*Aulonocephalus pennula*]) have been identified as potential causes for these declines. An interesting spatial-gradient pattern occurs in the prevalence of these parasites: eyeworms exhibit decreasing prevalence from northern Texas (50-90%) to southern Texas (4-10%) whereas cecal worms do not (80-90% prevalence across the N-S gradient). We hypothesized that species abundance of intermediate hosts–species required for the helminth development–varies from north to south. Our objective was to identify drivers of spatial patterns of helminth prevalence in northern bobwhite, specifically intermediate-host diversity (i.e., grasshoppers, crickets, wood cockroaches, and other insects). We collected insects during June–July 2025 across the entire N–S gradient of Texas ($n = 8$ counties) using sweep nets and pitfall traps ($n = 20$ sampling points per county). Grasshopper diversity decreased from northern Texas (53 species; Hemphill County) to southern Texas (20 species; Hidalgo County), as did grasshopper abundance (950 grasshoppers vs. 200 grasshoppers, respectively). We will use molecular techniques to screen insects for the presence of eyeworms and cecal worms and calculate prevalence for each helminth by insect species. These findings will shed light on the drivers of the spatial patterns of quail parasitism and help guide quail conservation efforts.

Climate change and extreme weather events to intensify West Nile virus activity

Friday, 31st July - 10:30: Wildlife Health - Avian II (O'Hare 1-2) - Oral

Desiree Bliss¹, Gracie Fischer¹, Leigh Combrink¹

1. University of Arizona

Transmitted by *Culex* mosquitoes, West Nile virus is the leading cause of arboviral disease in the United States. Arizona's record-breaking 2021 West Nile outbreak, with 1,715 reported human cases and 127 documented deaths, exemplifies this growing threat. The pathogen additionally has resulted in mass die-offs of avian host species, especially corvids. Here we present the first operational framework for predicting vector-borne disease seasonal increases at weekly temporal and landscape spatial scales. Using a decade of mosquito surveillance data coupled with time-lagged weather patterns in a random forest framework, we created spatial models to predict both mosquito abundance and West Nile Virus vector occurrences across Arizona. Our weighted models achieved 98.9% accuracy for occurrence and explained 65.3% of weekly variation in county-level human cases with a predictive time lag of one week. Drought and monsoon cycling emerged as primary drivers of West Nile occurrences; these patterns will intensify under all climate change scenarios. We are additionally in the process of adding West Nile avian host distributions to our existing models to improve accuracy in congruence with the whole disease system. Our framework represents the first landscape-scale, weekly disease prediction system with demonstrated human case correlation, providing a revolutionary decision-support tool for infectious disease forecasting that can be replicated globally and adapted to other vector-pathogen systems. Our work, which includes database building and Shiny App development, is already being shared with state vector control managers to improve outcomes for upcoming West Nile seasons.

Surveillance for influenza A virus H5-specific antibodies in Canada Geese (*Branta canadensis*) in Pennsylvania

Friday, 31st July - 10:45: Wildlife Health - Avian II (O'Hare 1-2) - Oral

***Justin D. Brown*¹, *David Stallknecht*², *Jeremy Stempka*³, *Andrew R. Di Salvo*³, *Amanda Hoyt*³, *Kyle Van Why*⁴, *Kevin D. Niedringhaus*⁵, *Lane Potts*⁵, *Erica Miller*⁵, *Emma Grunwald*⁵, *Madison Stevens*⁵, *Luke Scherer*⁵, *Whitney Kistler*⁶, *Nate Brown*⁷, *Rebecca Poulson*⁸**

1. Pennsylvania State University, **2.** Southeastern Cooperative Wildlife Disease Study, **3.** Pennsylvania Game Commission, Bureau of Wildlife Management, **4.** United States Department of Agriculture, Animal Plant Health Inspection Service, Wildlife Services, **5.** Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, **6.** Lincoln Memorial University, **7.** SCASD, **8.** Southeastern Cooperative Wildlife Disease Study, University of Georgia

Wild waterfowl serve as reservoirs for low pathogenic (LP) avian influenza viruses (AIV), maintaining a diversity of viral subtypes; however, infection with the H5 subtype has historically been uncommon in most species. This changed with the emergence of H5N1 highly pathogenic (HP) AIV in North America during 2021–2022, substantially altering AIV ecology in wild birds. Prior to H5N1 HPAIV emergence in North America, Canada geese (*Branta canadensis*) exhibited a high seroprevalence to H5 LPAIV relative to other waterfowl. During 2009–2012, 24% of Canada geese sampled in Pennsylvania during June had antibodies to AIV nucleoprotein (NP). Though antibodies to multiple hemagglutinin subtypes were detected, the most common were to H5. To assess changes in AIV exposure following H5N1 HPAIV introduction, blood samples from Canada geese throughout Pennsylvania were collected in June 2025, with antibodies to AIV NP detected in 33% of the geese. Among NP-seropositive samples, 52% had H5 antibodies. Of these, 48% reacted to a North American H5 LPAIV antigen, 18% to a Eurasian H5 HPAIV antigen, and 14% to both antigens. Among samples positive to both H5 antigens, 75% had North American H5 antibody titers that were equal or higher than to Eurasian H5. These results suggest Canada geese in Pennsylvania are being exposed to H5 HPAIV, although seroprevalence remains lower than to historic North American H5 LPAIV. Collectively, these findings improve our understanding of H5 AIV exposure and immunity in Canada geese and help clarify the role of this species in the evolving epidemiology of H5N1 HPAIV.

Predicting Wildlife Disease Risk from Space: Avian Tick Parasitism and Land-Use Change Across the Colombian Andes

Friday, 31st July - 11:00: Wildlife Health - Avian II (O'Hare 1-2) - Oral

Sreeja Puthumana¹, **Gustavo A. Londoño**², **Julie M. Allen**³, **Mohamed Sallam**¹

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Department of Biological Sciences, Virginia Tech

Wild birds disperse immature ixodid ticks and their pathogens across landscapes, making avian–tick infestation a critical but underused indicator of wildlife disease risk in fragmented tropical ecosystems. Yet the environmental and host drivers structuring these interactions across changing Neotropical landscapes, and their implications for avian conservation and pathogen surveillance, remain poorly resolved. Across 12 years (2008–2019), we screened 1,164 birds (12 orders, 204 species) for ixodid ticks at 15 Colombian Andean localities spanning ~500–3,121 m a.s.l. across Eastern, Western, and Middle slopes. Macrohabitat predictors, seven Sentinel-2 land-use/land-cover (LULC) classes (10-m resolution, Google Earth Engine), elevation, and climate, were extracted within 10-km buffers, with decadal LULC change quantified in ArcGIS Pro. Three Random Forest models (host-trait, macrohabitat, integrated) partitioned drivers of tick prevalence across ecological scales. Infestation peaked in the Eastern Andes (up to 46.5% of birds at 3,120 m) and was lowest in mid-elevation valleys, spatially overlapping known regional foci of spotted-fever group rickettsiae. LULC trajectories diverged: Evergreen Broadleaf Forest expanded across Western sites while grasslands encroached on the Eastern slope (net shift -1.530 km²), reshaping habitat suitability for off-host tick survival in opposite directions. The integrated model achieved near-ceiling discrimination (AUC = 0.98); elevation and vegetation structure dominated, with host traits (mixed-flock participation, bill morphology, foraging stratum) acting as secondary modulators. These findings identify Andean elevational and LULC-change hotspots where avian ectoparasite burdens and the tick-borne pathogens they mediate concentrate, offering a satellite-based One Health framework to prioritize wildlife disease surveillance and conservation of vulnerable montane avifauna.

Comparative Transmission Dynamics, Viral Shedding, and Pathobiology of Clade 2.3.4.4e H5N6 Highly Pathogenic Avian Influenza Virus in Mallards and Mandarin Ducks

Friday, 31st July - 11:15: Wildlife Health - Avian II (O'Hare 1-2) - Oral

Sun-Hak Lee¹, Andrew Y Cho¹, Tae-Hyeon Kim¹, Seo Jeong An¹, Heesu Lee¹, Yun-Yeong Choi¹, Ju Ho Song¹, Chang-Seon Song¹, Dong-Hun Lee¹

1. konkuk university

Mallards are well-known natural reservoirs of avian influenza viruses and help maintain viruses in wild bird populations. Mandarin ducks are often detected among early cases during HPAI outbreaks in East Asia, suggesting a role in local amplification and transmission. We compared infection dynamics and transmission potential of HPAI H5N6 between these species.

Ten mandarin ducks and ten mallards were experimentally inoculated with HPAI H5N6. For transmission studies, five naïve conspecific or heterospecific birds were co-housed with infected individuals. Oropharyngeal and cloacal swabs were collected at 1, 3, 5, 7, 10, and 14 days post-challenge (dpc), and viral shedding was quantified by qRT-PCR. Transmission was confirmed by viral RNA detection and seroconversion using NP-ELISA, and HI titers were measured in survivors. Two birds per species were euthanized after high-dose infection for necropsy, and tissue titers were determined by DF-1 cell-based TCID₅₀.

All surviving birds were NP-ELISA positive. HI titers were significantly higher in mallards ($\approx 2^8$) than in mandarin ducks ($\approx 2^6$) ($p < 0.05$). Peak shedding in inoculated birds occurred at 3 dpc, whereas contact birds peaked at 5–7 dpc. The highest viral titers were observed in inoculated mandarin ducks ($\approx 10^{7.0}$ EID₅₀/mL), and oropharyngeal shedding declined more gradually than in mallards. Estimated doses differed (mandarin ducks: logBID₅₀ 2.0, logBLD₅₀ >6.0; mallards: logBID₅₀ 3.0, logBLD₅₀ >6.0). Highest tissue titers were detected in mandarin duck cecal tonsil and pancreas and in mallard cecal tonsil and kidney.

These results indicate species-specific differences in shedding and immunity relevant to HPAI H5N6 transmission dynamics.

Posters

“Effects of rumen fluid contamination on anthrax-specific antibody detection in serum samples”

Poster - Poster Board 11

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Anthrax is a lethal zoonotic disease, primarily effecting herbivores, caused by the bacteria *Bacillus anthracis*. Surveillance of anthrax exposure in wildlife is determined by measuring the anthrax-specific antibody titers in blood samples using enzyme-linked immunosorbent assays (ELISAs). Occasionally, the blood samples collected via hunter-harvest for surveillance of anthrax can be accidentally mixed with rumen fluid, which may affect the detection of anthrax-specific antibodies. There is no current literature addressing if serum contaminated with rumen fluid effects the validity of serological assays. In this study, Brangus steers (n = 5) were vaccinated with the commercially available Anthrax Spore Vaccine for use as a positive control to generate anthrax-specific antibodies. Blood and rumen fluid were collected from the steers at weekly, biweekly, and monthly intervals. At the time of sample collection, blood was mixed with rumen fluid at varying concentrations of blood to rumen fluid (100%:0%, 75%:25%, 50%:50%, 25%:75%, and 0%:100%). Then, the anthrax-specific antibody levels of each sample were measured to determine the effect rumen fluid contamination has on ELISA readings compared to uncontaminated serum. Expected outcomes are that the detection of anthrax-specific antibodies will be negatively affected by contamination from rumen fluid due to ruminal proteases breaking down the antibodies present in the blood. Results of this study will allow wildlife disease surveillance researchers to determine the viability of rumen fluid contaminated serological samples and evaluate the long-term immune response of the commercially available anthrax vaccine in cattle.

A retrospective review of Tularemia cases in Wyoming, USA (2019-2024)

Poster - Poster Board 14

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In 2024, there was a sharp increase in human reports of tularemia, a zoonotic bacterial disease, in Wyoming, USA. To investigate current tularemia patterns in Wyoming, we collected and described tularemia data from two state agencies over a 5-year period (2019-2024). Wildlife data came from the Wildlife Health Laboratory (Wyoming Game and Fish Department (WGFD), Veterinary Services) and human reports from the Wyoming Department of Health (WDH). Tularemia status was determined based on the sample type available for testing, and was assigned positive/negative based on fluorescent antibody (FA), Polymerase Chain Reaction (PCR) or culture, or seropositive/seronegative based on the microagglutination test (MAT).

A total of 278 cases were submitted to the WGFD, with the majority of submissions being from *Sylvilagus* spp. (64.4%; n=179/278), during the Spring (March-May) (41.0%; n=114/278), and from Laramie County (25.2%; n=70/278). Ten wildlife samples (FA or PCR) were positive for tularemia (n=270; 3.7%; 95% CI: 1.8-6.7%), and only one (MAT) was seropositive (n=8; 12.5%; 95% CI: 0.3-52.7%). Of the positive wildlife submissions (FA or PCR), the highest prevalence was from Niobrara County (66.7%; n=2/3), and the most submissions were during the Summer (June-August) (8.2%; n=8/97). Eighteen human cases (ELISA or culture) were reported to the WDH, with the majority during the Summer (55.6%; n=10/18) and from Sheridan County (38.9%; n=7/18). No spatial or temporal overlap was identified between the two datasets. In addition to disease surveillance, this investigation helps to identify risk factors and strengthen relationships between agencies, with the potential for future management implications.

Adenoviral infection in a free-ranging moose calf in Wyoming, USA

Poster – Poster Board 26

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Adenoviral hemorrhagic disease (AHD) was first documented in mule deer (*Odocoileus hemionus*) in Wyoming, USA, in 1999, and has been sporadically detected in free-ranging and captive animals throughout the state since then. AHD presents similarly to other viral hemorrhagic diseases of cervids and pronghorn including epizootic hemorrhagic disease (EHD) and bluetongue (BTV). Mule deer are most commonly and severely affected by AHD. Between 1999-2025, over 65 cases were recorded through opportunistic surveillance, with fawns showing the highest mortality rates. Moose (*Alces alces shirasi*) cases are comparatively rare, with positive singular detections observed in 1999, 2010 and 2021.

A free-ranging female moose calf mortality was investigated in August 2025 in Albany County, Wyoming. Wyoming Game & Fish Department biologists conducted a field necropsy and submitted tissues and digital photographs for evaluation. AHD was considered a differential diagnosis based on gross observations of pulmonary edema and pleural effusion.

Molecular tests (qPCR) detected Deer adenovirus A (previously OdAdV-1) in a pooled sample of lung and spleen, while tests for EHD and BTV were negative. Histopathologically, there was acute segmental fibrinoid necrosis and vasculitis and resultant hemorrhage of multiple organs, most notably in the papillary muscle of the heart. Positive immunohistochemical staining for deer adenovirus was observed in a few cells in the intima and media of affected arteries. Genome sequencing of the adenovirus is currently underway.

Further investigations into the virus causing mortality in free-ranging moose can help in understanding the etiology and future impact on populations around the state.

Anatomical Determinants of Host Preference for Ixodid Ticks: A Comparative Study on Dermal Characteristics between Water Deer (*Hydropotes inermis*) and Roe Deer (*Capreolus pygargus*)

Poster – Poster Board 44

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This study investigated the morphological and histological mechanisms driving the differential host preference of Ixodid ticks between Water deer (*H. inermis*) and Roe deer (*C. pygargus*) in Inje, Gangwon Province. From July to October, ectoparasites were collected and analyzed alongside host-specific dermal traits, including hair diameter, inter-follicular distance, and epidermal thickness. Statistical analysis using the Mann-Whitney U test showed that Roe deer harbored significantly higher numbers of both total and fully engorged adult ticks, specifically *Haemaphysalis longicornis* and *H. flava*, compared to Water deer ($p < 0.05$). Morphometric analysis revealed that the ratio of tick thickness to inter-hair distance was 48.16% in Roe deer, whereas it was only 5.31% in Water deer, indicating that the denser and thicker hair of Water deer acts as a primary physical barrier against tick navigation and attachment. Although the tick hypostome length ($229.89 \pm 1.23 \mu\text{m}$) was more than triple the epidermal thickness of both species, no significant difference was found in the epidermal thickness itself, suggesting that hair density and diameter are the critical determinants of attachment success. During engorgement, ticks on Water deer must overcome the mechanical resistance of approximately 17 thick hairs ($363.30 \mu\text{m}$ diameter), presenting a significantly higher physical challenge than that encountered on Roe deer. These findings demonstrate that the pronounced host preference for Roe deer is fundamentally driven by its lower hair density and thinner hair diameter, which facilitate easier movement and successful engorgement for the ticks.

Are Wild Boar Spreading Disease in Alberta, Canada? Emerging Risks in Agricultural Landscapes

Poster – Poster Board 73

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As wild boars are rapidly expanding across agricultural landscapes in Alberta, understanding their pathogen burden is critical for managing disease risk at the wild–livestock–human interface.

The study aims to provide an overview of key pathogens circulating within the Alberta invasive wild boar population.

From 2018–2024, we opportunistically sampled 331 individuals. Pathogens were screened by serological, molecular and coprological assays. *Escherichia coli* isolates underwent antimicrobial susceptibility testing using the Sensititre NARMS Gram Negative CMV3AGNF panel.

Wild boars were infected with 13 pathogens.

Viral detections include porcine reproductive and respiratory syndrome (PRRS) (1%; 1/96), porcine circovirus (PCV1) (0.3%; 1/331), PCV2 (33%; 109/331), PCV3 (27%; 90/331), rotavirus (27%; 25/92), and influenza A virus (IAV) (4%; 5/120).

Evidence of exposure to HPAI H5N1 was identified during a widespread epizootic of clade 2.3.4.4b circulating in wild and domestic birds, suggesting incidental spillover into wild boars.

Bacterial detections included *Mycoplasma hyopneumoniae* (2%; 2/96), *Salmonella* spp. (3%; 2/66), and *Erysipelothrix rhusiopathiae* (100%; 120/120). *Salmonella*-positive were identified as *S. enterica* subsp. *diarizonae* serotype 61:k:1,5,(7) and *S. enterica* serotype Montevideo, both recognized foodborne pathogens.

Parasites identified include *Metastrongylus* spp. (26%), *Trichuris* spp. (6%), and *Ascaris* spp. (6%), all with limited zoonotic potential.

Antimicrobial resistance was observed across fluoroquinolones and second- and third-generation cephalosporins, which are critically important in human medicine.

Alberta wild boars carry multiple pathogens including of zoonotic importance. Their expanding presence in the province highlights the need for continued surveillance to safeguard livestock, wildlife, and public health within a One Health framework.

Assessing the Use of a Rapid, Point-of-Care Test for *Leptospira* in Free-Ranging Raccoons (*Procyon lotor*) in Washington State

Poster – Poster Board 25

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Leptospirosis, caused by pathogenic *Leptospira* spp., is a globally significant zoonotic disease. Raccoons (*Procyon lotor*) are reservoirs to some *Leptospira* spp., have adapted to urban environments, and are frequently seen in wildlife rehabilitation. Rapid diagnosis of infections is essential in guiding treatment and reducing transmission risk to staff and patients. However, the gold-standard serologic assay, the microscopic agglutination test (MAT), can take days and the IDEXX SNAP Lepto test (SNAP), a point-of-care ELISA which provides rapid results, is only validated in dogs. We assessed the use of the SNAP in 22 raccoons admitted to PAWS Wildlife Rehabilitation Center (WA) from 2024-2025. Sera were tested by MAT and SNAP. MAT titers were converted into binary results using two cutoffs: $\geq 1:100$ (17/22 positive) and $\geq 1:6400$ (5/22 positive), and 7/22 were SNAP positive. We calculated the positive percent agreement (PPA) and negative percent agreement (NPA) between the MAT and SNAP with MAT as the reference test. PPA and NPA are analogous to sensitivity (PPA) and specificity (NPA) when the true state is unknown. At MAT $\geq 1:100$, PPA=41.2% (7/17) and NPA=100% (5/5); at MAT $\geq 1:6400$, PPA increased (100%; 5/5) and NPA decreased (88.2%; 15/17). The high PPA at a high titer cutoff, which is likely more predictive of current versus prior infection, suggests that the SNAP correctly detects high MAT titers and may be useful as an initial screening tool in raccoons in this setting.

Bacterial Diversity and Antimicrobial Resistance in Wildlife and Client-owned Reptiles: A One Health Perspective

Poster – Poster Board 62

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Reptiles presented to wildlife rehabilitation centers and veterinary teaching hospitals frequently suffer from trauma or infectious disease, with secondary bacterial infections complicating clinical management. Understanding bacterial diversity and antimicrobial resistance (AMR) patterns in these cases is essential within a One Health framework, particularly at the wildlife-domestic-human interface. We evaluated causes of admission, bacterial isolates, and antimicrobial susceptibility profiles in reptiles presented to a southeastern U.S. veterinary teaching hospital during 1 year. Free-ranging reptiles were most commonly admitted due to vehicular trauma and domestic dog attacks, with box turtles (*Terrapene carolina*) and black rat snakes (*Pantherophis alleghaniensis*) predominating. In contrast, client-owned reptiles presented for respiratory and reproductive disease, many associated with suboptimal husbandry. Common captive species included pond sliders (*Trachemys scripta*), bearded dragons (*Pogona vitticeps*), iguanas (*Iguana iguana*), and leopard geckos (*Eublepharis macularius*). Gram-negative organisms predominated (77.05%), followed by gram-positive bacteria (21.31%) and acid-fast organisms (1.64%). Nearly 45% of isolates were not identified by MALDI-TOF mass spectrometry, suggesting substantial undercharacterized microbial diversity. Frequently isolated genera included *Pseudomonas*, *Aeromonas*, *Citrobacter*, *Pasteurella*, *Myroides*, *Morganella*, *Serratia*, *Salmonella*, *Stenotrophomonas* and *Comamonas*. Chelonians with dog bite wounds exhibited polymicrobial infections consistent with mammalian oral and reptilian skin microbiota. High resistance rates were observed to multiple commonly used antimicrobials, which were higher in previously treated client-owned reptiles. These findings highlight reptiles as potential environmental sentinels and reservoirs of AMR, reinforcing the need for culture-guided therapy with susceptibility analysis, antimicrobial stewardship, and integrated wildlife-companion animal-human health surveillance strategies.

Baylisascaris procyonis infection in Tennessee raccoons in relation to population density

Poster – Poster Board 58

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Baylisascaris procyonis, or raccoon roundworm, is a nematode parasite of raccoons that can be transmitted to humans and other animals. Raccoons (Procyon lotor) are the definitive host, and do not usually show signs of disease when infected. In paratenic hosts, larvae can migrate to the eyes or brain and cause disease. There is a small body of work associating raccoon B. procyonis infection with human population density, but results have been mixed. Additionally, few studies have quantified infections of B. procyonis in Tennessee. The purpose of this study was to investigate B. procyonis infections in TN raccoons and compare rural (defined as counties with <100,000 people) and urban (defined as counties with >100,000 people) areas. Thirty-six Tennessee raccoons were opportunistically acquired from the United States Department of Agriculture Animal and Plant Health Inspection Service National Rabies Management Program. Raccoons were necropsied, parasites extracted from the gastrointestinal tract and morphologically identified to species. Data for human population density was acquired from the University of Tennessee Institute for Public Service website. B. procyonis was identified in 41.7% of raccoons. In rural areas, B. procyonis was identified in 55.6% (5/9) of raccoons and in urban areas 37.0% (10/27) of raccoons. Other papers have found similar patterns and theorize this is because of a decreased reliance on paratenic hosts, such as squirrels. Future work should investigate abnormal hosts such as coyotes and dogs. The findings of this work emphasize the important ecological connection between wildlife and human populations.

Black Bear Mange Memoirs: Communication and management of a public-facing wildlife disease

Poster – Poster Board 70

***Raquel Francisco*¹, *Elizabeth Pienaar*¹, *Marcelo Jorge*¹, *Michael J. Yabsley*²**

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The management of sarcoptic mange in North American wildlife, particularly American black bears (*Ursus americanus*), presents challenges for wildlife agencies navigating public and hunter expectations. Because mange produces highly visible clinical signs in a charismatic species, management decisions often occur under public scrutiny, making stakeholder perceptions an important component of disease management. We surveyed 2,019 individuals, including 616 hunters and 1,403 non-hunters, to assess knowledge, concern, reporting behavior, and support for agency management actions. Respondents were recruited using quota-based sampling to represent the U.S. adult population, with targeted sampling in regions with varying histories of mange emergence. Support for management actions varied by mange severity, with most participants supporting euthanasia of bears with severe mange and opposing intervention for mild cases. Emotions, perceived ability of bears to recover, disease knowledge, and trust in wildlife agencies significantly influenced support for management decisions. Awareness of mange and willingness to report affected bears differed between hunters and non-hunters, highlighting differences in stakeholder engagement and surveillance participation. Messaging that addressed disease outcomes, treatment limitations, and logistical constraints improved alignment between public expectations and agency-supported management strategies. Our findings suggest that communication strategies emphasizing the scientific realities of mange progression, including the potential for mild and moderate infestations to resolve without intervention, may improve public understanding and support for evidence-based management. Integrating communication with disease surveillance and management efforts may strengthen stakeholder trust and improve implementation of wildlife health policies.

Body condition, metabolic indicators, and blood-parasite infection of European starlings (*Sturnus vulgaris*) across agricultural landscapes in East Lansing, MI

Poster – Poster Board 39

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Agricultural landscapes can alter wildlife health by modifying resource availability, energetic demands, and exposure to pathogens. Body condition is used as a measure of avian health; its mechanistic links to metabolic state and pathogen presence remain under-researched in agricultural environments. We examined variation in body condition and its associations with metabolic indicators and pathogen detection in wild birds sampled across four agricultural sites (Beef, Dairy, Sheep, and Horse) in East Lansing, Michigan, between May and August 2025. Using mist nets, we captured 57 birds, which were banded, sexed, aged, and sampled for morphometric and blood-based analyses. Plasma glucose and ketone concentrations were measured as indicators of metabolic state. Pathogen detection was assessed by bacterial growth from cloacal swabs to detect *Escherichia coli* and by blood smear microscopy screening for haemosporidian parasites (*Haemoproteus* spp.) and microfilariae. Body condition differed significantly among agricultural sites; birds from the Beef site exhibited the highest average condition and birds from the Dairy site the lowest, while Sheep and Horse sites were intermediate. In multivariable models, body condition was negatively associated with plasma glucose concentration, consistent with elevated glucose reflecting increased energetic demand or physiological strain. These results demonstrate strong context dependence of avian body condition across agricultural environments and suggest that metabolic indicators provide more insight into physiological variation than pathogen detection alone. Ongoing completion of blood-smear screening and planned molecular diagnostics will improve detection of blood-borne parasites and enable more comprehensive assessments of how metabolic stress and infection shape wildlife health in agricultural landscapes.

Camera trapping as a tool for monitoring dynamics of a visually apparent disease across land use gradients

Poster - Poster Board 18

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As a discipline, landscape epidemiology seeks to understand how environmental heterogeneity shapes infectious disease dynamics. However, its application to wildlife ecology remains limited by logistical challenges coinciding with pathogen detection across broad spatial scales. Visually apparent wildlife diseases, such as sarcoptic mange, provide an opportunity to overcome these barriers by enabling noninvasive surveillance. Here, we examine the landscape epidemiology of sarcoptic mange in red foxes (*Vulpes vulpes*), a ubiquitous species known to occupy virtually all urban-rural-natural landscape gradients. This study aims to quantify relationships between fox occurrence, mange prevalence, and land use while accounting for temporal trends such as seasonality. We deployed 102 camera traps across Athens-Clarke County, Georgia, one-third of which are hosted by community volunteers recruited through neighborhood-based outreach. Between June 2025 and February 2026, these cameras generated more than 1,600 confirmed fox detections from over 400,000 images, and we will present preliminary analyses of these detections. By combining noninvasive disease surveillance, fine-scale landscape data, and community participation, this work will advance wildlife landscape epidemiology and contribute to Urban One Health by fostering shared stewardship and improving understanding of disease dynamics in resilient, human-engineered ecosystems.

Can't outrun reoccurrence: Long-term outcomes of treating American black bear sarcoptic mange

Poster – Poster Board 77

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The growing incidence of sarcoptic mange in American black bears (*Ursus americanus*) has become a concern for wildlife managers in the eastern United States. Single-dose treatments like fluralaner have shown promise in treating mange in captive settings, but long-term post-release outcomes in mange-rehabilitated bears remain poorly understood. We evaluated the survival and movement patterns of 14 black bears treated for mange at the Wildlife Center of Virginia (WCV) between 2016 and 2023, including four GPS-collared adult and subadult individuals monitored via telemetry. All individuals were released only after negative serial skin scrapes and gross clinical recovery, defined by resolution of alopecia and scabbing, improved condition, and improved hematologic values relative to WCV reference ranges. Movements were analyzed for the four collared bears, all of which exhibited marked declines in movement, with three requiring euthanasia due to reoccurrence of severe mange lesions and one found dead with no gross lesions and no definitive cause of death identified. Among the 10 uncollared bears, three experienced mortality events presumably unrelated to mange reoccurrence, and seven had unknown outcomes. In all four collared bears, reduced movement following den emergence preceded euthanasia due to severe reoccurrence of mange lesions, suggesting that failure to resume typical post-denning activity may serve as an early indicator of mange relapse. Our findings indicate that although clinical recovery was achieved short-term in captivity, protection did not persist post-release into mange-endemic environments. These results highlight reinfestation risk, drug withdrawal considerations, and post-release behavioral ecology in disease management.

Causes of Death in Farmed White-tailed Deer (*Odocoileus virginianus*) in Florida during 2016-2025

Poster – Poster Board 50

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White-tailed deer (*Odocoileus virginianus*) are one of the most abundant wildlife species in North America. Deer farming offers a unique opportunity to study this important species in a controlled setting. One of the largest threats to captive and wild deer populations alike is pathogenic disease. Understanding the etiological agents responsible for pathogen-associated mortality is critical to improving the health and management of captive and wild deer. The Cervidae Health Research Initiative serves to address this issue through disease diagnostics and surveillance. This retroactive analysis of mortality data from 2016-2025 aims to identify major pathogens, susceptibility across age groups, and seasonality of outbreaks in Florida deer farms. The most prevalent pathogens include bacteria (detected in 62.9% of cases), and hemorrhagic disease viruses (42.8%). Many deer (25.2% of all cases) were found to have coinfection of viruses and bacteria. A higher percentage of bacterial detections were seen in fawns (36.0%) than yearlings (29.3%) and adults (34.7%). Conversely, a higher percentage of HD virus detections were seen in yearling (51.1%) than fawns (16.6%) and adults (32.1%). Pathogen associated fatalities varied annually, but showed clear seasonality, with outbreaks occurring in late summer. These findings will not only allow for target management solutions in Florida deer farms but also have implications for wild deer management. These findings will improve health measures and disease management strategies for both wild and captive deer, serving as an important tool in One Health management approaches in Florida.

Causes of mortality in Fiordland crested penguins (*Eudyptes pachyrhynchus*): A retrospective analysis of 2004-2024 postmortem records.

Poster – Poster Board 38

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1. Massey university

Background/Rationale: The Fiordland crested penguin (*Eudyptes pachyrhynchus*), also known as tawaki, are endemic to South Westland, Fiordland and Steward Island regions of New Zealand. The remoteness and difficulty in accessing the breeding habitat of these penguins has resulted in ongoing uncertainty regarding population size, though recent studies have estimated it to be between 12,500 to 50,000 mature individuals. Despite this, these penguins are experiencing a 20% to 29% population decline over a 35 year period and are classified as Near Threatened by the IUCN. Although conservation efforts and population demographic surveys have been in place for the last few decades, knowledge surrounding causes of mortality in this species is lacking. To the author's knowledge, there have been no large-scale retrospective studies quantifying causes of death in Fiordland crested penguins and thus gaps in understanding infectious and non-infectious contributors to their decline.

Aims: To assess causes of mortality of Fiordland crested penguins submitted to Massey University between 2004 and 2024 according to location, age groups and captivity status across New Zealand.

Methods: This retrospective study examined postmortem findings in Fiordland crested penguins using 70 reports obtained from the Massey University/Te Kunenga ki Pūrehuroa School of Veterinary Science Pathology Register, spanning the period from 2004 to 2024. The data from reports was exported, categorised and analysed using Microsoft Excel.

Characterizing Alphaherpesvirus in Diamondback Terrapins

Poster - Poster Board 20

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Diamondback terrapins are a turtle species native to coastal tidal marshes along eastern North America. A mortality event in a population of diamondback terrapins (*Malaclemys terrapin*) along the coast of New York coincided with an algal bloom, prompting an investigation into potential infectious causes. Preliminary PCR screening detected herpesvirus DNA in several individuals; however, no sequencing confirmation was performed. As herpesvirus infection has not been previously documented in this species, the objectives of this study were to clarify herpesvirus presence, evaluate genetic and host-microbe variation among individuals, and assess potential ecological implications. Two-round PCR, gel electrophoresis, band extraction, purification, and quantification of the sample DNA were performed, followed by fragment analysis and Sanger sequencing at the Cornell Biotechnology Resource Center. Of 20 samples tested, we found three exhibited PCR amplification consistent with Alphaherpesvirus, and two produced bands corresponding to the positive control of known Alphaherpesvirus DNA. Sequencing results showed *Bacteroidales* bacterium, MAG *Haliceaceae*, and MAG *Gammaproteobacteria* in two samples. These findings suggest that Alphaherpesvirus may not be present in this sample of diamondback terrapins. Our ongoing efforts include phylogenetic analysis of turtle herpesvirus and investigation of *Mycoplasma* infection. These findings provide an initial framework for disease surveillance in diamondback terrapins and contribute to broader conservation strategies to mitigate infectious disease threats in vulnerable reptile populations. This study highlights the value of sample archiving for reliable infectious disease analysis years after sample collection.

Community-based wildlife health surveillance system in Nunavik, Quebec

Poster – Poster Board 1

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A community-driven wildlife health surveillance program, targeting subsistence species, is being piloted across the 15 communities of Nunavik, Quebec. The approach utilizes standardized sampling kits, distributed through Anguvigait (Nunavik Hunting, Fishing, and Trapping Association) managers, which contain materials for organ, fecal, and blood collection, along with instructions in both English and Inuktitut. Harvesters are compensated for submissions, and samples are frozen locally before transferring to the Nunavik Research Centre (NRC) for diagnostic testing, including necropsy, microscopy, and molecular assays. Additional support is provided by the Canadian Wildlife Health Cooperative (Quebec).

Two complementary project streams are operational: one focusing on caribou and freshwater fish, and the other on marine mammals. To build long-term capacity, NRC staff provide training to Anguvigait managers on kit use and sample handling, as well as bi-monthly infographics summarizing results and observations to maintain engagement. The system also allows *ad hoc* submissions of unusual animal cases from the public, with costs covered by the NRC.

To date, three participatory workshops have been held to gather community perspectives on an ideal wildlife health monitoring system. This initiative aims to establish (i) a sustainable, participatory model of wildlife health monitoring that integrates Inuit harvesters, (ii) regional research capacity, and (iii) academic expertise. The program may allow for the detection of emerging pathogens, support food security, and generate early ecological indicators of environmental change by generating standardized diagnostic data on subsistence species. This approach would guide a long-term wildlife health surveillance framework in Nunavik, focusing on frequently observed diseases.

Comparison of qPCR and dPCR for Sensitive Detection and Quantification of Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) in Ticks from Wildlife Hosts

Poster - Poster Board 5

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Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne zoonosis caused by SFTS virus (SFTSV) in East and Southeast Asia, primarily transmitted by *Haemaphysalis longicornis*. Although qualitative PCR (qPCR) is widely used to detect SFTSV in humans, ticks, and vertebrate hosts, reported prevalence varies across studies. We compared digital PCR (dPCR) with qPCR for SFTSV detection in ticks from Korean wildlife hosts to evaluate analytical sensitivity and quantitative performance.

In 2025, ticks were collected from 37 Korean water deer (KWD) and 8 Asiatic black bears (ABBs). From KWD, 480 ticks were grouped into 97 pools (75 male and 22 female pools) and screened by qPCR; positive pools were serially diluted (10^{-1} – 10^{-6}) and tested by dPCR in duplicate to assess quantitative linearity. From ABBs, 55 ticks were grouped into 15 pools (1 male, 11 female, and 3 nymph pools) and tested by both assays in a single run to compare detection rates.

In KWD ticks, only one pool was qPCR-positive. qPCR detected SFTSV down to 10^{-3} (Ct 21.14–38.54 across 10^0 – 10^{-3}), whereas dPCR quantified SFTSV down to 10^{-4} (1,818,191.5 to 10.1 copies/ μ L across 10^0 – 10^{-4}). In ABB ticks, all pools were qPCR-negative, while dPCR detected four low-copy positives (11.3 or 14.7 copies/ μ L).

Overall, dPCR demonstrated superior sensitivity and more consistent quantification than qPCR, extending the limit of quantification in KWD ticks and detecting low-copy SFTSV in ABB ticks missed by qPCR. These results support the application of dPCR for sensitive and quantitative surveillance of SFTSV in wildlife-associated ticks.

Deer neighbors: A case study in multi-jurisdictional, urban deer management

Poster – Poster Board 35

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Management of white-tailed deer (*Odocoileus virginianus*; hereafter deer), in metropolitan areas is complicated by differing public interests, overlapping or disjunct jurisdictions, and varied management approaches that are often not in coordination with each other. These challenges are amplified by the spread of chronic wasting disease (CWD), a fatal deer disease that threatens deer populations and can require adjusting management strategies. There is limited research that investigates the interplay between different organizations in geographic proximity, each responsible for deer management, but with different stakeholders. Past research demonstrates that wildlife disease management that is inconsistently implemented across a geographic area can worsen outcomes. Relative to CWD, if insufficient numbers of deer are culled because one agency is intensively culling while neighbors do not, it may decrease the culling's efficacy and increase the opportunity for disease spread between neighboring deer social groups.

For this case study, we examined the Minneapolis and St Paul, Minnesota metro area (MSP), the 16th most-populated urban area in the United States, which saw its first detection of CWD in early 2025. We use a series of semi-structured interviews with deer managers in MSP to understand 1) how deer management strategies changed in the first year since CWD was detected and 2) variation in decision-making processes among actors involved in deer management across MSP. These results will relate urban deer management and CWD to consider how each influences the other. Thus allowing researchers to adapt local risk assessments to integrate the patchwork of management practices.

Determination of prominent tick species found on American black bears (*Ursus americanus*) in the Great Smoky Mountain region

Poster – Poster Board 27

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The American black bear (*Ursus americanus*) is a sentinel for wildlife health due to its generalist lifestyle, expansive home ranges, and ability to host several different species of ticks. Bears could play a prominent role in tick-borne pathogen transmission of One Health diseases, an ever-expanding concern in regions of growing development and tourism, such as the Great Smoky Mountains, where human- and domestic animal-bear interactions are on the rise. Evaluation of tick burden was performed on 155 American black bears that presented to either the necropsy or zoological medicine services at the University of Tennessee College of Veterinary Medicine from August 2021 - November 2024. Ticks (n = 862) were observed and removed from 86 bears, and species and sex determined based upon morphological characteristics. Ticks were considered as unknown if damaged (n = 23). *Dermacentor variabilis* (n = 818; 94.9%) was the most prominent species of tick removed, followed by *Amblyomma maculatum* (n = 17; 1.97%), and *Ixodes scapularis* (n = 4; 0.46%). Male (n = 411; 47.7%) and female (n = 428, 49.7%) ticks were observed in similar amounts across all species. This is a stark contrast to American black bear populations in Louisiana and Pennsylvania where *Amblyomma maculatum* and *Ixodes scapularis* are the most prominent tick species reported, respectively. These data illustrate the difference in tick species burden on American black bear populations across geographically disparate regions from the Gulf Coast to the Northeastern United States, which will guide a better understanding of possible tick-borne pathogen spread.

Development and Validation of a Novel Quantitative PCR Assay for Detection of Emydid Herpesvirus 1

Poster – Poster Board 34

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Herpesviruses are among the most widely understood and detrimental pathogens affecting chelonian populations worldwide. Mortality is not an uncommon consequence of these viruses, as seen with infection of emydid herpesvirus 1 (EmyHV-1) in an eastern river cooter (*Pseudemys concinna concinna*), three western pond turtles (*Actinemys marmorata*) and a northern map turtle (*Graptemys geographica*). Due to the lack of targeted studies and available diagnostic tests for detection, the true occurrence and prevalence of EmyHV-1 is largely unknown. To aid in the epidemiological characterization of this virus, this study aimed to develop a sensitive and specific quantitative PCR (qPCR) assay for the detection of EmyHV-1 DNA in chelonian samples. A TaqMan-MGB FAM-dye labeled primer-probe set was designed to target a 56 bp segment of the EmyHV-1 DNA polymerase gene. This assay was specific for EmyHV-1 DNA, having failed to amplify eight other chelonian herpesviruses and demonstrating a dynamic range of 1.0×10^7 to 1.0×10^1 copies per reaction, a slope of -3.43, and an R² of 0.999. Assay efficiency was unimpeded in clinical sample matrices of combined cloacal/oral swab DNA samples. The limit of detection for this assay was 101 copies per reaction, compared to 106 for the conventional PCR assay. As a result, the qPCR assay outlined in this study demonstrates enhanced utility in the epidemiological characterization of EmyHV-1 in chelonians.

Early-Stage Human–Wildlife Interaction: An Ecophysiological Baseline from a Newly Formed Penguin Colony

Poster – Global Voice

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Establishing baseline physiological reference values is essential for evaluating the health and conservation status of wildlife populations, particularly in colonies exposed to emerging anthropogenic pressures. Recently formed breeding colonies provide a unique opportunity to characterize physiological conditions before long-term cumulative impacts become entrenched. El Pedral, a Magellanic penguin (*Spheniscus magellanicus*) colony with a relatively short history of tourism, represents such a system and may reflect an earlier stage in the trajectory of human–wildlife interaction. Here, we present the first physiological parameters for adult females (N=21) and males (N=27) breeding at El Pedral. Hematocrit was slightly higher in females (50.3%) than in males (48.6%). Glucose was higher in males (131.3 mg/dl) than in females (121.3 mg/dl). Total proteins were similar between sexes (5.67 vs 5.64 g/dl). Red blood cell counts were higher in males (9333.3) than in females (780.9). Reticulocytes were comparable (14.3% females; 13.2% males). Total WBC was higher in females (182.6/mm³) than in males (161.7/mm³). Heterophils predominated in both sexes (46% females; 45.5% males), followed by lymphocytes (36.1% females; 37.6% males), while eosinophils represented ~16–17%. H/L ratios were similar (1.30 females; 1.29 males). Thrombocytes were higher in males (221.6) than in females (188.5). Overall, moderate variability was observed, with slight sex differences. This data offers a strong reference for future comparisons and health evaluations, facilitating the identification of changes related to stress, disease, or resource shifts.

Epidemiological Helminth, Disease, and Toxicant Survey of Northern Bobwhite Quail (*Colinus virginianus*) in South Carolina, United States

Poster - Poster Board 6

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Epidemiological surveys are essential in determining the health status of wildlife populations and are considered a step for future risk and conservation management. Operation Idiopathic Decline (OID), a comprehensive and collaborative research initiative, demonstrated that helminth infections, specifically the eyeworm (*Oxyuris petrowi*) and cecal worm (*Aulonocephalus pennula*), are an underlying cause of Northern bobwhite quail (*Colinus virginianus*) decline in West Texas and Oklahoma. It is essential to determine if parasites, pathogens, and/or toxicants are playing a critical role in the decline in bobwhite in understudied regions of their range, such as the southeastern United States. The main objectives of this study are to (1) identify the prevalence, abundance, and intensity of all ectoparasites (ticks, mites, lice) and endoparasites (protozoa and helminths), (2) detect the prevalence of bacterial, viral, and/or fungal infections, (3) survey for selected toxicants (pesticides, heavy metals), and (4) collect overall health measurements (mass, age, injuries, etc.). Hunter-harvested bobwhite quail collected during the 2025-2026 hunting season in South Carolina are assessed following full necropsies, including helminth and tissue (liver, heart, spleen, lungs, and kidneys) collection and storage. Preliminary results (n=14) have indicated that helminths have been predominantly found in the ceca (abundance = 15.71, intensity = 20, prevalence = 78%, range = 0-67) and proventriculus/gizzard (abundance = 2.4, intensity = 3.4, prevalence = 71%, range = 0-10). This study will provide a baseline health assessment and aid in determining any underlying factors that are contributing to the population decline of bobwhite in southeastern United States.

Establishment of an AI-Assisted CT-Based Cross-Sectional Anatomical Atlas in Raccoon Dogs (*Nyctereutes procyonoides*)

Poster – Poster Board 42

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Accurate diagnosis is fundamental to effective treatment and welfare improvement in wildlife medicine. Advanced imaging modalities, particularly computed tomography (CT), provide detailed cross-sectional visualization of skeletal and internal structures; however, standardized cross-sectional anatomical references remain limited for many wild carnivores. The raccoon dogs (*Nyctereutes procyonoides*), one of the most frequently admitted species to wildlife medical rescue centers in Korea, lack a comprehensive CT-based anatomical atlas to support clinical interpretation. This study aimed to develop an artificial intelligence (AI)-assisted cross-sectional anatomical atlas of clinically normal raccoon dogs using CT imaging. CT scans from clinically stable individuals were analyzed, and AI-based segmentation algorithms were applied to delineate major skeletal structures and internal organs automatically. Following expert validation, representative cross-sections from the head, thoracic, abdominal, lumbar, and sacral regions were selected to construct a standardized anatomical atlas. Quantitative morphometric measurements were also integrated to enhance anatomical precision and reproducibility. The resulting atlas provides systematically labeled, high-resolution cross-sectional images of normal raccoon dog anatomy and establishes a foundational reference for clinical diagnosis, surgical planning, and research applications. The integration of AI-assisted segmentation improves objectivity, efficiency, and scalability in atlas development. This study demonstrates the utility of AI-driven imaging analysis in wildlife medicine and provides essential baseline anatomical data to improve diagnostic accuracy and welfare outcomes in raccoon dogs. This work was supported by the National Institute of Wildlife Disease Control and Prevention through the “Specialized Graduate School Support Project for Wildlife Disease Specialists”.

Estimating Contacts of Deer Mice from Long Term Trapping Grids to Track Sin Nombre Virus Transmission

Poster – Poster Board 71

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Contact rates between animals are key factors in disease transmission, and represent the easiest and fastest interventions for disease prevention or control. However, quantifying contact rates in any population of wild animals is challenging, especially for small or cryptic rodent species. Sin Nombre Virus, a North American hantavirus, causes a chronic infection in deer mice (*Peromyscus maniculatus*) and can be fatal in humans. Despite being common hosts for zoonotic diseases around the globe, small rodents like deer mice have been excluded from more rigorous contact studies due to their size and the limits of tracking technology.

We estimated contact rates of deer mice using spatial-mark-recapture models built from data collected on long term trapping grids in Montana over 8-10 years. The first step is to determine deer mouse home range size, and whether sex, age, season, conspecific density and SNV status influence mouse behavior. Our results show that males have larger home ranges than females, but females are more likely to be found near the center of their home ranges. Mouse density was not positively correlated with home range size, suggesting density dependent transmission may be responsible for SNV transmission. We will use this information to predict home range overlap as a proxy for contacts between individuals. Our approach to track potential contacts between cryptic individuals will potentially allow us to predict trends in disease transmission of SNV. However, as trapping grids are common techniques to monitor small mammals, this approach is applicable in taxa and disease systems beyond SNV.

Evaluating the Role of Wildlife Rescue Data in Disease Surveillance: Fourteen Years of Insights from Chungbuk Province, Republic of Korea

Poster – Poster Board 23

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This study evaluates the utility of wildlife rescue center (WRC) data as a disease surveillance tool by analyzing fourteen years of records (2011–2024) from the Chungbuk Wildlife Center. Macro-analysis of total admissions revealed that natural causes (Orphaning, disease, starvation) accounted for 40.2%, followed by other or unknown factors (30.0%). And anthropogenic causes (29.8%). These findings suggest that rescue data is heavily skewed toward incidents occurring in human-populated ecotones rather than representing cryptic disease cycles in sylvatic habitats. Among mammals, Water deer (*Hydropotes inermis*) and Raccoon dogs (*Nyctereutes procyonoides*) accounted for 86% of admissions, yet their primary threats showed a stark contrast: 56% of Water deer cases were attributed to vehicle collisions, whereas 66% of Raccoon dog cases involved Sarcoptic mange, representing a rare clear disease signal within the system. In avian species (n=4,446 for the top five species), natural factors such as orphaning (41.4%) and anthropogenic collisions (14.7%) predominated. Infectious disease cases remained negligible across most taxa, with the exception of localized viral infection clusters in Oriental Turtle Doves. The spatial concentration of cases near human settlements indicates a significant reporting bias, as the dataset relies almost exclusively on public discovery and notification. Consequently, while WRC records serve as a robust metric for monitoring physical trauma—such as vehicle strikes and habitat-induced orphaning—they possess inherent limitations for comprehensive disease surveillance. We conclude that active field-based monitoring is essential to complement the “visible” trauma captured by passive rescue networks and to accurately assess the overall health of wildlife populations in their natural environments.

Fetal anomalies of *Meleagris gallopavo silvestris* (Eastern Wild Turkey) in the United States during the 2024 and 2025 nesting seasons

Poster – Poster Board 48

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The Eastern Wild Turkey (*Meleagris gallopavo silvestris*) is a native inhabitant of the contiguous United States. Over the past two decades, turkey populations have been steadily declining, and mitigation strategies have been unsuccessful at improving reproductive success. The purpose of this work is to document unique cases of hatching failure with abnormally presenting fetuses. During the 2024 and 2025 nesting seasons, wild turkey hens from across the United States were transmitter tagged and nests monitored as part of alternative studies. Unhatched eggs were opportunistically collected from inactive nests and submitted for fertility and embryonic mortality evaluation. Of 625 eggs submitted, 166 eggs had fetuses aged three days of development or later, of these, 18 had fetal anomalies. Of the ten state participants, four (Connecticut, Iowa, Ohio, and Oklahoma) had cases of abnormality. Abnormal fetuses were necropsied, fixed in 10% buffer neutral formalin, and subjected to histology or radiography as appropriate. Abnormalities observed in individual fetuses from independent nests include splayed leg conformation with contracted tendons in the feet, cross-beak paired with malformation of the rhinotheca, gastroschisis, anencephaly, and caudal duplication syndrome. Cases involving more than one fetus include one enlarged egg containing twin embryos with separate yolk sacs, and eleven fetuses from one nest with petechiae throughout the caudal coelom and extremities. This report serves to describe occurrences of fetal abnormalities over time. If documented regularly, fetal abnormalities can serve as indicators for environmental toxins, disease, or gene pool health in wild populations and inform management strategies for declining species.

Flea Dispersal Following Poisoning of Black-tailed Prairie Dogs: Implications for Plague Dynamics.

Poster – Poster Board 75

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Sylvatic plague, caused by the bacterium *Yersinia pestis* and vectored by fleas, is the primary biological threat to the endangered black-footed ferret (*Mustela nigripes*) and also kills their prey, black-tailed prairie dogs (*Cynomys ludovicianus*) with epizootic mortality rates surpassing 95%. Prairie dogs are subjected to chemical poisoning, which can rival the mortality rate of plague. We investigated how flea dispersal and feeding patterns are affected by poisoning events. We sampled fleas from prairie dog burrows across two paired prairie dog colonies before and after a targeted poisoning event at Badlands National Park in July 2025. We used a before-after control-impact (BACI) framework, designating one of two adjacent colonies as the treatment (poisoned) site and a separate pair of adjacent colonies as controls. These paired colonies were separated by a road and tall vegetation, significantly limiting prairie dog movement between colonies. We swabbed and collected fleas from burrows and categorized blood meal status of each flea. We hypothesized that burrows in the poisoned plot would have lower flea abundances and lower bloodmeal levels after the poisoning event. We analyzed our data using generalized linear models to model burrow flea abundances before and after poisoning. We did not detect a change in the number of fleas after poisoning, but fewer female fleas were found in the poisoned plot. Additionally, fleas in the poisoned plot contained lower bloodmeal scores after poisoning. Because poisoning mirrors the effects of plague on prairie dog colonies, our study provides insight into flea dispersal following plague epizootics.

Flea Reloading: Tracking the rate fleas return to hosts after initial flea removal in black-tailed prairie dogs.

Poster – Poster Board 67

***Holly Gilchrist*¹, *Jacob Linsmeyer*¹, *Jason Fly*¹, *Madisen Hartlaub*¹, *Seth Gerberding*¹, *Travis Livieri*²,
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Plague, caused by the bacterium *Yersinia pestis*, poses a deadly threat to many species, including black tailed-prairie dogs (*Cynomys ludovicianus*). Prairie dogs are highly susceptible to plague with mortality rates nearing 100%. Prairie dogs become infected with plague via contact with infected fleas. To control plague on prairie dog colonies, land managers use insecticides that reduce flea populations. After flea removal, there is knowledge lacking in how quickly prairie dogs are reinfested with fleas. We aimed to better understand flea reinfestation rates of prairie dogs after a flea removal event. We hypothesized that fleas would recolonize prairie dogs within two days after being combed, because they occupy burrows and take blood meals every 24 to 48 hours. To conduct this experiment, we trapped prairie dogs in Badlands National Park, South Dakota in June and July 2025. Captured prairie dogs were anesthetized and vigorously combed for 2 minutes over a white bin. Fleas were then collected and removed from the environment. When recapturing the prairie dogs, we repeated this process and documented the number of fleas that had colonized each individual. In total 53 prairie dogs were captured at least twice. We will use a binomial model to access the timeline it takes for fleas to begin reappearing on prairie dogs. We will also use a Quasi-Poisson linear regression model to assess variables that may affect the rate that fleas reappear. This research will provide insights for managers of ecologically important prairie dog colonies, insecticide developers, and plague researchers.

Flea Tracking: Biomarking prairie dogs as a novel approach to tracking flea and plague movement in grassland ecosystems

Poster – Poster Board 45

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Plague is a serious biological threat to many species, including prairie dogs (PDs; *Cynomys* spp.) and endangered black-footed ferrets (*Mustela nigripes*). Fleas are key plague vectors in mammal communities. However, the mechanisms of plague spread across the landscape are largely unknown. To understand plague spread, we measured flea movements within PD colonies in Badlands National Park, SD, considering PDs and smaller mammals as flea transporters. We used rhodamine B, a biomarker delivered orally to PDs, to mark and track flea movements. Prairie dogs live in family groups called “coterie.” We targeted one prairie dog hosting many fleas within a coterie (>10 fleas) and dosed it with rhodamine B. We then trapped other members of that coterie, removed their fleas, and assessed those fleas for presence of rhodamine B using fluorescent microscopy. Concurrently with PD trapping, we trapped small mammals, such as northern grasshopper mice (*Onychomys leucogaster*) and deer mice (*Peromyscus sonoriensis*) and removed their fleas for rhodamine B detection. We used general linear mixed models ANOVA to characterize factors influencing the proportion of fleas exhibiting rhodamine B fluorescence. We determined the duration after dosing that rhodamine B is detectable in fleas by examining fleas collected 1, 3, 5, 8, and 11 days post-dosing. This research provides innovative tools to monitor flea movements, assess the roles that different host and flea species play in plague spatial ecology, and determine how flea movements influence the success of current and forthcoming plague mitigation strategies.

Gastropod Surveillance of Grant Park and a nearby zoological institution to evaluate for the invasive zoonotic parasite, rat lungworm (*Angiostrongylus cantonensis*)

Poster – Poster Board 47

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Rat lungworm (*Angiostrongylus cantonensis*) is an invasive zoonotic parasite that utilizes gastropods (snails and slugs) as intermediate hosts, rats as definitive hosts, and numerous species as paratenic hosts. Globally, this parasite is the leading cause of eosinophilic meningitis in people and causes mortality in numerous wildlife species. In the USA, mortality has been documented in humans, armadillos, domestic dogs, horses, and numerous captive non-human primates. *A. cantonensis* utilizes gastropods as intermediate hosts and paratenic hosts, including frogs and lizards. This study documented gastropod species that could be intermediate hosts for *A. cantonensis* found in Grant Park in Atlanta, GA and a nearby zoological institution following the recent death of a lemur at the zoo due to rat lungworm and the detection of rat lungworm in rats at the zoo. We collected 169 snails from Grant Park and the surrounding area. Snails were weighed, measured, photographed and identified through sequence analysis of the COI gene. Results documented several species of mollusks around enclosures at the zoological park that are potential hosts for *A. cantonensis*. To date, 109 gastropods have been assigned based on sequence analysis. The most common species included 34 *Ventridens ligera*, 15 *Ambigolimax valentianus*, and 10 *Physella acuta*. Other species included 9 *Zachrysia provisoria* and 7 *Deroceras leae*. Although these data are preliminary, we discovered several known rat lungworm intermediate hosts, several of which are invasive species. The results provide data on hosts of *A. cantonensis* in urban Atlanta that can be used to implement surveillance and management plans.

Gut microbiome characterization of endangered ocelots and sympatric mesocarnivores using long-read metagenomics in southern Texas

Poster – Poster Board 31

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Microbiome composition plays a key role in host health, immune system function, and disease susceptibility, yet remains poorly characterized in endangered wildlife species. In fragmented landscapes, increased contact among sympatric species and exposure to anthropogenic stressors may influence microbial communities and shape disease risk. In southern Texas, the endangered ocelot (*Leopardus pardalis*) persists in small, isolated populations that overlap with abundant sympatric mesocarnivores such as bobcats (*Lynx rufus*) and coyotes (*Canis latrans*), providing an opportunity for contact and sharing of microbes in a multi-host carnivore community. This study aims to characterize and compare the gut microbiome of free-ranging ocelots, bobcats, and coyotes sampled between 2020 and 2025 in the Lower Rio Grande Valley, Texas. We hypothesize that microbiome composition and functional potential will differ among host species, with greater similarity between ocelots and bobcats in these fragmented landscapes. Fecal samples were collected during capture events and preserved for molecular analyses. Microbial DNA was extracted using standardized protocols and is currently being sequenced using long-read metagenomic sequencing on the Oxford Nanopore Technologies (ONT) platform. Unlike shortread shotgun approaches, ONT sequencing enables improved taxonomic resolution, recovery of complete genes and operons, and characterization of functional pathways and antimicrobial resistance potential. This work will generate baseline microbiome data for endangered ocelots and cooccurring mesocarnivores, and provide novel insights into host-microbiome structure in a fragmented, multi-host system. Results will inform future research on microbiome mediated disease processes and support wildlife disease surveillance and conservation planning.

Haemosporidian parasitemia and sex predict body condition in Brown-headed Cowbirds (*Molothrus ater*) across agricultural landscapes

Poster – Poster Board 40

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Body condition is a valuable integrative metric of avian health, reflecting how individuals balance nutritional/energetic demands, physiological stress, and pathogen pressures. Variation in body condition can also arise from intrinsic factors such as sex and age, as well as extrinsic factors including habitat quality. Haemosporidian blood parasites are ubiquitous in birds and may impose energetic costs, but to date little is known in most avian species about links between malarial infection, body condition, and other life-history and ecological variables. Here, we examined how body condition in Brown-headed Cowbirds varies with sex, age, agricultural context, and haemosporidian parasitemia across livestock farms in Michigan. We predicted that individuals with higher parasitemia would exhibit lower body condition, and that juveniles would be in poorer condition than adults. Given limited prior evidence in this system, we made no *a priori* directional predictions for sex- or farm-specific effects on body condition. We mist-netted, sexed, aged, measured and sampled cowbirds during the 2025 breeding season at several farms. We used residuals from a body mass v. tarsus length regression to calculate body condition and examined blood smears with microscopy for haemosporidian parasite identification. We found that body condition declined with increasing haemosporidian parasitemia, and that males were, on average, in better condition than females. These results suggest that variation in body condition among cowbirds is shaped by both infection intensity and sex-specific energetic demands during the breeding season, even in a brood-parasitic species like cowbirds (i.e. females still have a disproportionate reproductive investment due to egg-laying).

Health assessment and pathogen prevalence of urban raccoons (*Procyon lotor*) in Cook County, Illinois, USA

Poster – Poster Board 32

***Eliza Baker*¹, *Aubrey Engel*², *Corinne Vaughan*³, *John Winter*⁴, *Michael Neri*⁵, *Charles Rizzo*⁵, *Chris Anchor*⁵, *Danielle Strahl*², *Laura Adamovicz*⁴, *Matthew Allender*⁶**

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Raccoons are mesocarnivores common throughout North America, and populations can grow to high densities in urban environments. The objective of this study was to determine pathogen prevalence, establish clinical pathology variability and associated physical abnormalities in raccoons in Cook County, Illinois, USA. We performed physical examination, pathogen testing, biochemical analysis, and hematology on 46 free-ranging raccoons. Physical examination abnormalities included dental disease (46%), obesity (40%), and chronic trauma (20%). Though all raccoons had at least one parasite identified on fecal flotation, only one (4%, 1/23) was shedding *Baylisascaris procyonis*. Seven raccoons (15%) were PCR positive for *Cryptosporidium* sp., four raccoons (9%) were positive for *Bartonella rochalimae*, and five raccoons (11%) were PCR positive for *Procyon lotor* gammaherpesvirus 1. Herpesvirus positivity was significantly associated with higher rectal temperature ($p=0.02$) and neutrophil count ($p<0.001$). All but one raccoon was PCR positive for apicomplexan parasites, with sequencing of six positives producing a sequence most similar to *Babesia microti*-like. One raccoon with neurologic signs had meningoencephalitis and was IHC positive for canine distemper virus. Both *B. rochalimae* and *Cryptosporidium* are zoonotic. Raccoons in Cook County had physical examination abnormalities like obesity and dental disease that may be linked to anthropogenic food supplementation, and they are infected with numerous pathogens of conservation, domestic animal, and human health concern. Overall, this study identified numerous health concerns that signify how this species is utilizing the environment and may be a sentinel for exposure to other wildlife and humans.

Health Assessment of Common Snapping Turtles (*Chelydra serpentina*) in Cook County, IL USA

Poster – Poster Board 43

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The common snapping turtle (*Chelydra serpentina*) is a widely distributed North American aquatic turtle species that commonly co-occurs with other aquatic species of critical ecological and conservation concern. Despite this, health is understudied in this species. Health assessments including physical examinations, hematology, and molecular surveillance for 34 pathogens were performed in 294 turtles from five populations in 2023 – 2025. Numerous clinical pathologic findings were observed, including higher heterophil: lymphocyte and lower total solids, WBC, eosinophils, erythrocyte sedimentation rate, and lymphocytes in spring. The prevalence of *Chelydra* herpesvirus 1 was higher in the spring (20.14%) vs. summer (2.31%, OR = 10.65, $p = 0.0002$) and fall (0.55%, OR = 45.74, $p = 0.023$). The prevalence of *Chelydra* *Mycoplasma* sp. was also higher in the spring (23.76%) compared to the summer (1.23%, OR = 24.93, $p < 0.0001$) and fall (1.26%, OR = 24.34, $p = 0.0007$). Our results show a clear seasonal difference of health metrics in *C. serpentina* during spring, marked by stress biomarkers and pathogen peaks. Because *C. serpentina* overlaps ecologically with at-risk species, these findings provide important context for further understanding disease dynamics in the community, while also offering seasonal reference values for assessing population health progressions in future studies.

Healthy Wildlife, Healthy Cities: Educating Urban Residents on Wildlife Health

Poster - Poster Board 13

Brooke Ezzo¹

1. Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine

The Wildlife Futures Program, a partnership between the University of Pennsylvania School of Veterinary Medicine and the Pennsylvania Game Commission, is dedicated to safeguarding the health and strengthening the resilience of Pennsylvania's 480 species of birds and mammals. This commitment extends to wildlife, which increasingly inhabits urban landscapes alongside humans. This cohabitation can lead to zoonotic health concerns, including rabies and highly pathogenic avian influenza.

Drawing on its expertise, resources, and a presence in Philadelphia, the Wildlife Futures Program has actively educated urban residents on a wide range of wildlife health topics. These include the benefits of healthy wildlife, indicators of potential health concerns, and community actions that can enhance local wildlife's well-being, packaged in engaging events and presentations to capture the audience's attention. This presentation will outline strategies we have employed to successfully engage, empower, and motivate the urban Philadelphia community to advocate for wildlife health.

Hepatic mineral concentrations in wild white-tailed deer (*Odocoileus virginianus*) within a high prevalence chronic wasting disease area

Poster - Poster Board 15

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Chronic wasting disease (CWD) is a prion disease currently spreading across North American cervid populations with spatial scattered distribution and variable prevalence. It is not understood how CWD emerges and becomes established, quickly reaching high prevalence in some areas where in others it smolders. Imbalances in trace minerals can lead to increased disease susceptibility and have previously been associated with prion diseases. We measured hepatic selenium in white-tailed deer (*Odocoileus virginianus*) within (n = 61) and outside (n = 52) a high prevalence CWD area in Pennsylvania, USA. We did not find an association between hepatic selenium and CWD status. Additionally, white-tailed deer within the high prevalence area did not have significantly lower hepatic selenium concentrations compared to three of four sites outside of the high prevalence area. However, hepatic selenium was significantly higher in white-tailed deer from one specific site outside of the high prevalence area, compared to the other four sampling sites. Seasonal differences in hepatic selenium could influence the results since the samples from outside the high prevalence area were collected during a short period of time. Conversely, the high prevalence area samples were collected periodically across three years. In summary, white-tailed deer living within and outside the established CWD area have relatively low hepatic selenium concentrations which is similar to what has been reported for other deer populations in the US. Future studies should include longitudinal sampling across geographic sites to determine whether hepatic selenium varies with season.

Holding The Line: Unraveling The Immunological Consequences of Pathogenic Infection On Invasive Cuban Treefrogs, *Osteopilus Septentrionalis*, In Central Florida

Poster – Poster Board 69

Juliette Rodrigue¹, Matthew Atkinson¹

1. University of Central Florida

Wildlife populations have declined as a direct result of pathogenic interactions; however, many invasive species appear tolerant of these infections and may serve as a pathogen reservoir on the landscape. The Cuban treefrog (*Osteopilus septentrionalis*) has invaded portions of the Southeastern United States and could potentially serve as a reservoir for multiple pathogens. However, the consequences of these infections in Cuban treefrogs remain poorly understood. Here, we sought to determine the impact of infection status on leukocyte ratios and Fulton's body condition in a wild population of Cuban treefrogs to determine if pathogenic infections influence fitness of this species. We calculated leukocyte ratios and body condition for 92 Cuban Treefrogs collected on the University of Central Florida's Main Campus in Orlando and determined infection status for these individuals for 3 different amphibian pathogens associated with mass mortality events (MME's) using established qPCR protocols. Pathogenic infection resulted in little to no impact on their body condition and leukocyte ratio, with only *Batrachochytrium dendrobatidis* (Bd) showing significantly higher lymphocytes and lower neutrophils, ($p=0.009$) in infected individuals. Instead, other factors not related to infection consistently impacted both body condition and leukocyte ratio including sex, with gravid females exhibiting higher body conditions ($p=0.009$) and higher ratios of neutrophils to lymphocytes ($p=0.02$), and the overall highest body conditions occurring in August ($p<0.001$) regardless of sex. Our study expands upon host consequences for infection in Cuban Treefrogs and greatly adds to the general body of knowledge regarding amphibian hematology and disease ecology.

Hoof Disease in the endangered Florida Key Deer (*Odocoileus virginianus clavium*)

Poster – Poster Board 41

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The Florida Key Deer (*Odocoileus virginianus clavium*) is a federally endangered cervid with cultural and conservation significance. During winter 2016, the Southeastern Cooperative Disease Study received distal limbs from Key Deer exhibiting hoof abnormalities. Limbs were opportunistically collected from deer that died or were euthanized during New World screwworm (*Cochliomyia hominivorax*) eradication efforts. To investigate lesion etiology, limbs were examined grossly, radiographically, and histologically. In total, 49 limbs from 17 individuals were grossly examined, and a subset (n=12) was longitudinally sectioned to assess internal structures. Radiographs (dorsopalmar/plantar and lateral) were obtained for 33 limbs with gross lesions along with seven grossly normal limbs. Histologic evaluation was performed on nine limbs (7 affected, 2 grossly normal). Gross abnormalities of the hoof, coronary band, or associated soft tissues were identified in 80% (39/49) of limbs, with multiple limbs involved in 63% of affected deer. Radiographic and gross findings were consistent with chronic laminitis in 52% of limbs, traumatic injury in 43%, or both (14%). Three deer with severe injuries had limbs infested with *C. hominivorax*. Histology supported chronic laminar disease and trauma in affected limbs. These results suggest that hoof disease, particularly chronic laminitis, is a common cause of morbidity in this population. Given the unique ecology of Key Deer, including reliance on anthropogenic food sources and residence within human-modified landscapes, dietary and environmental factors associated with human activity are suspected contributors to hoof disease. Overall, morbidity and mortality in this endangered population appear strongly influenced by direct and indirect anthropogenic factors.

Host Lineage Shapes Gut Microbiome Structural Architecture at the Poultry–Wildlife Interface of Avian Influenza

Poster – Poster Board 33

Christina Naesborg-Nielsen¹, MHM Mubassir¹, Ludy Registre Carmola¹, Sihua Peng¹, Oluwatosin Babasola¹, Mohammed Bakheet¹, Justin Bahl¹

1. University of Georgia

Avian influenza viruses (AIV) circulate at the dynamic interface between waterfowl and domestic poultry, where spillover can drive major agricultural and public health impacts. Yet infection outcomes differ markedly among host lineages: Anseriformes typically exhibit limited pathology, while Galliformes often develop severe disease. We asked whether host lineage predicts consistent patterns of gut microbiome architecture and response to AIV infection at this poultry–wildlife interface.

We performed a comparative re-analysis of publicly available 16S rRNA datasets from wild ducks and whooper swans, and domestic chickens and turkeys with known AIV infection status. Sequences were processed using standardized QIIME2 workflows, and microbial functional potential was inferred using PICRUSt2. Across datasets, host lineage emerged as the dominant driver of microbiome composition, while infection effects were host-dependent rather than universal.

We identified three distinct microbiome response modes associated with host lineage: (i) **resilient** communities in ducks, characterized by stable diversity and minimal core microbiome turnover; (ii) **remodeled** communities in poultry, showing compositional shifts with partial retention of core taxa; and (iii) **collapsed** communities in whooper swans, marked by pronounced diversity loss and disruption of core microbiome structure. Functional predictions suggested lineage-specific shifts in microbial metabolic potential.

Together, these results show that host lineage structures gut microbiome architecture at the poultry–wildlife interface and shapes how microbial communities respond to AIV infection. These host-specific microbiome response modes provide a framework for applying machine learning approaches to test whether microbiome can predict host susceptibility and resilience to AIV infection, with potential applications in surveillance and risk assessment.

Host physiological variation in a wild reservoir of Sin Nombre virus

Poster - Poster Board 17

Nelle Jenkins¹

1. University of Montana

Physiological stress is widely hypothesized to influence immune function and disease susceptibility in a variety of systems, yet empirically testing this relationship remains limited in free-ranging wildlife. The Sin Nombre virus (SNV) – Deer mouse (*Peromyscus maniculatus*) system provides a natural framework for exploring how host physiology relates to infection status under ecologically relevant conditions. In this study, we assessed variation in physiological stress, immune metrics, and condition among wild-caught deer mice sampled across multiple sites in Western Montana. We quantified stress and condition using circulating corticosterone responses to a standardized suppression challenge, hematocrit, white blood cell profiles, and biometric measurements to explore their relationship with SNV infection status. Using these data, we explore whether physiological indicators differ between infected and uninfected individuals, and whether these relationships vary across sites. Across the study period, SNV prevalence was 13.5%, and stress-regulation phenotypes differed among hosts. Females – particularly lactating females – more frequently exhibited altered stress regulation. By integrating endocrine and immune data, this work aims to characterize how individual-level physiological variation may be associated with SNV infection patterns in natural populations.

Hunting for Histomonas: Surveillance of birds and their nematodes from Pennsylvania, USA

Poster – Poster Board 65

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Histomoniasis (blackhead disease) is caused by the protozoan *Histomonas meleagridis* and can cause high mortality rates in some species of gallinaceous birds. These protozoans can be transmitted by ingesting the eggs of cecal worms (*Heterakis gallinarum*), with the protozoans surviving in *H. gallinarum* eggs in the environment for years. *H. meleagridis* infects the cecum and liver of birds, resulting in lesions and necrotizing these organs. Surveillance efforts often focus on birds that are clinically ill or found dead, missing detections in subclinical individuals. Additionally, non-target tissues and samples are typically not tested. The primary goal of this study was to conduct surveillance of *H. meleagridis* in gallinaceous birds throughout Pennsylvania. Various tissues were tested for *H. meleagridis* via PCR, targeting the partial 5.8S rRNA region. Tissues included: 1) liver samples (n=62) from wild turkeys (*Meleagris gallopavo*) that were clinically ill and euthanized, or dead and presumed clinically ill; 2) venous blood samples (n=62) from subclinical wild turkeys. Additionally, an effort was made to test multiple species of *Heterakis* cecal worms for *H. meleagridis* to better understand the vectors responsible for transmission. Worms were recovered from subclinical wild turkeys, ruffed grouse (*Bonasa umbellus*), ring-necked pheasants (*Phasianus colchicus*), and domestic chickens (*Gallus gallus domesticus*). Results are ongoing but will help document the occurrence and distribution of *H. meleagridis* in Pennsylvania birds. Given the high susceptibility of wild turkeys to *H. meleagridis* and the impact on the poultry industry, establishing a baseline of this parasite in wild gallinaceous birds remains an important goal.

Infectious Disease Exposure Surveillance of Wildlife Populations in Texas

Poster – Poster Board 57

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Texas contains 12 distinct ecoregions that support diverse wildlife populations. Interactions among these populations can facilitate the transmission of infectious diseases such as *Bacillus anthracis* and *Brucella spp.* These diseases present complex management issues and can pose significant threats to wildlife, livestock, and potentially human health. In Texas, *B. anthracis* is historically confined to an area known as the Anthrax Triangle, where annual outbreaks can cause substantial mortality and ecological disruption. Though *Brucella spp.* is highly regulated in livestock, it can also infect various wildlife species and is known to comingle with livestock populations. Therefore, effective wildlife management requires a clear understanding of disease ecology across differing ecoregions. This study aims to investigate the spatial and temporal patterns of exposure to *Bacillus anthracis* and *Brucella spp.* in wildlife. Serum samples will be collected year-round through safe live capture methods, collaborations with external institutions, and opportunistic sample sharing. Repeated sample collection will be conducted to recognize region and season-specific disease patterns across Texas. Serological assays, including enzyme-linked immunosorbent assays (ELISAs) and buffered acidified plate antigen (BAPA), will be used to assess pathogen exposure. Sampled locations and serological results will then be mapped to visualize seroprevalence distribution for each disease. Preliminary results indicate that deer outside the Anthrax Triangle region have been exposed to *B. anthracis*, highlighting the need for continued disease surveillance. Findings from this study will provide landowners and managers with critical information on disease dynamics to support ongoing efforts in reducing disease risk in wildlife populations.

Invasive Wild Pig (*Sus scrofa*) Wallows as Microbial Hotspots: Assessing Pathogen Transmission Risk at the Wildlife-Livestock Interface

Poster – Poster Board 24

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Invasive wild pig (*Sus scrofa*) wallowing behavior creates environmental conditions conducive to pathogen persistence and transmission among wildlife, livestock, and humans. This ongoing study characterizes wallow use patterns and evaluates transmission risk for *Escherichia coli*, *Salmonella* spp., *Leptospira* spp., and antimicrobial-resistant bacteria at five forested sites across Georgia, USA. Using dual camera systems (n=22 cameras), we have monitored 11 active wallows, recording 199 animal detections over 55 trap nights to date. White-tailed deer (*Odocoileus virginianus*) were the most frequently detected species overall (48%, 96/199), followed by feral swine (35%, 69/199), with additional detections of raccoons (*Procyon lotor*), grey squirrels (*Sciurus carolinensis*), passerines, coyotes (*Canis latrans*), bobcats (*Lynx rufus*), and opossums (*Didelphis virginiana*). Site-specific variation was noted: feral swine comprised 68% of detections at Cohutta Wildlife Management Area (WMA) versus 14% at Paulding Forest WMA, while one site (Sheffield WMA) had no detections of swine activity despite wallow presence. Multi-species visitation patterns suggest wallows function as congregation sites for numerous wildlife species with potential for interspecies pathogen transmission. Environmental sampling protocols for water and soil are being optimized for pathogen detection. Future work includes monitoring cattle farm sites to quantify livestock-wildlife interactions, conducting network analysis modeling to assess transmission dynamics, and trapping wildlife at three enhanced surveillance sites beginning Fall 2026. Preliminary findings demonstrate that wallows attract diverse wildlife communities beyond feral swine, potentially amplifying pathogen transmission networks. Understanding these interaction dynamics is critical for developing targeted prevention measures and managing emerging pathogen risks at the wildlife-livestock-human interface.

Linking space-use and pathogen exposure in Minnesota white-tailed deer

Poster - Poster Board 19

***David Dayan**¹, Tyler Garwood¹, Tiffany Wolf¹, James Forester¹, Julia Pritchard¹, Anna Jaeger¹, Matthew Aliota¹, Meggan Craft¹*

1. University of Minnesota

White-tailed deer are widespread, synanthropic, and are sentinels for pathogens relevant to animal and human health. Using paired serological and GPS tracking data from three sites in the Twin Cities Metro Area, we aimed to 1) investigate if probability of pathogen exposure varied by sex, age class, and site and 2) examine whether individual home range size and landscape cover selection differed by serostatus. Testing has focused on three tick-borne pathogens: *Borrelia burgdorferi*, *Anaplasma phagocytophilum*, and Powassan virus. Seroprevalence was 45.5% (46/101) for *B. burgdorferi* and 17.8% (18/101) for *A. phagocytophilum*. For Powassan virus, 115 individuals were tested; 35 were tested twice (initial capture and recapture); 7.8% (9/115) of individuals were seropositive at least once. Based on logistic regression, there was no significant effect of sex, age class, or site on probability of exposure to *B. burgdorferi* or *A. phagocytophilum*; logistic regression for Powassan virus-exposure was not conducted due to complete separation. Accounting for site and sex, home-range areas did not differ significantly by serostatus for each pathogen, and selection ratios differed by serostatus for open habitats (agriculture, grassland, shrubland, and barren cover) for *B. burgdorferi*, developed areas for *A. phagocytophilum*, and open habitats for Powassan. These analyses provide initial insight into links between space use and pathogen exposure in suburban white-tailed deer. Inclusion of other pathogens can be used to explore patterns across pathogen transmission mode and habitat type.

Liver minerals associated with elk hoof disease in California, USA

Poster - Poster Board 10

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Trace minerals are nutrients obtained from environments which are essential to animal growth, development, and immunity. In ungulates, copper (Cu), selenium (Se), and zinc (Zn) are essential for immune function, as well as hoof development and maintenance. Trace minerals may influence the occurrence or severity of treponeme-associated hoof disease (TAHD), a debilitating infectious disease of free-ranging elk (*Cervus canadensis*). To investigate associations between mineral levels and TAHD, we collected postmortem liver and hoof samples from free-ranging elk during TAHD surveillance from 2020 to 2021 in Del Norte and Humboldt counties, California, USA. We analyzed mineral levels in liver samples ($n=81$; 41 TAHD positive, 40 TAHD negative) to improve baseline information on the range of trace mineral concentrations for elk in the region. Using TAHD surveillance data, we constructed regression models to examine associations between TAHD occurrence and TAHD lesion severity and liver mineral concentrations. We did not find support for our hypothesis that lower mineral levels contributed to higher TAHD occurrence in the sampled populations; however, Cu and Se levels in elk were below previously reported reference ranges, so lower levels of these minerals may still pose potential risk factors for TAHD in elk in the region. Contrary to our expectations, higher Zn levels were associated with TAHD occurrence and worsening lesion severity, which may be evidence of a host-mediated nutritional immune response to infectious disease. Further investigation is needed to understand broad-scale variation in mineral levels and their impact on wildlife health before mineral supplementation can be recommended.

Looking hard or hardly looking? Multifaceted chronic wasting disease surveillance for improved detectability

Poster – Poster Board 28

***Krysten Schuler*¹, *Brenda Hanley*¹, *Nicholas Hollingshead*¹, *Jue Wang*², *Carlos Gonzalez Crespo*³, *Noelle Thompson*⁴, *Landon Miller*⁵, *James Booth*¹, *Kevin Hynes*⁵**

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Historic disease surveillance metrics focus solely on the number of samples collected, assuming independence and equal values across all animals. In wildlife, we know animals live in groups, not all are equally susceptible to disease, and anthropogenic factors may be responsible for pathogen introduction. Leveraging auxiliary information can improve our confidence in freedom-from-disease and power to detect disease at low levels, providing the best opportunity for successful management. Using examples developed through Surveillance Optimization Project for Chronic Wasting Disease (SOP4CWD) partnerships, we will discuss newly developed models that offer mechanisms to develop long-term sampling strategies, utilize resources to minimize risk, predict new outbreak locations, and identify areas ripe for epizootics. However, implementation will require wildlife agencies to collect additional data streams. These tools are sensitive, scalable, and operationally useful information to support early discovery and target management goals, but require agency buy-in and participation to produce the most accurate and actionable surveillance recommendations.

Mapping Diversity: *Saprolegnia* Species and Strains Across the Great Lakes Region

Poster – Poster Board 22

Suhaylah Ahmad Ali¹, Bartolomeo Gorgoglione¹, Réka Vámosi², Edit Eszterbauer², Cahya Fusianto¹

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Saprolegnia is a common and widespread oomycete, although its genetic diversity and species/strains distribution throughout the Great Lakes region remain poorly characterized. Species within this genus cause saprolegniosis to freshwater fish and eggs, leading to significant ecological and economic impacts in fish hatcheries. Although *Saprolegnia parasitica* is widely recognized as the primary pathogen, variation in infection prevalence and morphological diversity among isolates suggests multiple species may contribute to disease dynamics. We hypothesize that *S. parasitica* will be the predominant species isolated from symptomatic fishes, while other *Saprolegnia* species may occur at lower frequencies across sites and sample types. The objective of this study is to culture *Saprolegnia* from environmental samples and fish farms collected across Michigan, aiming at species identification and genetic diversity assessment. Samples were collected from riverine locations and hatchery tanks, mucus swabs from skin lesions of symptomatic fish. Mucus samples were cultured on glucose-yeast agar supplemented with penicillin and streptomycin. Water samples were processed using micropore filtration, or with the seed baiting techniques, prior to culture. Primary cultures were incubated at room temperature for 3-5 days, sub-cultured, isolated, and stored at 4°C for genetic analysis. Thirty-seven isolates from seven locations were successfully cultured, with most originating from fish skin lesions at Little Manistee. Cultures exhibited notable morphological variation, with sequencing analysis revealing species such as *S. australis*. To further resolve this diversity, ongoing phylogenetic analyses will characterize genetic variation and identify potentially highly pathogenic strains.

Abstract Withdrawn from Conference

Microfilariae of a *Dirofilaria* sp. in *Linnaeus's* two-toed sloth, *Choloepus didactylus*, at the Greenville Zoo, SC.

Poster – Poster Board 66

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Filarioid nematodes parasitizing wildlife are understudied; many are not formally described or are lacking descriptions paired with modern molecular techniques. Animals imported and housed in zoos may be infected with parasitic helminths and other vector-borne infections, which are generally discovered incidentally upon medical exams or at necropsy. Filarioid nematodes such as *Dirofilaria* sp. may present a risk of infecting native and imported wildlife or have zoonotic potential. At least 5 known filarioids have been described infecting sloths, including *Dirofilaria incrasata*, *Dirofilaria macrodemos*, *Dirofilaria panamensis*, *Dirofilaria freitasi*, and *Dipetalonema spiralis*, none of which have published sequence data. In the present case, an imported two toed sloth had blood microfilariae during a routine exam in March 2022 and tested canine heartworm antigen positive. Blood tested from April 2024 was antigen positive, with no microfilariae detected in 2 ml of blood by filtered modified Knott's test. Additional testing in May of 2025 was antigen negative, and antibody positive, with no microfilariae detected in 2 ml of blood using a filtered modified Knott's test. Molecular testing of whole blood from 2022 targeting the COI gene was performed followed by Sanger sequencing. A search of NCBI Genbank using BLASTN showed a percent identity of 93.1% to a canine *Dirofilaria* sp. from Argentina, 92.7% *D. asiatica*, 92.1% *Onchocerca skrabinii*, 91.5% *D. repens* and 91.24% *D. striata*. This species appears to cross react serologically with *D. immitis*. More research is needed on filarioids of wildlife, incorporating both molecular characterization and morphological descriptions.

Modeling Avian Hotspots of Potential West Nile Virus Outbreaks: A Case Study in Arizona

Poster - Poster Board 2

Gracie Fischer¹, Leigh Combrink¹, Desiree Bliss¹

1. University of Arizona

West Nile Virus (WNV) is an arbovirus that infects birds and is spread by *Culex* mosquitoes. West Nile Virus has been detected in over 250 bird species, with morbidity and mortality of avian hosts varying significantly between clades. Changing climate, land use and biodiversity loss will influence the distribution of both avian hosts and mosquitoes, impacting the spread of vector-borne diseases. To identify potential hotspots of WNV outbreaks, we used MaxEnt species niche distribution modeling and ArcGIS Pro to model the habitat distribution of twenty-two avian host species of WNV of varying vertebrate host competence indices throughout the state of Arizona. We included eleven environmental and climatic variables influencing habitat use and distribution, such as temperature, rainfall, normalized difference vegetation index, and elevation, and then projected those likely suitable habitats with four Shared Socioeconomic Pathways (SSPs) under two different climate models. Understanding how the distributions of hosts shift under different climatic scenarios will allow both wildlife conservation and public health professionals to identify potential transmission 'hotspots' and perform proactive measures to mitigate future outbreaks. Presentation will also include photographs and preliminary data from bird banding, mosquito trapping, and sampling field work.

Modeling control of an introduced ectoparasite (*Otodectes cynotis*) in Channel Island foxes (*Urocyon littoralis*) using topical ivermectin

Poster – Poster Board 29

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Island foxes (*Urocyon littoralis*) are an endemic carnivore found on six of the Channel Islands located off the coast of Southern California, USA. As is the case for many endemic island species with restricted ranges, introduced pathogens are a major threat to island fox populations. The ear mite, *Otodectes cynotis*, is commonly found on domestic cats (*Felis catus*) and dogs (*Canis familiaris*) and was introduced to Santa Catalina (SCA) and San Nicolas (SNI) Islands, likely by feral cats. Infection with *O. cynotis* has been associated with severe otitis externa, gross proliferative lesions, and ceruminous gland hyperplasia and carcinoma in island foxes. A study on SCA found that topical, otic application of ivermectin was highly effective at reducing mite prevalence and these otic pathologies. Annual routine treatment with ivermectin was adopted on SCA in 2008. Island-wide mite prevalence was 84.1% in 2008, and by 2012 had dropped to 9.3% in treated foxes and 25.5% in untreated foxes, demonstrating a degree of herd immunity protecting untreated animals. Ear mite prevalence on SNI was 99.5% in 2024, the year that ivermectin treatment began. Feral cats were removed from SNI in 2010, providing a unique opportunity to monitor mite prevalence changes on a smaller island that only has one *O. cynotis* host. We will present possible demographic parameters which may drive mite prevalence in fox populations and compare these findings between islands with different *O. cynotis* host communities.

Molecular Surveillance of AIV and NDV in Captive Blue-Naped Parrots and Visayan Tarictic Hornbills, Philippines

Poster – Global Voice

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Avian influenza virus (AIV) and Newcastle disease virus (NDV) are significant pathogens affecting poultry health, with major economic and conservation implications. Wild birds serve as natural reservoirs for both viruses and may play important roles in viral maintenance and evolution. This study investigated the presence of AIV and NDV in two endemic Philippine avian species housed at Talarak Foundation Incorporated in Negros Occidental: blue-naped parrots (*Tanygnathus lucionensis*) and Visayan tarictic hornbills (*Penelopides panini*). Eighteen captive blue-naped parrots were sampled using fecal swabs pooled into five samples, while twelve apparently healthy hornbills were sampled using cloacal swabs pooled into three samples. Viral RNA was extracted and subjected to reverse transcription polymerase chain reaction (RT-PCR) for AIV detection, targeting the nucleoprotein gene, and RT-PCR or nested RT-PCR assays targeting the fusion and matrix genes for NDV detection. All pooled samples tested negative for both AIV and NDV. The absence of viral detection may be attributed to the captive-bred status of the birds, limited exposure to other animals, existing preventive measures, and the reported absence of AIV cases in Negros Occidental. Nevertheless, both viruses remain highly contagious and continue to circulate in the Philippines, with previous reports documenting NDV positivity in captive blue-naped parrots in other facilities. These findings underscore the effectiveness of current biosecurity measures while emphasizing the need for continuous surveillance, expanded testing, and further research to strengthen disease prevention strategies in conservation medicine and captive wildlife management.

More Testing, More Culling?: Accounting for Imperfect Detection in Disease Management Strategies of *Mycoplasma bovis* in North American Bison (*Bison bison*)

Poster - Poster Board 16

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North American bison (*Bison bison*) restoration increasingly relies on translocation among herds to preserve genetic diversity, raising concern about pathogen spread, particularly for *Mycoplasma bovis*, which can persist in asymptomatic carriers. Current test-and-remove strategies rely heavily on PCR diagnostics, yet imperfect detection may allow for infected individuals to persist and seed future outbreaks. We developed hierarchical occupancy models for *M. bovis* using PCR data from 2022-2026 from six bison herds to estimate detection probability, pathogen persistence, and optimal sampling strategies while accounting for herd-specific variation and irregular sampling intervals. Monthly PCR sensitivity was lower than expected, while specificity remained high (false-positive rate <2%). Persistence analyses indicated strong month-to-month retention of infection status, with most positive individuals remaining positive in subsequent months. Detection probability varied among herds, with some populations requiring more than twice the sampling effort to achieve comparable confidence in detection. At the individual level, a single negative PCR result left significant residual infection risk, whereas consecutive monthly negatives markedly improved confidence in clearance. Following outbreak periods, infection risk declined rapidly but still required repeated annual testing to reach residual-risk thresholds. These findings indicate that single-test clearance protocols may underestimate infection risk and highlight the importance of sequential surveillance for translocation decisions. Our framework provides a quantitative, adaptable approach for designing wildlife management strategies that account for imperfect diagnostic detection and pathogen persistence. As wildlife translocations accelerate globally, failure to account for detection uncertainty threatens to turn conservation tools into inadvertent networks for pathogen dispersal.

Navigating a morbidity event in the pet trade

Poster- Poster Board 76

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In late 2025, a private amphibian hobbyist and breeder reported concern about sick salamanders. Although grossly the lesions presented similar to *Batrachochytrium salamandrivorans* (*Bsal*) chytridiomycosis, diagnostic testing ruled out *Bsal*. Trade of animals to other private hobbyists resulted in similar morbidity occurring at these sites, causing concern for a transmissible infectious agent. Animals were submitted to multiple laboratories for concurrent testing. Chilled, frozen, and formalin-fixed animals from both the initial site and at least one of the secondary sites were examined by microscopy. Gross findings were not consistent in all animals but variably included sloughing skin, varying numbers of randomly distributed pinpoint to 1 mm diameter flat dark red to black foci throughout the body, and occasional up to 5 mm diameter ulcerations. General microscopic findings included multifocal epidermal necrosis with occasionally one or more of fungal hyphae, bacteria, or nematode larvae. Culture results from frozen tissues revealed multiple fungal and bacterial colonies. Ongoing investigations include metagenomics and virus isolation. This case highlights the importance of working as teams to tackle morbidity events.

Novel *Mansonella ozzardi*-like nematode in black bears and raccoons of east Tennessee

Poster – Poster Board 53

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Mansonella ozzardi-like nematodes have been reported sporadically in black bears in Japan and the United States (U.S.), and, most recently, have been reported in raccoons in the U.S. *Mansonella ozzardi* is a human filariid that can cause mansonelliasis in humans. Little is known about the *M. ozzardi*-like parasite that infects bears and raccoons. We analyzed blood samples from 93 American black bears (*Ursus americanus*) and 47 raccoons (*Procyon lotor*) in eastern Tennessee from 2022 to 2025. A modified Knott's test was performed on all samples. Microfilaria was found on a total of 66 (66/93, 71%) bears and 15 (15/47, 32%) raccoons. For both bears and raccoons, microfilaria sizes ranged from 225 and 275µm long and 2.5 to 5µm wide. Average length and width for microfilaria found in bears was 254.4µm (± 16µm), and 4µm (± 1.2µm). For raccoons, average length and width was 255µm (± 8.5µm), and 2.5µm (± 0µm). Conventional PCR using filarial ITS F (5'- TTCCGTAGGTGAACCTGC-3') and filarial ITS R (5'-ATATGCTTAAGTTCAGCGGG-3') primers was performed on a select number of positive samples. PCR samples sent to sequencing came back as 85.57% to 92.61% similar to *Mansonella ozzardi*. The relatively high prevalence in bear and raccoon populations of this region emphasizes the need to address knowledge gaps about this novel filarial nematode, including its life cycle, anatomical location of the adult nematodes, its pathologic impact on host species, and its zoonotic potential.

Outbreak of deadly clostridiosis in Chacoan peccaries (*Catagonus wagneri*) within a captive breeding program in the Chaco region of Paraguay.

Poster – Poster Board 49

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Clostridium perfringens is a gram-positive anaerobic bacillus that is commonly found in the microbiota of humans and animals. It is considered a typical enteric inhabitant, but pathogenesis and predisposing factors for the disease can vary between host species. An outbreak of necrotic enteritis caused by *Clostridium perfringens* type A, C, and *Clostridium sordellii* was diagnosed in captive Chacoan peccaries (*Catagonus wagneri*) raised in large pens within their natural habitat at the Chaco Center for Conservation and Research in the department of Boquerón, Paraguay. A total of 51 Chacoan peccaries of various ages (ranging from 20 days to 16 years) and sexes were affected. For all affected animals, symptoms included lethargy and inappetence, followed by sudden death within 1 to 6 hours. The diagnosis was confirmed by cultures of the organ, intestinal contents, and feces as *C. perfringens* and *C. sordellii*. Toxins were detected by immunochromatographic and conventional PCR, indicating the presence of toxins A and C. The animals were administered ampicillin, activated charcoal, and trimethoprim-sulfamethoxazole orally. The cause of the outbreak is not entirely clear. Still, it is attributed to high temperatures and humidity; the consumption of pumpkin and squash seeds, which contain trypsin inhibitors; excessive water consumption; stomach content fermentation; and the possible introduction of pathogenic bacteria by vultures. Preventive measures are recommended, including vaccination, dietary modifications during the summer, and the use of activated charcoal with appropriate antibiotics if required.

Parelaphostrongylus tenuis detection in hunter-harvested white-tailed deer (*Odocoileus virginianus*) in Colorado, USA

Poster – Poster Board 55

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Parelaphostrongylus tenuis (*P. tenuis*) is a nematode parasite commonly referred to as the meningeal worm or brain worm. This parasite has an indirect lifecycle, using gastropods as intermediate hosts and white-tailed deer (*Odocoileus virginianus*) as definitive hosts. White-tailed deer typically do not show clinical signs of infection; however, *P. tenuis* infections in aberrant hosts (e.g., moose and mule deer) can result in serious disease. *P. tenuis* has historically presented a concern for wild and domestic ungulates in eastern North America; however, recent detections suggest expansion in parasite distribution.

Due to detections in neighboring states, Colorado Parks and Wildlife (CPW) began passive surveillance efforts for *P. tenuis* in hunter-harvested white-tailed deer in 2022. Over three hunting seasons (2022-2024), CPW detected *P. tenuis* in 9/217 (4.1%) white-tailed deer heads from hunter-harvested animals. Detections of *P. tenuis* occurred in the northeastern region of Colorado along riparian corridors of the South Platte River (8/9; 88.9%) and the South Fork of the Republican River (1/9; 11.1%). Presence of *P. tenuis* was determined by gross examination of the brain tissue, pituitary recess, and cranial cavity with and without the dura mater.

To date, CPW has not detected *P. tenuis* in any species in Colorado other than white-tailed deer. These detections confirm the westward spread of this parasite into Colorado's free-ranging white-tailed deer population in the northeastern region of the state. Future efforts include continued surveillance to increase sample size and targeted surveillance in areas where white-tailed deer overlap with aberrant hosts of concern (e.g., moose).

Pathogens in Ocelots: A Patchwork of Published Records

Poster – Poster Board 21

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Disease risk is a critical consideration for species conservation as it can drive small or isolated populations to extirpation. Assessing disease risk in vulnerable populations includes understanding what pathogens a particular host species may be susceptible to, and which pathogens are present—and even enzootic—in a given population. Ocelots (*Leopardus pardalis*) are small felids that originally ranged from the southern United States (U.S.; Louisiana, Arkansas, Arizona, and Texas) to Peru and Brazil in South America. Their northern limit has receded, with the northern-most contemporary occurrence documented in the southern tip of Texas, consisting of two small populations isolated from the robust core of the range that exists in Central and South America. This study synthesizes peer-reviewed articles reporting infectious agents in free-ranging and captive ocelots. We utilized the Web of Science platform to conduct a literature review using the following search terms and Boolean operators: (“*Leopardus pardalis*” OR ocelot) AND (disease OR pathogen OR infection OR parasite) which returned 161 primary research articles as of June 2025. Filtering steps included review of the title and abstract for relevance, followed by full article review for final inclusion or exclusion. Extracted data includes pathogen identity, pathogen type, diagnostic methods, host context (i.e., wild vs. captive), and geographic location. The resulting database will provide a standardized, citable resource to support disease risk assessments, guide biosecurity screening priorities pre-transport for animals in the U.S. breeding and release program, and contribute to broader efforts to integrate wildlife disease knowledge into applied conservation planning.

Physiological correlates of body condition in house sparrows (*Passer domesticus*) across agricultural landscapes

Poster – Poster Board 72

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Agricultural environments impact wild avian health through altered diets and exposure to stressors. Although body condition is commonly used to assess bird health, its relationship with physiological markers is not fully understood. We studied house sparrows (*Passer domesticus*), a common wild bird, and hypothesized that body condition was associated (a) positively with carotenoid, vitamin, and glucose levels; (b) negatively with ketones and parasitemia; was (c) higher in males; and (d) lower during peak breeding season. Using mist nets, we captured 106 sparrows at four Michigan State University livestock farms from May-August 2025. We banded, aged, and sexed sparrows, and, using residuals from a body mass/tarsus regression, quantified body condition. We measured parasitemia via microscopy; glucose and ketone levels with point-of-care devices; and carotenoid and vitamin concentrations using high-performance liquid chromatography. We found that body condition declined through the breeding season and that males were in better condition overall. Body condition differed among farms, with sparrows from the sheep farm in better condition than those from an adjacent beef farm. We also found body condition to correlate positively and negatively with plasma vitamin A and vitamin E levels, respectively. Carotenoid levels were unrelated to body condition. These patterns likely reflect higher energetic investment of females relative to males, farm-specific differences in resource availability and disturbance, and increases in reproductive effort throughout the breeding season. Future study will focus on hematology and PCR to quantify parasitic and bacterial infections in *P. domesticus* to further investigate drivers of passerine health on farms.

Population viability analysis of Davis Mountains cottontail amidst potential rabbit hemorrhagic disease virus 2 re-emergence and vaccination

Poster - Poster Board 4

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The Davis Mountains cottontail (DMC; *Sylvilagus holzneri robustus*) is a subspecies of Holzner's cottontail designated in 2015 as a Species of Greatest Conservation Need in Texas. Within Texas, the DMC is endemic to the Trans-Pecos region, with its full historic distribution spanning from southern New Mexico to northern Mexico. DMCs are montane specialists, only known to occupy the pinyon-oak-juniper "sky islands" at >1500m in elevation. While current population estimates for the subspecies are unknown, anecdotal evidence suggests populations are declining. It is believed that the DMC has historically persisted in small population sizes and densities, making them particularly sensitive to stochastic events. In 2020, rabbit hemorrhagic disease virus 2 (RHDV2) emerged in the region, threatening the DMC's survival. While an RHDV2 vaccine produced by Medgene has proven to be successful in preventing disease in domestic rabbits, the vaccine's efficacy is unknown in wild lagomorphs. Our objective was to conduct a population viability analysis for the DMCs occupying the Davis Mountains in western Texas, aiming to determine which management strategies are most likely to promote the subspecies' persistence. Using the program *Vortex* v10.11.0, we ran simulations to predict the effects of deterministic forces and stochastic events on DMC populations. Simulation parameters were determined from in-field data collection, published DMC literature, and published information on eastern cottontails (*S. floridanus*) when DMC-specific information was unavailable. We varied survival, reproduction, and recruitment within scenarios of drought, habitat loss, RHDV2 re-emergence, vaccination, and combinations of each scenario to determine best management strategies for the DMC.

Raccoons from a One Health Perspective: Evaluation of Zoonotic and Sylvatic Disease in Rehabilitation Patients

Poster – Poster Board 68

William Funk¹, Jared Taylor¹, Kathryn Duncan¹

1. Oklahoma State University

Northern raccoons (*Procyon lotor*) are a common patient in rehabilitation throughout their range. These mesocarnivores have adapted well to the urban-wildlife interface, increasing potential for disease spillover events between humans, domestic animals, and other urban-adapted wildlife. Rehabilitation centers can act as a conduit for disease surveillance in these urban environments for a wide range of pathogens or disease presentations. A multifaceted research program was established to evaluate the prevalence of neurologic, gastrointestinal, and respiratory disease in raccoons admitted to a large rehabilitation center in Oklahoma using retrospective data as well as an opportunistic surveillance program to evaluate the prevalence of endoparasites through fecal analysis. Improving surveillance and diagnostic capacity is essential to fully understand the One Health implications of these findings and guide management and mitigation practices in the future.

Ranavirus (Frog Virus 3) identified in Missouri turtle species, with a focus on three-toed box turtles (*Terrapene mexicana triunguis*)

Poster – Poster Board 36

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In recent years, the ranavirus Frog Virus 3 (FV3) has emerged as a threat to reptile conservation. It has been recognized for its impact on fish and amphibian health; however, less is understood about its effects on reptile health. We have identified FV3 in both aquatic and terrestrial turtle species in Missouri since 2020. Our first positive case was identified by PCR in an eastern snapping turtle in north St. Louis County. No clinical signs were present at the time of sampling. As of February 2026, we have identified 15 positive cases of FV3 in three-toed box turtles. Of these 15 cases, 8 had clinical signs (e.g., ocular, nasal, and oral discharge, oral plaques, edema, lethargy, open-mouth breathing), 3 had low-level infections, and 4 were PCR positive on banked swabs. We also have extensively described FV3 infection in two cases of three-toed box turtles from the Wildlife Rescue Center (WRC, Ballwin, MO), in which differences in clinical signs between the cases may have been due to differences in the temporal course of FV3 disease at the time of necropsy. Failure to detect this infection previously in Missouri reptiles may have been due to lack of surveillance, although cases may also represent a novel spillover to turtles. Our findings reiterate previous suggestions that the range of FV3 infection may be greater than previously documented and that infection may occur in host species yet to be tested. Next steps include developing guidelines at the state level.

Relationship between Haemosporidian Parasitemia and Body Condition in Black-capped Chickadees (*Poecile atricapillus*)

Poster - Poster Board 12

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Avian malaria, caused by haemosporidian parasites, is widespread in songbirds and causes chronic parasitemia with potential physiological and fitness costs. Body condition reflects energetic balance, immune investment, and has been linked to avian malaria in multiple species, yet associations between haemosporidian infection, body condition, and other physiological metrics (e.g., circulating nutrients, immune cells) remain poorly understood in passerines. We investigated relationships among body condition, parasitemia, and physiological metrics in Black-capped Chickadees (*Poecile atricapillus*), a common backyard bird in the northern USA. We hypothesized that individuals in better body condition would have (a) lower blood glucose and ketone concentrations and heterophil/lymphocyte ratios (HL), (b) reduced global leukocytes (GL), (c) lower parasitemia, and that adults would be in better condition than juveniles. From May-August 2025, we captured, sampled, and measured 66 chickadees across Michigan State University natural areas (Baker Woodlot, Toumey Woodlot, Inland Lakes, and a residential area). We quantified blood glucose and ketone concentrations using point-of-care devices, and screened 100 fields per blood smear for leukocytes, erythrocytes, and blood parasites at 100x magnification. We estimated body condition as the residuals of a body mass vs. tarsus length regression, and analyzed data using linear models incorporating location, parasitemia, and aforementioned physiological metrics as predictors. We found that *Haemoproteus* parasitemia was negatively associated with body condition, but no other variables of interest were related to body condition. These results suggest that chickadees infected with malaria may experience a decline in condition, or that birds in worse condition are more susceptible to *Haemoproteus* infection.

Same Habitat, Different Constraints: Designing Noninvasive Pathogen Surveillance in Sympatric Marine Mammals

Poster – Poster Board 74

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Less invasive tools, such as drone-based sampling, can minimize disturbance and improve antemortem diagnostics in marine mammals. However, feasibility varies widely across taxa and settings. Defining these constraints is critical for designing realistic surveillance programs.

We evaluated the feasibility and diagnostic potential of noninvasive surveillance approaches during the 2025-2026 austral summer on Guafo Island, Chile, a remote island ecosystem supporting dense pinniped colonies and seasonal aggregations of large cetaceans. Shore-based drone flights documented cetacean presence and behavior and attempted respiratory sampling. Concurrently, sampling was conducted in a South American fur seal (*Arctocephalus australis*) rookery, including mucosal and fecal swabs from pups, paired blood and serum from a subset of individuals, and necropsy tissues collected opportunistically.

Blow samples were obtained from only two humpback whales (*Megaptera novaeangliae*), demonstrating that shore-based drone respiratory sampling depends on animal proximity and environmental factors. In contrast, pinniped sampling yielded consistent, high-quality samples. Drone footage documented spatial overlap between pinnipeds and cetaceans at foraging sites, highlighting a potential pathogen exposure interface.

To interpret low-biomass samples, laboratory analyses follow a staged framework. Initial screening targets priority respiratory and enteric pathogens and is supported by sensitivity and inhibition testing. Necropsy tissues will be used to benchmark noninvasive sample performance, and PhIP-Seq antibody profiling will characterize circulating antibody repertoires in pups to infer maternal pathogen exposure and population-level circulation.

Findings emphasize that shared habitat does not imply shared feasibility. Integrating behavioral observation, veterinary-supervised sampling, and molecular diagnostics provides a framework for context-appropriate surveillance strategies in remote marine mammal systems.

Select pathogen serology and fecal parasite identification results from raccoons captured at an Anthropology Research Facility in Eastern Tennessee

Poster – Poster Board 60

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The University of Tennessee Knoxville is home to the longest operational body donation program and human decomposition facility in the world. The UTK Anthropology Research Facility (ARF), which is a resource of the Forensic Anthropology Center (FAC), is on an approximately 3-acre woodlot. As opportunistic scavengers, the raccoons frequently consume donor soft tissue and have become accustomed to researcher presence at the ARF. Given that the ARF is used nearly every day for research and professional forensic training courses, it was of utmost importance to determine the potential for zoonotic disease transmission. To investigate this question, we live trapped, chemically immobilized, and collected biological samples from raccoons from the ARF in 2024. Samples included blood, serum, feces, ectoparasites, hair, ear punches, and nasal, oral and fecal swabs. Samples were analyzed for infection or exposure to select pathogens including *Toxoplasma gondii*, microfilariae, and fecal parasites by serology, modified Knott's, or fecal floatation. In total, 17 individual raccoons were captured and sampled. Of the 17 tested serum samples, 8 (47.1%) were seropositive for *Toxoplasma gondii* antibodies. Microfilariae were detected in 5 (29.4%) raccoons and microfilariae were most closely related to *Mansonella ozzardi*. Seven (4.1%) of the 17 fecal floats samples were positive for *Sarcocystis* spp. cysts and one raccoon was positive for *Baylisascaris procyonis*. Collectively, our results demonstrated raccoons from the ARF are exposed to various pathogens with some being zoonotic, including *B. procyonis*. Further metagenomic sequencing is being performed with collected samples to understand pathogen transmission and determine risk factors.

Severe Multispecies Parasitic Infection and Comprehensive Histopathology on a Wild Northern Bobwhite Quail (*Colinus virginianus*) in the Rolling Plains Ecoregion of Texas.

Poster – Poster Board 54

Henry Valencia¹, Scott Trasti¹, Shelly Briscoe¹, Ronald Kendall¹

1. Texas Tech University

Parasitic infections are increasingly recognized as important contributors to sublethal disease and population impacts in upland game birds; however, detailed histopathological descriptions of severe infections in free ranging individuals remain rare. We report a unique case of a wild adult male Northern bobwhite quail (*Colinus virginianus*) exhibiting severe multispecies parasitism and associated ocular and intestinal pathology. The individual was live captured in Garza County, Texas during routine disease surveillance and had corneal opacity. The bird was humanely euthanized and submitted for complete necropsy, histopathology, and parasitological evaluation. Gross examination revealed near complete corneal opacity with extensive neovascularization of the affected eye. Numerous nematodes consistent with ocular helminths (*Oxyspirura petrowi*) were observed within the sclera and adjacent conjunctival tissues. The gastrointestinal tract contained heavy burdens of both nematode (*Aulonocephalus* spp.) and cestode (*Raillietina* spp.) parasites with both parasites embedded in the intestinal wall. Histologic evaluation of ocular tissues revealed severe keratitis with neovascularization while intestinal sections demonstrated associated inflammation, fibrosis, and adhesions between intestinal loops. With extensive parasitism and damage this highlights the potential for severe localized pathology. This case provides rare documentation of parasitic burden affecting multiple organ systems in a free ranging bobwhite quail and signifies the capacity for ocular helminths and gastrointestinal parasites to induce significant tissue damage. Although limited to a single individual, these findings underscore the importance of incorporating pathology and histology into wildlife disease surveillance and suggest that parasitic infections may exert elevated individual level impacts than commonly noted in upland game bird populations.

Skunk Variant Rabies in Indiana: A One Health Approach

Poster - Poster Board 8

*Janetta Kelly*¹

1. Indiana Department of Natural Resources

In recent decades, the One Health movement has demonstrated an undeniable link between human, animal, and environmental health. For this reason, One Health promotes transdisciplinary, collaborative approaches to solving pressing health issues that exist at the human-animal interface. One such issue is rabies. Rabies is a wide-spread and vaccine-preventable viral disease that is fatal in all mammal species, including humans. Due to increased rates of habitat degradation and urbanization, interactions between wildlife, humans, and domestic animals are increasing; therefore, rabies continues to be a growing concern for humans and domestic animals. By employing a One Health approach, Indiana is currently addressing this important public health issue.

Indiana has been free of terrestrial rabies since the last skunk in southern Indiana tested positive in 2004. In January 2024, a skunk in Clark County, Indiana tested positive for north central skunk variant rabies after having an altercation with a domestic dog. A few weeks later, another skunk tested positive in Washington County, within 10 miles of the initial detection and since then 2 more positive skunks have been identified in Washington County. Indiana Department of Natural Resources (DNR) has been actively collaborating with multiple agencies including Indiana Department of Health (DOH), Indiana's Board of Animal Health (BOAH), and the Centers for Disease Control and Prevention (CDC) to conduct surveillance and provide outreach materials. This successful collaborative effort exemplifies how a One Health framework is integral to state agencies in addressing critical multisectoral health concerns.

Spatial Variation in *Giardia* spp. and *Cryptosporidium* spp. Infections in African Buffalo in Kruger National Park

Poster – Poster Board 61

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Landscape connectivity and shared grazing and water resources at the wildlife–livestock interface surrounding Kruger National Park (KNP), South Africa, create opportunities for pathogen transmission between African buffalo (*Syncerus caffer*) and domestic cattle. *Cryptosporidium* spp. and *Giardia* spp. are zoonotic enteric protozoan parasites with a global distribution and may be transmitted across this interface. In KNP specifically, *Cryptosporidium* has been detected in African buffalo, particularly near the western boundary; however, examinations of neither the spatial nor temporal distributions of this pathogen within KNP have been conducted. Consequently, any existing geographic hotspots and their associated environmental drivers have yet to be identified. With regards to *Giardia*, there exists no published literature on infection in African buffalo within KNP, despite documentation of this pathogen in other hosts across South Africa. This lack of information on parasite hotspots, host demographic predispositions, environmental reservoirs, and potential geographic hotspots of transmission limits our understanding of the epidemiology and spillover potential of these parasites in this host.

Fecal samples from approximately 600 African buffalo captured in KNP in 2023 (cross-sectional) and from repeatedly recaptured individuals sampled every six months over two years (longitudinal) was analyzed using digital PCR (dPCR). Utilizing cross-sectional data, we first assessed spatial patterns of both *Cryptosporidium* and *Giardia* and identified key areas within KNP that pose the greatest spillover risk to both domestic livestock and human populations. Longitudinal data was then used to build upon our first model and evaluate temporal changes in these potential spillover areas and identify their associated environmental drivers.

Spatiotemporal distribution of ticks on a southern Texas rangeland

Poster – Poster Board 64

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The risk of tickborne illness depends on tick presence and activity patterns, as well as tick pathogen carriage: all of which vary with tick life stage. Some land cover types may create favorable environments (e.g., humid and warm) which could facilitate tick activity and survival. Southern Texas is characterized by warm temperatures and woody encroachment, yet, regional ecological data regarding tick presence, phenology, land cover use, and pathogen carriage remain limited despite important management implications in this prominent cattle-ranching region. We conducted monthly drag surveillance over two years (2023-2025) across two land cover types (mottled perimeter and grassland) for all active life stages (larvae, nymph, adult) of hard ticks. Further, collected ticks were collected and tested for a panel of tick-borne pathogens. Our study had two major objectives: (i) to determine the phenology and land cover associations of each active tick life stage and (ii) to assess which pathogens are circulating in these vectors. Our findings revealed distinct land cover associations and seasonal trends in both tick presence and questing densities across life stages. Adult ticks were active year-round, while immature life stages exhibited a fall diapause. Further, ticks quested at significantly higher densities around mottled perimeters relative to open grassland. Pathogen carriage was low in this system, and *Borrelia* was undetected. The results from this study suggest that encroached rangeland environments in the ecoregion likely provide favorable conditions for year-round tick activity, and that woody mottles aid in supporting these populations.

Spatiotemporal Risk Assessment of SFTSV in Korean National Parks: Establishing Evidence-Based Prevention Strategies

Poster – Poster Board 30

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Severe Fever with Thrombocytopenia Syndrome (SFTS) is a major tick-borne disease in South Korea, with a case fatality rate of 18.5% (2013–2024). National parks represent critical human–wildlife interfaces where visitor exposure to ticks is high. This study investigated tick distribution and SFTS virus (SFTSV) prevalence across 22 national parks to establish a systematic surveillance framework and provide evidence-based risk communication.

Ticks were collected via flagging along main trails and campsites in May, July, and September 2025. Specimens were identified morphologically and tested for SFTSV using real-time RT-PCR. Tick pools were defined by collection site and sampling session and stratified by life stage (and sex for adults); pool sizes were 30 larvae/nymphs and 5 adults. Minimum infection rate (MIR, %) was calculated as (positive pools / ticks tested) × 100, assuming one infected tick per positive pool.

A total of 13,666 ticks were collected, with *Haemaphysalis longicornis* accounting for 96.7%. Nymphs peaked in May, adults in July, and larvae in September. SFTSV was detected in 21 pools, exclusively from July collections across 10 parks. The overall MIR was 0.15%, with Chiaksan National Park exhibiting the highest localized risk at 4.00%.

The exclusive detection of SFTSV in July, coinciding with adult tick activity peaks, identifies mid-summer as a period of significantly elevated risk. These findings support July-focused risk communication, bite prevention, and enhanced vector surveillance for visitors and staff, particularly around high-use trails and campsites.

Successful Treatment of Severe Sarcoptic Mange using a Single Oral Dose of Fluralaner in a Reintroduced Red Fox (*Vulpes vulpes*) in South Korea

Poster - Poster Board 3

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Sarcoptic mange is a highly contagious zoonotic disease caused by *Sarcoptes scabiei*. It is a primary cause of morbidity and mortality in wild red foxes (*Vulpes vulpes*), posing a significant threat to the red fox restoration project in South Korea.

Addressing the need for efficient and long-acting treatment protocols, this case report describes the treatment of severe sarcoptic mange in a male red fox born in captivity in 2022 and released in July 2024. In August 2025, the fox was rescued exhibiting lethargy and severe dermatologic abnormalities. Physical examination revealed emaciation (5.3 kg), generalized alopecia, and severe hyperkeratosis. Laboratory analyses indicated severe anemia, hypoproteinemias, and elevated hepatic and renal parameters, while skin scrapings confirmed *Sarcoptes* mites and eggs. A single dose of oral fluralaner (Bravecto®) was administered alongside intensive supportive care. Clinical signs improved within 14 days, and cutaneous lesions resolved with no mites detected by day 36. One month post-release, the fox was recaptured via an illegal snare, confirming satisfactory hair regrowth and successful rehabilitation. This case is the first to demonstrate the effectiveness of single-dose oral fluralaner as a practical treatment for severe mange in reintroduced red foxes, contributing to the establishment of disease management protocols in the red fox restoration project for both wildlife conservation and public health.

Surveillance of *Chlamydia psittaci* and *Giardia duodenalis* in Wild Birds Across Greece

Poster – Global Voice

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Wild birds are increasingly recognized as contributors to the circulation and environmental dissemination of zoonotic pathogens; however, data from Greece remain scarce, particularly for raptors, corvids, and water birds. This study presents selected molecular findings on *Chlamydia psittaci* and *Giardia duodenalis* in a subset of free-living wild birds originating from various regions of Greece and admitted to two wildlife health care facilities. Cloacal swabs from 150 injured or sick birds were collected between November 2023 and January 2025 and examined by quantitative PCR.

Chlamydia psittaci was detected in 8 birds (5.3%), while *Giardia duodenalis* was identified in 2 birds (1.3%). *C. psittaci* was detected across different bird groups, with higher occurrence among corvids, whereas *G. duodenalis* was exclusively detected in water birds. To the best of our knowledge, this study provides the first detection of both *C. psittaci* and *G. duodenalis* in free-living wild birds in Greece, as well as the first evidence worldwide of *G. duodenalis* in *Ardea* spp. and *C. psittaci* in *Botaurus stellaris* and *Plegadis falcinellus*.

These findings highlight wild birds as potential reservoirs of zoonotic pathogens, with relevance for avian conservation. The results underscore the importance of One Health-oriented surveillance and conservation-focused monitoring of understudied bird taxa.

Survey of parasite products observed during Zinc fecal flotation of frozen banked elk (*Cervus canadensis*) feces

Poster – Poster Board 37

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We examined 210 elk feces that were opportunistically collected in western North Carolina in 2020 and 2021 and kept frozen at -20°C until thawed for processing. Approximately 2 grams of feces were used for each Zinc Sulfate (specific gravity = 1.18) fecal flotation with centrifugation at 1800xg for 10 minutes. As expected, we found and photographed many parasite products. Parasite products were observed in 13.3% (28/210) of feces examined. From the positive fecal flotations, we observed Trichostrongyle-type eggs in 14.3% (4/28), *Strongyloides* spp. in 28.6% (8/28), *Capillaria* spp. in 10.7% (3/28), *Trichuris* spp. in 7.1% (2/28), *Moniezia* spp. in 7.1% (2/28), *Eimeria* spp. in 25.0% (7/28). Larvae were noted in 28.6% (8/28) of the samples with dorsal spines identified in at least two parasites from one sample. We also found an incidental carnivore *Sarcocystis*-like sarcocyst in one elk and a *Cystoisospora*-like oocyst in another, likely not representing infection, but ingestion from the environment. Surprisingly, we found some specimens of *Strongyloides* still alive and mobile within their eggs, indicating parasite survival during prolonged freezing. This research is ongoing with over 200 samples yet to be processed and molecular work is ongoing.

Take the ibex by the horns: A mechanistic basis for sarcoptic mange dynamics in Iberian ibex populations

Poster – Poster Board 63

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Studies on wildlife diseases have been shifting interest towards wildlife conservation focusing on intervention and management actions to minimize epizootic's consequences in host populations. Descriptions of mechanistic processes driving wildlife diseases systems are of significant value for understanding host-pathogen dynamics and assessing management strategies. However, this framework based on modelling-before-acting is not yet deeply rooted in the wildlife community. Here, we developed a mechanistic model for the well-studied and challenging case of the Iberian ibex (*Capra pyrenaica*) and sarcoptic mange (caused by *Sarcoptes scabiei*) aiming to inform and guide species disease management and research. We created a state-based deterministic model segregating ibex by sex and using their seasonal behavior to shape transmission events. We performed two different sensitivity analysis to assess the relative importance of uncertain parameters included in the model. The resulting five-year model showed an infection peak at two years after mange detection with 42.0% of individuals affected, and 86.2% of total population decline by five years. These epidemiological outcomes are comparable to field observations. Sensitivity analysis demonstrated strong monotonic relationship for most parameters, and that output variability arose almost entirely from interactions among parameters. Our model represents a fair mechanistic description of sarcoptic mange in Iberian ibex, including seasonal mating behaviors, forming a foundation for quantitatively assessing strategies for future management actions, and being potentially translatable to other mountain ungulate species. We illustrated modelling feasibility with parameter uncertainty requiring little modelling experience willing to inspire and motivate wildlife managers and researchers to endeavor this line of work.

THE IMPACT OF TRADE RELATIONSHIPS AND BUSINESS CHARACTERISTICS ON BIOSECURITY BEHAVIORS: A CASE STUDY OF THE AMPHIBIAN PET TRADE

Poster – Global Voice

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The global amphibian trade has been identified as a primary pathway of disease spread to naive amphibian populations in captivity and the wild. Three OIE reportable diseases, Bd, Bsal, and Ranavirus are of particular concern because of their virulence and pathogenesis. These diseases have been spread around the world through human activities. Improper or a lack of biosecurity actions performed by amphibian pet trade stakeholders are at least partially responsible for introducing these diseases and subsequent population declines. Understanding what motivates an amphibian pet trade business to partake in or prohibit biosecurity practices is critical to developing behavior change interventions. Here, we explore how a business' trade network centrality and position affect how many biosecurity practices they perform. We found that the percentage of animals sold to different places, mode of selling, importer status, and concern for public image had significant relationships with how many biosecurity practices a business performs. Additionally, we identify three distinct kinds of amphibian pet trade businesses. This information is useful in identifying what strategies will encourage more biosecure behaviors and which subpopulations to target for outreach.

Toxic Effects of the “Eagle-Killer” Aetokthonotoxin (AETX) in Mice

Poster – Poster Board 46

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Aetokthonotoxin (AETX) is a neurotoxic compound produced by the *Aetokthonos hydrillicola* cyanobacterium found throughout the southeastern United States. AETX causes vacuolar myelinopathy (VM) and is typically associated with mass die-offs of bald eagles (*Haliaeetus leucocephalus*) and aquatic birds on man-made reservoirs with dense populations of the submerged aquatic plant *Hydrilla verticillata*. Previous research has demonstrated toxicity of AETX to many terrestrial and aquatic species, but the direct effects of AETX to mammals have yet to be confirmed. Characterization and synthesis of the AETX molecule in 2021 presented the opportunity for toxicological studies of this unique cyanotoxin. We performed a pilot study using laboratory mice to observe the acute oral toxicity of AETX to mammals. Ten mice were dosed with AETX (0, 2, 5, 10, 20 mg/kg) via oral gavage and monitored for two weeks. All mice that were dosed with AETX developed vacuolar lesions in the white matter of the central nervous system, but clinical signs were only observed in a single mouse that received the highest dose (20 mg/kg). This study shows that mammals are susceptible to AETX toxicity as evidenced by vacuolar lesions in white matter tracts at environmentally relevant concentrations without clear behavioral neuropathy. This study is the first step toward demonstrating that AETX has the potential to affect a wide range of species in freshwater ecosystems containing *A. hydrillicola*, and VM should be considered in cases of wildlife mortality in the southeast.

Toxoplasma gondii in corvid species

Poster – Poster Board 59

Hannah Bleecker¹

1. University of Chicago

Toxoplasma gondii is a widespread protozoan parasite capable of infecting nearly all warm-blooded vertebrates, including corvid birds. This literature review synthesizes research examining *T. gondii* detection methods, seroprevalence, and epidemiological factors in corvids. Individuals from 14 corvid species have been tested for *T. gondii* or *T. gondii* antibodies across 23 different studies worldwide, producing a data set that allows for consideration across methods, locations, and species. When a reliable test is used, corvids often display higher seroprevalence compared to other avian species tested in the same study, perhaps due to their diet, gregarious social behavior, and presence in urban areas, suggesting that they may be useful bioindicators of *T. gondii* prevalence in cities. While most corvids appear to act as asymptomatic reservoirs, there has been mortality documented in endangered Hawaiian crows (*Corvus hawaiiensis*), demonstrating important conservation implications. As human and wildlife populations become more urbanized, a good understanding of urban environmental contamination, transmission dynamics, and host susceptibility is critical. This research highlights ecological and epidemiological insights from urban environments and calls for further scholarship regarding *T. gondii* risk in conservation translocation programs.

Trueperella pyogenes, a Lethal Pathogen of Farmed White-Tailed Deer (Odocoileus virginianus) in Florida

Poster – Poster Board 51

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White-tailed deer (*Odocoileus virginianus*) farming is a growing industry in Florida, but bacterial infections and viral hemorrhagic diseases significantly contribute to mortality and production losses. Coinfection complicates diagnosis and treatment by adversely affecting the immune response. This study focuses on the spatial distribution, transmission routes, and antimicrobial resistance genes of *Trueperella pyogenes*, a prevalent bacterial pathogen in farmed white-tailed deer. The University of Florida Cervidae Health Research Initiative (CHeRI) provides diagnostic services to farmers, analyzing submitted deceased deer and tissues from 2016 to 2023. Our data show that *Escherichia coli* and *T. pyogenes* are the most common bacteria found. Since 2018, cases of *T. pyogenes* have increased, particularly in North Florida, revealing two clades: one linked to pigs and another to cattle. The diversity of *T. pyogenes* in Florida's farmed deer suggests multiple transmission routes. Many isolates carry antimicrobial resistance genes, including those for tetracycline, indicating that antimicrobial resistance may play a significant role in the high mortality rates seen in farmed white-tailed deer. These findings will help enhance health measures and management strategies for both wild and captive deer in Florida.

Using a One Health Approach to Investigate a Black Crappie Die-Off Event at Silver Lake, Indiana

Poster – Poster Board 52

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Silver Lake is a popular fishing lake for anglers in northeast Indiana that hosts a variety of game fish. In 2024, the Indiana Fish and Wildlife Health Program received reports from anglers of black crappie *Pomoxis nigromaculatus* with red lesions on their bodies and poor fishing in the lake. We collected five Black Crappie and three Largemouth Bass *Micropterus nigricans* in September of 2025 from Silver Lake in Kosciusko County, Indiana. The fish were packaged on ice and shipped to the La Crosse Fish Health Center (LFHC) in Wisconsin for diagnostic testing, including a physical examination, bacteriology and virology. The predominant bacteria isolated from these samples was *Plesiomonas shigelloides* and no findings were reported on virology. This bacterium is typically associated with tropical and subtropical environments and has the potential to cause large scale fish morbidity and mortality events in the wild and in aquaculture settings. It is also linked to foodborne illness in humans from improperly prepared fish. While relatively common in freshwater and estuaries in Asia and Africa, *P. shigelloides* is less common in North America. The Indiana DNR continues to monitor this detection with the goal of understanding the distribution of *P. shigelloides* in the state and its potential impact on fish and human health.

Using a One Health Approach to responding to Corvid Health Events in Indiana

Poster – Poster Board 56

Eli Fleace¹

1. Indiana Department of Natural Resources

Purpose:

Since 2022, Indiana has seen mortality events in crows and other corvid species. Many of the diseases that affect Corvid health are zoonotic in nature and pose risks to human and domestic animal health. Indiana DNR has formed a partnership with other One Health agencies to respond to such events in a cohesive and organized manner.

Methods:

Indiana DNR receives reports of sick and dead wildlife from the public. Biologists review these reports and investigate reports of concern such as: large mortality events, events with zoonotic disease potential, or reports that help collect data for surveillance or research projects.

Indiana DNR works closely with One Health sister agencies to keep health officials informed of events happening in the state, and to communicate with the public in a cohesive manner.

Indiana DNR and other One Health agencies meet regularly to discuss events that are happening in the state, and to plan ahead for events that may occur in the future.

Results:

This One Health collaboration helps the State communicate a cohesive and inclusive message to citizens in the state, and bolsters the State's ability to respond quickly and appropriately to One Health concerns as they arise.

Conclusion:

Indiana has developed a successful One Health collaboration in the State, which has allowed the State to respond to One Health events such as Corvidae mortalities in a quick and unified way.

Validation of a commercially available H5N1 rapid antigen test in wild waterbirds in California

Poster - Poster Board 9S

***Elizabeth Ashley*¹, *Rebecca Duerr*², *Kelly Beffa*², *Christine Kreuder Johnson*³**

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Detecting and mitigating high pathogenicity avian influenza virus (HPAIV) in wildlife requires coordinated, systematic surveillance, yet executing large-scale early detection systems presents logistical and financial challenges. Further, as treatment and control options are severely limited, the ethical and biosafety considerations of investigating disease outbreaks are complex. While various influenza A virus (IAV) point-of-care (POC) tests are used in animal production and human hospital settings, these platforms are currently not designed or validated for use in wildlife. Rapid POC tests detecting IAV and/or H5/H7 subtypes can help bridge individual animal welfare and population-level conservation decision making for wild birds and mammals affected by HPAIV. We screened aquatic birds (numerous gull, shorebird, and waterfowl species) with a commercially available and affordable H5N1 rapid antigen test in the field and at International Bird Rescue centers near San Francisco and Los Angeles, California, USA, in 2025-2026. We present test agreement with laboratory RT-qPCR, sensitivity, specificity, and predictive values, stratified by waterbird species and by symptom and/or postmortem status. We additionally share safe operating procedures, practical constraints, and considerations for confirmatory testing and reporting, as relevant to diverse wildlife monitoring, research, response, and care operations.

Wildlife Health, Disease, and Indigenous Communities: A Scoping Review of Ecological, Governance, and Community Impacts

Poster - Poster Board 7

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Wildlife diseases influence conservation policy, ecosystem management, and public health, yet their relationships with Indigenous communities and systems remain fragmented in the scholarly literature. This project presents a scoping review examining how wildlife disease and wildlife health issues are framed, studied, and addressed in relation to Indigenous peoples and lands in North America.

Drawing on research across environmental science, wildlife health, policy studies, and Indigenous studies, we systematically mapped peer-reviewed articles and selected grey literature, including government reports and Indigenous-led research. The review examines patterns in how scholarship addresses ecological impacts on wildlife and subsistence systems, decision-making authority, and community-level dimensions such as cultural continuity, food security, and sovereignty. We also assess whether and how studies engage Indigenous knowledge systems and ethical research practices, and how zoonotic versus non-zoonotic diseases are framed.

As a scoping review, this project also maps the breadth of existing scholarship to identify dominant framings, methodological patterns, and persistent gaps in research on wildlife disease and Indigenous communities. Our synthesis demonstrates that Indigenous authority and stewardship roles are inconsistently represented and that Indigenous knowledge systems are often acknowledged but infrequently integrated into study design, analysis, or decision-making frameworks. By clarifying these patterns, the project advances ongoing conversations about wildlife health, environmental stewardship, and Indigenous sovereignty and highlights areas for more collaborative and ethically grounded research.

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5. Comparison of qPCR and dPCR for Sensitive Detection and Quantification of Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) in Ticks from Wildlife Hosts
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6. Epidemiological Helminth, Disease, and Toxicant Survey of Northern Bobwhite Quail (*Colinus virginianus*) in South Carolina, United States
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7. Wildlife Health, Disease, and Indigenous Communities: A Scoping Review of Ecological, Governance, and Community Impacts
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8. Skunk Variant Rabies in Indiana: A One Health Approach
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10. Liver minerals associated with elk hoof disease in California, USA
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30. Spatiotemporal Risk Assessment of SFTSV in Korean National Parks: Establishing Evidence-Based Prevention Strategies
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