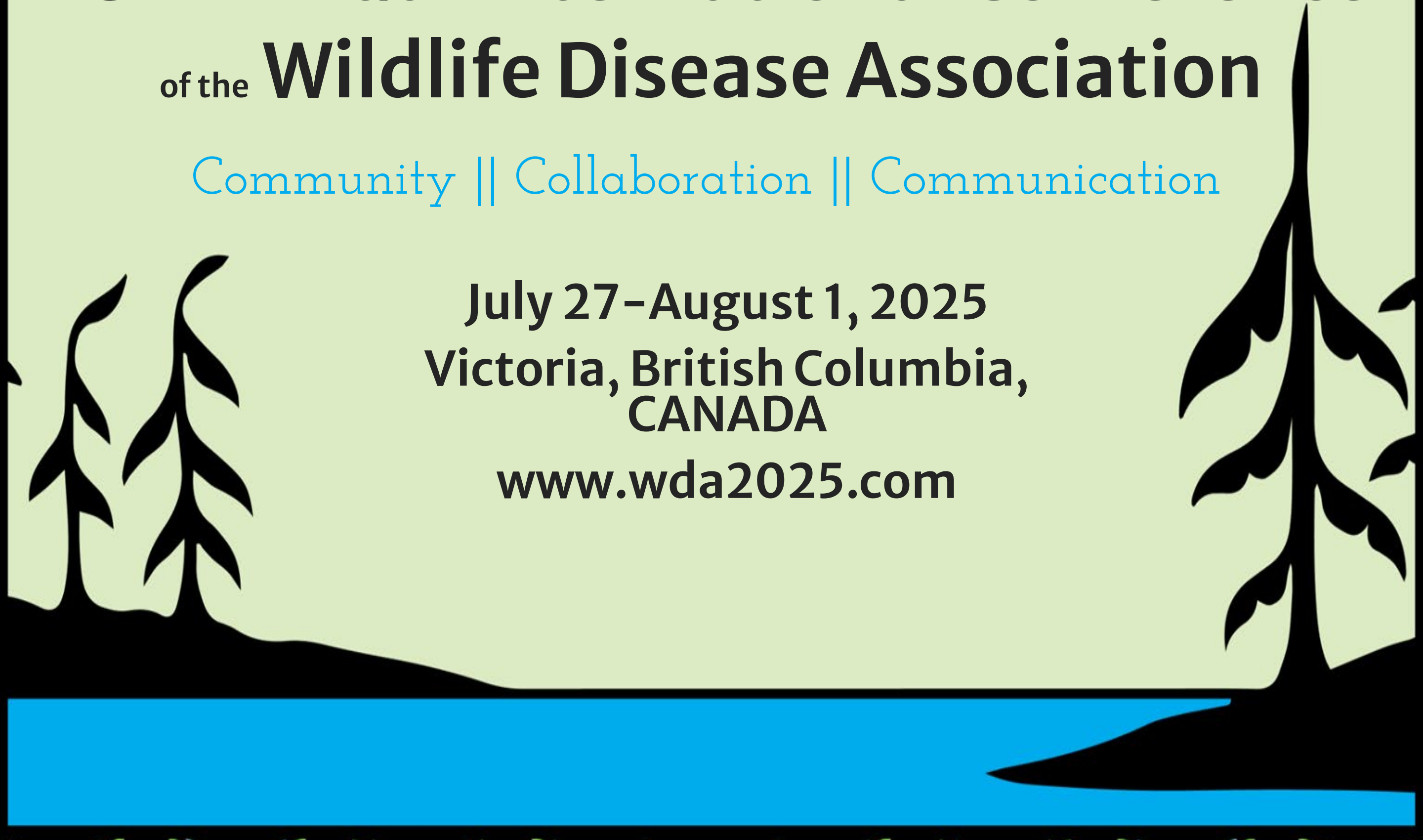
WDA

73rd Annual International Conference of the Wildlife Disease Association

Community || Collaboration || Communication

July 27–August 1, 2025
Victoria, British Columbia,
CANADA
www.wda2025.com



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WELCOME FROM THE LOCAL ORGANIZING COMMITTEE

Dear attendees,

Welcome to Victoria, British Columbia, Canada for the 73rd annual International Conference of the Wildlife Disease Association. We acknowledge and respect the Lək̓ʷəŋən (Songhees and Xʷsepsəm/Esquimalt) Peoples on whose territory the conference is held, and the Lək̓ʷəŋən and W̱SÁNEĆ Peoples whose historical relationships with the land continue to this day. Look around you at this unique maritime ecosystem we share with people, animals from the air, land, and water and explore as much as you can while you are here. Our conference graphics say it all!

The theme for this year's conference is "Communication, Collaboration, & Community". We've added "for Change" since everyone can agree that action must happen to deal with today's challenges. In keeping with the themes, we have invited speakers from diverse backgrounds to challenge you to think beyond the office, lab or your fieldwork.

In addition to the in-person science program, WDA 2025 is continuing some groundbreaking adventures with our hybrid online sessions, now known as Global Voice, as well as the Dialogues and Science Cafes. Look further into the program for a full description of these opportunities for those who cannot join in-person and for those can come, a more intimate and in-depth way to communicate and collaborate.

As with most WDA conferences, there are workshops, social events, and all are networking opportunities. In addition to traditional general and student sessions we have several poster sessions spread throughout the week during breaks. The Wednesday afternoon break provides off-site activities or time on your own to explore more of the local environment, community and what Vancouver Island has to offer.

This meeting is a little different than others since there is no sponsoring institution. Instead, we reached out to many who may not be traditional supporters of WDA but are integral in research and operational wildlife health in this country, on this continent, and beyond. We can never thank them enough for stepping up in the name of wildlife health, collaboration and community! 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 volunteers who have helped keep conference registration costs down. Many local and WDA family members, artists and businesses provided donations for the Student Auction, and we are so thankful to them. I contacted an indigenous-owned event company in 2024, and Indigenous Management Solutions (IMS) has been an incredible partner to help us celebrate the peoples of the coast, their art and concepts – thank you IMS for seeing our vision. And finally, the venues, their staffs and caterers have been stupendously patient with our requests. We know that you will appreciate their efforts to keep each and every one of you fed, watered and cared for.

Every volunteer is wearing a custom black WDA 2025 t-shirt. They are students and they are also just generous and interested locals. When you see a volunteer during the workshops, social events, field trips, auction, photo contest, student-mentor mixer or just wandering the hallways, please extend a warm thanks. Please use them for questions – if they do not know they will find out!

Enjoy the conference and have a lovely time in Victoria!

Your Organizing Committee is Helen Schwantje (host), Peri Wolff, Sonia M. Hernandez, Cat Vendl, Michael Miller, Craig Stephen, Lyndell Whyte, Roxann Corpuz and the amazing Damien Joly.

WELCOME FROM THE PRESIDENT

Welcome to the 73rd annual international conference of the Wildlife Disease Association! If this is your first time, I hope you find WDA is not just your professional home where you get Continuing Education credits and learn things to use in your job, but also where people share your ***passion for wildlife*** and understand the challenges of working with wildlife. Please find me or any of our staff and leadership-we want to get to know you, and we want you to know us. We are about advancing wildlife health, but wildlife health does not take place in a vacuum, and we cannot advance it without the constant and enthusiastic participation from everyone. Thus, fittingly, this year's theme is ***Building Communities to Promote Collaboration and Communication for Change***.

We live in uncertain times; wildlife health solutions should be based on scientific evidence, but scientific enterprise is facing unprecedented challenges. As well the various anthropogenic factors influencing health (habitat loss, fragmentation, invasive species, the pet trade, intensive agriculture, etc), society is challenging whether science has the answers. It is going to take a myriad of perspectives to devise creative solutions to maintain healthy wildlife populations and continue the hard work of educating the public about why healthy wildlife translates to healthy people and healthy economies. There are many roles to play in this puzzle—research, education, management—but like it or not, we will all have to advocate for science harder than ever.

Luckily, the WDA Futures Committee foresaw this. In 2021 they finalized the Strategic Plan to move the WDA to a public-facing association that capitalizes on the hard work of its members and is a reference for the public and other agencies working on wildlife health. Our most engaged members have worked hard to expand its international base, become more inclusive, expand our voice, engage new partners and, if the members support it, rebrand. Change is difficult, but it is also a huge opportunity for growth.

The amazing conference you're about to enjoy was, almost single-handedly, put together by the hard work of Helen Schwantje—it is unusual to host a conference without institutional support, but Helen managed it, with good cheer and laughter! The scientific program was led by Damien Joly, Mike Miller and Craig Stephen and the Global Voice by Cat Vendl—they all deserve a heartfelt thanks. Please know the entire WDA Council, Communications Officer Lyndell Whyte and Executive Manager Peri Wolff also work tirelessly to put together this wonderful event. Every decision is carefully considered, as are all of your opinions, but if there is something you don't like, don't go home disappointed - we want to know!

As you enjoy this conference, take a moment to look around and think about where WDA "has been"—there are many seasoned members here eager to share their stories. But also reflect on where it is going—what do we want WDA to look like in five, ten and twenty years? Take time to read the 2021 Strategic Plan—I think you will find it charts a path for thoughtful growth. If you are not involved in a committee, know that we can use your energy and passion. If you want to learn more about being involved in the direction of WDA, come to the WDA Council meeting on July 27th at 1pm (open to all) or the scheduled Business Meeting. The Business Lunches also will give you a sense of all the behind-the-scenes work and the wonderful people with whom I've had the pleasure to work with the past few years.

I hope the conference challenges you to think critically about the direction of wildlife health in the world, but that you also enjoy yourself, enjoy your time with friends, and make some new friends!

Sincerely,

Sonia Hernandez,
President, Wildlife Disease Association

MEET OUR GENEROUS SPONSORS

Without their amazing support, this conference would not be possible

PLATINUM

WILD SHEEP
Foundation

Founded in 1977, the Wild Sheep Foundation (WSF) is dedicated to restoring wild sheep populations that dwindled to historical lows in North America in the 1950s and ‘60s. The Wild Sheep Foundation and its Chapters and Affiliates actively fund initiatives throughout North America and its overarching strategic goal is to ensure wild sheep populations and their habitats worldwide are effectively managed, accessible, utilized and supported by interested stakeholders.

WILD SHEEP SOCIETY
OF BRITISH COLUMBIA

The Wild Sheep Society of British Columbia is dedicated to the protection and enhancement of wild sheep and wild sheep habitat throughout British Columbia as an iconic symbol of BC’s wilderness. Formed in 1992 the WSSBC funds wild sheep science and research projects, habitat enhancement and protection projects, and transplantation of sheep into unoccupied or historically occupied areas with the goal of “Putting More Sheep On The Mountains”.

GOLD

Cornell
K. Lisa Yang Center
for Wildlife Health

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.

SILVER

AAWV

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.

ALASKA
WILD SHEEP FOUNDATION

The Alaska Wild Sheep Foundation (AK WSF) was established in 2014 and chartered by the Wild Sheep Foundation (WSF) in January 2015. Its purpose is “Keeping sheep on the mountains of Alaska”. With members throughout Alaska, the United States, and an increasing number of international members, this volunteer-driven organization facilitates science-based management of wild sheep throughout the state. Approximately 25% of all the wild sheep in North America live in Alaska.

Government of
Northwest Territories
Gouvernement des
Territoires du Nord-Ouest

The Department of Environment and Climate Change ensures the land, water, wildlife, and environment in the NWT are well-managed and sustainably used and is the territorial lead for climate action. It promotes, plans, and supports the sustainable use of land and natural resources, and protects, restores, and stewards the environment in a balanced manner, a responsibility shared with Indigenous and community governments, federal and territorial departments, boards, agencies, and NWT residents.

GUIDE OUTFITTERS
Association of British Columbia
Wildlife First™

Guide outfitters are the founders of the tourism industry and an important part of the outdoor heritage of British Columbia, starting in the late 1800s. Legislation in 1961 gave guide outfitters exclusive rights to guide non-resident big game hunters and became the foundation of the guide outfitting industry in British Columbia. The Guide Outfitters Association of British Columbia is a non-profit society established in 1966 to represent the guide outfitting industry.

IDAHO
WILD SHEEP
Foundation

The Idaho Wild Sheep Foundation was founded in 1982 by two dozen concerned sportsmen who wanted to “put more bighorns on Idaho’s mountains.” From that core group, many of which are still very active on our board and committees, we have grown to a thriving organization with more than 1500 committed members.

One Health
Concepts

One Health Concepts - Moving One Health to Policy and Practice

MEET OUR GENEROUS SPONSORS

Without their amazing support, this conference would not be possible

SILVER

San Diego Zoo Wildlife Alliance is a non-profit conservation organization integrating wildlife health and care, science, and education to develop sustainable conservation solutions. Over 105 years we have honed a unique skillset and strengths that are a significant part of greater conservation efforts globally. We have an army of scientists, vets, EMTs, caregivers, strategists, and more, contributing to a host of efforts and initiatives on behalf of wildlife.

The Texas Bighorn Society (TBS) is a prominent advocate for wildlife conservation in the Lone Star State. For over four decades, our organization has remained steadfast in its commitment to safeguarding the iconic bighorn sheep and their natural habitat across Texas. Today, nearly 1500 bighorns roam the West Texas mountains, but the society remains dedicated to returning bighorns to all their native ranges and increase their numbers to approximately 3000.

The Utah Wild Sheep Foundation promotes increasing populations of indigenous wild sheep in Utah, safeguards against the decline or extinction of such species, and funds programs for professional management of these populations. Vigorously involved in the conservation, propagation, and intensive management of the remaining wild sheep populations and their habitats, the foundation funds a variety of essential projects encompassing wildlife enhancement, management, the re-establishment of wild sheep, and sportsmen's rights.

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.

Genome BC is a not-for-profit organization supporting world-class genomics research to grow globally competitive life sciences sectors and deliver sustainable benefits for British Columbia, Canada and beyond. Its initiatives are improving the lives of British Columbians by advancing health care and addressing environmental and natural resource challenges. Genome BC supports responsible research and innovation and fosters an understanding and appreciation of the life sciences among educators, students and the public.

The Outer Circle Wild Bunch Club has been associated with the Foundation for North American Wild Sheep, followed by the Wild Sheep Foundation (WSF) for decades. The unique club initiation was a mandatory preserved human toe "cocktail" or "toe shot" and the membership fee was $100. Funds from merchandise sales and membership fees support a project/recipient. In January 2025, one evening session raised almost $5000 and WDA 2025 was the recipient.

There are 37 national parks, and 11 national park reserves in Canada protecting approximately 343,377 square kilometres. They range from mountains and plains, to boreal forests and tundra, lakes, glaciers, and more. Its scientists and Indigenous knowledge holders work together to conserve nature. It creates and manages protected areas. It protects species and habitats. It helps nature adapt to climate change. It restores natural areas.

The Abbotsford Rod and Gun Club is a hunter and angler organization based in Abbotsford BC that actively fundraises for BC-based wildlife management and research projects. The club hosts many annual events and many sub-club tournaments. Also, many of the sub clubs host tournaments. The club offers, from time to time depending on demand, the "CORE Program" (Conservation and Outdoor Education) and a variety of other course offerings.

ADDITIONAL SPONSORS

CURRENT WDA OFFICERS

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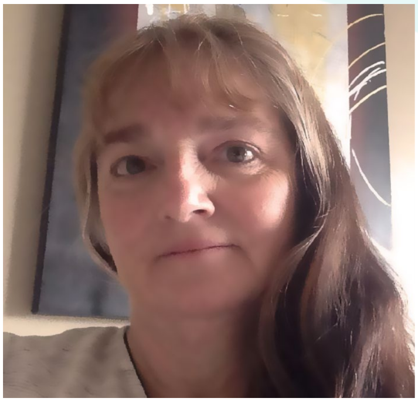

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MISSION STATEMENT

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 affect 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 will take place in 2025

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**

WE WANT TO HEAR FROM YOU!!

Share your thoughts on the process (and informally vote for a new name) by:

- **Visiting the WDA Rebranding poster and leaving a comment there OR**
- ***Sending the WDA leadership an email***

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.

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.

WILDLIFE DISEASE ASSOCIATION CODE OF CONDUCT cont'd

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-a-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 Victoria, British Columbia, Canada!

We ask that all attendees of the 73rd 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 2025 mug! The Victoria Conference Centre is award winning for their sustainability and we hope you see them and us trying our best. Wherever possible we have sourced locally or from Canada, 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 many of the auction items were specifically chosen for their eco-friendly materials and durability. We thank our participating artists for their creativity, love of wildlife and wild places, and sustainability ethic.

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.

Local community Conservation Project

What was started after at the Cuenca conference and continued in Madison, is the identification of a local conservation project by the local conference organizers, that WDA will support financially support as a meaningful, impactful and appropriate carbon off-set measure.

This year the support will go to the Habitat Acquisition Trust (HAT), a regional land trust dedicated to conserving nature on south Vancouver Island and the southern Gulf Islands. HAT is a registered charity and society that works to protect ecosystems and habitats permanently through land acquisition, education, and community engagement. Their vision includes a future where the full array of natural habitats in the region are healthy and conserved. Once the conference finances have been tallied, this project, and a request for WDA's financial support will be brought before Council.

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

A GUIDE TO YOUR 2025 WDA BADGE

20 25

WDA

JAEDEN DOE
University of Victoria
Canada
Add appropriate dots from below here

●	●	●	●	●
ALL WEEK	**ONE DAY**	**TWO DAYS**	**THURSDAY BANQUET**	**MONDAY PICNIC HATLEY CASTLE**
●	●	Wristband	●	●	●
TUESDAY STUDENT MENTOR MIXER - COURTYARD	**TUESDAY AUCTION STICKY WICKET**	**WEDNESDAY WHALE WATCHING**	**WEDNESDAY KAYAKING**	**WEDNESDAY SKYWALK**	**WEDNESDAY OFF THE EATEN TRACK**

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 fernando.vilchez.d@upch.pe with the subject line **"WDA Photo Contest 2025."**

REGISTRATION

Anyone attending the conference can participate in the photo contest.
A maximum of 3 photos **per** person can be submitted via the **official WDA Photo Contest website by July 30** in one or all the following categories

1. Wildlife – free ranging
2. Wildlife – captive or at the urban interface
3. Landscapes/Flora – can either contain animals or not

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

Register for the photo contest, pay your participation fee, and turn in your photos when you arrive at the meeting **OR** Register and pay ahead of time via the WDA 2025 Ex Ordo website. If you have already registered but would like to enter, you can edit your registration and add the contest to your activities (under Social Events list)

Entry fees:	
	Regular members – $6 for 1 photo ($5 each if submitting >1 photo)
	Student members – $5 for 1 photo ($4 each if submitting >1 photo)

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 30**

DISPLAY FORMATTING

- All photos should be printed or cropped to an 8″ x 10″ (20 cm x 25 cm) format.
- If you require photo printing services, there are several stores near the conference centre

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. 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

PHOTO EVALUATION

The contest will be judged by a group of WDA members with a "popular vote" by conference attendees. Judges' decisions are based on image clarity, color, lighting, contrast, composition, and "wow factor."

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

WDA 2025 Overview of Events

July 26 – Aug 1, 2025

Repeated events:

Legend:

Global Voice	**Oral presentations**	**Poster Sessions and Breaks**	**Social events**	**Science Café**

Times	Event	Room
7:30 AM – 5:00 PM	WDA Office & Storage Rooms	West Coast
Sun: 7:30 AM – 5:00 PM, M: 7:30 AM – 2:00 PM, T: 7:30 AM – 1 PM, W: 7:30 AM – 12:00 PM, Th: 7:30 AM – 7:00 PM, F: 8:00 – 11:30 AM	Registration	Pre function 1A
Sun-Th: 8:00 AM – 5:00 PM F: 8:00 AM – 12:00 PM	Quiet Room	Victoria
M-Th: 8:30 AM – 5:00 PM	Exhibitors	Pre function 2A
M -Th 8:30 AM - 5:00 PM	Photo Contest	Pre function 2A
M-Th: 8:30 AM – 5:00 PM F: 8:00 AM – 12:00 PM	Speakers Room	Metchosin
M-Th: 9:00 AM – 4:00 PM	WDA Oral History Project	Sooke
M: 10:45 AM – 5:00 PM T-Th: 8:30 AM – 5:00 PM F: 8:30 AM – 12:00 PM	**Science Café** See the board outside Colwood for the menu of each day's topics, or to schedule your own!	Colwood
M.T,Th: 8:30 AM – 5:00 PM F: 8:30 AM – 12:00 PM	**Global Voice** View the program stream	**Langford**
	Global Voice presenters	**View Royal**

Program:

Pre Conference	**Saturday, July 26**	Room
8:00 AM - 5:00 PM	**WDA/Davis Thompson Foundation Annual Wildlife Pathology Workshop**	**Oak Bay 1**

Day 1	Sunday, July 27	Room
8:00 AM - 5:00 PM	Oiled Wildlife Readiness and Response: Conservation, Command, Capture & Care	Oak Bay 1
8:00 AM – 4:30 PM	Western Association of Wildlife Agencies Wildlife Health Committee Technical Meeting	Oak Bay 2
8:00 AM - 5:00 PM	American College of Zoological Medicine Exam Preparation and Study Course	Colwood 1
10:00 AM - 12:00 PM	WDA Editorial Board Meeting	Esquimalt
12:00 PM - 1:00 PM	Joint Lunch – Editorial Board & Council & Oiled Wildlife Workshop	Saanich
1:15 PM – 5:00 PM	WDA Council Meeting	Esquimalt
5:30 PM - 7:30 PM	Welcome Reception/Icebreaker	VCC Courtyard

Day 2	Monday, July 28	Room
8:15 AM - 10:00 AM	Welcomes and Keynote Address	Salon BC
10:00 AM – 10:45 AM	Morning Break and poster set up (poster set up can start at 8:00 AM)	Salon A
Concurrent Sessions		
Session A 10:45 AM - 12:00 PM	Avian Influenza	Salon BC
Session B 10:45 AM - 12:00 PM	Collective Action and Collaboration	Saanich
Session C 10:45 AM - 12:00 PM	Mechanisms of Harm	Oak Bay
12:00 PM – 1:30 PM	Lunch & Business Meeting #1	Salon BC
Concurrent Sessions		
Session A 1:30 PM - 2:45 PM	Aquatic Animal and Marine Health	Salon BC
Session B 1:30 PM - 2:45 PM	Dialogue Session: Shared Ground: Community Collaborations in Wildlife Health Monitoring	Saanich
Session C 1:30 PM - 2:45 PM	Wildlife Rehabilitation	Oak Bay
3:00 PM – 3:45 PM	Afternoon break & Poster Session Innovations in Wildlife Disease Detection	Salon A
Concurrent Sessions		

Session A 3:45 PM – 5:00 PM	Aquatic Animal and Marine Health (continued)	Salon BC
Session B 3:45 PM – 5:00 PM	Dialogue Session: Navigating the Policy Ecosystem	Saanich
Session C 3:45 PM – 5:00 PM	General Wildlife Health	Oak Bay
5:30 PM – 10:00 PM	**Picnic at Hatley Castle - http://hatleycastle.com/** Buses will leave Victoria Conference Centre at **5:45 PM**, **6:00 PM**, and **6:15 PM**, returning at **9:15 PM**, **9:30 PM** and **9:45 PM**	

Day 3	Tuesday, July 29	Room
7:00 AM – 7:50 AM	American Association of Wildlife Veterinarians Business Meeting	Sidney
8:00 AM – 8:30 AM	General Session: Student Keynote	Salon BC
8:30 AM – 10:00 AM	Student Presentations: Small mammals and vectors	Salon BC
10:00 AM - 10:45 AM	Morning Break & Student Poster Session	Salon A
10:45 AM - 12:30 PM	Student Presentations: Hoofstock	Salon BC
12:30 PM - 1:30 PM	Lunch with Business Meeting #2	Salon BC
1:30 PM - 3:00 PM	Student Presentations: Non-mammal	Salon BC
3:00 PM - 3:45 PM	Afternoon Break & Student Poster Session	Salon A
3:45 PM - 5:15 PM	Student Presentations: Spillover and Transmission	Salon BC
5:15 PM - 6:30 PM	Student-Mentor Mixer	Upper Pavillion
6:30 PM - 11:00 PM	Auction: Wicket Hall at Strathcona Hotel, 919 Douglas St, Victoria BC	

Day 4	Wednesday, July 30	Room
9:00 – 12:00 PM	Global Voice Plenary	Salon BC
10:30 AM – 10:45	Morning (Networking) Break	Salon A
2:40 PM – 7:40 PM	Global Voice studio	View Royal
8:00 AM – 8:50 AM	WDA Wildlife Veterinary Section Business Meeting	Sidney
12:00 PM - 1:00 PM	WDA Section and Committee Chair Meeting (with box lunch)	Salon BC
1:00 PM on	Activities for Afternoon/Dinner on Own	

Day 5	Thursday, July 31	Room
7:00 AM – 8:00 AM	CANUSA Student Chapter Meeting	Sidney
8:15 AM - 10:00 AM	General Session Carlton Herman Founders Fund Invited Speaker AAWV, Al Franzmann Award Invited Speaker	Salon BC
10:00 AM - 10:45 AM	Morning Break & Poster Session: Disease Ecology in Changing Environments	Salon A
Concurrent Sessions		
Session A 10:45 AM - 12:00 PM	Ecology and Management	Lecture Theatre
Session B 10:45 AM - 12:00 PM	Dialogue Session: Future-Ready Wildlife Health: Building Resilience, Driving Change	Saanich
Session C 10:45 AM - 12:00 PM	Transboundary Wildlife Health Management	Oak Bay
12:00 PM – 1:00 PM	Lunch & Business Meeting #3	Salon BC
12:00 PM – 1:00 PM	Journal of Wildlife Diseases Associate Editors Lunch	Salon BC
12:45 PM – 1:30 PM	Poster Session: Host-Pathogen Dynamics and Co-Infection	Salon A
Concurrent Sessions		
Session A 1:30 AM - 3:00 PM	Northern and Mountain Ungulates	Lecture Theatre
Session B 1:30 AM - 3:00 PM	Dialogue Session: WHIN: Connecting the Global Community at the Frontline of Wildlife Health Surveillance	Saanich
Session C 1:30 AM - 3:00 PM	Education and Communication	Oak Bay
3:00 PM - 3:45 PM	Afternoon Break & Poster Session: Case Studies and Regional Surveillance Insights	Salon A
3:45 – 5:00 PM	Poster, Photo, Exhibitor take down	Salon A
Concurrent Sessions		
Session A 3:45 PM - 5:00 PM	Northern and Mountain Ungulates continued	Lecture Theatre
Session B 3:45 PM - 5:00 PM	Dialogue Session: Using Wildlife Health Research in Agency Decision Making	Saanich
Session C 3:45 PM - 5:00 PM	Pathogen Discovery	Oak Bay

5:00 PM - 6:00 PM	WDA Annual Business Meeting	Sidney
6:00 PM - 7:30 PM	Cocktail Hour(-ish)	Pre function 2
7:30 PM - 11:00 PM	Banquet, Awards Ceremony	Salon BC

Day 6	Friday, August 1	Room
8:30 AM – 9:30 AM	General Session Lessons Learned in Dialogues and What's Next?	Salon BC
9:30 AM – 10:15 AM	Morning Break	Salon A
Concurrent Sessions		
Session A 10:15 AM - 11:15 AM	Pathogen Discovery	Saanich
Session B 10:15 AM - 11:15 AM	Ecology and Management	Oak Bay
Session C 10:15 AM – 11:15 AM	Mechanisms of Harm	Salon BC
11:30 AM - 12:00 PM	Closing Remarks and Ceremony	Salon BC

JUMP TO THE DETAILED PROGRAM

Welcome to Victoria!!

Nestled between the waters of the Salish Sea and the mighty rainforests of Vancouver Island, Victoria is an unparalleled destination. It's a unique place where natural wonder sits side by side with cultural treasurers both traditional and contemporary.

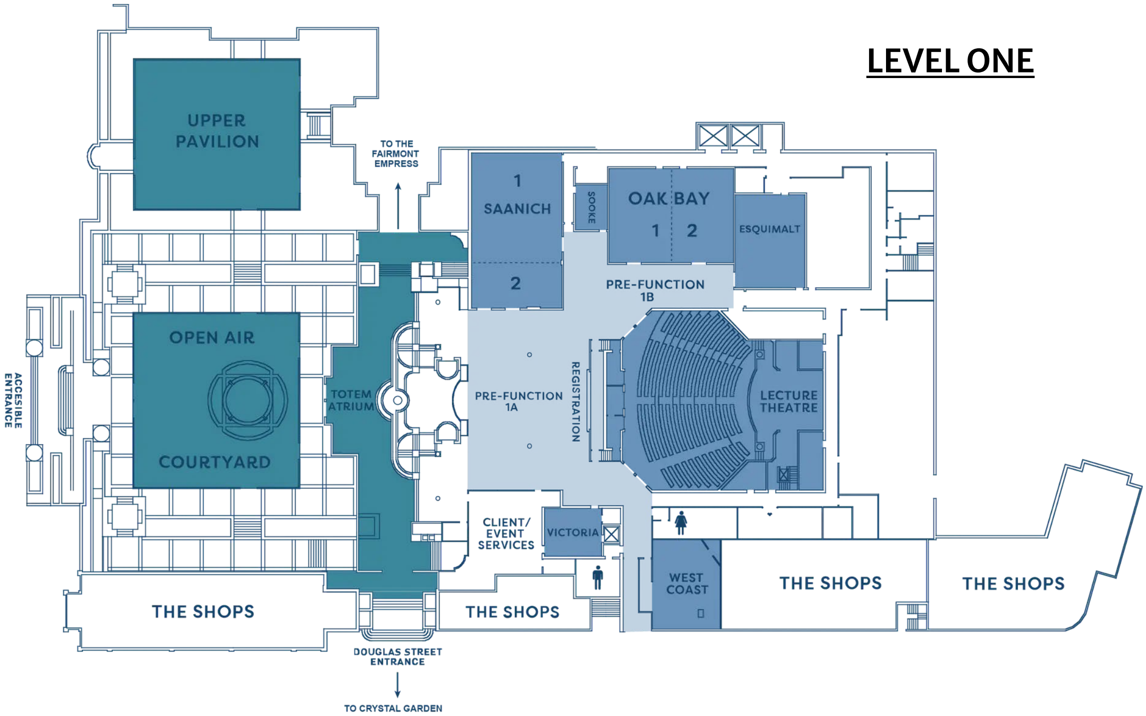
For all the details on where to go and what to see, visit our travel partner Tourism Victoria

POINTS OF INTEREST

1 Abkhazi Garden
2 Art Gallery of Greater Victoria
3 The Bay Centre
4 Beacon Hill Children's Farm
5 Belfry Theatre
6 Cameron Band Shell
7 Carr House
8 Chinatown
9 Craigdarroch Castle
10 The Fairmont Empress
11 Fisherman's Wharf
12 Government House
13 Helmcken House
14 IMAX Victoria
15 Langham Court Theatre
16 Market Square
17 McPherson Playhouse
18 Mile 0
19 Miniature World
20 Parliament Buildings
21 Point Ellice House
22 Royal BC Museum
23 Royal Theatre
24 St. Ann's Academy
25 Save-on-Foods Memorial Centre
26 Terry Fox Memorial Statue
27 Victoria Bug Zoo
28 Victoria Public Market

VICTORIA
CONFERENCE
CENTRE

LEVEL ONE



WDA Rooms

Colwood 1
Colwood 2
Esquimalt Room
Langford

Lecture Theatre
Metchosin Room
Oak Bay 1 Room
Oak Bay 2 Room

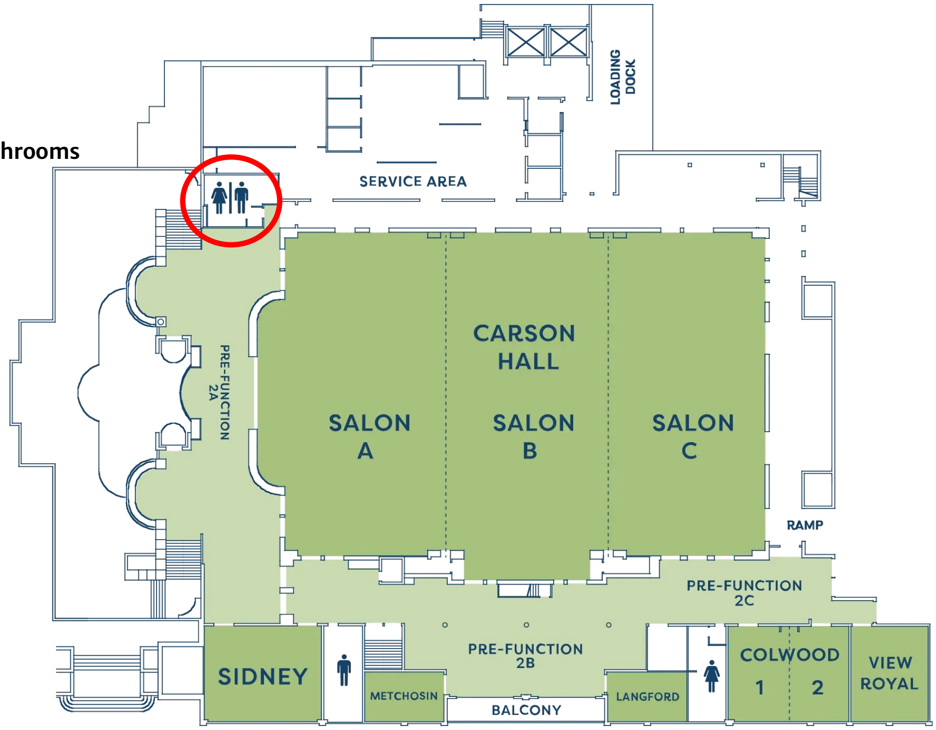
Oak Bay Room
Salon A
Sooke Room
Salon BC

Saanich Room
Sidney Room
Upper Pavillion
Victoria CC Courtyard

Victoria Room
View Royal Room
West Coast Room
Prefunction 1A
Prefunction 2A

LEVEL TWO

○ – Gender neutral bathrooms



HEALTH GUIDELINES

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 2025

If you need local assistance:

Overall concerns and program enquiries contact:
- Helen Schwantje **+1 (250) 710-6026**
- WDA Exec Manager Peri Wolff **+1 (805) 857-5809**

Scientific program enquiries contact:
- Damien Joly **+1 (250) 616-4961**

Field trips enquiries contact:
- Helen Schwantje **+1 (250) 710-6026**

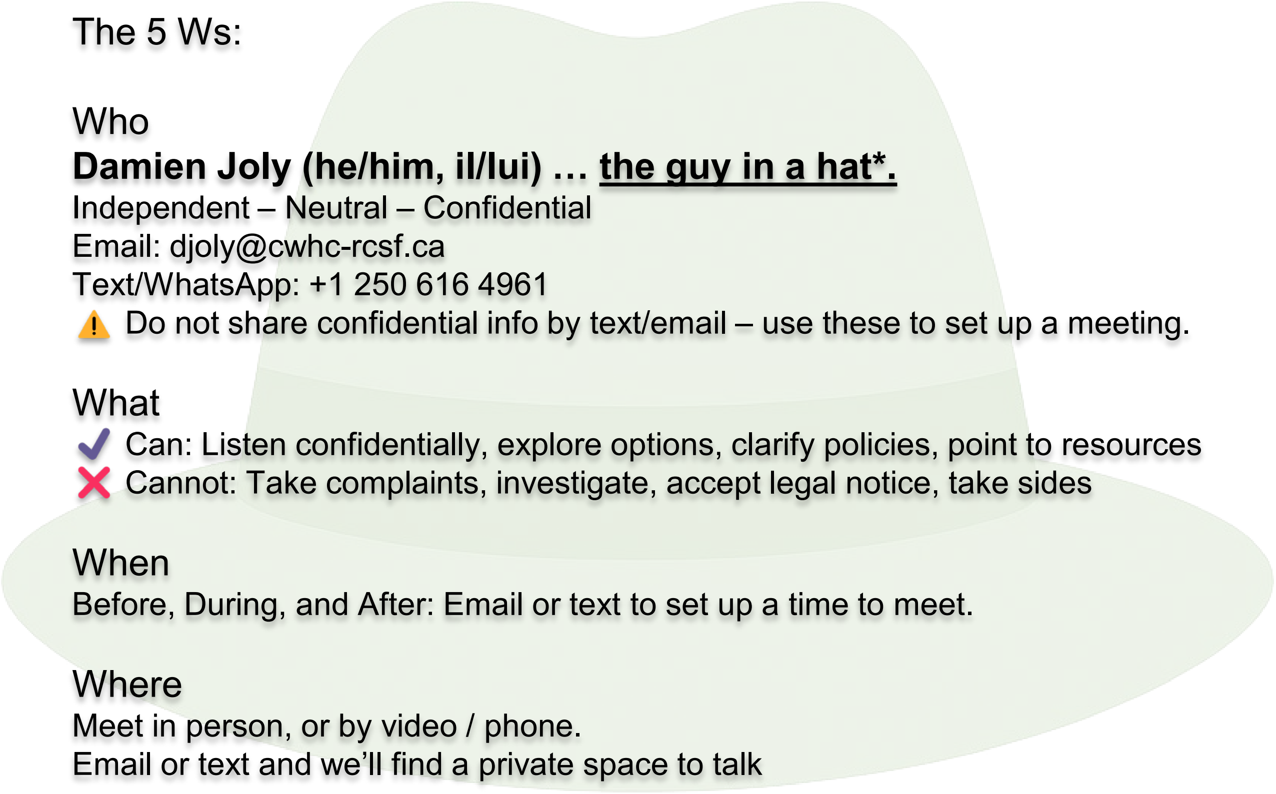
Ombudsman enquiries contact:
- Damien Joly **+1 (250) 616-4961**

For emergencies *within* the Victoria Conference Centre, call +1 (250) 361-1011 or +1 (250) 361-1013

For emergencies *outside* the conference centre, call 911

Ombuds at WDA 2025

ombuds *[ˈäm-ˌbudz]* (*noun*, plural also *ombuds*)
Definition: A neutral and independent individual appointed to provide confidential, informal assistance in resolving concerns, addressing conflicts, and promoting fair practices within an organization or event. Ombuds do not take sides, conduct investigations, or accept formal complaints. Shortened from *ombudsman*, borrowed from Swedish *ombudsman*, meaning “representative” or “proxy” — from *ombud* (“agent, representative”) + *-man* (“person”).



The 5 Ws:

Who

Damien Joly (he/him, il/lui) … the guy in a hat*.
Independent – Neutral – Confidential
Email: djoly@cwhc-rcsf.ca
Text/WhatsApp: +1 250 616 4961
⚠ Do not share confidential info by text/email – use these to set up a meeting.

What

✓ Can: Listen confidentially, explore options, clarify policies, point to resources
✗ Cannot: Take complaints, investigate, accept legal notice, take sides

When

Before, During, and After: Email or text to set up a time to meet.

Where

Meet in person, or by video / phone.
Email or text and we’ll find a private space to talk

Why

You feel unsafe or unsure
You saw something concerning
You want a confidential sounding board
You care about a respectful event

* To help identify him, Damien will wear a fedora, pork pie, or flatcap throughout the conference

ACTIVITIES – WEDNESDAY, JULY 30

OFF THE EATEN TRACK

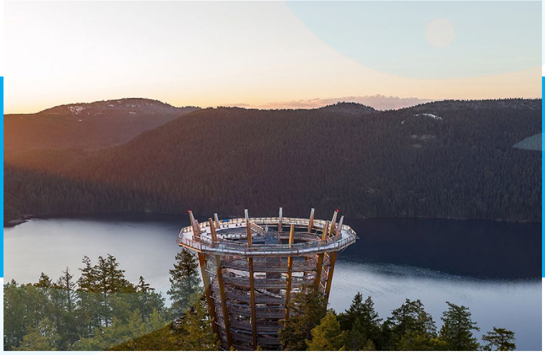
Times updated in activity emails

EAGLE WING TOURS

Times updated in activity emails

OCEAN RIVER KAYAKING

Times updated in activity emails



MALAHAT SKYWALK

Times updated in activity emails

Quiet Room – need a place for prayer, meditation, or peaceful reflection?

We have a room for you.

The Victoria Room is located on Level One of the Victoria Conference Centre

CONTINUING EDUCATION CREDITS

Continuing Education credit for Veterinarians

Thanks to the American Association of Wildlife Veterinarians for compiling and submitting the CE program, and the American College of Zoological Medicine for approving the CE credits for both the in-person and Global Voice scientific programs.

The Veterinary CE certificate for the in-person meeting can be found HERE

The Veterinary CE certificate for Global Voice can be found HERE*

*Note for Global Voice attendees: To receive CE credits, you must watch the presentation **in real time**. There will be no opportunity to review recorded presentations and take a quiz to receive CE. You will only receive CE credits for the talks listed on the certificate.

Continuing Education credit for Certified Wildlife Biologists®

For the in-person conference, The Wildlife Society has reviewed and approved up to **26 CEUs** for Category I of their Certified Wildlife Biologist®/Professional Development Certificate Program.

One CEU can be earned for every hour of classroom-style learning, whether in-person or live-streamed.

For the Global Voice virtual meeting, participants can earn up to **23.5 CEUs** on the renewal application. One CEU can be earned for every hour of learning.

Download your in-person CE certificate HERE

Download your Global Voice CE Certificate HERE

20 25

WDA

SCHEDULE AND ABSTRACTS

Community || Collaboration || Communication

WDA 2025 Schedule of Presentations

Monday AM, July 28

Plenary Session Venue: Salon BC	
08:15	Welcome and Opening Remarks - Helen Schwantje, Conference Host & Sonia Hernandez, WDA President
08:30	Welcome and Land Acknowledgement - Diane Sam, Cultural Advisor, Songhees Nation
08:55	Opening Remarks - WDA 2025 Scientific Program - Craig Stephen, Scientific Program Cochair
09:00	WDA Oral History Project - Randy Zarnke, Lead for Oral History
09:05	Plenary Keynote Introduction - Peri Wolff, WDA Executive Manager
09:15	Keynote Address: Shane Mahoney, Conservation Visions/Wild Harvest
10:00	**Morning Break and Poster Set up. Venue Salon A**

Concurrent Sessions

Session:	**Avian Influenza**	**Collective Action and Collaboration**	**Mechanisms of Harm**
Venue:	**Salon BC**	**Saanich Room**	**Oak Bay Room**
10:45	WildAlert 2.0: Advancing Wildlife Disease Surveillance with AI-Driven Anomaly Detection Pranav Pandit	Bridging Science and Community: A Collaborative Approach to Baird's Tapir Health Investigation in Costa Rica Jorge Rojas Jimenez	Investigating Phaeohyphomycosis in Salmonids of Northern Quebec, Canada: Past, Present, and Future Perspectives Benjamin Jakobek
11:00	Highly Pathogenic Avian Influenza Virus (H5N1, clade 2.3.4.4b) Outbreak in Birds of Prey from Québec, Canada Chloé Stefanopoulos	By Our Powers Combined: Recommendations for Collaboration between Wildlife Rehabilitators and Wildlife Health Researchers Stephanie Herman	Impact of human contact on critically endangered mountain gorilla health Kathryn Harper
11:15	Utilizing serology to better understand trajectory and impacts of highly pathogenic avian influenza in wildlife Rebecca Poulson	A multi-species determinants of health approach for nanuk (polar bear) co-management Andrea Hanke	Prevalence, Diversity, and Intensity of Trichinella spp. in Wildlife from Northern Canada and Alaska: New Geographic and Host Records for Trichinella chanchalensis Cody Malone
11:30	Long-term temporal dynamics of influenza A virus antibodies in black vultures (*Coragyps atratus*) after an H5N1 highly pathogenic influenza A virus outbreak Justin Brown	GPS mapping and community-based interviewing for One Health Surveillance in Kasongoire forest region, Uganda Victoria Priester	The other shoe drops: emergence of *Salmonella enterica var Weltevreden* in critically endangered Christmas Island Reptiles Karrie Rose
11:45	Highly Pathogenic Avian Influenza (HPAI) in Canadian Species at Risk Damien Joly		Causes and Contributors to Bat Mortality: 47 Years of Diagnostic Data at the Southeastern Cooperative Wildlife Disease Study Mattison Green

Monday PM, July 28

12:00	Lunch & Business Meeting #1. Venue: Salon BC		
	Concurrent Sessions		
Session	**Aquatic Animal and Marine Health**	**Dialogue Session**	**Wildlife Rehabilitation**
Venue:	**Salon BC**	**Saanich Room**	**Oak Bay Room**
13:30	Autopsy findings in sea otters found along the British Columbia coast from 2000 to 2024. Trent Bollinger	Shared Ground: Community Collaborations in Wildlife Health Monitoring Led by Naima Jutha & Erica Suitor	Guess what is in my cadaver freezer: wildlife rehabilitation as an under-utilized resource in wildlife diseases surveillance Chantal Theijn
13:45	Emergence of virulent toxoplasmosis in southern sea otters (*Enhydra lutris nereis*) due to the COUG strain of Toxoplasma gondii Karen Shapiro		Long-Term Monitoring of Chronic Oiling in California Seabirds: Trends, Impacts, and Conservation Implications Jamie Sherman
14:00	Identifying a causative agent for sea star wasting disease Melanie Prentice		Wildlife Rehabilitation Facilities, an Essential Partner in One Health Collaborative Networks: SARS-CoV-2 Surveillance in Native U.S. Mammals and Assessment of Biosecurity Practices Jeff Gruntmeir
14:15	Determining the best predictors of body condition in leatherback turtles (*Dermochelys coriacea*) Heather Harris		Retrospective Hematological Analysis of Raccoon Dogs (*Nyctereutes procyonoides*) with Sarcoptic Mange Rescued in Gangwon State Sohwon Bae
14:30	Is Tularemia an emerging marine zoonosis in Washington marine mammals? Erin D'Agnese		Pre-Release Health & Post-Release Fate of Rehabilitated Macropods (Kangaroos and Wallabies) Joanne Connolly
14:45	Contaminants of emerging concern and antimicrobial resistance in Great Lakes fish: implications for One Health Bridget Baker		Bridging the Gap: Research Opportunities in Wildlife Through Partnerships with Wildlife Rehabilitators Angelika Langen

Monday PM, July 28, Continued

15:00	**Poster Session: Innovations in Wildlife Disease Detection with Afternoon Break. Venue: Salon A**		
Concurrent Sessions			
Session:	**Aquatic Animal and Marine Health continued**	**Dialogue Session**	**General Wildlife Health**
Venue:	**Salon BC**	**Saanich Room**	**Oak Bay Room**
15:45	Health and food borne parasite assessment of East Beaufort Sea Beluga (*Delphinapterus leucas*) in the Inuvialuit Settlement Region: A Collaborative Approach Émilie L. Couture	Navigating the Policy Ecosystem Led by Charlie Booher	Framework for assessing chemical immobilization in free-range darted mule deer Emma Lantz
16:00	Survey of pathogens in Antarctic pinnipeds: a decade of health monitoring Florencia Soto		Understanding Wildlife Health Metrics Under the Threat of Climate Change Sabrina Greening
16:15	Dead but not forgotten - Drivers of cetacean necrobiome and their importance in understanding carcass decomposition and circumstances of death Catharina Vendl		Understanding Antibody Dynamics in the Wild Anna Jolles
16:30	Using Models to Evaluate the Efficacy of Management Actions for Reducing the Risk of Salmon Disease Julie Alexander		How Can We Get to Wildlife Health Intelligence? Krysten Schuler
16:45	Land use impacts movement and pathogen transmission of a wetland bird Sonia M. Hernandez		

Tuesday AM, July 29

Plenary Session **Venue: Salon BC**	
08:00	**Student Keynote Speaker - SSRA Winner** Land use and soil characteristics are associated with increased risk of treponeme-associated hoof disease in elk (*Cervus canadensis*) Steven Winter
	Student Presentations - Small Mammals and Vectors
08:30	Wake up and fight!? Effect of torpor on immunity in eastern bent-winged bats (*Miniopterus orianae oceanensis*) Anna Langguth
08:45	Identification and deep sequencing of potentially zoonotic Bartonella from wild small mammals in urban parks and green spaces of Toronto, Ontario, Canada Simon P. Jeeves
09:00	Mosquito and Culicoides vector breeding ecology in feral swine (*Sus scrofa*) wallows in Georgia and South Carolina Taylor Fisher
09:15	Multi-State Investigation of Pathogen and Contaminant Exposure in Declining Eastern U.S. Muskrat (*Ondatra zibethicus*) Populations Nicholas Friedeman
09:30	Incriminating vectors of deer malaria (*Plasmodium odocoilei*) at a Florida deer farm Morgan Rockwell
09:45	Impacts of wildfire on rodents (*Peromyscus maniculatus*) and hantavirus dynamics (Sin Nombre virus, SNV) in the Sierra Nevada mountains of California Ariel Loredo
10:00	**Student Posters and Morning Break. Venue: Salon A**
	Student Presentations - Hoofstock
10:45	Old Nodes, New Tricks: Novel Diagnostics for Chronic Wasting Disease in Preserved Retropharyngeal Lymph Nodes Avery Munster
11:00	Genetic Epidemiology of North Dakota Deer: Identifying Polymorphisms Influencing Chronic Wasting Disease Ethan Baker
11:15	An Agent-Based Modeling Approach to Simulating Chronic Wasting Disease Transmission among Three Sympatric Cervid Species Ashlyn Halseth-Ellis
11:30	The next stage of environmental surveillance for chronic wasting disease: What can we learn from testing scrape sites? Miranda Huang
11:45	Development of a rapid and reliable experimental infection model for an emergent hoof disease in elk (*Cervus canadensis*) Holly Drankhan
12:00	Incisor pathology in muskoxen from the Canadian Arctic Erica Suitor
12:15	Investigating Pestivirus Infections in Barren-Ground Caribou: Strain Identification and Diagnostic Test Refinement Jessie Olson
12:30	**Lunch and Business Meeting - Student Activities Committee Update. Venue: Salon BC**

Tuesday PM, July 29

Student Presentations - non-mammal	
13:30	An occupancy analysis to determine the unbiased prevalence of three pathogens in free-ranging eastern box turtles (*Terrapene carolina carolina*) in central Illinois Maris Daleo
13:45	How's the Weather in There? Impacts of extreme weather events on parasitism in riverine fishes Connor Whalen
14:00	Exploring St. Louis encephalitis and West Nile virus infection kinetics and host immunity within House sparrows (*Passer domesticus*) Jennifer Buczek
14:15	Harbor porpoise predation by grey seals in the St. Lawrence Estuary, Québec, Canada Amélia Dalpé
14:30	Adenovirus and Herpesvirus Detection in Ornate Box Turtles (*Terrapene ornata ornata*) in Illinois Erika Suniga
14:45	COMPARATIVE GENE EXPRESSION OF THREE SEA STAR SPECIES WITH VARYING SUSCEPTIBILITY TO SEA STAR WASTING DISEASE Grace Crandall
15:00	**Student Posters and Afternoon Break. Venue: Salon A**

Student Presentations - Spillover and transmission	
15:45	Surveillance and Management of Invasive Marmosets (*Callithrix* sp.) as a Strategy to Minimize Risks Associated with the Buffy-Tufted Ear Marmoset (*Callithrix aurita*) Conservation Translocation to Atlantic Forest Fragments in Southeastern Brazil Isabela Mascarenhas
16:00	Prevalence of canine distemper virus in wild carnivores of North Carolina submitted to a public health laboratory for rabies virus testing Seth Lattner
16:15	Applying a Continuum of Care Framework to Convention on Migratory Species Resolutions: Strategic Opportunities for Wildlife Health Management Caroline Kern-Allely
16:30	Feeders, Feathers, and Feces: Finding Ways to Prevent Salmonella Infections in Birds and People Kimberly Perez
16:45	Gut feelings: Exploring gastrointestinal parasite sharing at the wildlife-livestock interface in Kenya Kim van de Wiel
17:00	Disease and Immunity: What do host inflammatory profiles tell us about unknown disease exposures in wild free-roaming bighorn sheep? Luke Weinstein

Wednesday, July 30

	Global Voice Plenary Session **Venue: Salon BC**
09:00	**Welcome**
09:15	**Invited talk - Rabies takes to sea: an outbreak in Cape fur seals in southern Africa** Lesley van Helden
09:45	Q&A
09:55	Announcements
10:00	The potential threat of Strongyloides spp. to mountain gorillas and public health in Bwindi Impenetrable National Park Bukamba Nelson
10:15	Methodologies and Techniques for Preemptive Detection of Avian Influenza in Wetlands via eDNA Andrew Hopkins
10:30	Networking break
10:45	**Invited talk - Primate trafficking in Colombia** Angela Maldonado
11:15	Q&A
11:20	Announcements
11:25	Does anthropogenic ecological disruption underlie chronic wasting disease's emergence, spread, and persistence? Brian Dugovich
11:40	Pathogenic Bacteria in Feces of the Violet-crowned (*Ramosomyia violiceps*) and Broad-billed (*Cynanthus latirostris*) Hummingbirds in Two Distinct Environments in West-central Mexico Lizeth Raygoza
11:55	Wrap-up
12:00	**WDA Section and Committee Chair Meeting (with box lunch)**

Thursday, July 31

Plenary Session Venue: Salon BC	
08:15	Announcements
08:30	**Carlton Herman Speaker:** Axel Moehrenschlager Embracing values, uncertainty, and fear to take science-based conservation action
09:15	**Al Franzmann Memorial Speaker:** Tom Besser Bighorn sheep pneumonia: Identifying the Cause of a Multifactorial Disease
10:00	**Morning Break and Poster session - Disease Ecology in Changing Environments. Venue: Salon A**

Concurrent sessions			
Session	**Ecology and Management**	**Dialogue Session**	**Transboundary Wildlife Health Management**
Venue:	**Lecture Theatre**	**Saanich Room**	**Oak Bay Room**
10:45	Flocking for Surveillance: Vulture Movement as a Sentinel for Anthrax Outbreaks Barb Wolfe	Future-Ready Wildlife Health: Building Resilience, Driving Change Led by Julie Ellis	Regional Coordination Advances Fish and Wildlife Health Across the US Ellen Haynes
11:00	Patterns, Processes and Prions: Modeling Chronic Wasting Disease Dynamics in Alberta Owain Barton		Building Wildlife Health and Zoonotic Disease Capacity Both Within and Beyond California's Borders Brandon Munk
11:15	Modeling Contact Dynamics to Understand Potential Disease Transmission Between Wild and Domestic Felids Alexandria Hiott		Managing health risks in translocations of displaced wildlife: New IUCN Guidelines on responsible Translocation of displaced Organisms Julie Sherman
11:30	Impacts of Winter Prescribed Fire on Tick Density and Tick-Borne Pathogen Diversity in the Gulf Coast Prairies and Marshes Ecoregion of Southern Texas, USA Rachel Walters		Stronger Together: US-Canada Wildlife Surveillance Initiative for Adaptive Management of Highly Pathogenic Avian Influenza Damien Joly
11:45	Spatial risk of chronic wasting disease in white-tailed deer: the role of habitat, minerals, and soil properties in the Midwest, U.S. Kristin Bondo		Viral Diversity in North American Bats: A Collaborative Multi-State Surveillance System Bridging Public Health Laboratories, Bat Biologists, and Wildlife Disease Researchers Mattison Green
12:00	**Lunch and Business Meeting #3. Venue: Salon BC** **Journal of Wildlife Diseases Associate Editors Lunch. Venue: Salon BC**		

Thursday, July 31 Continued

12:45	**Poster session - Host-Pathogen Dynamics and Co-Infection. Venue: Salon A**		
Session	**Northern and Mountain Ungulates**	**Dialogue Session**	**Education and communication**
Venue:	**Lecture Theatre**	**Saanich Room**	**Oak Bay Room**
13:30	Developing field-based assays for the detection of Mycoplasma ovipneumoniae Kate Huyvaert	WHIN: Connecting the Global Community at the frontline of Wildlife Health Surveillance Led by Mathieu Pruvot	Application of immersive technology and other learning approaches in the wildlife sector Justin Brown
13:45	Fatal interactions: pneumonia in bighorn lambs following experimental exposure to carriers of Mycoplasma ovipneumoniae Logan Weyand		Chronic Wasting Disease Concerns Among First Nations in British Columbia Irina Borgos
14:00	Cross-Sectional Serosurvey of Sarcoptic Mange in Wild Mountain Ungulates in Kyrgyzstan Martin Gilbert		See one, do one, teach one - global connections in One Health Woutrina Smith
14:15	Parasite Burden Without Physiological Cost? Investigating Fascioloides magna in Austrian Red Deer Friederike Pohlin		All Stories Great and Small: The Power of Science Communication Eunah Preston
14:30	Twenty years of ungulate disease surveillance by the Canadian Wildlife Health Cooperative (2002–2023) Kerry Schutten		Study Abroad Courses are Essential Tools in Creating Future Health and Disease Practitioners Sonia M. Hernandez
14:45	Assessing the health-fitness dynamics of endangered mountain caribou and the influence of maternal penning Clayton Lamb		
15:00	**Afternoon Break and Poster session - Case Studies and Regional Surveillance Insights. Venue: Salon A**		
15:45-17:00	**Poster and Exhibit Removal**		

Thursday, July 31 Continued

15:45	**Northern and Mountain Ungulates Continued**	**Dialogue Session**	**Pathogen Discovery**
Venue:	**Lecture Theatre**	**Saanich Room**	**Oak Bay Room**
15:45	Health Survey of Migratory and Boreal Caribou (*Rangifer tarandus*) in Québec and Labrador, Canada Laura Van Driessche	Using Wildlife Health Research in Agency Decision Making Led by Nancy Wilkins, Brett Elkin, & Theresa Burns	Real-time quaking induced conversion (RT-QuIC) in a state wildlife management agency: examples of projects utilizing this tool in Wyoming, USA Brie Hashem
16:00	Neosporosis, an emerging parasitic threat to free-ranging caribou (*Rangifer* sp.)? Kimberlee Beckmen		A multi-omics approach to health surveillance and translocation success in Sonoran pronghorn Natalie Payne
16:15	Mathematical models evidence the importance of alternative hosts and environmental transmission for bacterial diseases affecting ungulates in the Arctic Juan Vargas		Novel betacoronaviruses in white-footed mice (*Peromyscus leucopus*) and deer mice (*Peromyscus maniculatus*) Jonathon D. Kotwa
16:30	Enhancing community-based wildlife health surveillance through advancing field-friendly methods Olivia Hee		Accumulation of benzotriazole UV-stabilizers in relation to ingested plastics and associated health metrics in Larus gulls feeding at a landfill in Atlantic Canada Kerry Schutten
16:45	Geographies of *Bacillus anthracis* Exposure: Converging Indigenous Knowledge and Remote Sensing to Map Cattle Anthrax Risk in Southern Africa Juan M Dabezies		

Friday, August 1

08:30	**Plenary Session: Lessons learned in Dialogue Sessions and What is Next?**		
09:30	**Morning Break. Venue: Salon A**		
10:15	**Mechanisms of Harm**	**Pathogen Discovery**	**Ecology and Management**
Venue:	**Salon BC**	**Saanich Room**	**Oak Bay Room**
10:15	Results from the first five years of the Carnivore Diseases Monitoring Program in Navarre (N Spain) Javier Millán	Role of wild coypu (*Myocastor coypus*) as sentinel, reservoir and vector of antimicrobial resistance in the aquatic environment: preliminary results Elisa Massella	Diverse and persistent impacts of West Nile virus on breeding bird populations in Pennsylvania Brock Geary
10:30	Parasite genotype, host, and environmental factors are associated with fatal *Sarcocystis neurona* infection in southern sea otters (*Enhydra lutris nereis*) Devinn Sinnott	Paranannizziopsis infections in garter snakes in the Pacific Northwest Nicki Rosenhagen	Five years of rabbit hemorrhagic disease virus 2 infections in wild lagomorphs in California, USA - tracking disease spread and mitigating impacts to an endangered species Deana Clifford
10:45	Toxoplasmosis outbreak in black howler monkeys in Chiapas, Mexico Elliott Chiu	Microbiomes As Biomarkers of Health in Wild Carnivores Leigh Combrink	A novel method of estimating badger population density for disease monitoring and vaccination delivery. Ruth Cox
11:00	Botulism, Fermentation, or Something More? Solving the Mystery of Lorikeet Paralysis Syndrome. Viviana Gonzalez Astudillo	Cracking the egg on sea turtle egg fusariosis in leatherback nests, an investigation of fungal burden Samantha Kuschke	Guinea worm Disease Surveillance and Home range Analysis of Olive Baboons: Inform Programmatic Decisions for Eradication in Ethiopia. Alexandra Sack
11:30	**Closing Remarks. Venue: Salon BC**		

Poster Session: Innovations in Wildlife Disease Detection

Monday, 3 pm. Venue: Salon A

Title	Author
Thermal Geography of Sylon Disease in Commercially Important Prawns Under a Changing Climate	Madeleine Abbott
Community pathogen surveillance in Chicagoland aquatic turtles	Laura Adamovicz
From surveillance to action – collaboration to manage Echinococcus hotspots in Sweden	Erik Ågren
HPAIV infection in peridomestic animals	Angela Bosco-Lauth
Occurrence and Genetic Characterization of Tick-borne Relapsing Fever Borrelia spp. in a Florida subspecies of soft ticks (*Ornithodoros turicata americanus*)	Nicholas Canino
Malagasy flea microbiota results from a combination of vertically transmitted and environmentally acquired microbes	Victoria Carcauzon
Hepatic Lipidosis in Bats in Pennsylvania, USA	Taylor Chan
Detection of Paranannizziopsis sp. in wild Swinhoe's japalure (*Diploderma swinhonis*) in Taiwan	Chiao-Wen Chen
Spontaneous amyloidosis is associated with endoparasitism in wild rabbits (*Sylvilagus* spp.)	Elliott Chiu
Regional surveillance for Echinococcus species in wild canids in the Eastern United States	Christopher Cleveland
Electrocardiographic examination of 16 eastern grey kangaroos (Macropus giganteus) and a red kangaroo (*Osphranter rufus*)	Joanne Connolly
Abdominal ultrasonographic evaluation of healthy juvenile eastern grey kangaroos (*Macropus giganteus*)	Joanne Connolly
Effect of prairie dog burrow density on tick abundance on small mammals in South Dakota	Shelli Dubay
Comparison of two sampling protocols for the detection of Mycoplasma ovipneumoniae in hunter-harvested desert bighorn sheep	Ann Fan
Performance Data Trends for Candidates Taking the American College of Zoological Medicine Board Examination (2012-2024)	Daniel Fredholm
Skua die-off from high pathogenicity avian influenza on Beak Island, Antarctica, 2023–2024	Anne Günther
Geographic Distribution and Neuropathology of *Elaeophora schneideri* in Shiras Moose (*Alces alces shirasi*) in Idaho, USA	Christine Haake
Emaciation and mortality in rough-skinned newts on the Olympic Peninsula, Washington State	Katherine Haman
Tracking Tularemia: Insights into Ferret Exposure and Tick Dynamics in South Dakota	Madisen Hartlaub
The Early Bird Catches the Parasite: Potential Invertebrate Pathway for *Baylisascaris Procyonis* to Infect Songbirds	Scott Henke
Clinical Management of H5N1 Avian Influenza in a Captive Flock of Red-Breasted Geese (*Branta ruficollis*)	Yousuf Jafarey
Thyroid Hyperplasia in Wild Brook Trout (*Salvelinus fontinalis*) from Lake Florentien (Quebec, Canada)	Marion Jalenques
Wild turkey infectious disease prevalence across Pennsylvania landscapes	Ryan Koch
Histopathologic Lesions of Free-Ranging Rats in Hong Kong	Lisa Lee
Health assessment of snow leopards through non-invasive techniques in Nepal	Nicole Lewis
Determinants of emerging disease at the global wildlife-human-livestock interface: a scoping review	Alaina MacDonald

Title	Author
Resource sharing of wallows by feral swine and native wildlife and the potential for interspecies disease transmission at Anahuac and Aransas national wildlife refuges, Texas, USA	Rachel Maison
Rabies in Early Life: A Case Report of a 10-week-old Aardwolf (*Proteles cristatus*)	Giovana Martins Miranda
Enterococcus faecalis and Enterococcus faecium from Wild Animals: Uncovering the Hidden Threat of Antimicrobial Resistance Pollution	Elisa Massella
Whole Genome Sequence Analysis of Brucella spp. from Human, Livestock, and Wildlife in South Africa	Koketso Desiree Mazwi
Tick distribution, phenology and hosts across altitudinal gradients in the central Pyrenees, Spain. Preliminary results	Javier Millán
Sarcoptic Mange in Rescued Raccoon Dogs (*Nyctereutes procyonoides*) of Chungcheongbuk-do, South Korea: Infection Prevalence, Mortality, and Urban Impact	Kwon Mirim
Antibody response of endangered riparian brush rabbits to vaccination against rabbit hemorrhagic disease virus 2	Megan Moriarty
Improving the surveillance of canine and feline coronavirus in domestic and wild carnivores to understand the risk of cross-species transmission and the emergence of recombinant variants	Ximena Olarte-Castillo
Community partnership for successful eradication of African Swine Fever: Challenges and lessons learned from the 2023 outbreak in wild boar in Sweden	Karin Olofsson-Sannö
Validation of an Indirect Fluorescent Antibody Test for *Sarcocystis neurona* infection in California sea lions.	Andrea Packham
Evaluating the Ability of a Rapid, Field-Deployable, PCR Test to Screen Deceased Avian Wildlife for Influenza A Virus	Lucie Pascarosa
Highly pathogenic avian influenza viruses in Mississippi Flyway dabbling ducks: a multi-season perspective	Rebecca Poulson
Validating portable X-ray fluorescence for bone lead measurements of Virginia opossums (*Didelphis virginiana*)	Amanda Rappaport
Fatal bronchopneumonia cases in California mountain lions with concomitant feline leukemia virus and Mycoplasma sp. infection	Jane Riner
Understanding the health of Texas ocelots from their microbiome and virome.	MAURICIO Rued
Investigating the Cause of Elevated Mortalities of Greater One-Horned Rhinoceros (*Rhinoceros Unicornis*) in Chitwan National Park in Nepal, 2004-2024	Carmen Smith
Tularemia in Utah beavers	Virginia Stout
Trichinella Spp. in Wolves (*Canis Lupus*), Red Foxes (*Vulpes Vulpes*) and Wild Boars (*Sus Scrofa*) in Emilia-Romagna Region (Italy) During 2020-2024.	Camilla Torreggiani
The cetacean virome: Expanding the range of RNA viruses in cetaceans with disease presentation	Kate Van Brussel
Cold Stress, Heart Failure, and Esophageal Occlusion Cause the Death of a West Indian Manatee Trichechus manatus in Alabama, USA	Jillian Western
Enterobacteriaceae and antibiotic resistance in howler monkeys (*Alouatta palliata*) from environments subject to high anthropogenic influence	Clara Maria Wiederkehr Bruno
Gut Inflammatory Consequences of Gastrointestinal Parasitism in Bighorn Sheep in SE Oregon	Marci Witczak
Non-zoonotic disease systems and the One Health framework: Tiny ticks have big impacts to moose biology, management and culture	Alaina Woods
Insights from a three-year observational study of High Arctic muskoxen (*Ovibos moschatus*) following an acute infectious disease epidemic	McCaide Wooten
Arrival and Expansion of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) in the Western United States and Mexico.	Cole Wzientek
Serological investigation of livestock infectious diseases in Long-tailed goral (*Naemorhedus caudatus*) in the Republic of Korea	Subo Yang

Student Poster Session

Tuesday Morning 10-10:45 AM and Afternoon 3-3:45 PM

Venue: Salon A

Session	Title	Author
Morning	Metabolic chemistry and hematology parameters as a proxy for body condition in Columbia River Sea lions	Louise Bishop
Morning	Impacts of agricultural disturbances on small mammal population and Sin Nombre Virus temporal dynamics	Laura Budd
Morning	Examination of pathogen shedding patterns, based on variation in temperature and housing groups, in confiscated eastern box turtles (*Terrapene carolina carolina*)	Maris Daleo
Morning	Egyptian fruit bats (*Rousettus aegyptiacus*) present functionally distinct proteomic profiles in serum during pregnancy	Brooke Genovese
Morning	Comparing the utility of nasal and conjunctival swabs to tissue samples for the detection of canine distemper virus in wild carnivores using real-time RT-PCR	Seth Lattner
Morning	Presence of Infectious Agents in Free-Ranging Urban Mice from the Metro Vancouver Regional District in British Columbia, Canada	Lisa Lee
Morning	Ocular Plague (*Yersinia pestis*) in a Mule Deer (*Odocoileus hemionus*) from Idaho, USA	Tiffany Lin
Morning	Prevalence, Diversity, and Intensity of Trichinella spp. in Wildlife from Northern Canada and Alaska: New Geographic and Host Records for Trichinella chanchalensis	Cody Malone
Morning	Retrospective and Prospective Evaluation of Mediastinal and Pulmonary Mineralization in Peninsular Pronghorn (*Antilocapra americana peninsularis*): Diagnostic Imaging, Clinical, and Pathological Findings	Abbie McGuire
Morning	Fatal Verminous Pneumonia and Airsacculitis Resulting From Diplotriaena Sp. Infection in A Pileated Woodpecker (*Dryocopus Pileatus*)	Jay Muir
Morning	A ‘Purr-sistent’ Problem: How Interactions Between Domestic Cats and Wildlife Contribute to the Spread of Canine Distemper Virus in an Urban Setting	Shayna Orens
Morning	Investigating Bartonella spp. in Fleas Parasitizing Voles from Interior Alaska	Tabitha Page
Morning	Prevalence of Leptospira spp. in mesocarnivores from North Carolina	Adam Rose
Morning	Investigating the top-down disease control of a recolonizing predator	Ishana Shukla
Afternoon	Spatial Dynamics of Zoonotic Pathogens in Bank Vole (*Myodes glareolus*) Populations from Northern Sweden	Alina Johanna Anton
Afternoon	Genetic Epidemiology of North Dakota Deer: Identifying Polymorphisms Influencing Epizootic Hemorrhagic Disease	Ethan Baker
Afternoon	Disease Considerations in Beaver Translocation	Reid Ballard
Afternoon	Efficacy of the “pouring over feed” oral administration method for the commercially available Bacillus anthracis Sterne strain 34F2 vaccine in white-tailed deer (*Odocoileus virginianus*)	Maeli Caudillo
Afternoon	The influence of baiting on the prevalence of avian influenza virus (AIV) in Ontario dabbling ducks	Samantha Dobson
Afternoon	What can microbiomes tell us about the health of wild birds?	Carolina Gutierrez
Afternoon	Monitoring of Viral Agents in Wild Mammals from an Urban Center in Brazil	Bruna Hermine de Campos
Afternoon	Retrospective Serological Study of *Toxoplasma gondii* in Bighorn Sheep	Laurel Hossler
Afternoon	Pathogen Detection of Wild Turkeys Across North Dakota	Cailey Isaacson

Afternoon	Carrier animals and viral persistence: a phylogenomic approach to foot-and-mouth disease in African buffalo	Cambrey Knapp
Afternoon	Bridging the gap: multi-sector perspectives on wildlife, domestic animal and human leptospirosis in Ontario, Canada.	Kellie Libera
Afternoon	Marine Birds as Early Sentinels of Harmful Algal Blooms: Identifying Key Indicator Species	Carmen Ross
Afternoon	Wild Pig-Livestock Interactions and their Consequences for Disease Transmission	Luis Salazar
Afternoon	Silent sentinels?: reptiles and birds as alternative host reservoirs in *Trypanosoma cruzi* ecology	Mycha Van Allen
Afternoon	Comparison of Canadian Wildlife Health Cooperative wildlife disease surveillance data streams in Ontario	Kaytlyn Wise

Poster Session: Disease Ecology in Changing Environments

Thursday, 10 am. Venue: Salon A

Title	Author
A Community-Driven Sperm Whale Health Assessment Program in Dominica	O. Alejandro Aleuy
Leveraging Clinical Wildlife Data for Enhancing Wildlife Health Monitoring and Research	Rachel Avilla
Gut microbiome as an indicator of Florida Manatee (*Trichechus manatus latirostris*) health across diverse ecosystems contaminated by microplastics	Tracie Baker
Collaboration in Wildlife Health Research & Surveillance	Michelle Benavidez Westrich
Bobcat population health in New York state	Jennifer Bloodgood
"Nematoes" – Identification of *Maseria vespertilionis* Associated with Swollen Toes in Rehabilitated Big Brown Bats (*Eptesicus Fuscus*)	Justin Brown
A Thousand Pelicans: California Brown Pelican Mass Stranding Event 2024	Rebecca Duerr
Wildlife Health Communications – A Walk through (Jurassic) Park	Brooke Ezzo
Interagency Collaboration for Increase Capacity and Response Time to HPAI	Ann Fan
Deep dive on cetacean health from New South Wales, Australia	Heather Fenton
Wildlife Rehabilitation: The Unseen Partner in Wildlife Health	William Funk
Disease Outbreaks & Vaccine Efficacy in Raccoons in Rehabilitation: A Pilot Study	William Funk
Detection of Leptospira in Oregon Wildlife: groundwork for investigating prevalence and diversity across a range of small mammals in contact with humans	Kacy Hayes
Detection of European haplotype of *Echinococcus multilocularis* in coyotes in Washington state and implications for global surveillance strategies	Yasmine Hentati
Development of an Optimized Capture and Anesthesia Protocol for Formosan Sika Deer (*Cervus nippon taiouanus*) in South Korea	Nari Kim
The wild sea lion gut ecosystem: characterizing host-microbe-parasite interactions and assessing links to health	Emma Little
Characterizing Wildlife Rehabilitation Centres in the British Isles: an Antimicrobial Use Perspective	Daniela Losada-Medina
Causes of Mortality in Captive, Captive-release and Wild Vancouver Island Marmots (*Marmota vancouverensis*)	Malcolm McAdie
Management and short-term monitoring of leishmaniosis (*Leishmania infantum*) in a European Mink (*Mustela lutreola*)	Javier Millán
Addressing the global gaps in wildlife health data management through a community-of-practice-supported database	Mathieu Pruvot
Improving Wildlife Disease Surveillance through Rehabilitation Center Partnerships: Focus on HPAI	Amanda Rappaport
Serosurvey of California mountain lions and implications for management and conservation	Jessica N. Sanchez
Increasing awareness of collaboration opportunities with your partners in wildlife rehabilitation	Sarah Sirica
Less Lethal Wildlife Deterrent Round Impacts on Simulated Tissue	Owen Slater
Collaboration, Communication, Education, and disease surveillance	Shelley Spanswick
Growing Art-Sci Pathways for Wildlife Conservation	Lucy Spelman

Poster Session: Host-Pathogen Dynamics and Co-Infection

Thursday, 12:45 pm. Venue: Salon A

Title	Author
Mycoplasma ovipneumoniae strain types in Arizona, USA: Spatiotemporal trends inform risk assessments	Anne-Justice Allen
Identifying and Diagnosing Two Distinct Species of Carotid Worms Infecting Wild Cervids in Wyoming, USA	Samantha Allen
Exploring *Toxoplasma gondii* prevalence and impact on survival and fawn quality of a popular game species	Kendall Bancroft
Contact Networks of White-tailed Deer and Their Scrapes: Implications for the Spread of CWD	Ian Burke
Epidemiological Features, Genome Characteristics, and Antimicrobial Resistance of *Trueperella pyogenes* Isolated from Farmed White-tailed Deer (*Odocoileus virginianus*) in Florida	Juan Campos-Krauer
Lack of Evidence For Eyeworm and Cecal Worm Driving Quail Condition and Population Dynamics	Maedean Cardenas
A landscape of disease: metapopulation dynamics structure the history of disease exposure in desert bighorn sheep	Sara Carpenter
New Techniques to Optimize Real-Time Quaking Induced Conversion for Chronic Wasting Disease Detection in White-Tailed Deer Feces	Madison Davis
Pathologic, serologic, molecular and preliminary epidemiologic characterization of leptospirosis in southern sea otters (*Enhydra lutris nereis*)	Padraig Duignan
An Overview of Prion Protein Gene Diversity in European wild Cervids	Sonja Ernst
Genetic Diversity Of Sarcoptic Mange Mites In American Black Bears	Raquel Francisco
Portrait of viral communities in deer upper respiratory tracts across the United States	Roderick Gagne
The science behind the scent – An interdisciplinary approach to understanding how chronic wasting disease influences feces from white-tailed deer leading to discrimination of disease status by canines.	Michelle Gibison
What's The Scoop on Vulture Poop: Investigating the Role of Avian Obligate Scavengers in the Spread of Chronic Wasting Disease (CWD) Infectious Prions	Ashlyn Halseth-Ellis
Are white-tailed deer in Pennsylvania dying with or of chronic wasting disease?	Jennifer Høy-Petersen
Evidence of Novel Gastric Helicobacter Species in Stranded Pygmy (*Kogia breviceps*) and Dwarf (*Kogia sima*) Sperm Whales on the East Coast of Florida	Wendy Marks
Development of Passive Viral eDNA Detection Methods for Mule Deerpox Virus	Lillan Maxwell
Sex-Ratio of Dioecious Acanthocephalan Endoparasites in Harbor Seal (*Phoca vitulina*) Hosts	Jasper Nevis
Wild Cats and Wiggly Critters: Parasitic Insights from the Scat of Ocelots (*Leopardus pardalis*) and Bobcats (*Lynx rufus*) of the Southern United States	Tiffany Pope
Mapping the Host Community of Leptospira in the Eastern Pacific Coastal Ecosystsem Using Novel Genomic Approaches	Katie Prager
From Theory to Action: Insights from a Systematic Review of Chronic Wasting Disease Management Strategies	Sarah Robinson
The Influence of Vegetation Structure on the Prevalence and Intensity of Strongyloid Nematodes Infecting Native Rodents in an African Savanna.	Thaleia Roda
Effects of parasite co-infection on disease dynamics of Sin Nombre hantavirus in deer mice (*Peromyscus maniculatus*)	Madeline Rowland

Title	Author
Population stability for Davis Mountain Cottontails (*S. robustus*) post-Rabbit Hemorrhagic Disease Virus 2 (RHDV2) outbreak in western Texas.	Hannah Shapiro
Wildlife disease research in Texas: Trends over the past three decades	Norelia Solis
Parasitism in Quail: What We Know and Should We Be Concerned?	Liza Soliz
A One Health Risk Framework Towards CWD Management in Saskatchewan	Iga Stasiak
Population genomics of white-tailed deer reveals major rivers and highways as potential barriers to chronic wasting disease spread in Kentucky and Tennessee, USA.	Sarah Tomke
Phthalate esters (plasticizers) in dead southern right whales (*Eubalaena australis*) at Península Valdes, Argentina.	Marcela Uhart
Acute multisystemic sarcocystosis due to *Sarcocystis alceslatrans* in a wild elk calf (*Cervus canadensis*) in Washington State, USA	Emmalina Wineland
California’s Chronic Wasting Disease Educational Outreach and Surveillance	Liberty Wood

Poster Session: Case Studies and Regional Surveillance Insights

Thursday, 3 pm. Venue: Salon A

Title	Author
Linking population modeling with a health assessment to determine the impact of an invasive acanthocephalan parasite in an island fox population	O. Alejandro Aleuy
Managing Shared Resources: Using Workshops to Increase Resources for Detecting and Responding to Wildlife Disease Events	Anne-Justice Allen
A retrospective summary of pronghorn (*Antilocapra americana*) morbidity and mortality in Wyoming, USA (2015-2023)	Samantha Allen
Dogs and Cats Infected with Bat Rabies Virus Variants—United States, 2012–2021	Natalie Bauer
20 years of research on SpayVac-equid, a multi-year, single-dose vaccine to control fertility of free-roaming horses	Ursula Bechert
Absence of Antimicrobial Resistance in Elasmobranchs (Elasmobranchii) in a Marine Management Area of the North Pacific Coast of Costa Rica	Gianmarco Bettoni
Collaborative Infectious Disease Notification Networks?	Diana Boon
The Role of Hookworm-Specific IgG and Antimicrobial Peptides on the Survival of South American Fur Seal Pup	Juntian Bu
RATical - Re-envisioning Rat-Management	Kaylee Byers
Investigating A Mysterious Necrotizing and Ulcerative Dermatologic Syndrome in Bull Elk (*Cervus Canadensis*)	Taylor Chan
Analysis of Stress Factors in Formosan Macaques: A Comparison Between Shoushan and Other Populations	AiMei Chang
Assessing health and feasibility of releasing confiscated eastern box turtles (*Terrapene carolina carolina*): A quantitative framework for informed conservation decisions	Maris Daleo
A molecular survey of zoonotic pathogens of public health importance in rodents/shrews and their ectoparasites trapped in Puducherry, India	Brenna Eikenbary
Predicting Avian Hotspots of Potential West Nile Virus Outbreaks: A case study in Arizona	Gracie Fischer
Expanding the plague-control toolbox: Edible flea-control baits show promise for plague mitigation	Jason Fly
A summary of investigations of Pasteurella multocida in bighorn sheep respiratory disease	Karen Fox
A One Health Response to the Eagle Gold Heap Leach Failure in the Yukon, Canada	Jane Harms
Retrospective Study of Causes of Mortality of Chelonians Submitted to the Southeastern Cooperative Wildlife Disease Study, 1981-2018	Ellen Haynes
Ecological Patterns of Chigger Mites and Small Mammals in Korea: Implications for Public Health	Kiyoon Kim
A first glimpse into the fungal microbiota on the skin of leatherback sea turtles	Samantha Kuschke
"What is this thing?" How Sample Management Plays a Pivotal Role in Ongoing and Future Research	Casey Maynard
Molt induction Using Levothyroxine in Five Captive Spheniscus Penguins	Ji-Hyung Park
Defining Population Health in Rewilding Projects by Stakeholder Engagement	Stuart Patterson
Identifying One Health Priorities and Collaborations in California using Cognitive Maps of Mental Models	Hannah Shapiro
Susceptibility and transmission potential of ectotherms and house sparrows to Japanese encephalitis virus (JEV)	Audrey Walker

Collaborative Approaches to Addressing Health Risks from Wildlife Trade in Guatemala and the Andes-Amazon-Orinoco region	Chris Walzer
Modelling human-rat interactions: A One Health investigation into the ecosocial determinants of rat-associated risks in urban neighbourhoods	Christine Yanagawa

Dialogue Session: Shared Ground: Community Collaborations in Wildlife Health Monitoring

Monday, 28th July 2025 - 1:30pm, Saanich Room

Chairs: Naima Jutha *(Government of the Northwest Territories, Department of Environment & Climate Change),* Erica Suitor *(University of Calgary)*

This dialogue session explores the power of community-driven and co-developed approaches to wildlife health monitoring, with a focus on northern and Indigenous-led initiatives. Through a series of short “Community Voices” lightning talks and an open discussion, the session highlights diverse experiences from harvesters, outfitters, wildlife officers, and researchers. Together, we will examine ethical considerations, practical challenges, and innovations emerging from collaborative work in the field. Centering community leadership and Indigenous knowledge systems, the session aims to foster deeper understanding and more effective, respectful partnerships in wildlife health research and practice.

This session will be chaired by Naima Jutha, a Wildlife Veterinarian and Chief Veterinary Officer with the Government of the Northwest Territories, and Erica Suitor, a PhD candidate at the University of Calgary, in the Faculty of Veterinary Medicine, under the mentorship of Dr. Susan Kutz.

Naima has a strong focus on community-engaged approaches to wildlife health. Her work in northern Canada, including her graduate work with northern BC guide outfitters and the Tahltan Nation, emphasizes the importance of transdisciplinary networks and bridging Local, Indigenous, and Western knowledge systems to support collaborative, responsive, and sustainable wildlife health surveillance systems. Erica's research is part of a long-standing, community-based wildlife health surveillance program in the Kitikmeot Region of the Canadian Arctic, developed in response to concerns about declining muskox and caribou populations. Rooted in collaboration with Inuit harvesters who collect samples, the program emphasizes respectful partnerships, knowledge sharing, and the co-production of locally relevant research. Erica’s doctoral work focuses on dental health and aging of muskoxen, using mandible analysis to generate insights into population demographics and broader indicators of health. As a hunter herself, she brings a grounded, relational understanding to her research and values reciprocal engagement with communities who rely on wildlife for food, culture, and livelihood.

Dialogue Session: Navigating the Policy Ecosystem

Monday, 28th July 2025 - 3:45pm, Saanich Room

Chair: Charlie Booher (Watershed Results)

Many wildlife students still don't have a meaningful opportunity to take a policy class. Those who do have the opportunity typically experience either a recitation of agency structure, enabling legislation, and treaties, or a collection of stories from folks who have worked in the business of wildlife policy for some time. While both are valuable, they lack important context and often leave students wondering what to do with the information that's been presented. This session aims to offer thoughts, guidance, and tools for understanding and influencing formal and informal policy in all its forms (private, public, local, corporate, state/provincial, federal, international). This session will utilize a combination of the speaker's own experiences in natural resource policy and an integration of current attendee research to provide attendees applicable skills for the practice of wildlife policy. Much like the scientific discussions biologists are used to, this session will introduce a systems view of policy in which participants can see the position they occupy now and the positions they can navigate toward or away from in their careers, and what options they'll be facing in each position.

The chair of this session, Charlie Booher is a Consultant at Watershed Results who specializes in natural resource conflict resolution. He has the great privilege of representing some of this country's oldest, largest, and most generous conservation organizations in Helena, MT and in Washington, DC. Charlie is an Associate Wildlife Biologist © and a Professional Member of the Boone and Crockett Club. Outside of the office, you can find him hiking in the mountains of Western Montana and re-learning how to hunt and fish in the Northern Rockies.

Dialogue Session: Future-Ready Wildlife Health: Building Resilience, Driving Change

Thursday, 31st July 2025 - 10:45am, Saanich Room

Chair: Julie Ellis *(Wildlife Futures Program, University of Pennsylvania)*

How do we build a thriving future for wildlife in a rapidly changing world?

This panel brings together a senior leader and an early-career innovator to explore the big questions and knowledge needs shaping the future of wildlife health. Through short talks and a dynamic discussion, panelists will share candid insights on driving meaningful change, navigating career challenges, and sustaining resilience and optimism. Designed to inspire early career professionals, this session offers practical advice and fresh ideas for building a future where wildlife and people can flourish.

Speakers:

Chris Cleveland and Chris Johnson

Dialogue Session: WHIN: Connecting the Global Community at the frontline of Wildlife Health Surveillance

Thursday, 31st July 2025 - 1:30pm, Saanich Room

Chairs: Sarah H Olson *(Wildlife Conservation Society)*, Mathieu Pruvot *(University of Calgary, Faculty of Veterinary Medicine)*

The Wildlife Health Intelligence Network (WHIN) a community of practice aiming to address the global gaps in wildlife health surveillance implementation will be introduced. Our model relies on the contribution of experts and practitioners like you, and we want to hear from you. Through interactive surveys, small group and plenary discussions, we hope to consult with the WDA community on interests, priorities, and directions for WHIN and its task forces, and identify what contribution you may be able to make to WHIN. We will also briefly introduce three additional opportunities to immediately contribute to this initiative in ways that advance resource sharing for capacity building, recognition of the value of wildlife health information, and management of wildlife health data.

Dialogue Session: Using Wildlife Health Research in Agency Decision Making

Thursday, 31st July 2025- 3:45pm, Saanich Room

Chair: Nancy Wilkin

This session will explore the information needs of wildlife health decisions makers and how they use evidence to make decisions. After brief introductory comments from the panelists, attendees will be encouraged to share experiences in how to move evidence into action and seek advice from the panelists and peers.

This session will be chaired by Nancy L. Wilkin, a retired senior public servant who served as Assistant Deputy Minister in British Columbia's Ministry of Environment and as Director of Sustainability at Royal Roads University. Over a 30-year career, she held leadership roles at all levels of government, including Chief Treaty Negotiator for the Province of BC, and built strong partnerships with First Nations and environmental stakeholders. She continues to volunteer on boards such as Ducks Unlimited Canada and the Galiano Conservancy Association, and currently co-chairs the Minister's Wildlife Advisory Council alongside Chief Harry Nyce. Nancy lives in Victoria and on Galiano Island with her husband and is a proud mother and grandmother.

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WildAlert 2.0: Advancing Wildlife Disease Surveillance with AI-Driven Anomaly Detection

Monday, 28th July - 10:45: Avian Influenza (Salon BC) - Oral

Pranav Pandit [1], ***Devin Dombrowski*** [2], ***Rachel Avilla*** [2], ***Soumya Ranjan*** [3], ***Terra Kelly*** [4]

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Participatory wildlife health surveillance programs enhance early disease detection and outbreak prevention. However, robust, scalable, and adaptable algorithms are necessary to forecast and detect disease events across diverse wildlife species and disease systems. We present WildAlert 2.0, a wildlife health surveillance system active in California, Florida, and Arizona. WildAlert leverages advanced large language models and anomaly detection algorithms to detect wildlife morbidity and mortality events in real time using pre-diagnostic Wildlife Rehabilitation Medical Database (WRMD) data.

NLP models (BERT) in WildAlert demonstrated excellent 85-97% accuracy in tagging multiple clinical classifications and circumstances of admission in rescued wildlife. The anomaly detection models (isolation forest and autoencoder regression) outperformed the currently deployed moving averages WildAlert model by better accounting for seasonality, significantly reducing false positives. Specifically, the isolation forest algorithm excelled at detecting rare events and both algorithms showed moderate agreement across different surveillance targets.

WildAlert 2.0 effectively detected morbidity and mortality events that after agency investigations were determined to be due to highly pathogenic avian influenza in waterfowl, harmful algal bloom toxicities, and extreme weather events in marine birds, West Nile virus outbreaks in raptors, Canine Distemper virus outbreaks in raccoons, and cold stress events in sea turtles, showcasing its ability to detect anomalies associated with both known and emerging threats.

WildAlert's success in early detection of unusual health events has informed monitoring efforts, public education, and outreach, highlighting its potential for broader geographic application. Integrating NLP and time-series forecasting models provides a cost-effective, efficient, and scalable solution for wildlife health surveillance, benefiting wildlife agencies, public health experts, and rehabilitators.

HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS (H5N1, CLADE 2.3.4.4b) OUTBREAK IN BIRDS OF PREY FROM QUEBEC, CANADA

Monday, 28th July - 11:00: Avian Influenza (Salon BC) - Oral

Chloé Stefanopoulos [1] ***, Stéphane Lair*** [1] ***, Guy Fitzgérald*** [2] ***, Ariane Massé*** [3] ***, Gabrielle Dimitri-Masson*** [4]

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In addition to being associated with significant mortality of waterfowl species, the emergence of a highly pathogenic avian influenza virus (HPAI) H5N1 clade 2.3.4.4b in North America has caused mortality among avian predators and scavengers, including birds of prey. We describe the epidemiology and pathology of the HPAI outbreak in raptors in the province of Quebec, Canada since the emergence of this virus in March 2022. From the 1 052 postmortem reports of Accipitriformes, Falconiformes or Strigiformes reviewed, 88 cases (8.4%) of fatal infections by HPAI-H5N1 were documented (CWHC-database). The annual prevalence of infection in the sample examined was the highest during the first year (17.9%) and decreased to 3.3% and 1.6% the second and third years respectively. Turkey vultures, bald eagles, rough-legged hawks, red-tailed hawks and peregrine falcons were the most frequently represented species, accounting respectively for 34.5%, 23.0%, 11.5%, 10.3% and 5.7% of the cases of infection documented. This species distribution supports the hypothesis that scavenging feeding strategy and predation on waterfowl are risk factors for this infection. The most frequently documented lesion associated with this viral infection was fibrinonecrotic splenitis (present in 84.5% of the cases examined), followed by encephalitis (53.7%), fibrinonecrotic hepatitis (47.2%), fibrinonecrotic pancreatitis (43.4%), enteritis (24.2%) and necrotizing myocarditis (23.9%). The decrease of case numbers in the two years following the initial mortality spike might be explained by a decrease in the exposure of raptorial birds to this virus consecutive to a decrease in the number of symptomatic infections in waterfowl.

Long-term temporal dynamics of influenza A virus antibodies in black vultures (Coragyps atratus) after an H5N1 highly pathogenic influenza A virus outbreak

Monday, 28th July - 11:15: Avian Influenza (Salon BC) - Oral

Tessa Bissett [1], ***Kyle VanWhy*** [2], ***David Stallknecht*** [3], ***Rebecca Poulson*** [3], ***Andrew Di Salvo*** [4], ***Lisa Williams*** [4], ***Erica Miller*** [5], ***Kevin Niedringhaus*** [5], ***Justin Brown*** [6]

1. *Penn State University,* ***2.*** *USDA APHIS,* ***3.*** *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***4.*** *Pennsylvania Game Commission,* ***5.*** *Wildlife Futures Program, University of Pennsylvania,* ***6.*** *Department of Veterinary and Biomedical Sciences, Penn State University*

Historically influenza A virus (IAV) exposure in black vultures (*Coragyps atratus*) was rare. However, in 2021, H5N1 highly pathogenic influenza A virus (HPIAV) clade 2.3.4.4b was detected in Canada and subsequently spread throughout North America, causing significant mortality in wild birds. The emergence of H5N1 HPIAV has changed the significance of IAV for raptors, but the long-term impacts of this disease are poorly understood. We characterized the temporal IAV antibody dynamics in black vultures associated with an outbreak of H5N1 HPIAV. In 2022, over 550 black vulture mortalities were reported in Pennsylvania in eleven southeastern Pennsylvania counties. Serum was collected from outwardly healthy black vultures in Southeastern Pennsylvania during 2016 (pre-outbreak; Lancaster County; n=51), 2023 (< 1-year post-outbreak; Dauphin County; n=93), and 2024 (1- to 2-years post-outbreak, Dauphin County; n=152). Samples were tested for antibodies to IAV nucleoprotein by ELISA, and seropositive samples were subsequently tested for antibodies to H5 and N1 using virus neutralization and enzyme-linked lectin assay, respectively. None of the black vultures sampled in 2016 had antibodies to IAV. The seroprevalence to IAV <1-year post-outbreak was 48.3% (45/93) and most seropositive samples were antibody-positive for H5 and N1. At 1- to 2-years post-outbreak, the seroprevalence was 17.8% and most samples remained antibody-positive for H5 and N1. The results of this study confirm long-term persistence of antibodies to H5N1 HPIAV in black vulture post-outbreak. Further research is needed to define the immunological significance of these data, both for individual animals and populations.

Utilizing serology to better understand trajectory and impacts of highly pathogenic avian influenza in wildlife

Monday, 28th July - 11:30: Avian Influenza (Salon BC) - Oral

Rebecca Poulson [1], ***Deborah Carter*** [1], ***Zijing Cao*** [1], ***Paige Palomaki*** [2], ***Victoria Hall*** [3], ***Jacqueline Nolting*** [4], ***David Stallknecht*** [1]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *The Raptor Center, University of Minnesota,* ***3.*** *One Health Institute, University of California, Davis,* ***4.*** *The Ohio State University*

Since introduction into North America in 2021, highly pathogenic (HP) H5N1 avian influenza A (IAV) has spread rapidly in wildlife, with infection confirmed in over 200 avian species, and mammals, across North and South America; it also continues to impact domestic animal health. An expanding list of impacted species highlights the need to better understand the potential seasonal, spatial, and species-related risks of HP H5N1 in wildlife. Actual rates of exposure and associated impacts are hard to estimate from observational and virologic data alone. In collaboration with state, federal, and academic partners, we have been testing pro- and retrospectively collected serum from a wide-range of wildlife species. Sera are screened by IAV bELISA, and then subsequently tested by virus neutralization and hemagglutination inhibition to detect antibodies to H5 (2.3.4.4b and North American origin low pathogenicity (LP)), and N1 enzyme-linked lectin assay. Thus far, in waterfowl, the observed patterns as related to prevalence of HP H5N1 and resultant immunologic responses, are similar to the seasonal dynamics of LP IAV which are driven by population immunity. In other species for which LP IAV trends have not been well-defined (ex. bald eagles, black vultures, mammals), serologic evidence supports potential resiliency in some populations after initial exposure to HP H5N1. Continued virologic monitoring of wildlife species, inclusive of both LP and HP IAV, is key to helping define viral prevalence and diversity; however, the context that serologic monitoring provides is critical to understanding the potential trajectory of HP H5N1 across North America.

Highly Pathogenic Avian Influenza (HPAI) in Canadian Species at Risk

Monday, 28th July - 11:45: Avian Influenza (Salon BC) - Oral

Damien Joly [1]***, Jolene A. Giacinti*** [2]***, Dayna Goldsmith*** [3]***, Nathan Hentze*** [4]***, Claire Jardine*** [5]***, Stéphane Lair*** [6]***, Ariane Massé*** [7]***, Samira Mubareka*** [8]***, Julie Paré*** [9]***, Cynthia Pekarik*** [10]***, Neil Pople*** [11]***, Margo Pybus*** [12]***, Brian Stevens*** [3]***, Trevor Thompson*** [10]***, Maeve Winchester*** [13]

1. *Canadian Wildlife Health Cooperative | Réseau Canadien pour la Santé de la Faune,* ***2.*** *Ecotoxicology and Wildlife Health Division, Science and Technology Branch, Environment and Climate Change Canada, Government of Canada, Ottawa, Ontario, Canada,* ***3.*** *Canadian Wildlife Health Cooperative,* ***4.*** *B.C. Conservation Data Centre / Ministry of Water, Land and Resource Stewardship,* ***5.*** *Department of Pathobiology, University of Guelph,* ***6.*** *Canadian Wildlife Health Cooperative / Centre québécois sur la santé des animaux sauvages, Université de Montréal, Faculté de médecine vétérinaire, 3200 rue Sicotte, St-Hyacinthe, Québec J2S 2M2, Canada,* ***7.*** *Direction générale de la gestion de la faune, Ministère de l'Environnement, de la Lutte contre les changements climatiques, de la Faune et des Parcs, Québec, Québec G1S 4X4, Canada,* ***8.*** *Sunnybrook Research Institute,* ***9.*** *Science Branch, Canadian Food Inspection Agency,* ***10.*** *Wildlife Management and Regulatory Affairs Division, Canadian Wildlife Service, Environment and Climate Change Canada, Government of Canada,* ***11.*** *Veterinary Diagnostic Services, Manitoba Agriculture,* ***12.*** *Fish and Wildlife Stewardship, Alberta Environment and Protected Areas,* ***13.*** *B.C. Ministry of Water, Land and Resource Stewardship*

Since its emergence in North America in late 2021, highly pathogenic avian influenza (HPAI) H5N* virus clade 2.3.4.4b has been associated with extensive mortality in wild birds and mammals, including species of conservation concern. We systematically assessed detections of HPAI in Canadian avian and mammalian species at risk by comparing surveillance data with provincial and territorial conservation status ranks. Between November 2021 and November 2024, HPAI was detected in 37 avian species at risk across 10 provinces, with no detections in the three territories and no mammalian species at risk. Affected taxa spanned 10 avian orders, including Accipitriformes, Anseriformes, and Charadriiformes. Three species detected with HPAI - Barn Owl (Tyto alba), Horned Grebe (Podiceps auritus), and Western Grebe (Aechmophorus occidentalis) - were also assessed as at risk nationally by COSEWIC. These findings highlight HPAI as an additional conservation threat for species already facing population pressures. However, limitations in surveillance, including biases in species detection, require further research to assess the full impact of HPAI on at-risk species in Canada.

Bridging Science and Community: A Collaborative Approach to Baird's Tapir Health Investigation in Costa Rica

Monday, 28th July - 10:45: Collective Action and Collaboration (Saanich Room) - Oral

Jorge Rojas Jimenez [1]**, *Sonia M. Hernandez*** [2]**, *Vilmar Villalobos*** [3]**, *Donald Varela-Soto*** [4]**, *Michael Yabsley*** [2]**,**
Elías Barquero-Calvo [5]**, *Roberto Olivares*** [6]**, *Emmanuel Rojas*** [7]

1. *Warnell School of Forestry & Natural Resources, University of Georgia; Tapir Vet Project, Costa Rica,* ***2.*** *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***3.*** *National System of Conservation Areas (SINAC), Costa Rica,* ***4.*** *Tapir Valley Nature Reserve, Bijagua, Costa Rica,* ***5.*** *Programa de Investigación en Enfermedades Tropicales (PIET), Escuela de Medicina Veterinaria, Universidad Nacional de Costa Rica,* ***6.*** *College of Veterinary Medicine, UC Davis,* ***7.*** *Tirimbina Biological Reserve*

Effective wildlife health programs require collaboration across disciplines, institutions, and communities. In response to emerging health threats and missed opportunities for tapir health investigations due to limited resources, we established the Tapir Health Program in Costa Rica. This initiative integrates disease surveillance with community engagement to monitor Baird's tapirs (*Tapirus bairdii*) in human-modified landscapes. Through partnerships with local stakeholders, conservation organizations, and research institutions, we have developed a community-inclusive framework for disease surveillance in tapirs.

The program has established effective collaborations among scientists, officials, park rangers, and local landowners, ensuring that research findings inform decision-making at multiple levels. Case studies from the Tenorio-Miravalles Biological Corridor (TMBC) demonstrate how local engagement has strengthened disease surveillance, improved human-wildlife coexistence strategies, and mobilized conservation action.

Recent findings highlight the importance of a systematic health program: A necropsy performed revealed an *Actinomyces israelii* infection, a bacterial pathogen relevant to both wildlife and human health, raising concerns about potential zoonotic transmission. Additionally, *Rickettsia belli*, a tick-borne pathogen, was isolated from tapir-associated ticks, underscoring the role of tapirs as a potential reservoir in disease ecology. These findings highlight the critical need for continued pathogen surveillance and interdisciplinary collaboration.

Beyond disease detection, our approach prioritizes mutual respect, active listening, and assertive communication to bridge gaps between scientific research and local ecological knowledge. By incorporating storytelling, participatory monitoring, and citizen science, we facilitate the empowerement of communities to co-create solutions for tapir conservation and health research to achieve human-tapir coexistence.

By Our Powers Combined: Recommendations for Collaboration between Wildlife Rehabilitators and Wildlife Health Researchers

Monday, 28th July - 11:00: Collective Action and Collaboration (Saanich Room) - Oral

Stephanie Herman [1]

1. *International Wildlife Rehabilitation Council*

Wildlife Rehabilitation facilities represent a vastly underutilized resource for wildlife health research and monitoring. Wildlife rehabilitators stand at the intersection between public health and wildlife health; with access to hundreds of thousands of living and dead wild animals annually around the world, as well as a direct line of communication with invested stakeholders in their communities through volunteer programs, wildlife education and conservation efforts, and compelling media stories. Despite a growing recognition by both wildlife rehabilitators and researchers that there is a great need for partnership and a wealth of data to be mined, the road to collaboration can sometimes be unnecessarily bumpy. In this talk, we will explore barriers that can arise during the collaboration process, and suggest resources and recommendations for avoiding many common pitfalls.

A multi-species determinants of health approach for nanuk (polar bear) co-management

Monday, 28th July - 11:15: Collective Action and Collaboration (Saanich Room) - Oral

Andrea Hanke [1], ***David Borish*** [1], ***Andrea Hicks*** [2], ***Agata Durkalec*** [2], ***Kaitlin Breton-Honeyman*** [2], ***Jamie Snook*** [1]

***1.** Cloudberry Connections, **2.** Polynya Consulting Group*

What is the issue?

Inuit and nanuk (polar bears; *Ursus maritimus*) coexist in a delicate balance, influencing one another and sharing the landscape with other species. As such, documented Inuit Knowledge is amongst the main data sources that inform conservation decisions for nanuk.

The Davis Strait nanuk subpopulation spans across Nunavut, Nunavik (Quebec), Nunatsiavut (Labrador), and Greenland. The documented Inuit Knowledge for this subpopulation is largely disconnected due to challenges in sharing and exchanging information across political borders.

How do you want to better understand the issue?

We reviewed and synthesized documented Inuit Knowledge of the Davis Strait nanuk population through a multi-species determinants of health lens, with the aim to support meaningful conservation discussions and decisions. The Inuit determinants of health focused on proximal, intermediate, and distal social determinants, and the nanuk determinants of health were drawn from Wittrock et al.'s (2019) wildlife health model.

What did you find?

By amplifying Inuit voices and wisdom, we highlight the vital connection between cultural heritage and nanuk health. We found that Inuit and nanuk determinants of health were highly interconnected, where each individual health factor was connected to the status of the other species.

How could your findings be used?

Conservation decisions for the Davis Strait subpopulation should consider the contrasting impacts to Inuit health. We emphasize that protecting nanuk is essential for both ecological wellbeing and the cultural vitality of Inuit communities; and vice versa, thriving Inuit communities support the wellbeing of nanuk.

GPS mapping and community-based interviewing for One Health Surveillance in Kasongoire forest region, Uganda

Monday, 28th July - 11:30: Collective Action and Collaboration (Saanich Room) - Oral

Victoria Priester [1]***, Julian Bement*** [2]***, Michael Jurua*** [3]***, Robin Radcliffe*** [4]***, Peter Apell*** [3]

1. *College of Veterinary Medicine, Cornell University,* ***2.*** *College of Agriculture and Life Sciences, Cornell University,* ***3.*** *Jane Goodall Institute,* ***4.*** *Department of Clinical Sciences, College of Veterinary Medicine, Cornell University*

Habitat fragmentation in the Kasongoire forest region of Uganda has resulted in chimpanzees (*Pan troglodytes*) leaving the forest and entering community gardens in search of food. Simultaneously, people enter the forest for water, medicinal plants and firewood, resulting in human-wildlife conflict and the potential for disease transmission. To further understand the scope of human-wildlife interactions, we visited over 70 households in seven villages bordering Kasongoire forest to ask interview-style questions and capture GPS coordinates. Community members were asked how often someone in their household visits the forest to collect water, how often they see chimpanzees in their daily routine, if they have observed signs of disease in their domestic animals, and if they have seen their domestic animals interact with wildlife. Every household reported that they, or someone in their household, visits the forest multiple times a day to collect water. Of the households with domestic animals, 65% had observed interactions between these animals and wildlife; 30% of people interviewed see chimps in their homestead at least once a week. In two villages, 40% of households reported seeing chimpanzees daily. By integrating villager responses and GPS coordinates, our goal is to create geographic heat maps of all the villages bordering Kasongoire that show where chimpanzees are most frequently seen and where wildlife and domestic animals interact. This data will be used to localize where disease surveillance is needed and to prioritize where One Health interventions can be implemented if an outbreak occurs in humans, wildlife or domestic species.

Investigating Phaeohyphomycosis in Salmonids of Northern Quebec, Canada: Past, Present, and Future Perspectives

Monday, 28th July - 10:45: Mechanisms of Harm (Oak Bay Room) - Oral

Benjamin Jakobek [1]***, Stéphane Lair*** [1]***, Géraldine Gouin*** [2]***, James Scott*** [3]***, Marie-Lou Gauthier*** [4]***, Patrick Vincent*** [5]

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Phaeohyphomycosis is an emerging and poorly understood fungal disease affecting a range of hosts, including salmonids. The impact of this condition, caused by pigmented hyphal fungi, on fish conservation and its zoonotic potential are unknown. Salmonids are an important food source for many Inuit and First Nations communities, making disease surveillance particularly relevant for food security and ecosystem health. This study investigates phaeohyphomycosis in Northern Canadian (primarily Nunavik) salmonids through retrospective case analysis (1995–2020) and prospective surveillance (2021–2023). A review of archived pathology cases from the CWHC database revealed cases of phaeohyphomycosis in Atlantic salmon (*Salmo salar*), Arctic cisco (*Coregonus autumnalis*), brook trout (*Salvelinus fontinalis*), and lake whitefish (*Coregonus clupeaformis*). Prospective surveillance led to detection of phaeohyphomycosis in 2.6% of the 156 Atlantic salmon examined. Gross and histologic examinations identified darkly pigmented cutaneous, muscular and visceral (mainly renal) lesions, with pigmented fungal hyphae associated with necrosis and histiocytic inflammation. Despite limited success in fungal culture and molecular identification, fungal isolates included species from the genus *Aureobasidium* spp., *Cladosporium* spp., *Ochroconis* spp., and *Alternaria* spp. This study represents the first report of phaeohyphomycosis in Arctic cisco and lake whitefish, expanding the known host range in Northern Canada. These findings emphasize the need for continued surveillance, improved diagnostics, and research into environmental drivers of disease emergence in Northern ecosystems, especially with climatic changes. Strengthening collaboration between scientific research and Indigenous traditional knowledge will be key to addressing future challenges in Northern salmonid health and conservation in a changing ecozone.

Impact of human contact on critically endangered mountain gorilla health

Monday, 28th July - 11:00: Mechanisms of Harm (Oak Bay Room) - Oral

Kathryn Harper [1], ***Natalie Payne*** [1], ***Leigh Combrink*** [1], ***Melanie Culver*** [2], ***Jennifer Verdolin*** [1]

1. *University of Arizona,* ***2.*** *USGS / University of Arizona*

Mountain gorillas (Gorilla berengei berengei) are the only non-human great apes with a growing population, yet they remain critically endangered. Understanding the relationship between their diet, microbiome, and parasite prevalence is vital for their conservation, particularly in light of varying degrees of human contact. This study, conducted in Bwindi Impenetrable National Forest, explores the impact of human proximity on gorilla health by analyzing fecal samples from five gorilla troops with different levels of human interaction. Combining diet, host genetics, microbiome composition, and parasite prevalence data, we aim to examine how human proximity influences gorilla health. Specifically, we ask (1) How does proximity to humans influence the diet of gorillas? and (2) Are differences in microbiome and parasite communities associated with human proximity? Our findings indicate differences in microbiomes between gorilla groups, highlighting the complex interplay between diet, microbiome, and parasites in mountain gorillas, and emphasizing the potential role of human proximity in shaping these factors. Understanding these dynamics is crucial for the conservation of mountain gorillas and other endangered great apes, as it informs management strategies aimed at mitigating anthropogenic impacts on their health and long-term survival.

Prevalence, Diversity, and Intensity of Trichinella spp. in Wildlife from Northern Canada and Alaska: New Geographic and Host Records for Trichinella chanchalensis

Monday, 28th July - 11:15: Mechanisms of Harm (Oak Bay Room) - Oral

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

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

A new species of the zoonotic nematode *Trichinella—T. chanchalensis* (T13)—was recently discovered in wolverines and an American marten in the Northwest Territories (NWT) and in wolverines from the Yukon, Canada. It is not currently known if T13 can infect wildlife species other than mustelids. This study aimed to further investigate the ecology of T13 to determine geographic and host ranges. We worked with northern partners to sample terrestrial carnivores and omnivores from Alaska, USA, and the three northern Canadian territories. The double separatory funnel method was used to recover larvae from tissues and all recovered larvae were genotyped using deep amplicon next-generation sequencing on the Illumina MiSeq. Animals positive for *Trichinella* spp were found in the Yukon (158/213 (74%)), Alaska (53/157 (33.8%)), the NWT (53/157 (33.8%)), and from Nunavut (41/50 (82%)). Co-infections with *Trichinella nativa* and *Trichinella* T6 (169/281, 60%) were most common, but the number of co-infections ranged significantly from 33% (Alaska) to 87% (NWT). T13 was detected in 41/158 (25.9%) animals in the Yukon, 2/31 (6.5%) in NWT, 9/41 (22%) in Nunavut, and 1/51 (2%) in Alaska. T13 was predominantly found in mixed infections 50/53 (94.3%) with one or more additional taxa. T13 was found in two lynx (*Lynx canadensis*), two wolves (*Canis lupus*), and one coyote (*Canis latrans*), all of which are new host records for T13. Moreover, T13 was also detected for the first time in Nunavut and Alaska. This study provides new geographic and host records for T13 and also contributes meaningful updates to *Trichinella* prevalence, diversity, and intensity in four geographic regions while using a novel metabarcoding. Research into host-specific differences in prevalence, intensity, and diversity of *Trichinella* spp. is essential to assess the risk for food safety and to support food sovereignty.

The other shoe drops: emergence of Salmonella enterica var Weltevreden in critically endangered Christmas Island Reptiles

Monday, 28th July - 11:30: Mechanisms of Harm (Oak Bay Room) - Oral

Karrie Rose [1]***, Jess Agius*** [2]***, Winkie Fong*** [2]***, Heather Fenton*** [3]***, Jane Hall*** [1]***, Alexia Jankowski*** [4]***, Kristen Shanygina*** [4]***, Brendan Tiernan*** [4]***, Mark Westman*** [5]***, Cheryl Jenkins*** [5]

1. *Australian Registry of Wildlife Health,* ***2.*** *Centre for Infectious Diseases and Microbiology – Public Health, Westmead Hospital AND Sydney Infectious Diseases Institute, Faculty of Medicine & Health, The University of Sydney, Westmead, New South Wales,* ***3.*** *Taronga Conservation Society Australia,* ***4.*** *Christmas Island National Park - Parks Australia,* ***5.*** *Elizabeth Macarthur Agricultural Institute, Biosecurity and Food Safety, Department of Regional New South Wales, Menangle, New South Wales*

Christmas Island (CI), an Australian external territory in the Indian Ocean, is rich in biodiversity, enjoying high levels of endemism of its flora and fauna. Natural vulnerabilities of small island populations and the introduction of invasive vertebrates and microbes have resulted in extinction in the wild of four of five endemic CI lizard species. The critically endangered Lister's gecko (*Lepidodactylus listeri*) now exists only within breeding colonies on CI and at Taronga Zoo.

Acute mortality within the captive breeding colony of Lister's geckos on CI was first observed in November 2021. Affected animals were found dead individually or in small clusters, often near water dishes. Some animals presented alive with emaciation (3) or paralysis (3) and were euthanased. Gross lesions included oral and intestinal erythema, rare cavitating soft tissue lesions, and mottled or nodular hepatic parenchyma. Histological examinations revealed a broad range of lesions, generally characterized by fine, Gram-negative bacilli associated with necrosis and acute to chronic inflammation within the respiratory, gastrointestinal, coelomic, skeletal muscle, reproductive and hepatic tissues. *Salmonella enterica* var *Weltevreden* was identified based on 99% sequence homology of the 16S rRNA gene and ITS regions conducted on ethanol-fixed liver tissues from six affected animals. Sequence data was used to generate a nested *Salmonella* genus and *S.Weltevreden* specific PCR test to confirm infection in a further 15 animals. Disease control includes quarantine and strict biosecurity measures. This finding follows the 2014 emergence of novel *Enterococcus lacertideformus* as a pathogen within the same captive colony of CI reptiles. These organisms have the potential to pose a significant threat to reptile biodiversity as the captive management of these species is critical to survival of this species and others in Australia and worldwide.

This conservation research reflects collaboration across multiple Australian state and commonwealth agencies and the community of Christmas Island.

Causes and Contributors to Bat Mortality: 47 Years of Diagnostic Data at the Southeastern Cooperative Wildlife Disease Study

Monday, 28th July - 11:45: Mechanisms of Harm (Oak Bay Room) - Oral

***Mattison Green* [1], *Kevin Keel* [2], *Heather Fenton* [3], *Justin Brown* [4], *Andrew Allison* [5], *Melanie Kunkel* [6], *Chloe Goodwin* [7], *Kevin Niedringhaus* [8], *Aidan O'Reilly* [1], *Rebecca Radisic* [9], *Mark Ruder* [1], *Xuan Teo* [1], *Nicole Nemeth* [1]**

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Despite their widespread geographic distribution and critical ecological roles such as pollination and insect population control, large scale, holistic, diagnostic analyses of microbats are scarce. Due to their small size, negative stigmas and zoonotic disease concerns, many deceased bats are likely not found or collected, or are solely submitted to public health laboratories for rabies virus testing. Since 1978, the Southeastern Cooperative Wildlife Disease Study at the University of Georgia has received >750 bats for diagnostic evaluation from across the southeastern United States. These records, which include 19 species of bats from 20 states and Puerto Rico, provide information regarding regional causes of morbidity and mortality, and diseases of bats found at the human-wildlife interface. Through evaluation of 47 years of diagnostic data, we determined contributors and causes of mortality, assessed demographic, taxonomic, temporal, habitat, and geographic patterns, and highlighted unusual and interesting cases (including parasitic infections, white-nose syndrome, toxicoses, and anthropogenic impacts). In some areas, traumatic injury from a variety of anthropogenic sources is commonly suspected (including from cat predations), while more recently, heat stress events associated with bat boxes have become more common. This information conveys a deeper understanding of regional, seasonal, and more all-encompassing threats to the health of a diversity of bat species in the southeastern United States. Using these datasets, we identified long-term patterns that highlight the need to reduce anthropogenic impacts on bat populations and can be used to facilitate future collaborations and integrative ways to evaluate bat health and inform conservation management.

Autopsy findings in sea otters found along the British Columbia coast from 2000 to 2024.

Monday, 28th July - 13:30: Aquatic Animal and Marine Health (Salon BC) - Oral

Trent Bollinger [1]***, Michael Pawlik*** [2]***, Paul Cottrell*** [3]***, Kazal Ghosh*** [2]***, Andrew Ross*** [4]***, Linda Nichol*** [5]***, Brendan Cottrell*** [6]***, Michael Grigg*** [7]***, Martin Haulena*** [8]***, Rhea Storlund*** [9]***, Andrew Trites*** [9]***, Stephen Raverty*** [10]

1. *Dept. of Veterinary Pathology, U. of S., Saskatoon, SK.,* ***2.*** *Animal Health Centre, Ministry of Agriculture, Abbotsford, BC,* ***3.*** *Fisheries and Oceans Canada, Fisheries and Aquaculture Management, Vancouver, BC,* ***4.*** *Fisheries and Oceans Canada, Institute of Ocean Sciences, Sidney, BC,* ***5.*** *Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo, BC,* ***6.*** *Department of Geography, McGill University, Montreal, Quebec,* ***7.*** *Laboratory of Parasitic Diseases, National Institute of Health, NIAID, Bethesda, MD,* ***8.*** *Vancouver Aquarium Marine Mammal Rescue Society,* ***9.*** *Marine Mammal Research Unit, The University of British Columbia, Vancouver, BC,* ***10.*** *Animal Health Centre*

Sea otters (*Enhydra lutris*) are a keystone species in near-shore marine environments. They require a high daily intake of food to survive and their effect on prey species impacts food-webs and ecosystems. The best studied is the effect of sea otter predation on sea urchin abundance which helps restore and maintain kelp beds and the associated ecosystems. Once numerous and wide-spread, sea otters were extirpated from the BC coast in the 1800s due to the fur trade; however, between 1969-1972, 89 sea otters from Alaska were re-introduced to the west coast of Vancouver Island, BC. Although this re-introduced population is currently increasing, some populations along the Pacific Coast of North America are not, due to disease, predation and other factors. To evaluate potential health threats to BC sea otters we reviewed the autopsy findings of sea otter carcasses submitted to the Animal Health Centre, Abbotsford, BC from 2000 to 2024. The number of submissions were relatively low due to the remoteness of these populations and frequently autolysis precluded detailed autopsy investigations. Slightly over 50 sea otter submissions were evaluated and using more recent case definitions and analytical testing techniques we were able classify the cause of death as: 30% septicemia/bacteremia; 18% trauma; 10% cardiovascular disease, with domoic acid toxicity as the presumptive cause; and 12% neuromuscular disease, primarily the result of protozoan infections. The remainder were classified as unknown. Although sample sizes are too low for direct comparisons to other populations of sea otters along the Pacific Coast, a few findings were noteworthy and warrant further study. First, the impact of domoic acid from diatom blooms appears to be greater than suspected, and second, mortality due to protozoan parasites, which are thought to cycle primarily in terrestrial systems, may be significant and the risk factors for exposure are unclear.

Emergence of virulent toxoplasmosis in southern sea otters (Enhydra lutris nereis) due to the COUG strain of Toxoplasma gondii

Monday, 28th July - 13:45: Aquatic Animal and Marine Health (Salon BC) - Oral

Devinn Sinnott [1]***, Melissa Miller*** [2]***, David Arranz-Solis*** [3]***, Francesca Batac*** [2]***, Katie Greenwald*** [2]***, Colleen Young*** [2]***, Angelina Reed*** [2]***, Michael Harris*** [2]***, Heather Harris*** [4]***, Mary Gomes*** [2]***, Karen Shapiro*** [1]

1. *University of California Davis,* ***2.*** *Marine Wildlife Veterinary Care and Research Center, California Department of Fish and Wildlife, Santa Cruz, CA, USA,* ***3.*** *SALUVET, Animal Health Department, Complutense University of Madrid, Spain,* ***4.*** *The Marine Mammal Center*

The COUG strain of *Toxoplasma gondii* was first reported in southern sea otters (*Enhydra lutris nereis*) in 2023, with affected animals exhibiting severe protozoal-associated steatitis, a lesion pattern not previously linked to toxoplasmosis in this species. Multilocus sequence typing confirmed infection with the COUG genotype, first isolated in the 1990s from mountain lions on Vancouver Island, British Columbia, Canada, after a human toxoplasmosis outbreak linked to contaminated drinking water. Historically, *T. gondii* infections in sea otters have been associated with Type II and Type X strains, with deaths primarily attributed to meningoencephalitis in otters infected with Type X or its variants. This study describes additional COUG infections in sea otters and explores the utility of serotyping for premortem strain differentiation. Since the initial cases were recognized, several more otters have been identified with COUG infections. Most presented with severe steatitis, though one died from meningoencephalitis without steatitis. Given the high prevalence of *T. gondii* exposure in sea otters, premortem identification of virulent strains responsible for clinical disease could inform diagnosis and treatment in rehabilitation centers. An ELISA serotyping test applied to sera from infected otters revealed distinct peptide reactivity profiles for COUG, Type X, and Type II strains, supporting its potential as a diagnostic tool. Over three decades of sea otter health surveillance has shown no prior evidence of COUG infections or similar lesion patterns, suggesting its recent introduction to California's nearshore marine environment as a new threat to sea otters, with implications for marine ecosystem health and zoonotic risk.

Identifying a causative agent for sea star wasting disease

Monday, 28th July - 14:00: Aquatic Animal and Marine Health (Salon BC) - Oral

Melanie Prentice [1], ***Grace Crandall*** [2], ***Amy M. Chan*** [3], ***Katherine M. Davis*** [4], ***Paul Hershberger*** [5], ***Jan F. Finke*** [1], ***Jason Hodin*** [6], ***Andrew McCracken*** [7], ***Colleen T. E. Kellogg*** [8], ***Rute Carvalho*** [8], ***Carolyn Prentice*** [8], ***Kevin X. Zhong*** [3], ***Drew Harvell*** [9], ***Curtis A. Suttle*** [3], ***Alyssa-Lois Gehman*** [8]

1. *The Hakai Institute & The University of British Columbia,* ***2.*** *University of Washington,* ***3.*** *The University of British Columbia,* ***4.*** *Washington Department of Fish and Wildlife,* ***5.*** *U.S. Geological Survey,* ***6.*** *University of Washington, Friday Harbor Laboratories,* ***7.*** *University of Vermont,* ***8.*** *The Hakai Institute,* ***9.*** *University of Washington, Friday Harbor Laboratories & Cornell University*

For over a decade, the marine epizootic known as sea star wasting disease (SSWD) has proliferated along the Pacific Coast of North America, affecting more than two dozen asteroid species. Among them, the sunflower sea star (*Pycnopodia helianthoides*) is most susceptible, with range-wide losses averaging 94%, initiating a trophic cascade involving un-checked urchin population growth, and the widespread loss of kelp forests. Despite much effort, the causative agent for SSWD has remained elusive, yet its identification remains imperative for the recovery of both sunflower sea star populations and kelp forest ecosystems. In this talk we present the results of controlled exposure experiments on *P. helianthoides* and genetic datasets generated from samples therein to identify candidates for the causative agent of SSWD. Exposure experiments using tissue homogenate and coelomic fluid inoculum prepared from wasting sunflower sea stars caused disease in 95% of exposed individuals, with no mortality observed in controls injected with heat-killed versions of the inoculum. Further, inoculum preparations that involved filtration through 0.22µm, 0.45µm or 0.8µm membranes did not cause disease, suggesting that the causative agent of SSWD is not viral. Metatranscriptomic and 16S rRNA gene amplicon sequencing is now being used to identify candidate causative agents in samples from controlled exposure experiments and field outbreaks of SSWD. Identification of a causative agent will facilitate continued research on SSWD and support recovery efforts of imperiled *P. helianthoides* populations by enabling pathogen monitoring across affected species and environments.

Determining the best predictors of body condition in leatherback turtles (Dermochelys coriacea)

Monday, 28th July - 14:15: Aquatic Animal and Marine Health (Salon BC) - Oral

Heather Harris [1], ***Justin Perrault*** [2], ***Scott Benson*** [3], ***George Shillinger*** [4]

1. Upwell/ The Marine Mammal Center, 2. Loggerhead Marinelife Center, 3. NOAA Southwest Fisheries Science Center, 4. Upwell

As facultative endotherms, leatherback turtles (*Dermochelys coriacea*) develop thick peripheral fat layers similar to the blubber of marine mammals. This adaptation allows them to forage in cold temperate waters and sustains them during long-distance migrations to nesting beaches. They undergo substantial cyclical changes in body condition, characterized by the relative prominence of their dorsal carapacial ridges and appendicular skeletal features. Previous research validated ultrasound as a non-invasive diagnostic tool for measuring subcutaneous fat layers in leatherbacks. Our study compared ultrasound fat depth measurements with morphometric and clinical data to determine the best predictors of body condition for the first time in a sea turtle species. To evaluate turtles across a broad array of physiological states, we sampled foraging, nesting, bycaught, and dead stranded leatherbacks from the Western Pacific and Atlantic populations. We developed a species-specific body condition scoring system to standardize subjective assessments of individuals. We compiled morphometric measurements (mass, straight and curved carapace length and width, neck circumference), calculated body condition index (mass/straight carapace length^3 x 10,000) and evaluated blood health parameters (complete blood count, plasma chemistries, lipid panels, beta-hydroxybutyrate). Preliminary analyses of data from nesting leatherbacks indicate that ultrasound fat depth is positively correlated with body condition index and beta-hydroxybutyrate levels. We will use a quantitative approach to evaluate the best predictors of body condition across the broader dataset and provide an objective framework for evaluating individuals and comparing them across populations and life stages. Body condition can serve as a valuable indicator of individual health status, suggest energetic thresholds that may predict the timing of remigration, provide context for interpretation of fluctuating lipophilic contaminant levels, and highlight periods of resource limitation, disease, and oceanographic change that impact this endangered species at a population level.

Is Tularemia an emerging marine zoonosis in Washington marine mammals?

Monday, 28th July - 14:30: Aquatic Animal and Marine Health (Salon BC) - Oral

***Dyanna Lambourn* [1], *Erin D'Agnese* [2], *Allan Pessier* [3], *Cathy King* [4], *EJ Verble* [4], *Beth Lipton* [5], *Hanna Oltean* [5], *Kevin Snekvik* [3], *Becca Wolking* [3], *Christina Haake* [3], *Katherine Haman* [1], *Casey Clark* [1]**

1. *Washington Department of Fish and Wildlife,* **2.** *Wild EcoHealth,* **3.** *Washington Animal Disease Diagnostic Laboratory, College of Veterinary Medicine, Washington State University,* **4.** *World Vets,* **5.** *Washington Department of Health*

Tularemia, caused by the facultative intracellular gram-negative bacteria *Francisella tularensis*, has occurred in at least two species of marine mammals in Washington state beginning with a case in 2023. The first case was identified after a necropsy technician developed an ulcerative lesion due to an *F. tularensis* infection at the site of a minor laceration that occurred during the necropsy of a harbor seal (*Phoca vitulina richardii*). The harbor seal was subsequently confirmed to be positive for *F. tualernsis* via PCR. In early 2025, a Northern Sea Otter (*Enhydra lutris kenyoni*) was also confirmed positive for *F. tularensis* upon submission for pathology, which coincided with the two researchers who performed the necropsy becoming ill. Lesions in the harbor seal included necrotizing lymphadenitis and evidence of septicemia whereas the sea otter had a necrotizing bronchopneumonia without lymphadenitis. These necropsy findings overlap significantly in appearance with other infectious diseases commonly observed in stranded marine mammals (e.g. disseminated mucormycosis). Given the potential for exposure to communities and researchers working with marine mammals, understanding the pathological signs and prevalence of *F. tularensis infection* in Washington State is critically important. To this end, our collaborative One Health team is conducting a retrospective analysis of archived necropsy samples from multiple species of marine mammals. We aim to conduct a seroprevalence survey using retrospective harbor seal serum from decades of captures and necropsies. We will present the pathological findings and any strain-level genetic information on the bacterium isolated from the confirmed cases, as well as any preliminary results related to the retrospective analysis of necropsied marine mammals and/or any serological testing. Our results will create a better understanding of the prevalence of this disease in Washington's marine mammals and the risks faced by people who work with them.

Contaminants of emerging concern and antimicrobial resistance in Great Lakes fish: implications for One Health

Monday, 28th July - 14:45: Aquatic Animal and Marine Health (Salon BC) - Oral

BRIDGET BAKER [1], ***Emma VanderMeulen*** [1], ***May Thongthum*** [1], ***Mallory Llewellyn*** [1], ***Alvin Wu*** [1], ***Joanne Wang*** [1], ***Aidan Keenan*** [1], ***Carol Miller*** [2], ***Benjamin Anderson*** [1], ***Tracie Baker*** [1]

1. *University of Florida*, **2.** *Wayne State University*

Contaminants of emerging concern (CECs), including PFAS and pharmaceutical and personal care products (PPCPs), in aquatic ecosystems are a significant threat to One Health. Our previous studies showed bioaccumulation and biomagnification of PFAS within the aquatic food web and environmental persistence of PPCPs, including antibiotics (e.g. sulmethoxazole), in the Lake Huron to Erie corridor (HEC) within the Great Lakes. The HEC is an international shipping route and border with Canada, includes the only International Wildlife Refuge in North America that serves as an important habitat for over 500 native fish, wildlife, plant, and freshwater mussel species, is the drinking water source for up to 4 million people, and a popular destination for recreational and sustenance fishing. To investigate One Health implications of these persistent CECs in this social-ecological system, we collected popular game fish to test: PFAS bioaccumulation in White Bass; and PPCPs bioaccumulation and occurrence of antibiotic resistant genes (ARGs) in Yellow Perch and Walleye across a gradient of known contamination. Results show that PFOS is most commonly implicated in PFAS bioaccumulation across game fish species. Azithromycin was the only antibiotic found in fish tissue. tetW was the most prevalent ARG, followed by sulI and sulIII. ARGs were more prevalent in areas with higher environmental contaminant burden. Controlling for organ type and location, Walleye had 2.52 more ARGs compared to Yellow Perch. PFAS, PPCPs, and ARGs pose a potential risk to aquatic food webs and public health via ingestion of game fish at environmentally-relevant doses.

Guess what is in my cadaver freezer: wildlife rehabilitation as an under-utilized resource in wildlife diseases surveillance

Monday, 28th July - 13:30: Wildlife Rehabilitation (Oak Bay Room) - Oral

Chantal Theijn [1], ***Alaina MacDonald*** [2], ***Claire Jardine*** [3], ***Jeff Bowman*** [4], ***Samira Mubareka*** [5]

1. *Hobbitstee Wildlife Refuge,* ***2.*** *Ontario Veterinary College,* ***3.*** *Department of Pathobiology, University of Guelph,* ***4.*** *Wildlife Research and Monitoring Section, Ministry of Natural Resources,* ***5.*** *Sunnybrook Research Institute*

Wildlife rehabilitators care for thousands of sick, injured and orphaned wildlife annually. Medical care and operating expenses of wildlife rehabilitation are often funded by donations, which limits diagnostics, outreach and conservation capacity. Using case studies and medical record data from the past 5 years of intakes at Hobbitstee, this presentation will highlight opportunities for collaboration between wildlife rehabilitators and the scientific community.

Hobbitstee Wildlife Refuge (Nanticoke, Ontario) cared for 14,861 wild-animals of 227 species from 2019-2024. Common causes of presentation include orphaned young (4865), trauma (9587) and confirmed or suspected infectious disease (409). The majority of infectious disease cases are unconfirmed, but are likely associated with pathogens which are zoonotic and/or have negative impacts on health and conservation of wild species.

Hobbitstee assisted with identifying the first case of ranavirus in common snapping turtles worldwide. Hobbitstee contributes to ongoing research investigating presence of SARS-CoV-2 in wildlife and cellular mechanisms of viral susceptibility in white-tailed deer. Additionally, the refuge developed and implemented an SOP to prevent incursion of highly pathogenic avian influenza into the facility and participates in ongoing HPAI surveillance. Regular public outreach activities include training of bylaw officers and SPCA employees as well as public health communication via social media.

Investing in laboratory diagnostics and improving communication between rehabilitators and researchers may offer opportunities in surveillance and support a One Health approach to studies of wildlife and human disease.

Long-Term Monitoring of Chronic Oiling in California Seabirds: Trends, Impacts, and Conservation Implications

Monday, 28th July - 13:45: Wildlife Rehabilitation (Oak Bay Room) - Oral

Jamie Sherman [1], ***Corrine Gibble*** [2], ***Laird Henkel*** [2], ***Lorraine Barbosa*** [1], ***Victoria Hall*** [1], ***Michael Ziccardi*** [3]

1. *Oiled Wildlife Care Network, UC Davis Wildlife Health Center,* ***2.*** *Marine Wildlife Veterinary Care and Research Center, California Department of Fish and Wildlife, Santa Cruz, CA, USA,* ***3.*** *One Health Institute, University of California, Davis*

Chronic oil pollution remains a persistent threat to marine wildlife, originating from natural petroleum seeps, shipwrecks, and unidentified anthropogenic discharges. Unlike catastrophic oil spills, chronic oiling occurs continuously, making it difficult to quantify and mitigate. In California, natural petroleum seeps contribute significant crude oil to the marine environment, leading to direct oiling of seabirds and creating wildlife agency response challenges. To address this, the Oiled Wildlife Care Network (OWCN), in collaboration with the California Department of Fish and Wildlife Office of Spill Prevention and Response (CDFW-OSPR), established the Individual Oiled Animal (IOA) monitoring program in 1998. This program collects real-time wildlife admission data from 45 rehabilitation centers across California, serving as both an early warning system for oil spills and a long-term monitoring initiative.

This study analyzed data from oiled birds admitted to California rehabilitation centers between 2005 and 2025 to assess spatial, temporal, and population-level trends in chronic oiling. Results indicate that species composition varies by region, with a higher prevalence of oiling near known natural seeps. Seasonal peaks, particularly in winter months, align with increased storm activity, which likely mobilizes seep oil. In combination, these trends can be used to distinguish chronic from catastrophic oiling events. Furthermore, patient disposition analysis revealed varying survival outcomes among species.

These findings highlight the value of long-term monitoring and interagency collaboration, and are essential to improving wildlife emergency response protocols. Strengthening data-sharing networks and integrating diverse knowledge sources will enhance proactive conservation strategies for at-risk marine species.

Wildlife Rehabilitation Facilities, an Essential Partner in One Health Collaborative Networks: SARS-CoV-2 Surveillance in Native U.S. Mammals and Assessment of Biosecurity Practices

Monday, 28th July - 14:00: Wildlife Rehabilitation (Oak Bay Room) - Oral

Jeff Gruntmeir [1]***, Hayley Yaglom*** [2]***, Beth Nielson*** [2]***, Katy Parise*** [2]***, Steven Rekant*** [3]***, Jessica Siegal-Willott*** [4]***,***
Jim Wellehan [5]***, David Engelthaler*** [2]***, Martha Keller*** [4]***, Maueen Long*** [6]

1. *University of Florida Emerging Pathogens Institute,* ***2.*** *Translational Genomics Research Institute (TGen North),* ***3.*** *USDA-APHIS-VS,* ***4.*** *USDA-APHIS-AC,* ***5.*** *University of Florida, College of Veterinary Medicine,* ***6.*** *University of Florida, Emerging Pathogens Institute*

Wildlife rehabilitation groups are overlooked partners in research and often find themselves on the front lines of endemic, emerging, and reemerging diseases of one health importance. Considerable human-animal interactions occur at wildlife rehabilitation facilities, where ill or injured wildlife are temporarily housed in human care. It is established that animals infected with SARS-CoV-2 can infect other animals and humans in close contact. This study further investigated susceptibility of US native wild mammals to SARS-CoV-2 infection and surveyed biosecurity practices at wildlife rehabilitation facilities. This effort required a collaborative team involving USDA-APHIS, TGen, UF-Emerging Pathogens Institute (UF EPI) and a network of over 69 wildlife rehabilitators across 39 states. Following acquisition of state permissions or permits, UF-EPI recruited U.S. facilities who collected respiratory swabs, rectal or fecal swabs, and blood samples from arboreal, terrestrial, or aquatic non-endangered native mammals. Samples submitted to TGen were screened by RT-qPCR (viral detection) and viral neutralization assays (antibody detection). Biosecurity surveys were completed by facilities to identify and formulate best practice guidelines for disease prevention at this human-wildlife interface. Since 2023, over >2400 swab samples and >950 blood samples from 62 species have been screened for antibodies against SARS-CoV-2 and shed virus. While the project is ongoing, so far virus was detected by RT-PCR in one eastern gray squirrel, and antibodies against SARS-CoV-2 detected in 10 white-tailed deer fawns, a bobcat, and a beaver highlighting species susceptibility and illustrating the importance of establishing One Health collaborative networks with the wildlife community.

Retrospective Hematological Analysis of Raccoon Dogs (Nyctereutes procyonoides) with Sarcoptic Mange Rescued in Gangwon State

Monday, 28th July - 14:15: Wildlife Rehabilitation (Oak Bay Room) - Oral

Sohwon Bae [1]***, Seri Hong*** [2]***, Minjae Jo*** [2]***, Jung Hoon Choi*** [2]***, Son-Il Pak*** [2]***, Sangjin Ahn*** [2]

1. *Gangwon Wildlife Medical Rescue Center,* ***2.*** *College of Veterinary Medicine and Institute of Veterinary Science, Kangwon National University*

Sarcoptic mange, caused by *Sarcoptes scabiei*, is a contagious skin disease that significantly impacts wildlife populations, including raccoon dogs (*Nyctereutes procyonoides*). This study retrospectively analyzes the hematological and biochemical parameters of raccoon dogs with sarcoptic mange rescued in Gangwon State, aiming to identify key prognostic indicators associated with survival outcomes. A total of 262 raccoon dogs with clinical signs of mange were examined between 2017 and 2024. The animals were categorized into two groups: those that survived rehabilitation and those that succumbed to the disease.

Hematological analysis revealed that deceased individuals exhibited significantly lower red blood cell counts, hemoglobin levels, and hematocrit values, indicating anemia. Elevated white blood cell and neutrophil counts suggested a strong immune response, while significantly lower glucose and albumin levels were associated with metabolic stress and poor prognosis. Logistic regression analysis identified hypoglycemia and elevated blood urea nitrogen (BUN) as key mortality predictors. Additionally, phosphorus imbalances and severe anemia further contributed to negative survival outcomes. Seasonal variations also played a role, with higher mortality rates observed in winter due to hypothermia and malnutrition.

Early intervention, including glucose supplementation and supportive therapy, is essential for improving survival rates in affected raccoon dogs. Routine hematological assessments upon rescue can serve as valuable prognostic tools to guide treatment strategies. These findings provide critical insights into the pathophysiological effects of sarcoptic mange in raccoon dogs and emphasize the importance of timely medical intervention to enhance wildlife rehabilitation efforts.

Keywords: Raccoon dog, Sarcoptic mange, *Sarcoptes scabiei*, Hematology, Wildlife disease, Prognostic markers

Acknowledgement: This research was supported by the Specialized Graduate Program for Training Wildlife Professionals through the National Institute of Wildlife Disease Control and Prevention, Ministry of Environment (20241104000003125600).

Pre-Release Health & Post-Release Fate of Rehabilitated Macropods (Kangaroos and Wallabies)

Monday, 28th July - 14:30: Wildlife Rehabilitation (Oak Bay Room) - Oral

Joanne Connolly [1]***, Geoffrey Dutton*** [1]***, Elle Deane*** [1]***, Deanna Duffy*** [1]***, Jacqueline Marlow*** [2]***, Ian Ralph*** [2]***, Lauren Suffling*** [3]***, Joan Reid*** [2]***, Lorraine Woodward*** [2]***, Margot Horder*** [2]***, Mikala Welsh*** [2]***, Margaret St Hill*** [4]***, Dianne Lane*** [5]***, John Palmer*** [5]

***1.** Charles Sturt University, **2.** Sydney Wildlife Rescue, **3.** The University of Sydney, **4.** Sydney Bushwalkers Club, **5.** Wildlife Information, Rescue and Education Service Inc (WIRES)*

Globally wildlife faces many threats from anthropogenic activities and climate change. In Australia 104,000 native animals are rescued and rehabilitated each year by 5,600 licensed volunteers in NSW. The goal in rehabilitating wildlife is not only to improve welfare, but to ensure animals successfully reintegrate into the wild and survive. Outcomes such as mortality and time till release are easy to define, but post-release survival longer term and breeding is the ultimate measure of successful rehabilitation. There is little literature to guide decision-making during rehabilitation and treatment of disease, with a noticeable lack of critical post-release monitoring. The aim of the study was to perform a pre-release health assessment (including behavioral, fitness, body condition and blood analysis), followed by post-release monitoring (ear tags, GPS/VHF collars, visual observations, camera traps) of rehabilitated orphaned macropods at carefully considered release sites to measure and improve outcomes. Reference ranges were determined for blood analytes from healthy, hand-reared sub-adult macropods (40 Eastern grey kangaroo and ten swamp wallaby). In the Riverina, 32 macropods were ear tagged prior to release, with trail cameras and landholders observing tagged animals. In Sydney, four swamp wallabies were released into bushland with ear tags and GPS/VHF collars and monitored for up to 12 months. The combination of spatial analysis, along with camera trap images and visual observations provided data on movements, interactions, home ranges and survival times. Swamp wallaby home ranges appeared smaller than anticipated, and prophylactic use of ectoparasiticides, fox control and predator training are recommended.

Bridging the Gap: Research Opportunities in Wildlife Through Partnerships with Wildlife Rehabilitators

Monday, 28th July - 14:45: Wildlife Rehabilitation (Oak Bay Room) - Oral

Angelika Langen [1]

1. *Northern Lights Wildlife Society*

This presentation explores the untapped potential of research collaborations with wildlife rehabilitators, highlighting the critical role they play in advancing wildlife health, conservation, and policy. Unlike traditional research models, our approach is uniquely self-funded, leveraging an extensive network of organizations, donors, and stakeholders to ensure accurate data collection, outreach, and implementation.

We have demonstrated our ability to sustain a dedicated position that navigates the intricate landscape of wildlife rearing professionals, academia, First Nations, industry leaders, enforcement agencies, biologists, government officials, NGOs, and the philanthropic public. This ability to “walk the line” across diverse sectors positions us as a bridge between science, practice, and policy, creating unparalleled opportunities for impactful research.

Key discussion points include:

- The need for stronger wildlife rehabilitator partnerships in research
- How self-funding and direct access to networks enhance data integrity and outreach
- Case studies demonstrating successful cross-sector collaboration
- The role of research in shaping policy, conservation, and wildlife care best practices

By fostering these partnerships, we can elevate the standard of wildlife research, ensuring that it is both practical and applicable to those working on the front lines of conservation.

Health and food borne parasite assessment of East Beaufort Sea Beluga (Delphinapterus leucas) in the Inuvialuit Settlement Region: A Collaborative Approach

Monday, 28th July - 15:45: Aquatic Animal and Marine Health continued (Salon BC) - Oral

Émilie L. Couture [1], ***Amélia Dalpé*** [1], ***Jasmine Brewster*** [2], ***Shannon MacPhee*** [3], ***Adrián Hernández-Ortiz*** [4], ***Sylvain Larrat*** [5], ***Raphaela Stimmelmayr*** [6], ***Emily Jenkins*** [4], ***Lisa Loseto*** [7], ***Stéphane Lair*** [8]

1. *Centre québécois sur la santé des animaux sauvages / Canadian Wildlife Health Cooperative, Faculté de médecine vétérinaire, Université de Montréal,* **2.** *Arctic Region, Inuvik, Fisheries and Oceans Canada,* **3.** *Arctic Region, Winnipeg, Fisheries and Oceans Canada,* **4.** *Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon S7N 5B4,* **5.** *Biodivet,* **6.** *North Slope Borough Department of wildlife management and Institute of Arctic Biology, University of Alaska Fairbanks, Alaska,* **7.** *Lisa Loseto (Pacific region, Institute of Ocean Sciences, Fisheries and Oceans Canada),* **8.** *Canadian Wildlife Health Cooperative / Centre québécois sur la santé des animaux sauvages, Université de Montréal, Faculté de médecine vétérinaire, 3200 rue Sicotte, St-Hyacinthe, Québec J2S 2M2, Canada*

Beluga whales (*Delphinapterus leucas*) are key health indicators of a rapidly changing arctic ecosystem and are culturally and nutritionally important to Inuvialuit communities. To track changes over time, we assessed the health of harvested Eastern Beaufort Sea beluga whales from the Tarium Niryutait Marine Protected Area in 2015–2016 (n=26) and 2023–2024 (n=35). We developed a population specific scaled mass index and conducted standard post-mortem examination. Overall, harvested whales appeared in good health and body condition, compatible with hunter selection practices. Degenerative changes, most likely age-related, were frequently observed in thyroid and adrenal glands. Helminths were commonly observed in mesenteric lymph nodes (unidentified trematodes) (2015–2016: 9/26, 2023–2024: 7/35), airways (pseudaliid nematodes) (2015–2016: 18/26, 2023–2024: 30/35), and stomachs (anisakid nematodes) (2015–2016: 8/26, 2023–2024: 14/35). The occurrence of renal nematodiasis (*Crassicauda* sp.) seem to have increased from 2015–2016 (8/26) to 2023–2024 (33/35). Sarcocysts were observed microscopically in skeletal muscles in 6/26 (2015–2016) and 15/24 individuals (2023–2024). In addition, *Sarcocystis* spp. DNA was detected in the skeletal muscle of 59% (n=46/78) of tested belugas from 2015 to 2021. DNA of *T. gondii* was detected in one heart sampled in 2015-2016. Larvae of *Trichinella* spp. were not detected in tongues from beluga in 2015–2016. The observed parasitic burden was as expected for healthy wildlife. Periodic longitudinal studies in partnership with indigenous communities, government, and academic partners contribute to a better understanding of beluga health in the face of a rapidly changing ecosystem.

Survey of pathogens in Antarctic pinnipeds: a decade of health monitoring

Monday, 28th July - 16:00: Aquatic Animal and Marine Health continued (Salon BC) - Oral

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Monitoring the health of key Antarctic species is essential amid emerging disease risks that threaten fragile ecosystems. However, knowledge of diseases affecting Antarctic pinnipeds remains scarce. Early serological studies began in the 1980s, but comprehensive data are still lacking. This study assesses the circulation of transmissible pathogens in Antarctic seal species, providing crucial conservation insights. Between 2014 and 2024, we collected serum from 19 southern elephant seals (SES) (*Mirounga leonina*) on Isla 25 de Mayo, 16 (WS) Weddell seals (*Leptonychotes weddellii*), 14 crabeater seals (CS) (*Lobodon carcinophaga*), and 8 leopard seals (LS) (*Hydrurga leptonyx*) on Danco Coast. We performed commercial ELISA tests to detected antibodies against *Brucella* sp. (SES=5%,WS=56%,CS=0%,LS=50%), *Coxiella burnetii* (SES=11%, WS=6%, CS=14%, LS=25%), *Paslahepevirus balayani* (SES=0%, WS=0%, CS=7%, LS=13%), *Alphainfluenzavirus influenzae* (SES=0%, WS=0%, CS=0%, LS=13%), *Orthoflavivirus nilense* (all negative), and *Betacoronavirus pandemicum* (all negative). Microscopic agglutination test was used to test antibodies against *Toxoplasma gondii* (SES=16%, WS=0%, CS=7%, LS=13%). Additionally, sera from 10 WS, 10 CS and 14 LS from Danco Coast were tested with ELISA for IgG antibodies against *Morbillivirus canis* (canine distemper; WS=90%, CS=0%, LS=100%). During summer 2024, we collected nasal swabs, from 42 Antarctic fur seals (*Arctocephalus gazella*), and 12 other pinnipeds from Isla 25 de Mayo and Danco Coast, all tested negative for H5 high pathogenicity avian influenza using RT-qPCR. Despite serological limitations, these findings provide baseline health data for Antarctic pinnipeds. As environmental changes and invasive species pose increasing threats, monitoring infectious agents is critical for biosecurity and conservation efforts in Antarctica.

Dead but not forgotten - Drivers of cetacean necrobiome and their importance in understanding carcass decomposition and circumstances of death

Monday, 28th July - 16:15: Aquatic Animal and Marine Health continued (Salon BC) - Oral

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The mammalian skin microbiome is intrinsically linked with its host. Strong evidence in human forensics suggests that this connection does not end upon the host's death. Changes of the necrobiome (microbiome of the dead host) may correlate with and even drive the body's decomposition process. To investigate the drivers of necrobiome as a promising forensic tool to define circumstances and timing of death for cetaceans, we collected skin samples from 10 fresh to moderately decomposed bottlenose dolphins (*Tursiops truncatus*) stranded dead in the northern Gulf of Mexico (Alabama, Florida). We used two different sampling techniques (skin swab, biopsy). Samples were analyzed by 2x250 Illumina MiSeq amplicon sequencing (V4 region of 16S rRNA gene). The most abundant phyla across samples were Proteobacteria (45% relative abundance), Firmicutes (36%) and Fusobacteriota (12%), all three previously found to dominate in the dolphin gut. The samples showed an average richness of 96 ASVs (ranging 16-255). Estimates of alpha diversity (ASV richness, Shannon-Wiener, Chao1, ACE) remained constant among individuals but differed between sample types and age classes (higher in swabs and adults). Beta diversity was driven by age class, decomposition code, and individual animal. Like the skin microbiome of live cetaceans and the relatively well-studied human necrobiome, the dolphin necrobiome is likely driven by multiple factors, including individual variation. Our findings suggest using skin swabs or collecting larger pieces of skin (> 1 cm diameter) will provide better necrobiome representation. This study is an important first step towards the use of cetacean necrobiome in forensic investigations.

Using Models To Evaluate The Efficacy Of Management Actions For Reducing the Risk of Salmon Disease

Monday, 28th July - 16:30: Aquatic Animal and Marine Health continued (Salon BC) - Oral

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Infectious diseases caused by parasites that have complex lifecycles are often poorly understood. Models can be useful tools for bridging data gaps and for evaluating efficacy of management actions, pre- or post- action. We developed a tandem modeling approach to evaluate flow manipulation (management actions) employed to reduce invertebrate hosts of *Ceratonova shasta* (myxozoan parasite) in the Klamath River, USA. *Ceratonova shasta* alternately infects *Manayunkia occidentalis* (freshwater annelid) and salmonids, and has been associated with salmon population declines throughout the Pacific Northwest. Our aims were to predict invertebrate host distribution in river sections characterized by elevated *C. shasta* densities. Two-dimensional hydraulic models (2DHMs) were developed for each river section and used to describe hydraulic variation and stratify invertebrate host sampling locations across gradients of depth and velocity within substrate classes. Benthic samples were used to build predictive distribution models; distribution was associated with substrate, as well as depths and velocities predicted from the 2DHMs during the previous water year's peak discharge. We evaluated model performance against independent datasets collected in multiple water years. Our results demonstrate that hydraulic conditions during peak discharge (natural or managed) drives invertebrate host distribution the following season, and distribution in turn influences *C. shasta* prevalence in, and risk of infection for, salmonids. Our study provides a tool that allows us to predict how invertebrate host distribution responds to flow manipulation at the study sites and evaluate the potential efficacy of proposed management scenarios for reducing the risk of salmon disease.

Land use impacts movement and pathogen transmission of a wetland bird

Monday, 28th July - 16:45: Aquatic Animal and Marine Health continued (Salon BC) - Oral

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White Ibis are nomadic wading birds that move across the landscape in Florida. Former studies have identified the movement patterns of and habitat use of adult ibises and found evidence that some ibis were becoming more sedentary and reliant on anthropogenic landscapes. Recently we studied the reproductive success, diet and pathogen load of urban-nesting ibis. Ibis move frequently between urban and natural coastal-freshwater environments, transporting pathogens across habitats. *Vibrio* is a relevant zoonotic pathogen responsible for causing disease in both birds and humans. We collected fecal samples from adult/fledgling ibis and water samples from urban parks/colonies where ibis are found for *Vibrio* isolation/sequencing between 2023-2024. We detected it, including disease-causing strains, in 42% of the 138 samples we tested, indicating that this pathogen is commonly circulating in urban spaces in Florida.

We also outfitted 30 ibis fledglings with GPS transmitters and followed their dispersal patterns for two years. Their movements were divided into “nomadic” and “resident” points using recursions based on the times an individual revisited an area. Integrated step selection function models suggested that urban-born fledglings selected for “low urban” and agricultural sites that are near bodies of water. *Vibrio* was detected in 17 fledglings and of significance, at a higher prevalence in those that died before leaving the colony (n=3/3) and in those that were predominantly nomadic (n=9/12), moving frequently across habitat types. Integrating animal movement data and pathogen surveillance can help us understand the impacts of pathogens on post-fledgling survival while better defining transmission pathways.

Framework for assessing chemical immobilization in free-range darted mule deer

Monday, 28th July - 16:00: General Wildlife Health (Oak Bay Room) - Oral

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Chemical immobilization is a crucial tool for studying and managing many free-ranging wildlife populations, the success of which depends on appropriate application of drug formulations. Although wildlife agencies regularly test new drugs and drug combinations to improve capture efficiency and animal welfare, the results of these efforts can be difficult to interpret. Trials on wild animals in captive settings can be valuable but are limited by sample size and may not reflect performance under field conditions. Studies in free-ranging populations can provide important insight into the performance of drugs in situ but the complexity of these systems can make results difficult to compare. Here we implemented statewide collection of an immobilization quality score (IQS) to standardize the assessment of three drug combinations in mule deer and black-tailed deer (*Odocoileus hemionus*): tiletamine-zolazepam/xylazine, butorphanol-azaperone-medetomidine (BAM), and nalbuphine-medetomidine-azaperone. California Department of Fish and Wildlife (CDFW) biologists immobilized 163 deer by free-range darting for population monitoring between August 2022 and April 2024. Biologists were instructed to grade six parameters related to each immobilization event on a five-point scale to complete the IQS. Morphometrics, vital rates, and induction and recovery times were also collected. In general, the quantitative IQS scores corroborated qualitative feedback and the standardization allowed for easier comparison across regions and subspecies. Refinements to consider include creation of a shorter and simpler IQS and incorporation of additional parameters such as habitat/cover and rate of non-recovered or multi-dosed animals. The results of this study were used to inform CDFW mule deer chemical immobilization protocols.

Understanding Wildlife Health Metrics Under the Threat of Climate Change

Monday, 28th July - 16:15: General Wildlife Health (Oak Bay Room) - Oral

Sabrina Greening **[1]** ***, Lucie Pascarosa*** **[2]** ***, Avery Munster*** **[1]** ***, Roderick Gagne*** **[1]** ***, Julie Ellis*** **[1]**

1. *Wildlife Futures Program, University of Pennsylvania,* **2.** *University of Pennsylvania School of Veterinary Medicine*

Climate-associated impacts on wildlife health are inevitable, making it essential for wildlife management to incorporate climate change into the response to other health threats (e.g., pathogens, contaminants) and to implement strategies that mitigate risks related to climate change. However, integrating climate change into health considerations is complicated by variations in the definition of health being used by management agencies and health practitioners. Recent wildlife health frameworks reflect our expanding understanding and definition of health – extending beyond disease and emphasizing the interaction of biological, social, and environmental determinants and their impact on health. The scale at which health is considered (e.g., individual, population, and ecosystem) also plays a role in how it is measured. In this presentation, we present findings from an ongoing series of literature reviews focusing on climate change impacts on wildlife health. We found researchers remained disease-centric in their approach and the literature was focused upon climate effects on the distribution and abundance of animals, vectors, and pathogen species. There is a need to identify wildlife health metrics that can move us beyond pathogens and their pathology toward management actions that help promote healthy and resilient populations. We hope this presentation will stimulate further discussion on how to add climate to the wildlife health agenda and expand current wildlife health frameworks so they may be used to help inform on-the-ground management actions.

UNDERSTANDING ANTIBODY DYNAMICS IN THE WILD

Monday, 28th July - 16:30: General Wildlife Health (Oak Bay Room) - Oral

Anna Jolles [1]**, *Ricardo Reyes Grimaldo*** [1]**, *Jan Medlock*** [1]**, *Brianna Beechler*** [1]

1. *Oregon State University*

The dynamics of adaptive immune responses against infectious diseases in natural host populations are poorly known because time series of antibody titers within individualhosts are hard to collect for most species.

We measured antibody responses to a suite of 10 respiratory pathogens in a herd of African buffalo icontained within a 900ha enclosure in Krueger National Park, South Africa. We sampled the study herd every 2-3 months for 3 years, resulting in a serological time series, which we utilized to (i) estimate the duration of immunity for our focal pathogens, (ii) test for positive (synchronized) or negative (prioritization) correlations in the timing of the loss of immunity, and (iii) evaluate demographic, environmental and physiological factors that might affect the timing/rate at which immunity to each pathogen is lost.

We demonstrate that antibody longevity is extremely variable across pathogens. For the acute pathogens we studied, correlations in the timing of antibody loss were overwhelmingly positive, indicating synchronization. By contrast, the three chronic pathogens we studied displayed opposite (negatively correlated) patterns. The loss of antibody protection was driven by seasonal variations in body condition and forage availability. Metabolic and behavioral host factors and associations in the incidence of some of the pathogens are likely to contribute to these patterns.

This study is one of the first to describe variation in antibody dynamics against a range of different pathogens in a natural mammalian population, addressing a critical empirical data gap that is foundational to construct meaningful disease dynamic models for infection risk forecasting and management.

How Can We Get to Wildlife Health Intelligence?

Monday, 28th July - 16:45: General Wildlife Health (Oak Bay Room) - Oral

Krysten Schuler [1], ***Brenda Hanley*** [1], ***Nicholas Hollingshead*** [1], ***Paul Adams*** [2], ***Landon Miller*** [3], ***Carlos Gonzalez Crespo*** [4], ***Noelle Thompson*** [5], ***Jue Wang*** [6], ***James Booth*** [7], ***Andreas Eleftheriou*** [8], ***Sonja Christensen*** [9], ***Kevin Hynes*** [3]

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With increasing importance on wildlife health, we need to ensure that data collected on diseases is maximized to the greatest potential. Antiquated data systems, lack of case definitions, non-standard terms, and unwillingness to share information all hamper our knowledge of disease systems and threats to wild populations. With examples we learned through the Surveillance Optimization Project for Chronic Wasting Disease (SOP4CWD), we discuss opportunities for better data leading to improved opportunities for learning. Using digital data with sample collection in the field, automatic results links from diagnostic labs, shared terminology and case definitions, and innovative quantitative methods, we can surpass the limitations of individual scientists or organizations. These changes can lead to improved confidence in disease status, time and cost savings in surveillance programs, and shared datasets. Beyond technological improvements, we found a diverse community of people interested in topics of disease transmission, sampling size estimation, and surveillance and prevention optimization that are joining this effort. Focusing on collaboration rather than competition, we see a path for wildlife health data that ultimately benefits the humans, animals, and environment.

Wake up and fight!? Effect of torpor on immunity in eastern bent-winged bats (Miniopterus orianae oceanensis)

Tuesday, 29th July - 08:30: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

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Australian microbats face a significant threat from the fungus *Pseudogymnoascus destructans*. This pathogen causes White Nose Syndrome (WNS), a disease responsible for millions of bat deaths in North America since 2006. The fungus infects bats during winter hibernation, when their metabolic processes slow as they enter torpor, a deep sleep state that helps conserve energy but weakens their immune system.

Despite the risk posed by WNS, little is known about the immune capabilities of Australian microbats, hindering the development of effective conservation strategies. This study therefore aimed to investigate to what degree torpor suppresses immune functions of a model Australian microbat species, how quickly suppression is reversed after arousal, and whether torpor duration influences this process.

In mid-2024, I conducted a laboratory study on 52 free-ranging Australian eastern bent-winged bats (*Miniopterus orianae oceanensis*), assessing immune parameters after 2 (n = 23) and 8 (n = 29) hours of torpor. Blood samples were collected before torpor, during torpor, and 30 minutes post-arousal.

Results showed a significant reduction in total white blood cell counts during torpor (LME: Sample, $\chi 2 = 32.78$, $p < 0.001$), with counts returning to baseline levels within 30 minutes after arousal. This change was primarily driven by neutrophils, indicating that cells of the innate immune system may be recalled more rapidly.

Plasma microbicidal activity was not significantly affected by torpor, but by the time of year, with greater potency observed during Australian autumn compared to winter (LME: Season, $\chi 2 = 13.98$, df = 1, $p < 0.001$).

These findings are the first to explore the impact of torpor on immune dynamics in Australian microbats. While the rapid recall of innate immune cells and stable microbicidal activity during torpor are promising, further research is needed to fully understand the immune resilience of these species against emerging threats like WNS.

Identification and deep sequencing of potentially zoonotic Bartonella from wild small mammals in urban parks and green spaces of Toronto, Ontario, Canada

Tuesday, 29th July - 08:45: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

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Background: Species of *Bartonella* are intraerythrocytic bacterial zoonotic pathogens that can cause disease in both humans and animals. Reservoirs of *Bartonella* spp. include wild small mammal hosts. Rodents and other small mammals are highly adaptable animals that can readily exist in peridomestic environments and can invade human dwellings. Previous studies have focused on *Bartonella* spp. infections of introduced hosts (e.g., *Rattus norvegicus*) in urban contexts or endemic hosts in non-urban contexts. We investigated *Bartonella* spp. infecting endemic small mammal species in green spaces of Toronto, Ontario, Canada – a major urban centre.

Methods: We employed live-trapping to collect blood via cardiac puncture from 230 wild small mammals. Screening for *Bartonella* spp. in clotted blood was completed with real-time PCR targeting the *gltA* gene. Metagenomic amplicon sequencing was conducted to identify bartonellae in PCR-positive samples. Differences in the odds of infection by sex and age were examined using Fisher's exact tests.

Results: Overall, 92/230 (40.0%) of animals were positive for *Bartonella* spp. via qPCR. At least one positive animal was collected from 30/35 (85.7%) urban parks sampled. Sequencing identified two species: *B. vinsonii* and *B. grahamii*. The odds of infection were significantly greater for adults vs juveniles (OR=6.61, 95% CI: 1.93-22.60, $p<0.001$); no difference in odds of infection was seen for females vs males.

Conclusion: Multiple *Bartonella* spp. with known zoonotic potential are harbored by endemic wild small mammals in green spaces of Toronto, Ontario, Canada. These findings build on existing knowledge of *Bartonella* reservoir ecology and aid in identifying risk areas in urban contexts.

Mosquito and Culicoides vector breeding ecology in feral swine (Sus scrofa) wallows in Georgia and South Carolina

Tuesday, 29th July - 09:00: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

Taylor Fisher [1]***, Lilyanne Callaham*** [2]***, James Beasley*** [3]***, Vienna Brown*** [4]***, Ellen Haynes*** [1]***, Erin Lipp*** [5]***, Bethany McGregor*** [6]***, Daniel Peach*** [7]***, Michael Yabsley*** [1]***, Christopher Cleveland*** [1]

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Feral swine (*Sus scrofa*), commonly referred to as wild pigs, function as ecosystem engineers and are a significant invasive species in the United States. They consume agricultural crops, native plants and animals, while their rooting and wallowing behaviors lead to extensive habitat modification. Specifically, wallowing creates ephemeral pools distributed throughout the landscape, which may serve as breeding sites for arthropods requiring aquatic or semi-aquatic conditions during development.

This study investigates whether feral swine wallows act as habitats for mosquito (Diptera: Culicidae) and biting midge (*Culicoides* spp.) vector species. Collections were conducted at feral swine wallows across three sites in South Carolina and Georgia from April 2024 to August 2025. Sampling methods include mosquito larval dipping and soil incubation for midge emergence. Preliminary morphological identification has yielded 200 mosquito larvae and 90 adult *Culicoides* midges across all sites. Notable species identified include *Culicoides variipennis*, a sister species of the primary North American bluetongue virus vector *C. sonorensis*, , as well as mosquitoes from the genera including *Anopheles*, *Culex*, *Aedes*, and *Psorophora*. Mosquito vectors identified morphologically have the capacity to transmit *Plasmodium* spp. (causative agents of malaria), *Dirofilaria immitis* (canine heartworm), and various Flaviviruses and Alphaviruses. This study highlights that feral swine-created wallows are used as breeding habitats for medically and veterinary important vectors. Furthermore, our results provide a framework for understanding vector driven pathogen transmission in *Sus scrofa*-modified landscapes and potential effects on population health. This study emphasizes the interconnectedness of invasive species, vector ecology, and pathogen transmission within a One Health framework.

Multi-State Investigation of Pathogen and Contaminant Exposure in Declining Eastern U.S. Muskrat (Ondatra zibethicus) Populations

Tuesday, 29th July - 09:15: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

Nicholas Friedeman [1], ***Christine Casey*** [2], ***Ellen Haynes*** [1], ***Mark Ruder*** [1], ***Michael Yabsley*** [1], ***Christopher Cleveland*** [1]

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Long- term population declines in muskrats (*Ondatra* zibethicus) have raised concerns among wildlife state agencies. Muskrats serve as ecosystem engineers, enhancing wetland habitat quality and diversity, while also providing economic value as furbearers. The causes of range-wide population declines remain poorly understood, and contemporary data on pathogen and contaminant exposure are limited. To address these knowledge gaps, we are conducting a regional study in collaboration with 14 state wildlife agencies across the eastern United States. This multi-state effort investigates the prevalence and distribution of pathogens and contaminants potentially affecting muskrat populations. Currently, we have tested 246 muskrats from 14 states for known causes of morbidity and mortality (*Francisella* tularensis, *Clostridium* piliforme, *Toxoplasma gondii*, *Versteria* spp., *Taenia* taeniaformis), and emerging concerns (volatile organic compounds (VOC), neonicotinoids). Preliminary results indicate *F. tularensis* is absent, or rare (0/246) in sampled populations, while *C.* piliforme shows variable prevalence (36 – 68%) across the sampling range with an overall prevalence of 48% (118/246). The high prevalence of *C.* piliforme likely represents subclinical infections rather than clinical Tyzzer's disease. VOC screens have yielded trace amounts of chemical intermediates m/p-cresol (>92% match) and detectable levels of the herbicide metribuzin (78% match). All muskrats have tested below levels of detection for neonicotinoid compounds, yet exposure to imidacloprid metabolites has varied between individuals and among states. Additional pathogen testing is ongoing, and results are forthcoming. This ongoing study will enhance our understanding of health threats affecting muskrats at a regional scale and provide insight into potential drivers of population declines.

Incriminating vectors of deer malaria (Plasmodium odocoilei) at a Florida deer farm

Tuesday, 29th July - 09:30: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

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Plasmodium odocoilei, the only nonhuman *Plasmodium* parasite affecting native mammals in North America, infects white-tailed deer (*Odocoileus virginianus*) across the eastern United States. While *P. odocoilei* does not cause significant disease in healthy deer, infection with *P. odocoilei* may increase the susceptibility to epizootic hemorrhagic disease virus infection and mortality in fawns. In this study, we partially incriminated the vectors of *P. odocoilei* by determining host use and *P. odocoilei* natural infection in mosquito species. At a deer farm with previous evidence of *P. odocoilei* transmission, mosquitoes were collected using carbon dioxide-baited light traps, aspirators, and resting shelters. White-tailed deer host use and *P. odocoilei* infection rates were quantified using polymerase chain reaction and Sanger sequencing in potential vectors. Diverse mosquito species (n=38) were found at the farm. Four mosquito species or species complexes specialized in feeding on the deer, taking at least 75% of blood meals from deer: *Anopheles quadrimaculatus* s.l. (88.9%), *Anopheles punctipennis* (83.3%), *Anopheles crucians s.l.* (81.4%), and *Culex erraticus* (87.7%). The highest infection rate of *P. odocoilei* was found in *An. quadrimaculatus s.l.* (9.7%), followed by *An. punctipennis* (4.1%), and *An. crucians s.l.* (0.91%). No other mosquito species were infected with *P. odocoilei*. *Anopheles quadrimaculatus s.l.*, *An. punctipennis*, and *An. crucians s.l.* specialized on feeding on white-tailed deer and were naturally infected with *P. odocoilei*. *Anopheles quadrimaculatus s.l.* and *An. punctipennis* were partially incriminated to be vectors of *P. odocoilei* in Florida, given their high percentages of deer blood meals (>83%) and relatively high infection rates (>4%). Implementing integrated pest management (IPM) strategies for *Anopheles* from this study may reduce the risk of infection in white-tailed deer across the eastern United States. Future studies can fully incriminate vector species by determining vector competence of *Anopheles* by experimentally transmitting *P. odocoilei* between deer in a laboratory setting.

Impacts of wildfire on rodents (Peromyscus maniculatus) and hantavirus dynamics (Sin Nombre virus, SNV) in the Sierra Nevada mountains of California

Tuesday, 29th July - 09:45: Student Presentations - Small Mammals and Vectors (Salon BC) - Oral

Ariel Loredo [1], ***Rebecca Radisic*** [1], ***Bruno Ghersi Chavez*** [2], ***Jalika Joyner*** [1], ***Julien Ferrero*** [3], ***Sarah Smith*** [4], ***Brooke Genovese*** [1], ***Amalie Luneng Solli*** [5], ***Peter Bowman*** [1], ***Ernesto Rojas-Sanchez*** [1], ***Frank Chilanga*** [1], ***Alexandre Tremeau-Bravard*** [1], ***Tracy Drazenovich*** [1], ***Woutrina Smith*** [1], ***Sharif Aly*** [4], ***Brian Bird*** [1]

1. *One Health Institute, University of California, Davis,* ***2.*** *Cummings School of Veterinary Medicine, Tufts University,* ***3.*** *VetAgro Sup - campus vétérinaire de Lyon,* ***4.*** *School of Veterinary Medicine, University of California Davis,* ***5.*** *School of Veterinary Medicine, UC Davis*

Wildfires are increasing in frequency and severity, with varied impacts to humans, wildlife, and the environment. Understanding the consequences of these fire events on wildlife populations and pathogen dynamics is an important part of risk communications to promote wildlife and public health. To explore this, we utilized an established field study area impacted by a severe wildfire (Dixie Fire 2021) at burned and unburned study sites. This observational study revealed dramatic effects on rodent population density and hantavirus shedding following the burn, over a two-year followup period. The proportion of animals SNV RT-qPCR-positive in excreta increased markedly at burned sites during the initial 6 months post-fire, and remained elevated compared to non-burned sites for nearly 2-years. This and other population-based factors were used in a logistic regression model that revealed 2.37-fold increased risk of virus shedding in rodents from burned sites during the first year post-fire (p=0.026). This risk coupled with significantly increased distances travelled per trap night for burned site animals suggests potentially increased risk of transmission and spillover to other species post-fire, including people. Genomic sequencing revealed at least two SNV lineages were present prior to the burn, with analyses underway to determine fire impacts on viral diversity at these study sites. Taken together, these data indicate that wildfire habitat alteration may significantly increase SNV transmission during a 2-year recovery period. Subsequent risk communication efforts can help address these wildlife and public health risks for similar communities impacted by fires.

Old Nodes, New Tricks: Novel Diagnostics for Chronic Wasting Disease in Preserved Retropharyngeal Lymph Nodes

Tuesday, 29th July - 10:45: Student Presentations - Hoofstock (Salon BC) - Oral

Avery Munster **[1]*, Jennifer Høy-Petersen*** **[1]*, Madison Davis*** **[1]*, Sarah Tomke*** **[1]*, Kevin Niedringhaus*** **[1]*, Roderick Gagne*** **[1]*, Michelle Gibison*** **[1]**

1. *Wildlife Futures Program, University of Pennsylvania*

Chronic Wasting Disease (CWD) is a highly transmissible prion disease of captive and wild cervids. The gold standard for detection of CWD is ELISA and Immunohistochemistry (IHC), but these diagnostic tools can yield discrepant results. IHC diagnostics require the RPLN to be formalin-fixed and paraffin-embedded, while ELISA requires a fresh or frozen RPLN thus, requiring two different storage protocols. Real-Time Quaking Induced Conversion, or RT-QuIC, is an amplification assay that is effective for diagnosing other prion diseases in a research setting. Here we optimize RT-QuIC for CWD diagnostics of formalin-fixed and formalin-fixed paraffin-embedded tissues. This enables testing of formalin fixed samples that can be stored for years at room temperature, particularly in situations when refrigeration or freezing of samples is not possible, such as field samples from wild cervid species. Additionally, this test would allow for confirmation of CWD status in tissue archives as well as when the IHC results are questionable or discrepant from prior ELISA-results. Results from this research indicate that formalin-fixed RPLN samples can be tested on RT-QuIC with 98% specificity and 95% sensitivity and formalin-fixed paraffin-embedded RPLN samples can be tested on RT-QuIC with 99% specificity and 93% sensitivity for CWD detection, a comparable result to testing fresh or frozen tissue. These results have the potential to improve disease management in regions with limited access to cold storage and allow surveillance and retesting on discrepant specimens where fresh tissue is unavailable.

Genetic Epidemiology of North Dakota Deer: Identifying Polymorphisms Influencing Chronic Wasting Disease

Tuesday, 29th July - 11:00: Student Presentations - Hoofstock (Salon BC) - Oral

Ethan Baker [1]**, *Sarah Daman*** [2]**, *Charlie Bahnson*** [3]**, *William Jensen*** [3]**, *Turk Rhen*** [1]**, *Susan Ellis-Felege*** [1]

1. *University of North Dakota,* ***2.*** *University of Victoria,* ***3.*** *North Dakota Game and Fish Department*

Wildlife disease is an increasingly prominent aspect in managing wildlife populations and requires an interdisciplinary approach to maintain population health. Genetic epidemiology focuses on how genetic variation in a species interacts with environmental factors, allowing us to better understand disease systems and manage them. In North Dakota, Chronic wasting disease (CWD) is has a limited distribution in the state, but it impacts two prominent cervid species, white-tailed deer (*Odocoileus virginianus)* and mule deer (*Odocoileus hemionus)*.Prion protein gene (PRNP) polymorphisms have been previously linked to slowing CWD progression at codons 95, 96, 116, and 226 in white-tailed deer and codon 225 within mule deer which may promote CWD within the environment. We collected and sequenced 1,248 deer tissue samples from across ND to identify and quantify these previously documented polymorphisms linked to CWD progression. We found at least one slow variant was present in 31 of the 37 ND hunting units (84%). We detected all 4 codons in ND across 756 white-tailed deer samples. Codon 96 was the most frequent polymorphism detected across white-tailed deer (15.2%). We did not find codon 225 in any of the 162 mule deer. Our results demonstrate that while CWD prevalence is low in white-tailed deer within ND, they present the potential of spreading CWD over a longer period compared to mule deer with the detection of these slow progression polymorphisms. This information can help wildlife managers better understand potential CWD progression using genetic epidemiological approaches.

An Agent-Based Modeling Approach to Simulating Chronic Wasting Disease Transmission among Three Sympatric Cervid Species

Tuesday, 29th July - 11:15: Student Presentations - Hoofstock (Salon BC) - Oral

Ashlyn Halseth-Ellis [1], ***Alynn Martin*** [1], ***Michael Cherry*** [1], ***Warren Conway*** [2], ***Austin Ibarra*** [1], ***David Hewitt*** [1], ***Walter Cook*** [3], ***Randy DeYoung*** [1], ***Justin French*** [4], ***Louis Harveson*** [4], ***Shawn Gray*** [5], ***Courtney Ramsey*** [2], ***Levi Heffelfinger*** [6]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***2.*** *Natural Resources Management, Texas Tech University,* ***3.*** *College of Veterinary and Biomedical Sciences, Texas A&M University,* ***4.*** *Borderlands Research Institute, Sul Ross State University,* ***5.*** *Mule Deer and Pronghorn Program Leader, Texas Parks and Wildlife Department,* ***6.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University- Kingsville*

Chronic Wasting Disease (CWD) is a fatal neurodegenerative disease affecting members of the cervid family. Regions where multiple susceptible cervid species coexist present unique challenges for understanding disease spread. The northernmost region of Texas (hereafter Texas Panhandle) has recently experienced growing numbers of white-tailed deer (*Odocoileus virginianus*) and elk (*Cervus canadensis*). This increase in sympatric cervid species to the region, along with existing mule deer (*Odocoileus hemionus*), means the Texas Panhandle contains free-ranging populations of three CWD-susceptible species. Since the first CWD case in the Texas Panhandle in 2016, positive cases have been documented in all three species. As CWD poses significant economic and ecological threats, understanding how these species contribute to disease spread is critical. To address this, we are launching a research project to assess movement and demographic rates of cervids in the Texas Panhandle CWD zone. Further, we developed an *a priori* agent-based model (ABM) that simulates site-, species-, age-, and sex-specific cervid movement as a preliminary forecast of CWD dynamics in this region. In each simulation, CWD was introduced via a single infected mule deer. Each model simulates 2 years with each time step representing one day. We ran 100 iterations of our model. Mean (±SD) prevalence after 100, 200, 300, 400, 500, 600 days was 2.90% (± 2.31%), 4.68% (± 3.59%), 5.57% (± 4.39%), 4.73% (± 3.86%), 2.97% (± 2.62%), 2.46% (± 2.07%), respectively. Our concurrent field-based research project will provide empirical data to enhance simulation inputs. This ABM is the first to model CWD dynamics in the Texas Panhandle while incorporating multi-species movement patterns. This model provides a framework for understanding how cervid behavior influences CWD spread and test proposed management options to inform decision makers.

The next stage of environmental surveillance for chronic wasting disease: What can we learn from testing scrape sites?

Tuesday, 29th July - 11:30: Student Presentations - Hoofstock (Salon BC) - Oral

Miranda Huang [1]***, Steve Demarais*** [2]***, Stuart S. Lichtenberg*** [1]***, Bronson Strickland*** [2]***, Tiffany Wolf*** [1]***, Eric Michel*** [3]***, Manuel Ruiz Aravena*** [2]

1. *University of Minnesota,* ***2.*** *Mississippi State University,* ***3.*** *Department of Wildlife, Fisheries and Aquaculture, Mississippi State University*

Environmental monitoring is an emerging tool in cryptic species detection (e.g., eDNA) and disease surveillance, such as wastewater testing during the SARS-CoV-2 epidemic. By testing environmental sources rather than individuals, surveillance can be more efficient, allowing the use of fewer tests to detect the species or pathogen of interest. Chronic wasting disease (CWD) costs millions of dollars for surveillance and management in the United States, Canada, and Europe. Detecting CWD early, while prevalence at the local population level is still low provides the best opportunity for management, however detection by sampling individual animals is labor-intensive and often relies on samples submitted voluntarily by hunters. In this study, we built upon previous work that demonstrated that real-time quaking-induced conversion (RT-QuIC) effectively detects CWD prions in environmental samples from natural areas of deer congregation called scrape sites. From November 2023 to April 2024, we collected samples from 950 scrape sites in 9 states with differing epidemiological histories and apparent CWD prevalence (from newly detected to nearly 50%). For each scrape, we tested soil and licking branches for presence of prion seeding activity. In addition to detecting prion seeding activity in areas with known CWD presence, we also found that environmental monitoring identified prion contamination at scrape sites up to 65 km away from the leading edge of a CWD zone. In this presentation, we will discuss the implications of our initial results and discuss the utility of scrape-site monitoring for informing wildlife disease management and surveillance strategies.

Development of a rapid and reliable experimental infection model for an emergent hoof disease in elk (Cervus canadensis)

Tuesday, 29th July - 11:45: Student Presentations - Hoofstock (Salon BC) - Oral

Holly Drankhan [1], ***Kyle Taylor*** [2], ***Devendra Shah*** [3], ***Charlie Park*** [1], ***Margaret Wild*** [1]

1. *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University,* ***2.*** *Washington Animal Disease Diagnostic Laboratory, College of Veterinary Medicine, Washington State University,* ***3.*** *Texas Tech University*

Treponeme-associated hoof disease (TAHD) causes foot lesions, lameness, and apparent increased mortality in free-ranging elk (*Cervus canadensis*) in Washington, Idaho, Oregon, and California, USA. TAHD is likely a polybacterial disease associated with *Treponema* spp., which are fastidious spirochetes. However, many details of disease etiology and pathogenesis are unknown but may be elucidated with a controlled experimental infection model. Our goal was to develop a model for rapid and reliable induction of TAHD lesions in captive elk maintained under approved animal welfare protocols. Inocula consisting of macerated tissue and cultures of mixed anaerobic bacteria including spiral-shaped bacteria resembling spirochetes were prepared from naturally occurring TAHD lesions and applied to the hind feet of treatment elk (n = 5), which were abraded and wrapped to expedite lesion development. Following inoculation, all treatment elk developed interdigital erosions or ulcers on both hind feet that were grossly indistinguishable from mild to moderate TAHD lesions in free-ranging elk. In 4/5 treatment elk, lesions were observed 14 days after initial inoculation, and histologic examination of biopsies collected on day 28 confirmed TAHD through identification of spirochetes within lesions on one or both hind feet. These lesions were not observed in mock-inoculated control animals (n = 2). 16S rRNA gene amplicon sequencing was used to characterize changes to the skin microbiome associated with lesion development and provide new insights into disease etiology. This experimental infection model can facilitate further investigations into host and environmental factors that may influence disease susceptibility and transmission in elk populations.

Incisor pathology in muskoxen from the Canadian Arctic

Tuesday, 29th July - 12:00: Student Presentations - Hoofstock (Salon BC) - Oral

Erica Suitor **[1], *John Scheels*** **[2], *Jamie L. Rothenburger*** **[1], *Fabien Mavrot*** **[1], *Ekaluktutiak Hunters and Trappers Organization*** **[3], *Kugluktuk Angoniatit Association*** **[4], *Olokhaktomiut Hunters and Trappers Organization*** **[5], *Lisa-Marie Leclerc*** **[6], *Douglas Whiteside*** **[1], *Tracy Davison*** **[7], *Susan Kutz*** **[1]**

***1.** University of Calgary, Faculty of Veterinary Medicine, **2.** Milwaukee County Zoo, **3.** Ekaluktutiak Hunters and Trappers Organization, **4.** Kugluktuk Angoniatit Association, **5.** Olokhaktomiut Hunters and Trappers Organization, **6.** Government of Nunavut, Department of Environment, **7.** Government of the Northwest Territories, Department of Environment & Climate Change*

Chronic dental lesions are painful and impairs digestive efficiency and overall productivity in mammals, leading to broader health issues. In the declining muskox (*Ovibos moschatus*) population from Victoria Island in the Canadian Arctic, an unusual occurrence of incisor abnormalities was detected through a community-based muskox health surveillance program. Here, we present the first comprehensive examination of dental lesions and anomalies in muskoxen, focusing on the incisors. We examined 243 mandibles from community-harvested muskoxen, collected from two distinct arctic locations: 124 individuals from Victoria Island and 119 from the adjacent mainland. Gross examination revealed that fractured incisors were the most frequent lesion, especially among adults (≥5 years old) on Victoria Island, where 83.6% (56/67) of individuals displayed at least one incisor with a complicated fracture. In contrast, the most frequent lesion in adults on the mainland was labial abrasion, with 68.1% (49/72) having at least one incisor worn, specifically the central incisors (I_1 and I_2) wearing to the dentine and, in severe cases, to the pulp. Other gross lesions included unerupted fourth incisors and drift/malposition. Radiographic analysis of a subset of 136 incisor arches, selected by presence of gross abnormalities, revealed additional lesions, such as root fractures and endodontic disease associated with crown and root fractures. Other radiographic lesions included hypercementosis, ankylosis, dilaceration, and retained primary tooth roots. These results highlight the high prevalence and severity of incisor pathology in muskoxen and will also be used to assess the epidemiology of these lesions and the subsequent impact on body condition and reproduction.

Investigating Pestivirus Infections in Barren-Ground Caribou: Strain Identification and Diagnostic Test Refinement

Tuesday, 29th July - 12:15: Student Presentations - Hoofstock (Salon BC) - Oral

Jessie Olson [1]***, Susan Kutz*** [2]***, Guido van Marle*** [3]***, Naima Jutha*** [4]***, Stephanie Behrens*** [5]***, Frank van der Meer*** [1]

1. *University of Calgary, Faculty of Veterinary Medicine,* ***2.*** *University of Calgary, Faculty of Veterinary Medicine, 3330 University Drive NW, Calgary, Alberta T2N 4N1, Canada,* ***3.*** *University of Calgary, Department of Microbiology Immunology and Infectious Diseases,* ***4.*** *Government of the Northwest Territories, Department of Environment & Climate Change,* ***5.*** *Tłı̨chǫ Government*

Community-based wildlife health surveillance is crucial for understanding wildlife health by combining Traditional Knowledge with scientific methods. One overlooked aspect of caribou-health is viral ecology, as virus research is limited by sampling challenges and lack of caribou-specific diagnostics. Pestiviruses are concerning as they are highly infectious, pathogenic and abortogenic in livestock. Although antibodies to pestiviruses have been found in Canadian-caribou, specific strains remain unidentified. This project aims to identify circulating pestivirus strains through RT-PCR and develop caribou-specific assays (ELISA).

Samples were collected with community collaboration and a hunter-sampler kit monitoring program through the Kutz-Research group, University of Calgary. Pestivirus presence was assessed in 100 spleens and 23 placentas using RT-PCR. Concurrently, a caribou-specific ELISA was developed for border disease virus (BDV) strains to detect caribou antibodies in filter-paper eluates and serum (n=200). Strains were expressed in eukaryotic cells using plasmid vectors and protein presence was confirmed by Western blot.

The ELISA has been optimized for antibody types, concentrations, and vector-protein tags. BDV E2 protein expression of strains 1,2,3 and 8 was successful, enabling detection of BDV antibodies in caribou filter-paper eluates. ELISA testing identified BDV antibody-positive caribou samples. RT-PCR analysis is in progress, a positive result has been sent for Sanger-sequencing.

The presence of antibodies against pestiviruses is concerning, as viral circulation may impact herd health. Further study is needed to determine if antibody reaction with multiple BDV strains reflects cross-reactivity or multiple strains circulating in caribou. This research aims to improve caribou health monitoring and foster dialogue with Northern communities on the implications of viruses in caribou populations.

An occupancy analysis to determine the unbiased prevalence of three pathogens in free-ranging eastern box turtles (Terrapene carolina carolina) in central Illinois

Tuesday, 29th July - 13:30: Student Presentations - non-mammal (Salon BC) - Oral

***Maris Daleo* [1], *Kirk Stodola* [2], *Laura Adamovicz* [1], *Thomas Benson* [2], *Chistopher Phillips* [2], *Matthew Allender* [1]**

1. *Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign,* ***2.*** *Illinois Natural History Survey*

Wildlife epidemiologists aim to understand how pathogens spread across landscapes; however, raw data without unbiased estimates is often reported, which may lead to ineffective management actions. In chelonian disease surveillance, prevalence is typically determined using quantitative PCR (qPCR), but if an animal is not shedding the virus during surveillance or viral load is too low for detection, the animal will appear qPCR negative; thus, occupancy modeling can provide a better estimation of the true prevalence within a population by accounting for false negative test results. We utilize dynamic occupancy models to generate unbiased disease parameter estimates for three pathogens in eastern box turtles (*Terrapene carolina carolina*). We analyzed *Terrapene* herpesvirus 1, box turtle *Mycoplasma* sp., and *Terrapene* adenovirus detection data from five sites in central Illinois. The unbiased prevalence for these three pathogens ranged from 43-63.5%, much higher than apparent prevalence values ranging from 7.84-13.1%. However, the detection probability for these pathogens in a single swab ranged from 18.3-37.7%, emphasizing the need for multiple sampling occasions to determine true pathogen status. Pathogen occupancy was not different between the sites surveyed, suggesting that some of these pathogens may be widespread in Illinois populations. Continued investigation of pathogen impact on health in free-living box turtles and their communities will fill knowledge gaps in shedding patterns and latent disease periods and promote effective conservation strategies.

How’s the Weather in There? Impacts of extreme weather events on parasitism in riverine fishes

Tuesday, 29th July - 13:45: Student Presentations - non-mammal (Salon BC) - Oral

Connor Whalen [1], ***Desmond Boyd*** [2], ***Shyanne Christner*** [3], ***Gabriella Commisso*** [1], ***Imani Jones*** [4], ***Katie Leslie*** [1], ***Jolee Thirtyacre*** [1], ***Armand Kuris*** [5], ***Justin Mann*** [6], ***Henry Bart Jr.*** [6], ***Dakeishla Diaz Morales*** [1], ***Chelsea Wood*** [1]

1. *University of Washington,* ***2.*** *University of South Carolina,* ***3.*** *Valdosta State University,* ***4.*** *Tuskeegee University,* ***5.*** *University of California Santa Barbara,* ***6.*** *Tulane University*

Extreme weather events (EWE) have increased in frequency and magnitude due to anthropogenic climate change. These extreme weather events, including hurricanes, floods, and droughts, can cause outbreaks of parasitic diseases in humans, but little is known about how these events impact parasite abundances in wildlife populations. Fish serve as hosts for several parasite groups and therefore represent an excellent model to understand parasite responses to EWE. We expected that parasites with complex life cycles and sensitive free-living larval stages would decrease in abundance after EWE, while spore-forming and direct life cycle parasites might withstand such conditions. We dissected 1,188 preserved fish across 7 fish species collected between 1963 and 2005 from the Pearl River in Louisiana and examined them for metazoan parasites. We also identified EWE that affected this river system during the focal time period, including 5 major droughts, 3 major floods, and 25 hurricanes. We evaluated the effect of EWE disturbances on parasite abundance using generalized linear mixed models, finding that change in parasite abundance in response to an EWE is dependent upon parasite type. By quantifying the impact of extreme weather events on parasitism in wildlife populations across this 42 year period, we are building an understanding of how these manifestations of anthropogenic climate change affect wildlife populations.

Exploring St. Louis encephalitis and West Nile virus infection kinetics and host immunity within House sparrows (Passer domesticus)

Tuesday, 29th July - 14:00: Student Presentations - non-mammal (Salon BC) - Oral

Jennifer Buczek [1], *Lark L. Coffey* [2], *Angela Bosco-Lauth* [1]

1. *Colorado State University,* **2.** *University of California Davis*

House Sparrows *(Passer domesticus)* are an overpopulated, invasive, passerine species that play a major role in the sylvatic cycling of West Nile (WNV) and St. Louis encephalitis viruses (SLEV) in the same geographical zones. WNV and SLEV are both flaviviruses that cause febrile illness and encephalitis in humans. Post 2015, a new genotype of SLEV was detected in California (CA) which has resulted in re-emergent SLEV human cases. Pre-2015, WNV seemingly outcompeted historical SLEV strains (hSLEV) in overlapping regions of CA; however, post-2015 contemporary SLEV (cSLEV) may escape this competition by an unknown mechanism. Our hypothesis was that cSLEV evades avian host immunity such that prior infection with WNV does not protect against cSLEV infection, thus promoting re-emergence. Sparrows (n=18) were challenged with WNV and then divided into 2 groups. After 28 days, surviving birds were challenged with hSLEV or cSLEV. Levels of viremia (1-5 and 7 days post-inoculation), clinical signs, mortality, and neutralizing antibody were measured after each challenge. Contrary to our hypothesis, we found that all birds challenged with either SLEV isolate were aviremic and had cross-neutralizing antibody titers ranging from 10-160 against SLEV. This observation suggests that WNV confers sterilizing protection against both cSLEV and hSLEV in the short term. These findings illustrate the complexity of viral infection kinetics, strain variability, and avian immunity that warrant further investigation. Furthermore, this study demonstrates effective use of a “pest” model to clarify these complexities while also enhancing wildlife biodiversity by removing an invasive species from the environment.

Harbor porpoise predation by grey seals in the St. Lawrence Estuary, Québec, Canada

Tuesday, 29th July - 14:15: Student Presentations - non-mammal (Salon BC) - Oral

Amélia Dalpé [1] ***, Émilie L. Couture*** [1] ***, Stéphane Lair*** [2] ***, Cristiane C. Albuquerque Martins*** [3] ***, Robert Michaud*** [4] ***, Geneviève Parent*** [5]

1. *Centre québécois sur la santé des animaux sauvages / Canadian Wildlife Health Cooperative, Faculté de médecine vétérinaire, Université de Montréal,* ***2.*** *Canadian Wildlife Health Cooperative / Centre québécois sur la santé des animaux sauvages, Université de Montréal, Faculté de médecine vétérinaire, 3200 rue Sicotte, St-Hyacinthe, Québec J2S 2M2, Canada,* ***3.*** *Parks Canada,* ***4.*** *Quebec Marine Mammal Emergency Response Network– Groupe de recherche et d'éducation sur les mammifères marins,* ***5.*** *Fisheries and Oceans Canada/ Maurice Lamontagne Institute*

Harbour porpoise (*Phocoena phocoena*) body parts are found floating or ashore in the St Lawrence Estuary and reported to the authorities of the St Lawrence Saguenay Marine Park every summer since 2004. Initially suspected to be remains from poaching activities, sections of skin and blubber (n=77) and whole carcasses (n=17) collected between 2008 and 2022 were assessed for the presence of distinctive grey seal (*Halichoerus grypus*) predation lesions as described in the southern North Sea. Indications of the antemortem occurrence of the interactions were sought and, when possible, age and nutritional condition of affected individuals were estimated. Lesions were swabbed for molecular detection of grey seal DNA using a dye-based qPCR method. Most samples met the diagnostic criteria proposed for suspected predation events by grey seals, including large (>5x 10 cm) full thickness blubber and skin defects in carcasses or isolated severed sections of skin and blubber presenting smooth edges and defined angles, as well as repeated punctures matching grey seal dental interval (0,5-2 cm). Grey seal DNA was detected in almost all cases. While discrimination between scavenging and predation could rarely be made, the generally low level of decomposition was suggestive of perimortem interaction. Immature individuals in good nutritional condition were most represented in suspected predation cases. As previously observed in the southern North Sea and UK waters, predation by grey seals appears to be a relatively common cause of death in immature well-conditioned harbor porpoises in the St. Lawrence Estuary.

Adenovirus and Herpesvirus Detection in Ornate Box Turtles (Terrapene ornata ornata) in Illinois

Tuesday, 29th July - 14:30: Student Presentations - non-mammal (Salon BC) - Oral

Erika Suniga [1], Laura Adamovicz [2], Madeline Brookings [1], Kaitlin Moorhead [1], Amber Simmons [3], Crystal Moreno-Garcia [1], Matthew Allender [4]

__1.__ Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign, __2.__ Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign, __3.__ Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign, __4.__ Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign; Veterinary Diagnostic Laboratory, Wildlife Epidemiology Section, University of Illinois Urbana-Champaign; Chicago Zoological Society/Brookfield Zoo

Herpesviruses and adenoviruses are significant chelonian pathogens worldwide. Ornate box turtles (*Terrapene ornata ornata*) are listed as endangered, threatened, or of special conservation concern in many US states, including Illinois. Knowledge of pathogen epidemiology and impacts is critical for designing effective recovery plans, however, surveillance for DNA viruses in wild ornate box turtles is lacking. The purpose of this study was to conduct state-wide surveillance for herpesviruses and adenoviruses in Illinois ornate box turtles. Radio tracked and incidentally encountered turtles (N = 160) were evaluated from 15 populations using physical examination, clinical pathology, and PCR testing of oral/cloacal swabs (N = 359). Overall, 43 samples (sample prevalence 12%) from 34 individuals (individual prevalence 21.25%) at seven sites tested positive for adenoviruses. Adenovirus prevalence was higher in spring vs. summer (OR = 3.92) and greatest in the largest population in the state (27.3%). Two novel adenoviruses were identified via DNA sequencing and were 85 – 94% identical to existing box turtle adenovirus sequences. Both viruses were present in some populations, while only one virus was detected in others. Intermittent shedding occurred in serially-sampled turtles and no clinical signs of illness were associated with adenovirus detection. One apparently healthy adult male from a site with sympatric eastern box turtles (*Terrapene carolina carolina*) tested positive for Terrapene herpesvirus 2, but all other herpesvirus testing was negative. Continued viral pathogen surveillance is helpful for characterizing potential disease risks to conservation management of free-ranging populations and will further enhance conservation efforts for this species.

COMPARATIVE GENE EXPRESSION OF THREE SEA STAR SPECIES WITH VARYING SUSCEPTIBILITY TO SEA STAR WASTING DISEASE

Tuesday, 29th July - 14:45: Student Presentations - non-mammal (Salon BC) - Oral

Grace Crandall [1], ***Melanie Prentice*** [2], ***Alyssa-Lois Gehman*** [3], ***Drew Harvell*** [4], ***Paul Hershberger*** [5], ***Samuel White*** [1], ***Steven Roberts*** [1]

1. *University of Washington,* **2.** *Hakai Institute,* **3.** *The Hakai Institute,* **4.** *University of Washington, Friday Harbor Laboratories & Cornell University,* **5.** *U.S. Geological Survey*

Sea star wasting disease (SSWD) has caused widespread mortality among many sea star species along the North American west coast since its initial outbreak in 2013/2014. Sea star species vary in vulnerability, though it is unknown why. We investigated this question with three species of varying susceptibility to SSWD, from highest to lowest - Pycnopodia helianthoides, Pisaster ochraceus, and Dermasterias imbricata. One individual of each species was co-housed in replicate tanks. To create an exposed treatment and initiate disease spread, half of the tanks (N=8) contained a second P. helianthoides that was wasting, and to create a control treatment, the other half of the tanks (N=8) contained a second P. helianthoides that was not wasting. Coelomocytes, the cells responsible for innate immunity in echinoderms, collected from Day 12 of the experiment, were selected for RNA extraction and total RNA sequencing. This time point was chosen based on phenotypic observational data from the experiment; day 12 is a time point prior to early disease signs and after heavy SSWD exposure in the exposed group, and stars are likely beginning to launch an immune response. By the end of the experiment, all SSWD-exposed P. helianthoides and some SSWD-exposed P. ochraceus progressed through disease signs to mortality. None of the exposed D. imbricata showed any signs of disease. The gene expression of the stars was compared across species in order to determine if there are any different genetic responses occurring that might relate to their differences in susceptibility.

Surveillance and Management of Invasive Marmosets (Callithrix sp.) as a Strategy to Minimize Risks Associated with the Buffy-Tufted Ear Marmoset (Callithrix aurita) Conservation Translocation to Atlantic Forest Fragments in Southeastern Brazil

Tuesday, 29th July - 15:45: Student Presentations - Spillover and transmission (Salon BC) - Oral

Isabela Mascarenhas [1]***, Larissa Jesus*** [1]***, Gabriela Assis*** [2]***, Cristiana Brito*** [2]***, Alex Pauvolid-Côrrea*** [1]***, Fabiano Melo*** [1]***, Fabiana Voorwald*** [1]

1. *Universidade Federal de Viçosa,* ***2.*** *Instituto Rene Rachou - Fiocruz Minas*

The buffy-tufted ear marmoset (*Callithrix aurita*) is an endangered Brazilian primate, threatened by habitat loss, competition and hybridization with its invasive congeners. The species is covered by the National Action Plan for the Conservation of Atlantic Forest Primates and the Maned Sloth (PAN-PPMA), directed by the Brazilian Ministry of Environment and Climate Change. The PAN-PPMA defined strategies for the species conservation, among them: manage *C. aurita* populations aiming at their viability; manage allochthonous primates in areas important for the *C. aurita* conservation; and evaluate important disease for Atlantic Forest primates. Our research aims to adhere those guidelines and minimize health risks related to the translocation of *C. aurita* from *ex situ* to Atlantic Forest fragments in southeastern Brazil. From April 2021 to September 2024, we captured 83 free-living invasive hybrids (*Callithrix* sp.) in Viçosa, state of Minas Gerais, an area evaluated for *C. aurita* reintroduction, and surveillance and management of invasive marmosets. Seventy-three individuals were sterilized through male deferentectomy and female salpingectomy. Neutralizing antibodies for yellow fever virus were detected in one of 71 individuals tested, and all 31 marmosets tested for mayaro virus were seronegative. Likewise, we have not detected DNA of *Plasmodium vivax*, *P. brasilianum* and *P. simium*, malaria etiological agents in humans and non-human primates. We intend to endorse information for the consolidation of a health risk analysis for *Callithrix aurita* translocation, establish a long-term project to evaluate the impact of pathogens in primate conservation, and indicate the risk of emerging infectious diseases to public health.

The authors gratefully acknowledge the financial support from CAPES, CNPq, and FAPEMIG

Prevalence of canine distemper virus in wild carnivores of North Carolina submitted to a public health laboratory for rabies virus testing

Tuesday, 29th July - 16:00: Student Presentations - Spillover and transmission (Salon BC) - Oral

Seth Lattner [1], ***Colleen Olfenbuttel*** [2], ***Kelly Douglass*** [3], ***Rebecca Pelc*** [4], ***John Bunting*** [4], ***Ellen Haynes*** [1], ***Michael Yabsley*** [1], ***Christopher Cleveland*** [1]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *North Carolina Wildlife Resources Commission,* ***3.*** *United States Department of Agriculture,* ***4.*** *North Carolina State Laboratory of Public Health, Department of Health and Human Services*

Canine distemper virus (CDV) is a highly infectious morbillivirus (Family Paramyxoviridae) that can cause morbidity and mortality in numerous mammalian species, especially carnivores. Neurologic disease from CDV infections is indistinguishable from that caused by rabies virus (RABV). Thus, many neurological wild animals are submitted to state public health agencies for RABV testing, without subsequent testing for CDV or other pathogens. We investigated the prevalence of CDV in wild carnivores submitted to North Carolina State Laboratory of Public Health (NCSLPH) for RABV screening from 2021-2024. Brain samples from RABV-negative wild carnivores were screened for CDV using real-time RT-PCR. Additionally, the hemagglutinin gene of CDV was amplified from a subset of positive samples for phylogenetic analysis. Overall, CDV was detected in 46% (174/381) of brain samples tested. By species, CDV was detected in 49% (137/281) of raccoons, 44% of foxes (28/63), 14% of skunks (4/29), and 63% of coyotes (5/8). Detection prevalence varied between years, with the highest prevalence in 2021 (55%, n = 60), and the lowest in 2023 (39%, n = 77). Annual variation in CDV prevalence likely resulted from increased raccoon submissions, as raccoons accounted for 85% of total samples in 2021 and 66% in 2023. Phylogenetically, 23 samples grouped with the North/South America-4 lineage. These results indicate that leveraging wildlife submissions from public health diagnostic labs improves CDV surveillance. Understanding CDV prevalence on the landscape is important for management and conservation of wild carnivores, including rare or endangered species such as the Eastern spotted skunk and red wolf.

Applying a Continuum of Care Framework to Convention on Migratory Species Resolutions: Strategic Opportunities for Wildlife Health Management

Tuesday, 29th July - 16:15: Student Presentations - Spillover and transmission (Salon BC) - Oral

Caroline Kern-Allely [1], ***Ruth Cromie*** [2], ***Craig Stephen*** [3]

***1.** Colorado State University,* ***2.** Wildfowl & Wetlands Trust, Convention on Migratory Species,* ***3.** McEachran Institute*

Wildlife health exists along a continuum, from thriving to coping to recovering. Tailoring a continuum of care, such that populations are met where they are in the continuum of health, can lead to more effective management. Our objective was to explore the utility of a continuum of care concept as a strategic framework for wildlife health program planning. We analyzed how the suite of 43 resolutions adopted at the most recent Conference of Parties (COP14) of the Convention on the Conservation of Migratory Species of Wild Animals (CMS) aligned with a continuum of care approach to wildlife health in addressing determinants of health and drivers of harm. We found the primary determinants of health addressed in the resolutions were (i) needs for daily living, (ii) human expectations, and (iii) sustaining root causes of health that maintained adaptive capacity. The primary drivers of harm addressed were (i) habitat loss or degradation and (ii) overexploitation. The CMS resolutions are well-aligned with a continuum of care approach, incorporating strategies aimed at addressing the root causes of harm, reducing immediate health risks, and promoting long-term resilience. Less attention focused on actions that will reduce population vulnerability in advance of harms. Using the continuum of care framework highlighted opportunities to clarify and expand robust wildlife health definitions, priorities and programs. The continuum of care framework could help decision-makers identify opportunities to integrate management approaches across the continuum and foster more effective and integrated wildlife health and conservation strategies.

Feeders, Feathers, and Feces: Finding Ways to Prevent Salmonella Infections in Birds and People

Tuesday, 29th July - 16:30: Student Presentations - Spillover and transmission (Salon BC) - Oral

Kimberly Perez *[1]*, ***Sonia M. Hernandez*** *[2]*, ***Nikole Castleberry*** *[2]*, ***Sarah Dean*** *[3]*, ***Raquel Francisco*** *[4]*, ***Nicole Kemon*** *[5]*, ***Elizabeth Pienaar*** *[5]*, ***Nikki Shariat*** *[6]*, ***Erin Lipp*** *[1]*

1. *Environmental Health Sciences, College of Public Health, University of Georgia,* ***2.*** *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***3.*** *Odum School of Ecology, University of Georgia,* ***4.*** *Warnell School of Forestry & Natural Resources, Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***5.*** *Warnell School of Forestry and Natural Resources, University of Georgia,* ***6.*** *Department of Population Health, Poultry Diagnostic and Research Center*

Globally, salmonellosis outbreaks are common in songbird populations. *Salmonella* outbreaks have caused significant mortality events in wild songbirds, with evidence suggesting increasing frequency and severity. *Salmonella* remains a public health concern—a 2021 *Salmonella* Typhimurium outbreak in humans was linked to handling bird feeders.

To address *Salmonella* transmission at backyard feeders, we developed a two-year study to identify birds shedding *Salmonella* from nine sites in three Georgia counties, for 10 months, across a gradient of landscapes and assess bird feeding motivations and disease prevention practices. *Salmonella* prevalence was 2% in birds (17/803) and 14% (10/72) in environmental samples consisting of a monthly swab of each feeder and the surrounding environment. None of the bird feed samples (0/26) resulted in positive cultures.

The birds from which we isolated *Salmonella* represented 12 species across all land-use gradients in all three counties and occurred year-round but more frequently in spring and summer. The highest prevalence occurred in Red-bellied Woodpecker (n=3), Northern Mockingbird (n=2), Tufted Titmouse (n=2), and Northern Cardinal (n=2). Notably, these are not species typically linked to outbreaks or mortality events. The remaining positives were evenly distributed over eight species. To understand human behaviors influencing transmission, we conducted in-depth interviews, identifying three feeding behavior types: Enthusiastic (n=19), who acknowledged risks and practiced prevention; Well-Intentioned (n=27), who cleaned feeders but lacked pathogen awareness; and Self-Interested (n=7), who dismissed disease concerns. Key to preventing future outbreaks is understanding transmission dynamics including the species transmitting *Salmonella*, environmental persistence, and the behavior of people influencing transmission.

Gut feelings: Exploring gastrointestinal parasite sharing at the wildlife-livestock interface in Kenya

Tuesday, 29th July - 16:45: Student Presentations - Spillover and transmission (Salon BC) - Oral

Kim van de Wiel [1], ***Benedict Karani*** [2], ***Amy Sweeny*** [3], ***Phil Toye*** [2], ***Fiona Kenyon*** [4], ***Andy Fenton*** [1], ***Jakob Bro-Jorgensen*** [1]

1. *University of Liverpool*, **2.** *International Livestock Research Institute*, **3.** *University of Sheffield*, **4.** *Moredun Research Institute*

Amid the golden savannas of Kenya's Maasai Mara, wildebeest and zebras graze alongside cattle and sheep. Beneath their hooves, a network of gastrointestinal parasites quietly thrives, moving unnoticed between hosts. Since these parasites can impact the health of both wildlife and livestock, this raises a question… What happens when these animals share the same pastures?

To unravel this, we collected faecal samples from 14 wild and domestic African herbivore species across landscapes where these animals either coexisted or grazed separately. We examined the samples for nematode eggs and coccidia oocysts, while DNA analysis helped us identify the specific nematode species present in each host.

Our findings reveal a surprising contrast: while living side by side does not change whether an animal carries parasites, it does influence the intensity of infection. Interestingly, animals in shared pastures experience higher nematode burdens, yet coccidia infections are lower when wildlife and livestock graze together. These patterns illustrate how some parasites may be diluted in mixed grazing systems while others are amplified. A closer look at nematodes reveals that the coexistence of wild and domestic animals does not affect the types of nematodes present. However, wildlife shows greater variation in nematode community composition, which may indicate the impact of farming practices on parasite dynamics.

These findings offer valuable insights into the complex interactions between wildlife and livestock in shared landscapes. Understanding how parasite dynamics unfold in these multi-host, multi-parasite systems is essential for striking a balance between conservation and pastoral livelihoods.

Disease and Immunity: What do host inflammatory profiles tell us about unknown disease exposures in wild free-roaming bighorn sheep?

Tuesday, 29th July - 17:00: Student Presentations - Spillover and transmission (Salon BC) - Oral

Luke Weinstein [1], ***Brianna Beechler*** [1], ***Anna Jolles*** [1], ***Brian Dolan*** [1], ***Clinton W. Epps*** [1]

1. *Oregon State University*

Cytokines, an important immune modulator, can provide informative signals to researchers about immune responses being mounted by the host and indicate active stress, trauma, autoimmune disease, or infection. They may be able to tell the researcher when an animal is undergoing an inflammatory response, and what type of response they are mounting. There are few studies about the variety of inflammatory states in wild free-roaming ungulates. To address this, we measured six cytokines (IL 4, IL6, IL10, IL17a, TNFa, IFNγ) in the plasma of 581 wild desert and Sierra Nevada bighorn sheep (*Ovis canadensis nelsoni* and *Ovis canadensis sierrae*, bighorn) across southern California, USA. We utilized a custom 6-plex magnetic bead assay developed for domestic sheep (SCTY1-91K, Millliplex® xMAP®, Merck-Millipore, France) and demonstrated its utility for studying wild bighorn. We describe three distinct inflammatory profiles in bighorn defined by extreme levels of IL6 or IL17a, and a coelevated status of TNFa and IL10. We discuss the implications of these inflammatory states in terms of parasite burden, serology and PCR results, constitutive immune measures, location, age, sex, and mortality. The IL6 and IL17a profiles were locally concentrated in specific metapopulations of desert bighorn sheep and suggest infection as well as long-term mortality risk. The coelevated animals were more geographically spread, representing a syndrome that associated with a higher neutrophil to lymphocyte ratio and the potential for a chronic condition. This work demonstrates the utility of such studies in wild animals and indicates the potential diagnostic role of cytokines in wild animals.

Regional Coordination Advances Fish and Wildlife Health Across the US

Thursday, 31st July - 10:45: Transboundary Wildlife Health Management (Oak Bay Room) - Oral

Ellen Haynes [1]***, Tolani Francisco*** [2]***, Tricia Fry*** [3]***, Anne-Justice Allen*** [4]***, Melanie Kunkel*** [5]***, Noelle Thompson*** [6]***, Sonja Christensen*** [7]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *Native American Fish and Wildlife Society,* ***3.*** *Midwest Association of Fish and Wildlife Agencies,* ***4.*** *Arizona Game and Fish Dept.,* ***5.*** *College of Veterinary Medicine, Cornell University,* ***6.*** *Western Association of Fish and Wildlife Agencies,* ***7.*** *Michigan State University*

In response to increasing threats to wildlife health and efforts to manage healthy free-ranging wildlife populations, Regional Fish and Wildlife Health Coordinator positions were established in 2022 in collaboration with the Midwest, Northeast, Southeastern, and Western Associations of Fish and Wildlife Agencies, as well as the Native American Fish and Wildlife Society. The Regional Coordinators have built relationships between state, federal, and academic partners to understand and address gaps in wildlife health, including some unique to their regions/tribes, and others shared across regions/tribes. Working with the national Fish and Wildlife Health Coordinator, the Regional Coordinators have contributed to a revised National Fish and Wildlife Health Initiative Toolkit and developed guidance for states to incorporate wildlife health into State Wildlife Action Plans. In addition, the Regional Coordinators lead regional wildlife health committees, provide training to state agency personnel, organize symposia, collaborate on grants, and coordinate with a variety of regional committees and working groups. Notable accomplishments include the establishment of a Northeast Fish and Wildlife Health Committee, development of an interdisciplinary Southeast Cervid Health Working Group, creation of Voluntary Best Management Practices for Reducing Unintended Ingestion of Lead Ammunition and Tackle Residues in Wildlife, and communication about CWD regulations and management actions across the West. These activities advance the Coordinators' mission to develop resources and partnerships among fish and wildlife agencies to strengthen capacity for fish and wildlife health through monitoring, research, and management, and to promote the health of fish and wildlife populations and the ecosystems they inhabit.

Building Wildlife Health and Zoonotic Disease Capacity Both Within and Beyond California's Borders

Thursday, 31st July - 11:00: Transboundary Wildlife Health Management (Oak Bay Room) - Oral

Brandon Munk [1]***, Hannah Shapiro*** [2]***, Mark Lubell*** [2]***, Deana Clifford*** [1]***, Alex Heeren*** [1]***, Will Schmelter*** [1]***, Garry Kelley*** [1]***, Kirsten Gilardi*** [2]

1. *California Department of Fish and Wildlife,* ***2.*** *University of California Davis*

Rapid detection, characterization and response is essential to minimize emerging pathogen and disease threats to wildlife populations and prevent potential zoonotic spillover. However, wildlife health resources remain insufficient despite increased interest, awareness and expectations for timely action. To identify weaknesses, inefficiencies, and capacity limitations for wildlife disease surveillance, diagnostics, outbreak response, forecasting and management, we invited wildlife and zoonotic disease experts from California and adjacent state agencies, institutions and organizations with either the mandate, need, capacity or expertise to detect, report or study wildlife diseases to participate in three, two-day workshops. In the first workshop, we introduced the project and used mental modeling exercises to explore the determinants of wildlife health (DoWH). At the second workshop, participants reported organizations' authorities, needs and capacity for wildlife health. We then used the DoWH mental models from Workshop 1 to identify the gaps and barriers to collaboration. In the third workshop participants identified solutions to the identified gaps and barriers (e.g. improve wildlife diagnostics by curating gold standard specimen sets, validating tests in wildlife species and developing disease or species agnostic testing platforms). Scattered throughout, invited talks highlighted different collaborative models and how they address challenges to collaboration. This work demonstrated broad interest and need amongst wildlife health professionals for increased collaboration and a strong desire to work towards increased collaboration. Next steps will be to develop and implement an operational framework to facilitate increased collaboration for wildlife health within California and then beyond to support regional wildlife health priorities.

Managing health risks in translocations of displaced wildlife: New IUCN Guidelines on responsible Translocation of displaced Organisms

Thursday, 31st July - 11:15: Transboundary Wildlife Health Management (Oak Bay Room) - Oral

Richard Kock [1], ***Julie Sherman*** [2], ***Vivek Menon*** [3], ***Sonja Luz*** [4], ***Tony King*** [5], ***Ashraf N.V.K.*** [3], ***Pritpal Soorae*** [6], ***Axel Moehrenschlager*** [7]

1. *Wildlife Disease Association,* ***2.*** *Wildlife Impact,* ***3.*** *Wildlife Trust of India,* ***4.*** *Mandai Nature,* ***5.*** *Aspinall Foundation,* ***6.*** *Environment Agency, UAE,* ***7.*** *Panthera*

Recent analysis of zoonotic disease by the International Union for the Conservation of Nature (IUCN) found that most modern zoonotic human infections are acquired proximally from domesticated animals and food systems, while disease acquired directly from wildlife is uncommon and usually indirect through insect vectors. The risk of acquiring zoonosis through wildlife is logically higher for captive wildlife, especially animals being translocated. The IUCN has developed a guideline on responsible translocation of organisms displaced by trade, human activities, climatic events and natural disasters, with a major focus on risk reduction and best practice in the face of increasing anthropogenically-driven wildlife dislocation. Experts acknowledge that wildlife translocations, while popular, poses health, behavioural and genetic risks to wild populations, but, when well-managed, can benefit individuals and conservation efforts. This paper introduces the guidance, using the example of orangutan (Pongo spp.) displacement and translocations to illustrate the problem scope, challenges and opportunities. More than 1800 Critically Endangered orangutans have been translocated since 2005 following displacement by the illegal trade, pet ownership and captures driven by human-orangutan conflict. Disease risks for translocated individuals and recipient wild populations, arising from translocated individuals that have been in direct contact or proximity with captive wildlife, peridomestic animals and humans, are relatively high, and mitigation measure have been applied inconsistently. The new guideline sets out practical steps to aid decision-makers and translocation practitioners in determining how to minimise risks and maximise potential for responsible release in these and other situations involving displaced wildlife.

Stronger Together: US-Canada Wildlife Surveillance Initiative for Adaptive Management of Highly Pathogenic Avian Influenza

Thursday, 31st July - 11:30: Transboundary Wildlife Health Management (Oak Bay Room) - Oral

Damien Joly [1]***, Sarah Bevins*** [2]***, Michael Brown*** [3]***, Shannon French*** [4]***, Jolene A. Giacinti*** [5]***, M. Camille Hopkins*** [6]***, Julianna B. Lenoch*** [2]***, Charles Nfon*** [7]***, Cynthia Pekarik*** [3]***, C. LeAnn White*** [8]

1. *Canadian Wildlife Health Cooperative | Réseau Canadien pour la Santé de la Faune,* ***2.*** *USDA APHIS,* ***3.*** *Wildlife Management and Regulatory Affairs Division, Canadian Wildlife Service, Environment and Climate Change Canada, Government of Canada,* ***4.*** *Animal Health Strategic Planning and Research, Canadian Food Inspection Agency, Government of Canada,* ***5.*** *Ecotoxicology and Wildlife Health Division, Science and Technology Branch, Environment and Climate Change Canada, Government of Canada, Ottawa, Ontario, Canada,* ***6.*** *USGS Headquarters, Ecosystems Mission Area,* ***7.*** *National Centres for Animal Disease, Canadian Food Inspection Agency,* ***8.*** *USGS National Wildlife Health Center*

The ongoing epizootic of highly pathogenic avian influenza (HPAI) poses complex threats to biodiversity, public health, agriculture, and the economy in both the United States and Canada. In response, the White House Office of Science and Technology Policy (OSTP) requested in April 2023 that US and Canadian HPAI experts enhance collaborations by first coordinating a virtual bilateral HPAI technical meeting in June 2023. As part of this initiative, a wildlife surveillance and data-sharing working group was formed, including representatives from the US Geological Survey, US Department of Agriculture, US Centers for Disease Control and Prevention, Canadian Food Inspection Agency, Environment and Climate Change Canada, and the Canadian Wildlife Health Cooperative, and tasked with recommending ways to enhance binational cooperation on HPAI wildlife surveillance and data sharing.

This initiative recognized that while surveillance and data sharing are essential for monitoring HPAI, they alone cannot mitigate its broader impacts. Effective management requires integrating surveillance data into a larger framework considering ecological, economic, and social factors. A coordinated binational program would improve early detection, standardize data collection, enhance risk assessment, and enable timely management responses. Aligning surveillance efforts would also reduce duplication, improve cost efficiency, and strengthen pandemic preparedness.

Key recommendations include formalizing cross-border collaborations, defining wildlife data needs, establishing adaptive surveillance strategies, and enhancing diagnostic capacity. Addressing regulatory and data-sharing challenges is critical to ensuring effective interoperability between US and Canadian systems. By fostering a unified approach, this initiative strengthens resilience against HPAI and other emerging threats, aligning with One Health principles to protect wildlife, livestock, and human populations.

Viral Diversity in North American Bats: A Collaborative Multi-State Surveillance System Bridging Public Health Laboratories, Bat Biologists, and Wildlife Disease Researchers

Thursday, 31st July - 11:45: Transboundary Wildlife Health Management (Oak Bay Room) - Oral

Mattison Green [1]***, Nicole Nemeth*** [1]***, Justin Brown*** [2]***, Andrew Allison*** [3]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *Department of Veterinary and Biomedical Sciences, Penn State University,* ***3.*** *Department of Comparative, Diagnostic & Population Medicine, University of Florida*

As bat-borne viruses increasingly fall under the global spotlight, there is a growing need to identify the viruses endemic in North American bats to determine the risk (or lack thereof) they may pose to public, veterinary, and/or wildlife health. Our project aims to create a surveillance system through which multiple states can contribute bat carcasses for targeted diagnostic evaluations and viral testing, increasing the efficiency of such tasks by having centralized labs with the capacity for more in-depth analysis of samples. Through this, we have conducted postmortem evaluations and obtained biological samples for characterization of viral diversity in these bats, in addition to the establishment of a long-term biobank of bat tissue samples. The project began in the northeast with samples from Pennsylvania, with more recent expansion to include seven additional states. Currently, over 2,000 rabies-negative bat carcasses have been obtained in collaboration with state public health and wildlife agencies across Pennsylvania, Florida, Tennessee, Kentucky, Arkansas, Rhode Island, South Carolina, and Washington. Collected samples include lung, heart, liver, spleen, kidney, gastrointestinal tract, furred skin and patagium, and are examined for gross changes, subjected to RNA-sequencing and virus isolation, and contribute to bat biobank development for future surveillance, genetics, taxonomic, and ecoepidemiologic studies. Through opportunistic sampling of rabies-negative bats that oftentimes may be discarded, our project creates a cost-efficient means to determine the diversity of viruses that infect native bat species, and has already begun to create a more accurate picture of the ecological and animal and public health implications of these viruses.

Flocking for Surveillance: Vulture Movement as a Sentinel for Anthrax Outbreaks

Thursday, 31st July - 10:45: Ecology and Management (Lecture Theatre) - Oral

Ayesha Hassim [1], Gareth Tate [2], John Davies [2], Andre Botha [2], Papie Hlalele [3], Nomkhosi Mathebula [3], Barb Wolfe [4], Louis van Schalkwyk [3], Meredith Gore [5], Henriette van Heerden [1]

***1.** University of Pretoria, **2.** Endangered Wildlife Trust, **3.** Department of Agriculture, Skukuza State Veterinary Office, **4.** Colorado State University, **5.** University of Maryland*

Bacillus anthracis, the causative agent of anthrax, has been monitored and studied in the wildlife and environment of Kruger National Park (KNP) for over half a century through passive surveillance and, more recently in Greater Limpopo Transfrontier Park. The disease is enzootic along the Limpopo River system, in northern KNP, with episodic outbreaks extending southward to central KNP. However, current outbreak data are largely confined to areas within KNP where the state surveillance system is active. Vultures play a crucial ecological role as scavengers, influencing disease dynamics both in spreading and limiting pathogen transmission. This was documented by sampling and GPS tracking of vulture movements that provided valuable insight into vultures' behaviour, carcass site locations and potential disease outbreaks, particularly anthrax. Additionally, vultures face growing conservation threats from poachers and wildlife traffickers. In this study, we examine the role of vultures in reducing bacterial inoculum during anthrax outbreaks and how their tracking and sampling can help identify undetected anthrax cases and other diseases, offering a complementary approach to disease surveillance and conservation.

Patterns, Processes and Prions: Modeling Chronic Wasting Disease Dynamics in Alberta

Thursday, 31st July - 11:00: Ecology and Management (Lecture Theatre) - Oral

Owain Barton [1], ***Evelyn Merrill*** [1], ***Anne Hubbs*** [2], ***Margo Pybus*** [2], ***Wiktor Adamowicz*** [1], ***Martin Luckert*** [1], ***Qin Xu*** [1], ***Philip Walker*** [1], ***Hans Martin*** [3], ***Josh Nowak*** [3]

1. *University of Alberta,* ***2.*** *Environment and Protected Areas, Government of Alberta,* ***3.*** *SpeedGoat Wildlife Solutions LLC*

Chronic Wasting Disease (CWD) poses a significant threat to cervid populations across North America with implications for wildlife conservation, ecosystem functioning, and maintenance of traditional cultural values. Integrated Population Models (IPMs) are powerful tools for studying wildlife population dynamics because they integrate multiple data sources and describe population-level patterns as functions of key ecological processes. IPMs are widely used to inform population management but have not traditionally incorporated disease transmission and its demographic impacts. We describe a collaborative effort to integrate disease transmission into an IPM and evaluate potential demographic and spatial harvest management scenarios for mule deer (*Odocoileus hemionus)* populations in Alberta, Canada.

Mule deer abundance estimates and composition from aerial surveys, along with changes in CWD prevalence from ongoing surveillance (2005–2022), were compiled as inputs for the IPM. We modified the IPM structure by partitioning the population into infected and non-infected compartments and modelled the force of infection (i.e., the probability of transitioning between compartments) as a function of demographic and environmental factors. We incorporated functions for winter severity on juvenile survival, movement of deer among Wildlife Management Units (WMUs), and disease-associated mortality to empirically estimate key parameters for simulations of alternative harvest management strategies. Results from the IPM show that the model accurately predicted historic rates of change in sex-specific prevalence for 63 WMUs in Alberta. We present several insights from sensitivity analyses on disease dynamics and preliminary results from comparing harvest strategies in the core disease area versus along the westward edge of CWD spread.

Modeling Contact Dynamics to Understand Potential Disease Transmission Between Wild and Domestic Felids

Thursday, 31st July - 11:15: Ecology and Management (Lecture Theatre) - Oral

Alexandria Hiott [1], ***Alynn Martin*** [2], ***Mason Fidino*** [3], ***Clayton Hilton*** [4], ***Ashley Reeves*** [5], ***Matthew Smith*** [1], ***Lisanne Petracca*** [2]

1. *Ceaser Kleberg Wildlife Research Institute, Texas A&M University Kingsville,* **2.** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* **3.** *Lincoln Park Zoo,* **4.** *Ceaser Kleberg Wildlife Research Institute,* **5.** *East Foundation*

Disease can have profound impacts on wildlife populations, and understanding the drivers of disease transmission is critical for managing spread among individuals. Disease transmission dynamics are of considerable interest when wild and domestic species interact, and even more so if a wild species is of conservation concern. When species are low-density or cryptic, simulations can provide additional insights on population dynamics and potential contact networks. We used integrated step selection analysis (iSSA), which simultaneously estimates movement and resource selection parameters and can incorporate environmental covariates, in combination with an agent-based model (ABM), to investigate potential contacts among sympatric endangered ocelots (*Leopardus pardalis*) and bobcats (*Lynx rufus*) and nearby domestic cats (*Felis catus*) in a wildland-urban interface in South Texas. We used iSSA to estimate movement and resource selection of GPS-collared ocelots, bobcats, and domestic cats and hypothesized that certain environmental covariates (e.g., habitat type, percent canopy cover, and distance to highway) would impact habitat selection and movement. We then built an ABM that incorporated ocelot, bobcat, and domestic cat selection and movement behaviors estimated from these models. Lastly, we manipulated density of each species, as well as environmental factors such as patch configuration and patch size, to determine how contacts among these three species would change. These findings have important implications for disease transmission dynamics in this system, such as Feline Immunodeficiency Virus and Feline Leukemia, and will inform habitat management and assessment of disease risk for ocelots being reintroduced to South Texas.

Impacts of Winter Prescribed Fire on Tick Density and Tick-Borne Pathogen Diversity in the Gulf Coast Prairies and Marshes Ecoregion of Southern Texas, USA

Thursday, 31st July - 11:30: Ecology and Management (Lecture Theatre) - Oral

Rachel Walters [1]***, Scott Henke*** [2]***, Sandra Rideout-Hanzak*** [2]***, Tammi Johnson*** [3]***, Ashley Reeves*** [4]***, Alynn Martin*** [5]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville,* ***2.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville, Kingsville,* ***3.*** *Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M AgriLife Research,* ***4.*** *East Foundation,* ***5.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville*

In southern Texas, prescribed fire is used to improve forage for livestock, enhance wildlife habitat, and combat woody encroachment. Additionally, fire may affect populations of pest species such as ticks. Studies on prescribed fire as a tick control method are limited, especially in this region; therefore, this study evaluates the efficacy of prescribed fires in decreasing hard tick density and tick-borne pathogen diversity. We hypothesize that tick density and pathogen diversity will be reduced following prescribed burning when compared to control treatments. This study uses randomly assigned prescribed fire treatments on patches ≥200 ha in the Gulf Prairies and Marshes ecoregion: 4 winter prescribed burn treatments (2 in 2023, 2 in 2024) and 2 non-burned control treatments. Vegetation within each patch was sampled monthly through February 2025 for questing ticks via dragging a 1-m^2 cloth across two landscape types: around tree mottes ($n = 3$-4 per patch) and through open range ($n = 2 \times 750$ m^2 transects per patch). Preliminary results show that woody tree mottes, which do not burn under prescribed fire conditions, support higher tick densities ($p<0.05$), likely due to both high host-utilization and more favorable microhabitat conditions including increased shade and moisture. Future analyses will include tick species identification and pathogen screening (*Rickettsia*, *Borrelia*, and *Anaplasma* species). Our findings will help determine if winter prescribed fire is an effective component of integrated tick management in southern coastal Texas and inform management decisions.

Spatial risk of chronic wasting disease in white-tailed deer: the role of habitat, minerals, and soil properties in the Midwest, U.S.

Thursday, 31st July - 11:45: Ecology and Management (Lecture Theatre) - Oral

Kristin Bondo [1]***, W. David Walter*** [2]***, Diana L. Karwan*** [3]***, Marc Schwabenlander*** [4]***, Peter Larsen*** [4]***, Tiffany Wolf*** [5]

1. *Department of Veterinary Population Medicine, University of Minnesota,* ***2.*** *U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University,* ***3.*** *Department of Forest Resources, University of Minnesota,* ***4.*** *Department of Veterinary and Biomedical Sciences, University of Minnesota,* ***5.*** *University of Minnesota*

Chronic Wasting Disease (CWD) is a contagious neurodegenerative disease affecting cervid populations, with significant implications for wildlife management. While the impact of environmental factors in the spread and persistence of CWD remains unclear, emerging research suggests that factors such as soil properties and habitat may play a role. Using Bayesian hierarchical spatial models with R-INLA (integrated nested Laplace approximation) and SPDE (stochastic partial differential equation) approach, we analyzed 20 years (2001–2021) of white-tailed deer (*Odocoileus virginianus*) CWD surveillance data throughout Minnesota, Wisconsin, Michigan, and Iowa. We examined relationships between CWD detection and deer demographic (age and sex) and environmental variables, including habitat (proportion agriculture or forest, elevation, slope, and distance to streams), minerals (copper, manganese, and zinc), and soil properties (percent clay, organic matter, cation exchange capacity, saturated hydraulic conductivity, and pH). Our analysis identified deer age and sex, habitat, and several soil characteristics as important factors influencing CWD detection. These results suggest minerals and soil properties other than percent clay may contribute to CWD persistence and transmission. Our findings provide new insights into the epidemiology of CWD that may be relevant for the indirect transmission of the prion.

Application of immersive technology and other learning approaches in the wildlife sector

Thursday, 31st July - 13:30: Education and communication (Oak Bay Room) - Oral

Justin Brown [1], ***Adrian Barragan*** [1], ***Daniel Getz*** [2]

1. *Department of Veterinary and Biomedical Sciences, Penn State University,* ***2.*** *Penn State University*

There is an increasing need in the wildlife sector to communicate with various audiences representing a diversity of demographics, learning styles, needs, backgrounds, interests, and subject knowledge. Consequently, both novel and traditional approaches should be considered to engage different audiences and enhance teaching, learning, and communication efforts. Immersive technology utilizes Virtual Reality, Augmented Reality, or Artificial Intelligence to place learners in an engaging simulated environment. Over the last four years, we have begun to incorporate immersive learning technology into our teaching and extension efforts at Penn State University, College of Agricultural Sciences. Specifically, we have created 360° videos of various livestock and wildlife experiences that can be viewed on standard screens or in virtual reality. In addition, we have developed and utilized 3-D models in various classes and extension events. In this talk, we will discuss these and other learning technologies, and highlight logistical considerations, lessons learned, and potential applications within the wildlife sector.

Chronic Wasting Disease Concerns Among First Nations in British Columbia

Thursday, 31st July - 13:45: Education and communication (Oak Bay Room) - Oral

Irina Borgos **[1]** ***, Katherine Wolfenden*** **[2]*****, Saulteau First Nations Treaty Rights and Environmental Protection Department*** **[3]*****, Kaylee Byers*** **[1]**

1. *Simon Fraser University,* ***2.*** *Fort Nelson First Nation Lands Department,* ***3.*** *Saulteau First Nations*

Chronic wasting disease (CWD) is an emerging neurodegenerative prion disease in BC that affects cervids such as deer, elk, and moose, and causes brain damage and death. There is currently neither cure nor vaccine for CWD in cervids, and management programs in BC are still being developed. While there is yet no evidence that CWD can be transmitted to humans, it is highly transmissible between animals via bodily fluids and CWD prions can remain on the landscape for years.

This project examines how the rise of CWD in BC may affect food sovereignty and cultural practices in British Columbia. Group conversations were conducted with community members in Nations in northern and eastern BC, including elders, guardians, conservation officers, and other knowledge holders. These conversations indicated that CWD in BC would negatively affect both food and culture. Major themes were the relationship between harvesting practices and identity, benefits of connection to land and food, and a lack of widespread understanding of CWD specifics. Community worries included the potential loss of healthy food sources and the threat of human transmission. In particular, Nations raised concern for recovery efforts supporting caribou populations, which are culturally significant. Communities expressed a need for clear and frequent communication from the scientific community and a desire to be directly involved in CWD management.

See one, do one, teach one - global connections in One Health

Thursday, 31st July - 14:00: Education and communication (Oak Bay Room) - Oral

Woutrina Smith [1]

1. *One Health Institute, University of California, Davis*

Amidst global turmoil, staying connected and committed to our shared values of wildlife health, public health, and planetary health is more important than ever. As wildlife and ecosystem health professionals, we face especially stark challenges of limited resources and political upheaval. But we have the power of trust and collaboration at our fingertips, and together we can change conversation strategies, and we can create communities of practice and knowledge exchange that result in strategic actions, outcomes, and impacts around the world. Many of us have built strong friendships and nimble working groups over many years, to address challenges in wildlife health using a One Health approach. These transdisciplinary and collaborative efforts recognize connections between animals, humans, and our shared environments, to help enact integrated solutions that make sense for communities. Examples will be given of globally connected professional networks in North America, South America, Africa, and Southeast Asia that have used a One Health 'see one, do one, teach one' training approach in the context of wildlife health, public health, and planetary health, to shift how we communicate and collaborate as we prepare the next generation of innovators and leaders to solve the problems of today and tomorrow. These Training of Trainer activities include technical and functional competencies within the twenty main One Health domains, and can integrate knowledge, systems thinking, and passion into bottom-up or top-down actions that promote population health.

All Stories Great and Small: The Power of Science Communication

Thursday, 31st July - 14:15: Education and communication (Oak Bay Room) - Oral

Eunah Preston [1]***, Michael Ziccardi*** [1]

1. *One Health Institute, University of California, Davis*

Wildlife health challenges are complex and urgent, requiring both scientific evidence and effective communication to drive meaningful action. Programs with larger budgets have greater flexibility to prioritize communications and reallocate funding accordingly; resource-limited programs must rely more heavily on shared services or refine their communications to meet budgetary constraints. Regardless, a smaller budget does not have to preclude the translation of scientific evidence into compelling stories to effect change. Particularly in wildlife conservation, strategic models used by larger programs can be successfully scaled down to fit the capacity of smaller programs when bolstered by their broader human and environmental health implications and the enduring appeal of their charismatic, wild patients. Through collaboration, cross-functional teams can distill complex concepts into targeted messaging and compelling narratives that are engaging, relatable, and relevant to audiences and that capture the interest and sustained investment of stakeholders. This case study compares four One Health Institute programs at the University of California at Davis: the Oiled Wildlife Care Network, Gorilla Doctors, California Raptor Center, and California Carnivores Program. Their contrasting trajectories illustrate the importance of adaptability, collaboration, storytelling, and engagement to advance initiatives, maximize growth, and impact wildlife and the communities and ecosystems they inhabit.

Study Abroad Courses are Essential Tools in Creating Future Health and Disease Practitioners

Thursday, 31st July - 14:30: Education and communication (Oak Bay Room) - Oral

Sonia M. Hernandez [1]***, Jose Aguirre*** [2]***, Amanda Rugenski*** [3]***, Maria Navarro*** [4]***, Jorge Rojas Jimenez*** [5]***,***
Emmanuel Rojas [6]***, Leslie Ragde Sanchez Talavera*** [7]

1. *Warnell School of Forestry & Natural Resources, Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *Universidad Complutense of Madrid,* ***3.*** *Odum School of Ecology, University of Georgia,* ***4.*** *College of Agriculture, University of Georgia,* ***5.*** *Research Professional,* ***6.*** *Tirimbina Biological Reserve,* ***7.*** *Universidad de Costa Rica*

Globalization is a reality that impacts all aspects of wildlife health and environmental stewardship. The interconnection of environmental and anthropogenic factors that lead to biodiversity loss and/or the emergence and facilitation of transmission of pathogens is a global phenomenon that requires understanding about the socioeconomic and cultural realities of each region. Successful study abroad programs provide platforms for broadening the minds of young professionals and can facilitate direct, invaluable experiences not possible in traditional classrooms. However, not all study abroad experiences are created equal. In order for these courses to transform from "extractive" to "immersive" experiences, they must move beyond focusing on techniques (e.g. hands-on chemical immobilization workshops) and be intentional in creating experiences and assignments that examine ethical, social, cultural, governmental, and value systems that influence wildlife management and health in each scenario. Furthermore, as students have less opportunities for connection with nature, many technological distractions and stressors, for study abroad courses to be successful, the student cohort must be carefully and holistically curated. We have conducted month-long field and study abroad courses for > 15 years serving hundreds of students from various institutions, with an emphasis on mixing under- grad- and veterinary students working towards careers in conservation medicine/biology. Courses provide a mixture of hands-on activities, opportunities to work with regional professionals, critical thinking discussions, various introspective exercises such as PhotoVoice and service-learning. Strategies for maintaining a positive team atmosphere, especially under in unfamiliar situations, rigorous physical conditions and intensive academic content, should be at the forefront of course design.

Developing field-based assays for the detection of Mycoplasma ovipneumoniae

Thursday, 31st July - 13:30: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Kate Huyvaert [1]***, Erik Hofmeister*** [2]***, Alexandra Thomas*** [3]***, Becca Wolking*** [4]***, Frances Cassirer*** [5]***, Thomas Besser*** [3]***, Daniel Walsh*** [6]

1. *Washington State University,* ***2.*** *U.S. Geological Survey National Wildlife Health Center,* ***3.*** *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University,* ***4.*** *Washington Animal Disease Diagnostic Laboratory, College of Veterinary Medicine, Washington State University,* ***5.*** *Idaho Department of Fish and Game,* ***6.*** *U.S. Geological Survey, Montana Cooperative Wildlife Research Unit, Wildlife Biology Program, University of Montana*

Epizootic pneumonia associated with *Mycoplasma ovipneumoniae* infection has been linked to declines of bighorn sheep populations across their range. Accurately identifying and removing persistently infected carriers of *M. ovipneumoniae* within bighorn sheep populations is important for effective disease management. Rapid, sensitive, and specific field-based assays could simplify logistics to identify carriers while reducing stressful effects on the animals. Questions about test accuracy, technical feasibility, relative costs, and availability of materials and reagents of alternative methods motivated us to conduct a formal, experimental comparison of alternative field-based assays, with a reference test, real-time PCR conducted by the Washington Animal Disease Diagnostic Laboratory (WADDL). Using nasal swabs collected from non-infected animals in the field, we treated sets of 18 swabs with one of three different strains of cultured *M. ovipneumoniae* at one of three concentrations (consistent with natural infection levels), for a total of 162 treated swabs per test set. One set of treated swabs and a set of untreated swabs (negative controls) each were tested by 1) real-time PCR using a portable thermocycler, 2) loop-mediated isothermal amplification (LAMP) using a portable incubator and detection system, and 3) real-time PCR at WADDL. Preliminary results for both real-time PCR tests show high detection for the high and medium concentration treatments of all strain types. We will compare sensitivity, concordance, and test costs for all methods as well as recommend best practices for potential animal-side, field-based use emerging from this project.

Fatal interactions: pneumonia in bighorn lambs following experimental exposure to carriers of Mycoplasma ovipneumoniae

Thursday, 31st July - 13:45: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Logan Weyand [1]***, Brandi Felts*** [2]***, Frances Cassirer*** [3]***, Jonathan Jenks*** [2]***, Daniel Walsh*** [4]***, Thomas Besser*** [1]

1. *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University,* ***2.*** *Department of Natural Resource Management, South Dakota State University,* ***3.*** *Idaho Department of Fish and Game,* ***4.*** *US Geological Survey National Wildlife Health Center*

We hypothesized that bighorn sheep ewes with chronic nasal *Mycoplasma ovipneumoniae* carriage are the source of infection that results in fatal lamb pneumonia. We tested this hypothesis in captive bighorn ewes at two study facilities over a 5-year period, by identifying carrier ewes and then comparing lamb fates in groups that did (exposed pens) or did not (non-exposed pens) include one or more carrier ewes. Most (23 of 30) lambs born in exposed pens, but none of 11 lambs born in non-exposed pens, contracted fatal pneumonia. In addition, surviving lambs in exposed pens showed obvious signs of respiratory disease while lambs in non-exposed pens did not. In crossover experiments, individual non-carrier ewes had lambs that experienced fatal pneumonia in years when housed in exposed pens, but not in years when housed in non-exposed pens. The results of these studies clearly associate lamb pneumonia to exposure to *M. ovipneumoniae* carrier ewes, consistent with a necessary role for this agent in epizootic pneumonia of bighorn sheep. These data specifically highlight the role of chronic *M. ovipneumoniae* carriage by some bighorn ewes in the epidemiology of this population-limiting wildlife disease.

CROSS-SECTIONAL SEROSURVEY OF SARCOPTIC MANGE IN WILD MOUNTAIN UNGULATES IN KYRGYZSTAN

Thursday, 31st July - 14:00: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Martin Gilbert [1]***, Dersuu Akparalyev*** [2]***, Salamat Chegirov*** [3]***, José Enrique Granados*** [4]***, Paulino Fandos*** [5]***, Zairbek Kubanuchbekov*** [6]***, Klara Kursanbaeva*** [3]***, Jorge Ramón López-Olvera*** [7]***, Carlos Martínez-Carrasco*** [8]***, Jesús M. Pérez*** [9]***, Luca Rossi*** [10]***, Jesús Salinas*** [8]***, Alina Seidakhmatova*** [6]***, Carmen Smith*** [1]***, Marta Valldeperes*** [11]***, Askat Zhakshylykov*** [2]***, Gregorio Mentaberre*** [12]

1. *Cornell K. Lisa Yang Center for Wildlife Health,* ***2.*** *Ministry of Natural Resources, Ecology and Technical Supervision of the Kyrgyz Republic,* ***3.*** *Kyrgyz Veterinary Research Institute named after A. Duysheev,* ***4.*** *Servicio Gestión del Medio Natural, Delegación Territorial Consejería de Sostenibilidad y Medio Ambiente,* ***5.*** *Madrid,* ***6.*** *Ilbirs Foundation,* ***7.*** *Universitat Autònoma de Barcelona,* ***8.*** *University of Murcia,* ***9.*** *Universidad de Jaén,* ***10.*** *University of Torino,* ***11.*** *Institute National de Recherche pour l'Agriculture, l'Alimentation et l'Ecologie„* ***12.*** *University of Lleida*

Outbreaks of sarcoptic mange, caused by the burrowing mite *Sarcoptes scabiei*, pose a significant threat to maintaining viable herds of Siberian ibex (*Capra sibirica*) in Kyrgyzstan and across Central Asia. Wildlife managers face challenges in diagnosing and monitoring disease threats in such remote regions, making it difficult to develop effective mitigation strategies. To improve diagnosis capabilities, we employed a low-tech approach by preserving dried blood samples on Nobuto© filter paper strips from animals harvested during managed trophy hunts, overcoming logistical difficulties associated with sampling in remote areas. A commercial ELISA using *S. scabiei* var. *canis* immunoglobulin G (AFOSA, GmbH®, Germany) with a biotin-avidin detection system was validated to detect antibodies against *S. scabiei* using reconstituted blood from Nobuto© strips collected from 15 infected and 10 healthy Iberian ibex (*C. pyrenaica*), with a sensitivity of 94.4% and specificity of 100%. This test was used to analyse Nobuto© strips obtained from 132 Siberian ibexes and 27 sympatric argali (*Ovis ammon*) from Kyrgyzstan. The seroprevalence was significantly (p=0.00012) higher in ibex (53.8%, 71/132; 95% CI: 45.3–62.3) than in argali (11.1%, 3/27; 95% CI: 0.0–23.0). Among Siberian ibexes, the seroprevalence was significantly (p=2.6e-06) higher in the Naryn region (77.6%, 45/58; 95% CI: 66.9–88.3) compared to Issyk-Kul (34.7%, 25/72; 95% CI: 23.7–45.7). To explore potential surveillance and management strategies, professional exchange visits between specialists from Europe and Kyrgyzstan examined approaches used to control ibex mange in Spain and Italy, assessing how these could be adapted to field conditions in Kyrgyzstan.

Parasite Burden Without Physiological Cost? Investigating Fascioloides magna in Austrian Red Deer

Thursday, 31st July - 14:15: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Sebastian Alexander [1], Aldin Selimovic [1], Anna Kübber-Heiss [1], Franz Schwarzenberger [2], Sarah Kugler [1], Levente Bago [1], Hanna Rauch [1], Jessica Cornils [1], Friederike Pohlin [1]

1. *Research Institute of Wildlife Ecology, University of Veterinary Medicine Vienna,* ***2.*** *Unit of Physiology and Pathophysiology, University of Veterinary Medicine Vienna*

Invasive parasites may pose health risks to naive host species. The giant liver fluke, *Fascioloides magna*, native to North America, was first detected in Austria in 1982. It was identified in red deer (*Cervus elaphus*) within the Allentsteig military training area (Lower Austria) in 2020, raising concerns about its health impacts. This study investigated the relationship between *F. magna* infection, physiological stress markers, and body condition in Allentsteig's red deer population. Three hypotheses were tested: (1) liver infestation correlates with fecal egg counts, (2) infestation severity correlates with elevated hair cortisol and fecal glucocorticoid metabolite (FGM) concentrations, and (3) infestation negatively affects body condition.

Liver, feces, and hair samples from 80 red deer were collected during driven hunts in the winters 2021 and 2022, though not all were suitable for every analysis. Livers were examined pathologically, and fecal egg counts analyzed via coproscopy (n=40). Stress levels were quantified from hair (n=48) and feces (n=43) using enzyme immunoassays. Body condition was assessed using the kidney fat index (KFI). Liver fluke burden was strongly correlated with fecal egg counts, supporting the first hypothesis. However, no relationship was found between infestation severity and hair cortisol or FGM concentrations. The KFI showed only a slight negative relationship with parasite burden, with age having the strongest effect. These results indicate that *F. magna* has no discernible effect on stress physiology or health in the red deer population studied using the methods employed. Long-term studies incorporating environmental factors are needed to assess the broader ecological consequences.

Twenty years of ungulate disease surveillance by the Canadian Wildlife Health Cooperative (2002–2023)

Thursday, 31st July - 14:30: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Kerry Schutten [1]***, Leonard Shirose*** [1]***, Erin Moffatt*** [2]***, Brian Stevens*** [1]***, Dayna Goldsmith*** [3]***, Owen Slater*** [4]***, Jamie L. Rothenburger*** [3]***, Susan Kutz*** [5]***, Stéphane Lair*** [6]***, Megan Jones*** [7]***, Laura Bourque*** [2]***, Scott McBurney*** [2]***, Margo Pybus*** [8]***, Iga Stasiak*** [9]***, Naima Jutha*** [10]***, Helen Schwantje*** [11]***, Larissa Nituch*** [12]***, Damien Joly*** [2]***, Claire Jardine*** [1]***, Trent Bollinger*** [13]

1. *Department of Pathobiology, University of Guelph; Canadian Wildlife Health Cooperative.,* ***2.*** *Canadian Wildlife Health Cooperative,* ***3.*** *University of Calgary, Faculty of Veterinary Medicine; Canadian Wildlife Health Cooperative,* ***4.*** *University of Calgary; Canadian Wildlife Health Cooperative,* ***5.*** *University of Calgary, Faculty of Veterinary Medicine, 3330 University Drive NW, Calgary, Alberta T2N 4N1, Canada,* ***6.*** *Canadian Wildlife Health Cooperative / Centre québécois sur la santé des animaux sauvages, Université de Montréal, Faculté de médecine vétérinaire, 3200 rue Sicotte, St-Hyacinthe, Québec J2S 2M2, Canada,* ***7.*** *Atlantic Veterinary College; Canadian Wildlife Health Cooperative,* ***8.*** *Environment and Protected Areas, Government of Alberta,* ***9.*** *Saskatchewan Ministry of Environment,* ***10.*** *Government of the Northwest Territories, Department of Environment & Climate Change,* ***11.*** *British Columbia Ministry of Water, Lands and Resource Stewardship (Emeritus),* ***12.*** *Wildlife Research and Monitoring Section, Ontario Ministry of Natural Resources,* ***13.*** *Western College of Veterinary Medicine; Canadian Wildlife Health Cooperative*

Wild ungulates are integral to the health and well-being of Canadian ecosystems, contributing various One Health benefits to the people and animals that coexist within these landscapes. Ungulates face a range of potentially synergistic threats to population health throughout their North American distributions, with particular and increasing concern regarding the resiliency of species at risk (SAR; caribou (*Rangifer tarandus*), wood bison (*Bison bison athabascae*), moose (*Alces americanus*)). To address knowledge gaps surrounding the health of Canadian ungulates, we conducted a retrospective analysis of 20 years of ungulate morbidity and mortality data collected through passive (aka scanning) disease surveillance conducted by the Canadian Wildlife Health Cooperative (CWHC). In total, 2525 submissions across 12 species were assigned a category of diagnosis by a CWHC veterinary pathologist. Infectious categories of diagnosis accounted for 53.0% of all cases, with two diseases detected most frequently: chronic wasting disease (22.2% of infectious cases) and *Parelaphostrongylus tenuis* (20.7% of infectious cases). Emerging diseases were also detected for the first time through our surveillance approach (e.g., the first cases of epizootic hemorrhagic disease virus in Ontario). Trauma (15.3%) and emaciation (8.9%) were the most frequently assigned non-infectious categories of diagnosis. The majority of SAR cases were infectious in origin, and we identified potential disease threats to SAR that may emerge secondary to changing distributions of sympatric ungulate species and the pathogens they carry. Our results highlight the strengths of on-going disease surveillance, as well as the need for an integrated, holistic wildlife disease surveillance approach in Canada.

Assessing the health-fitness dynamics of endangered mountain caribou and the influence of maternal penning

Thursday, 31st July - 14:45: Northern and Mountain Ungulates (Lecture Theatre) - Oral

Clayton Lamb [1]***, Evgenia Dubman*** [2]***, Scott McNay*** [2]***, Line Giguere*** [2]***, Yasmine Majchrzak*** [3]***, Caeley Thacker*** [4]***, Owen Slater*** [5]***, Bryan Macbeth*** [6]***, Naomi Owens-Beek*** [7]***, Bruce Muir*** [8]***, Adam Ford*** [9]

1. *Biodiversity Pathways,* ***2.*** *Wildlife Infometrics,* ***3.*** *University of Alberta,* ***4.*** *Government of British Columbia,* ***5.*** *University of Calgary,* ***6.*** *Parks Canada,* ***7.*** *Saulteau First Nations Treaty Rights and Environmental Protection Department,* ***8.*** *West Moberly First Nations,* ***9.*** *University of British Columbia*

The health of wildlife plays a crucial role in population demography by connecting habitat and physiology. Southern mountain caribou, a population of woodland caribou (*Rangifer tarandus caribou* (Gmelin, 1978)) found in the mountains of southwest Canada, are facing significant threats. We evaluated the health of the Klinse-Za subpopulation within the central group of southern mountain caribou, which is part of an Indigenous-led conservation initiative aimed at enhancing caribou population growth through seasonal maternal penning. We collected health metrics from 46 female Klinse-Za caribou between 2014 and 2021. The health metrics included trace minerals, cortisol, biomarkers for inflammation, and pathogen prevalence. We compared these health metrics between penned and non-penned animals, reproductive and non-reproductive females, and nearby subpopulations. We provide correlative evidence linking reproductive success to trace nutrients but find no evidence for relationships with stress, exposure to pathogens, or biomarkers of inflammation. Based on the health metrics considered, Klinse-Za caribou were generally healthy relative to neighboring subpopulations and repeat capture for penning did not appear to create accumulated health issues. Penned caribou had lower fecal cortisol levels and inflammation markers compared to free-ranging animals. This work provides a baseline assessment of southern mountain caribou health and provides guidance on maternal penning activities in support of caribou recovery.

Real-time quaking induced conversion (RT-QuIC) in a state wildlife management agency: examples of projects utilizing this tool in Wyoming, USA

Thursday, 31st July - 15:45: Pathogen Discovery (Oak Bay Room) - Oral

Brie Hashem **[1]*, ***Brett Ralston*** **[1]*, ***Stuart S. Lichtenberg*** **[2]*, ***Robert Michitsch*** **[3]*, ***Daniel Pinneo*** **[1]*, ***Eric Newkirk*** **[1]*, ***Jennifer Malmberg*** **[4]*, ***Samantha Allen*** **[1]*, ***Peach Van Wick*** **[1]**

1. *Wyoming Game and Fish Department,* ***2.*** *University of Minnesota,* ***3.*** *University of Wisconsin-Stevens Point,* ***4.*** *USDA National Wildlife Research Center*

Chronic wasting disease (CWD) is a fatal, transmissible spongiform encephalopathy characterized by an accumulation of abnormal prion protein in the central nervous system and lymphoid tissues of cervids. Real-time quaking-induced conversion (RT-QuIC) is a highly sensitive assay developed to detect amyloid fibrils formed by proteins, such as $\mathrm{PrP}^{\mathrm{CWD}}$. While early RT-QuIC studies focused on detection of CWD in post-mortem tissues, more recent works aim to assess its utility for CWD detection in live animals and their environments. The Wyoming Game and Fish Department, with collaborators, are utilizing RT-QuIC to contribute to this more recent area of study. Two projects currently underway use Rocky Mountain elk (*Cervus canadensis nelsoni*); the first uses fecal samples to better understand CWD transmission, while the second uses environmental samples to evaluate disposal options for CWD-positive carcasses. For the first project, feces were collected every six months from captive elk with the 132LL genotype and known CWD-infection status from rectoanal mucosa-associated lymphoid tissue (RAMALT) testing via immunohistochemistry (IHC). For the second project, environmental samples were collected following composting trials of whole carcasses and butchered waste of four CWD-positive and two CWD-negative elk. Results from the fecal project show sporadic prion seeding activity at each time point, indicating potential capacity for fecal detection of CWD via RT-QuIC. Results of composted environmental samples are pending. These projects demonstrate potential uses of RT-QuIC by state wildlife management agencies and contribute to the knowledge of CWD transmission and RT-QuIC's capacity for detection of CWD in live cervids and their environments.

A multi-omics approach to health surveillance and translocation success in Sonoran pronghorn

Thursday, 31st July - 16:00: Pathogen Discovery (Oak Bay Room) - Oral

Natalie Payne [1] ***, Leigh Combrink*** [1]

1. *University of Arizona*

Translocations and captive breeding and release programs are increasingly important tools for wildlife conservation. However, introducing wildlife to novel environments can lead to changes in microbiome composition and function, and translocations could facilitate pathogen spread between introduced and resident individuals.

However, health, behavioral, and physiological impacts are not solely due to shifting microbial communities, as individual hosts can exhibit phenotypic plasticity in response to changing environmental contexts. The interaction of host molecular responses and microbial community dynamics likely plays a critical yet underexplored role in shaping the overall health of hosts, with unknown implications for the success of translocations.

We seek to disentangle the roles of interacting host and microbial community responses to translocation in the endangered Sonoran pronghorn (*Antilocapra americana sonoriensis*). Sonoran pronghorn undergo annual releases from captively managed herds in Arizona, USA, with future reintroductions planned to California, USA. This project integrates multiple ‘omics’ datasets (microbiomics, viromics, population genomics, and functional genomics) to (1) investigate host (e.g., genomic/immunological) and environmental drivers of microbiome and virome composition and (2) assess host and microbial responses to translocation.

We have generated fecal microbiome (16S/ITS) data from 130 pronghorn samples, with additional host genomic and fecal metatranscriptomic data for a subset of these samples. We have detected major shifts in microbiome composition between annual captures, along with differences between captive source populations. These findings could have major implications for future supplementation of captive herds or release efforts, as well as captive management strategies (such as routine administration of antibiotics at captures).

Novel betacoronaviruses in white-footed mice (Peromyscus leucopus) and deer mice (Peromyscus maniculatus)

Thursday, 31st July - 16:15: Pathogen Discovery (Oak Bay Room) - Oral

Jonathon D. Kotwa [1], ***Simon P. Jeeves*** [2], ***Winfield Yim*** [1], ***Lauren Crawshaw*** [3], ***Lily Yip*** [1], ***Phuc Tran*** [1], ***Will Zhang*** [1], ***Albrecht Schulte-Hostedde*** [4], ***Finlay Maguire*** [5], ***Jeff Bowman*** [6], ***Samira Mubareka*** [1], ***Claire Jardine*** [2]

1. *Sunnybrook Research Institute,* ***2.*** *Department of Pathobiology, University of Guelph,* ***3.*** *Wildlife Research and Monitoring Section, Ontario Ministry of Natural Resources,* ***4.*** *School of Natural Sciences, Laurentian University,* ***5.*** *Faculty of Computer Science, Dalhousie University,* ***6.*** *Wildlife Research and Monitoring Section, Ministry of Natural Resources*

Introduction:

Rodents are known reservoir hosts for coronaviruses, some of which pose spillover risk for humans and other animals. Surveillance for rodent coronaviruses in North America remains limited, particularly in Canada. Through the Wildlife Emerging Pathogens Initiative (WILD-EPI), we screened for endemic coronaviruses among *Peromyscus* spp. in Ontario, Canada.

Methods:

Rectal or oral swabs were collected from 357 *Peromyscus leucopus* from parks and green spaces within Toronto and 336 *Peromyscus maniculatus* from Algonquin provincial park from 2021-2024. Extracted RNA were analyzed using a pan-coronavirus RT-PCR targeting the RNA-dependent RNA-polymerase (RdRp). Partial RdRp and whole genome sequencing was conducted on positive samples. Phylogenetic analyses were performed using partial RdRp, whole genomes, and spike. Recombination analysis was conducted using RDP4.1.

Results:

Overall, 35/693 (5.1%) were PCR positive; 11 were *P. leucopus* and 24 were *P. maniculatus*. All partial RdRp sequences were betacoronaviruses. Six whole genomes and seven near complete or partial genomes were generated revealing two divergent betacoronaviruses preliminarily denoted as *Peromyscus* coronavirus (PCoV) A and B; PCoVA included sequences from both species while PCoVB only included *P. leucopus*. Both were *Betacoronavirus* 1, a species that includes human coronavirus OC43, bovine coronavirus, and porcine hemagglutinating encephalomyelitis virus. A statistically significant recombination event in the spike involving PCoVB and a bovine coronavirus was detected.

Conclusion:

Our work provides preliminary insights into coronavirus diversity in *Peromyscus* spp. in Ontario. The relatedness of PCoV to known human and livestock coronaviruses underscores the need for more surveillance at the human-wildlife-livestock interface to further investigate the evolutionary relationships among these viruses.

Accumulation of benzotriazole UV-stabilizers in relation to ingested plastics and associated health metrics in Larus gulls feeding at a landfill in Atlantic Canada

Thursday, 31st July - 16:30: Pathogen Discovery (Oak Bay Room) - Oral

Kerry Schutten [1]***, Andre Morrill*** [2]***, Zhe Lu*** [3]***, Akshaya Chandrashekar*** [4]***, Joshua Cunningham*** [2]***, Greg Robertson*** [2]***, Mark Mallory*** [5]***, Claire Jardine*** [1]***, Jennifer F. Provencher*** [2]

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Benzotriazole UV-Stabilizers (BZT-UVs), compounds added to plastics to reduce ultraviolet degradation, are considered contaminants of emerging concern given their environmental persistence and documented toxicity in humans and animals. UV328 is a BZT-UV that has been recently listed to Annex A of the Stockholm Convention; therefore, understanding species exposure is critical information to fulfill international and domestic regulatory obligations. We evaluated hepatic accumulation of 12 plastic additives (including nine BZT-UVs) in Larus gulls in Atlantic Canada. BZT-UV accumulation was assessed in relation to ingested plastics, hepatic heavy metal accumulation, and body condition. Ninety-six percent of gulls had at least one BZT-UV at detectable hepatic concentrations. The most frequently detected BZT-UVs were UVP (91.4 %) and UV328 (76 %), suggesting ubiquitous exposure across individuals. We demonstrated interspecific differences in the relationship between ingested plastics and accumulated contaminants, with a positive relationship detected between ingested plastics and both UVP and UV328 in American herring gulls (Larus argentatus smithsonianus), and a positive relationship between hepatic UV328 and Pb concentrations detected in great black-backed gulls (Larus marinus). We provide evidence that Larus gulls feeding at a coastal landfill are highly exposed to BZT-UVs, and that the relationship between ingested plastics and plastic-associated contaminants varies across sympatric species.

HEALTH SURVEY OF MIGRATORY AND BOREAL CARIBOU (RANGIFER TARANDUS) IN QUEBEC AND LABRADOR, CANADA

Thursday, 31st July - 15:45: Northern and Mountain Ungulates Continued (Lecture Theatre) - Oral

Laura Van Driessche [1], ***Stéphane Lair*** [1], ***Joëlle Taillon*** [2], ***Vincent Brodeur*** [3], ***Susan Kutz*** [4], ***Sara McCarthy*** [5], ***Sabrina Plante*** [2], ***Falk Melzer*** [6], ***Kerstin Wernike*** [6], ***Patricia König*** [6], ***Gereon Schares*** [6]

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Caribou (*Rangifer tarandus*) is the focus of major conservation efforts, with most populations significantly declining over the last decades. Health monitoring is imperative to better understand the dynamics of these populations facing habitat loss and deterioration. From 2019 to 2024, 167 boreal caribou (Quebec) and 121 migratory caribou (Quebec-Labrador) were screened. Serum was used for trace mineral analyses and pathogen exposure detection, either by serology or PCR. Based on published reference values for caribou, potential trace mineral deficiencies for copper, selenium and zinc were detected in 94.1%, 19.1% and 87.5% respectively for boreal caribou and in 95.7%, 7.4% and 91.5% respectively for migratory caribou. Additionally, serum levels for copper, iron, manganese and molybdenum in the majority of the animals were lower than those reported from caribou from British Columbia. Trace mineral deficiencies have been associated with increased susceptibility to infection, suboptimal performance and a decreased fertility, which can all contribute to population declines. All sampled animals were negative on PCR for *pestivirus* and seronegative for *Brucella* spp., *Coxiella burnetii* and *Neospora caninum*. Seroprevalence for *Besnoitia tarandi*, cervid herpesvirus 2, *Erysipelothrix rhusiopathiae* and *Toxoplasma gondii* was 8.4%, 14.6%, 27.3% and 0.0% respectively in boreal caribou and 66.0%, 12.7%, 9.9% and 2.5% respectively in migratory caribou. The individual and population health impact of exposure to *B. tarandi*, cervid herpesvirus 2 and *E. rhusiopathiae* are currently unknown. These results could contribute to a better understanding of the interactive effects of nutritional deficiencies and infectious disease on population dynamics of a species at risk.

Neosporosis, an emerging parasitic threat to free-ranging caribou (Rangifer sp.)?

Thursday, 31st July - 16:00: Northern and Mountain Ungulates Continued (Lecture Theatre) - Oral

Kimberlee Beckmen [1] ***, Camilla Lieske*** [1]

1. *Alaska Department of Fish and Game*

Neospora caninum is the major cause of reproductive loss in cattle and has been shown to cause clinical disease in cervids. The importance of *Neospora caninum*-associated disease in wildlife (such as caribou) has not been determined, but it is a potential concern as a source of reproductive failure. Alaska F&G surveillance data (samples collected 1994-2007) found low seropositivity (10-20% seropositive with no difference in age groups) in the Western Arctic (WAH) and Porcupine herds and 0-30% seropositivity in all Alaska caribou herds. However, during the June 2024 routine health assessment of blood sampled from the Central Arctic caribou herd (CAH) a much higher than expected percentage caribou >2 years old were found to have antibody titers against *Neospora caninum*. Due to the potential for negative effects on reproductive success and population recruitment in caribou, and to help assess if this potential change in exposure to *Neospora* contributed to the decline in the CAH population that started in 2010, we analyzed archived serum from 2008 and 2017 (when the population was at its lowest point). We found that for both years 80-90% of the caribou over 1 year-old had titers to *Neospora*, while only 16-22% of the caribou under a year had titers for *Neospora*. The significantly higher seropositivity in the older animals is consistent with a horizontal exposure (ingestion of oocytes from contaminated forage/water). The number of detections in adults in 2024 was lower than in 2008 and 2017, but the difference was not significant (p=0.22). We did not identify a time period for the CAH when exposure to *Neospora* was closer to historic levels in other arctic caribou herds (0-20%). We are continuing to analyze archived and current caribou sera from both arctic and Interior caribou herds to better understand the potential impacts of *Neospora* on caribou.

Mathematical models evidence the importance of alternative hosts and environmental transmission for bacterial diseases affecting ungulates in the Arctic

Thursday, 31st July - 16:15: Northern and Mountain Ungulates Continued (Lecture Theatre) - Oral

***Juan Vargas* [1], *Marina Reyne* [1], *McCaide Wooten* [2], *Sreejith Radhakrishnan* [3], *Fabien Mavrot* [4], *Taya Forde* [3], *Susan Kutz* [2], *Eric Morgan* [1]**

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The rising threat of emerging diseases is a significant cause of concern for vulnerable wildlife populations worldwide. Understanding and managing this threat is particularly challenging in systems with multiple hosts and environmental transmission, but mechanistic models can provide insights into their dynamics and identify critical processes and host roles even with limited data.

Here, we built a multi-species model of *Erysipelothrix rhusiopathiae*, a bacterium that has caused mass mortalities of muskoxen (*Ovibos moschatus*) in the Canadian Arctic. We parameterized the model with data from the literature and analyzed it to assess the role of different hosts (muskoxen and arctic foxes) and the importance of different environmental transmission sources (carcasses and feces). We estimated the system R_0 under multiple transmission scenarios, quantified parameter sensitivity to identify critical processes and solved the model numerically to predict how disease could affect population abundance.

Our model predicted bacteria to establish only in scenarios that included direct transmission or transmission from feces, with or without multiple hosts, and not in carcass-only scenarios. Environmental transmission processes like shedding and decay were the most influential for the system R_0. Disease-induced mortality could produce strong population declines in muskoxen, consistent with empirical observations, and these would be accelerated by the contribution of alternative hosts.

Our research highlights the need to understand contamination in the soil and other potential reservoirs like ponds, and spatio-temporal overlap among species; this is particularly relevant given the wide array of potential hosts, which includes wolves, polar bears, caribou, and crows. Our modelling approach combining multiple data sources provides a flexible and efficient framework to generate actionable insights that guide specific research and guide management of similarly complex wildlife diseases.

Enhancing community-based wildlife health surveillance through advancing field-friendly methods

Thursday, 31st July - 16:30: Northern and Mountain Ungulates Continued (Lecture Theatre) - Oral

Olivia Hee [1]***, Mathieu Pruvot*** [1]***, Fabien Mavrot*** [1]***, Eleanor R. Dickinson*** [1]***, Gabriela F. Mastromonaco*** [2]***, Kugluktuk Angoniatit Association*** [3]***, Olokhaktomiut Hunters and Trappers Organization*** [4]***, Ekaluktutiak Hunters and Trappers Organization*** [5]***, Lisa-Marie Leclerc*** [6]***, John Blake*** [7]***, Carla Willetto*** [7]***, Jan Adamczewski*** [8]***, Susan Kutz*** [9]

***1.** University of Calgary, Faculty of Veterinary Medicine, **2.** Toronto Zoo, Reproductive Sciences Unit, **3.** Kugluktuk Angoniatit Association, **4.** Olokhaktomiut Hunters and Trappers Organization, **5.** Ekaluktutiak Hunters and Trappers Organization, **6.** Government of Nunavut, Department of Environment, **7.** University of Alaska, Fairbanks, **8.** Government of the Northwest Territories, Department of Environment & Climate Change, **9.** University of Calgary, Faculty of Veterinary Medicine, 3330 University Drive NW, Calgary, Alberta T2N 4N1, Canada*

Community-based wildlife health surveillance that draws on harvester-based or non-invasive sampling is an efficient means to track and predict health of wildlife populations. To maximize information gained while minimizing work required by sample collectors, validated diagnostic tests that can be applied to these field samples are key.

As part of a community-based muskox health surveillance program in the Canadian Arctic, we assessed the use of harvester-collected samples for determining pregnancy status. First, we used 12 captive muskoxen to evaluate the efficacy of pregnancy-associated glycoproteins (PAG) from filter paper blood samples and fecal progesterone and estrogen metabolites (FPM, FEM), for determining pregnancy. Filter paper blood PAG analyses were highly sensitive and specific throughout gestation and comparable to serum results, while FPM and FEM were only accurate mid-gestation and late-gestation, respectively.

We then applied these tests to muskox samples submitted by Inuit harvesters. Pregnancy rates were lower in a declining population (Victoria Island) than in a stable population (mainland). We evaluated associations between pregnancy and seropositivity to *Brucella*, an emerging disease in muskoxen, and found that *Brucella* negatively affected odds of being pregnant.

We conclude that filter paper blood PAG analysis in muskoxen is accurate for pregnancy diagnosis and useful for collections by harvesters; fecal analyses are useful at certain stages of gestation for non-invasive collections and when blood is not available. We illustrated the importance of considering test type, animal biology, and sampling feasibility for wildlife health monitoring, and the potential population-limiting effect of disease in an important Arctic ungulate species.

Geographies of Bacillus anthracis Exposure: Converging Indigenous Knowledge and Remote Sensing to Map Cattle Anthrax Risk in Southern Africa

Thursday, 31st July - 16:45: Northern and Mountain Ungulates Continued (Lecture Theatre) - Oral

Juan M Dabezies [1]***, Kevin Curtin*** [2]***, Crhistian Fohringer*** [3]***, Maria Zubkova*** [1]***, Nathan Delong He*** [1]***, Meredith Gore*** [1]

1. *University of Maryland,* ***2.*** *University of Alabama,* ***3.*** *Marie Curie Fellow*

Anthrax, caused by *Bacillus anthracis*, poses significant challenges to wildlife conservation and livestock management in southern Africa. This study integrates indigenous ecological knowledge with remote sensing techniques to map anthrax risk for cattle in the human-wildlife interface zones of Limpopo National Park (LNP), Mozambique. We employed a novel approach combining participatory mapping with local communities and ecological suitability modeling to identify high-risk areas for anthrax transmission. Participatory mapping sessions were conducted with livestock-owning families in three communities within LNP's buffer zone. Local knowledge on cattle management practices, wildlife interactions, and perceived disease hotspots was spatially documented. Concurrently, we developed an ecological suitability model for B. anthracis using high-resolution environmental data, including soil types, elevation, vegetation indices, and proximity to water bodies. GIS analysis was used to integrate community-derived risk perceptions with the ecological suitability model. This approach revealed distinct spatial patterns of perceived and modeled anthrax risk across the study area. Our findings highlight the value of combining local ecological knowledge with scientific modeling to enhance understanding of zoonotic disease dynamics in complex socio-ecological systems. This integrated approach provides a more comprehensive assessment of anthrax risk, accounting for both environmental factors and human-wildlife-livestock interactions. The resulting risk maps offer valuable tools for targeted anthrax surveillance, prevention strategies, and community-based disease management.

Results from the first five years of the Carnivore Diseases Monitoring Program in Navarre (N Spain)

Friday, 1st August - 10:15: Mechanisms of Harm (Salon BC) - Oral

Javier Millán [1]***, Marta Canuti*** [2]***, Rocío Checa*** [3]***, Annalisa Guercio*** [4]***, Efrén Estévez-Sánchez*** [3]***, Isabel G. Fernández de Mera*** [5]***, Javier Marco*** [6]***, Diana Marteles*** [6]***, Francesco Mira*** [4]***, Guadalupe Miró*** [3]***, Alberto Moraga-Fernández*** [5]***, Clara Muñoz-Hernández*** [5]***, María-Paz Peris*** [6]***, Ruth Rodríguez-Pastor*** [1]***, Marta Sánchez-Sánchez*** [5]***, Fermín Urra*** [7]***, Sergio Villanueva-Saz*** [6]***, Diego Villanúa*** [7]

1. *Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA),* ***2.*** *University of Copenhagen,* ***3.*** *Universidad Complutense of Madrid,* ***4.*** *Istituto Zooprofilattico Sperimentale della Sicilia,* ***5.*** *Instituto de Investigación en Recursos Cinegéticos, IREC (CSIC-UCLM-JCCM),* ***6.*** *Universidad de Zaragoza,* ***7.*** *Navarra environmental management (GAN-NIK)*

Wild carnivores, closely related to domestic dogs and cats, share various pathogens and parasites, some of which threaten their conservation while, for others, act as reservoirs. Here, we present the initial findings of a monitoring program launched by the Regional Government of Navarre (Northern Spain), which focuses on the collection and analysis of road-killed carcasses from both protected and invasive carnivore species. Since 2020, 415 carcasses from 11 species within the Mustelidae, Viverridae, Canidae and Felidae families have been recovered and necropsied. A wide range of samples, including serum, ectoparasites, and major organs, are routinely collected. Serological screening detected antibodies against *Leishmania* and *Dirofilaria* in 3 and 9 out of 171 animals, respectively, and against FeLV and FIV in 9 and 0 out of 55 European wildcats. Molecular analyses identified *Carnivore protoparvovirus 1* in 2 of 171 individuals, specifically FPV in a badger and CPV-2 (Asian lineage) in a wildcat. Amdoparvoviruses were detected in 6 of 171 animals, including four distinct viral strains, one of which represents a novel species found in a stone marten. *Cytauxzoon europaeus*, *Hepatozoon felis*, and *Babesia vulpes* were detected in 41, 29, and 1 out of 63 wildcats, respectively. Cardio-respiratory nematodes, identified by morphological and molecular methods, included *Angiostrongylus chabaudi* (a new record for the Iberian Peninsula), *A. daskalovi*, *Oslerus rostratus*, *Troglostrongylus brevior*, *Crenosoma* sp., *Aelurostrongylus abstrusus*, and *Eucoleus aerophilus*. Ticks included *Rhipicephalus sanguineus s.l., Ixodes hexagonus*, *I. ricinus*, *I. ventalloi, and Dermacentor reticulatus*. These findings highlight the value of this monitoring program in detecting new or previously unreported pathogens and parasites.

Parasite genotype, host, and environmental factors are associated with fatal Sarcocystis neurona infection in southern sea otters (Enhydra lutris nereis)

Friday, 1st August - 10:30: Mechanisms of Harm (Salon BC) - Oral

Devinn Sinnott [1], ***Melissa Miller*** [2], ***Elizabeth VanWormer*** [3], ***Colleen Young*** [2], ***Padraig Duignan*** [4], ***Margaret Martinez*** [4], ***Cara Field*** [4], ***Michael Harris*** [2], ***Heather Harris*** [4], ***Mary Gomes*** [2], ***Karen Shapiro*** [1]

1. *School of Veterinary Medicine, University of California Davis,* ***2.*** *Marine Wildlife Veterinary Care and Research Center, California Department of Fish and Wildlife, Santa Cruz, CA, USA,* ***3.*** *School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln,* ***4.*** *The Marine Mammal Center*

The protozoal parasite *Sarcocystis neurona* is an important cause of mortality for southern sea otters (*Enhydra lutris nereis*) and has been associated with mass mortality events. Little is known about the role of parasite genotype in the outcome of infection in sea otters. The objective of this study was to evaluate effects of parasite genotype and specific host and environmental factors such as animal age class and sex, stranding location, and season of stranding on disease outcome in *S. neurona*-infected otters that stranded in California. A multi-locus sequence typing (MLST) approach was used to characterize the S. neurona genotype in fatal (n=92) and non-fatal (n=33) sea otter infections as determined by histopathology. For otters recovered along the northern end of the population's geographic range, detection of the IIg/j genotype was associated with fatal infections, while IIi and VIu/hh genotypes were associated with non-fatal infections. Along the southern end of the range, the Ia and Ib/c/d/gg genotypes were the dominant genotypes implicated in fatal infections and these same genotypes caused two mass-mortality events in 2004 (Ib/c/d/gg) and 2021 (Ia). Subadult sea otters were more likely to die from *S. neurona* than adults. Stranding during the wet season following rainfall events that facilitate land-to-sea flow of infective sporocysts was also more likely to result in fatal infection. These findings suggest that parasite genotype and host and environmental factors all contribute to disease outcome following *S. neurona* infection in southern sea otters.

Toxoplasmosis outbreak in black howler monkeys in Chiapas, Mexico

Friday, 1st August - 10:45: Mechanisms of Harm (Salon BC) - Oral

***Elliott Chiu* [1], *Edith Fernández-Figueroa* [2], *Laura Backus* [3], *Tania Leal* [4], *Andres Lopez* [4]**

1. *City University of Hong Kong,* **2.** *Núcleo B de Innovación en Medicina de Precisión, Instituto Nacional de Medicina Genómica,* **3.** *Animal Science Department, College of Agriculture, Food and Environmental Sciences, California Polytechnic State University,* **4.** *Red de Biología y Conservación de Vertebrados. Instituto de Ecología A.C.*

Seven black howler monkeys (*Alouatta pigra*) from a primate rehabilitation center located in Chiapas, southern Mexico died in a 15-day period between 5-19 February 2024. All the monkeys died within four to six days after the onset of the clinical signs. The main clinical signs were lethargy, anorexia, fever (39-40.8^o C), and pale oral mucosa. Some of the monkeys showed a decrease in platelets; those with thrombocytopenia had platelet counts ranging from 11 to 67 x 10^3/ul. Five individuals showed hemorrhage from the mouth and nose before they died. Gross necropsy revealed multifocal, acute, discrete ecchymoses and hemorrhages affecting the small intestine, mesentery, lungs, liver, heart, and spleen. Histology of three animals confirmed hemorrhage within numerous organs. More importantly, all animals displayed a mild to moderate, multifocal, acute, necrotizing hepatitis with myriad of apicomplexan zoites and shizonts. Numerous organs had abundant dark brown pigment deposition. Histopathology strongly supported toxoplasmosis; but malaria was also considered as a differential diagnosis. DNA was extracted from two lung samples, one spleen sample, and one intestinal sample, each from different individuals. PCRs were performed for *Plasmodium* spp. and *Toxoplasma gondii* targeting mtDNA *cytochrome b* and 18s ribosomal RNA and ITS1 genes, respectively. *Toxoplasma gondii* was identified in all four samples; all samples were negative for *Plasmodium* spp.

Botulism, Fermentation, or Something More? Solving the Mystery of Lorikeet Paralysis Syndrome.

Friday, 1st August - 11:00: Mechanisms of Harm (Salon BC) - Oral

Viviana Gonzalez Astudillo [1]***, Claude Lacasse*** [2]***, Rachele Wilson*** [3]***, Lauren Bassett*** [4]***, David Phalen*** [5]

1. *The University of Queensland,* ***2.*** *Royal Society for the Prevention of Cruelty to Animals,* ***3.*** *Griffith University,* ***4.*** *Wildlife Health Australia,* ***5.*** *The University of Sydney*

Paralytic syndromes of unknown etiology are impacting multiple species of Australian birds and flying-foxes. One of these, Lorikeet Paralysis Syndrome (LPS), is devastating lorikeets (*Trichoglossus* spp.) in eastern Australia overwhelming wildlife health resources. An initial study of LPS (Lacasse *et al.*, AVJ, 2021) showed that LPS affects adult birds of both sexes, occurs predominately in summer, and most birds will recover with prolonged care. This study also ruled out infectious diseases and many anthropogenic toxins as the cause of LPS, leaving a small set of toxins as likely candidates for LPS. A second syndrome in flying-foxes closely resembles LPS clinically and may be caused by the same etiology (https://wildlifehealthaustralia.com.au/News-Room/News-Media-Releases/incident-flying-fox-paralysis-syndrome-south-east-qld-northern-nsw-ongoing).

Our continued research into the etiology of LPS uses citizen science, targeted testing for toxins, and metabarcoding of droppings from lorikeet cases and controls. With these, we have identified 10 taxa on which lorikeets feed that could contain toxins that can cause neurologic signs. We also have evidence that lorikeets feed on overripe native and commercially-grown fruit and nectar and fruit that smell fermented. Tests for *Clostridium botulinum* type C neurotoxin, while not definitive, increasingly point to LPS being a form of botulism. Other potential causes are still being ruled out as LPS cases have been shown to consume large numbers of insects, arachnids and fungi. Evidence for ricin and blue-green algae exposure has also been documented. Additional studies using day-old chickens to screen for sources of toxins and an improved botulism toxin assay are being developed.

Role of wild coypu (Myocastor coypus) as sentinel, reservoir and vector of antimicrobial resistance in the aquatic environment: preliminary results

Friday, 1st August - 10:15: Pathogen Discovery (Saanich Room) - Oral

Elisa Massella **[1]*****, Simone Russo*** **[1]*****, Sara Castaldo*** **[1]*****, Stefano Bussolari*** **[2]*****, Stefano Martini*** **[2]*****, Alessandro Morabito*** **[2]*****, Tommaso Mazzini*** **[2]*****, Pier Francesco Fontana*** **[2]*****, Fabrizio Mezzetti*** **[2]*****, Giacomo Gallerani*** **[2]*****, Manuel Gamberini*** **[2]*****, Martina Munari*** **[1]*****, Mario D'Incau*** **[1]*****, Silva Rubini*** **[1]*****, Virginia Carfora*** **[3]*****, Maria Sampieri*** **[1]*****, Andrea Luppi*** **[1]**

1. *Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna,* ***2.*** *Polizia Locale Città Metropolitana di Bologna,* ***3.*** *Istituto Zooprofilattico Sperimentale del Lazio e della Toscana*

The wild coypu (*Myocastor coypus*) is an invasive semi-aquatic species, increasingly becoming synanthropic by sharing common habitats and interacting with humans and domestic animals.

This study aims to investigate its role i) as sentinel of antimicrobial resistance (AMR) spread through surface waters, focusing on resistance to critical antimicrobials (i.e. third-generation cephalosporins - 3GCs, carbapenems and colistin), ii) as potential reservoir and vector of multidrug resistant (MDR) pathogens for humans and other animals.

Between December 2024 and February 2025, 34 faecal samples were collected along the Reno river, Italy. Microbiological analysis was implemented to isolate strains belonging to the *Enterobacteriaceae* family, identified by MALDI-TOF. AMR profiles were assessed determining Minimal Inhibitory Concentration, interpreted according to EUCAST epidemiological cut-off values. Strains phenotypically resistant to critical resistances were screened for related AMR genes with PCRs.

We isolated 39 enterobacteria belonging to 9 different species, of which *Escherichia coli* was the most common (17/39, 43.59%). Interestingly, 19/39 (48.72%) isolates were MDR. The most common resistance frequencies were to sulphonamides (34/39, 87.18%), ampicillin (21/39, 53.85%) and trimethoprim (10/39, 25.64%).

Notably, 7/39 (17.95%) strains were resistant to the critical antimicrobials 3GCs, associated with bla_{SHV} (*Enterobacter cloacae*, n=2), bla_{TEM}-bla_{CTX}-bla_{CMY} (*Escherichia coli*, n=4) and bla_{CMY} (*Escherichia coli*, n=1) genes.

Our preliminary results suggest wild coypu as an effective AMR indicator, potentially useful for future AMR surveillance programs in aquatic environments. Additionally, wild coypu may play a role in maintaining and transmitting MDR pathogens to humans and other animals, posing a significant threat to public health.

Paranannizziopsis infections in garter snakes in the Pacficic Northwest

Friday, 1st August - 10:30: Pathogen Discovery (Saanich Room) - Oral

Nicki Rosenhagen [1]***, Katherine Haman*** [2]***, Ryan Munes*** [3]***, Allan Pessier*** [4]

***1.** PAWS Wildlife Rehabilitation Center, **2.** Washington Department of Fish and Wildlife, **3.** U.S. Fish and Wildlife Service, **4.** Washington State University*

The Progressive Animal Welfare Society (PAWS) Wildlife Rehabilitation Center recently admitted several garter snakes from the greater Seattle area with external lesions suspicious for fungal disease. In collaboration with the Washington Department of Fish and Wildlife, US Fish and Wildlife Service, and the Washington Animal Disease Diagnostic Laboratory (WADDL) at Washington State University, the snakes were confirmed to be infected with fungus from the genus *Paranannizziopsis*. Since diagnosis, the veterinarians at PAWS have been managing the disease with nebulized terbinafine with excellent clinical success and intend on releasing the snakes to their points of origin. Surveillance efforts at the Nisqually Wildlife Refuge are currently underway to understand the prevalence of this disease in wild snakes in the Pacific Northwest, and the information gleaned from the care of these patients will help dictate future care and management of clinically affected individuals.

Microbiomes As Biomarkers Of Health In Wild Carnivores

Friday, 1st August - 10:45: Pathogen Discovery (Saanich Room) - Oral

Natalie Payne [1], Karla Vargas [1], Cheryl Mollohan [2], Ronald Day [2], Leigh Combrink [1]

***1.** University of Arizona, **2.** Wildlife Capture and Research*

The links between gut microbiomes and host health are well established in humans and model animal systems. However, comparatively little is known about microbiomes in wildlife. The ability to survey microbes in wildlife from non-invasively collected feces would greatly improve early detection of disease threats to wildlife, humans, and domestic animals. Here, we describe a multiomics approach to investigate microbial associations with health, environment, and kinship in two carnivore species. We integrated microbiome, virome, and host genomic datasets from bobcats (Lynx rufus) at the wildland urban interface (WUI) in Tucson, Arizona, USA, to investigate how relatedness and urbanization influence microbial communities. Our bobcat virome characterization results revealed numerous pathogens with the potential to impact wild and domestic carnivore health at the WUI. Models of virome and microbiome composition along with host location and genomic datasets reveal key roles of kinship and urbanization in shaping communities of host-associated taxa. We are also generating microbiome and parasite data from coyotes (Canis latrans) in wild ecosystems in Arizona to determine microbial associations with coyote health. We highlight the potential for studying interactions between individuals and within wildlife holobionts to yield important insights into disease spread, organismal health, and environmental change. With the current rate of anthropogenic ecosystem alteration, 'omics technologies provide a high-throughput solution for identifying key disease threats, allowing critical management decisions to preserve wildlife populations and "One Health."

Cracking the egg on sea turtle egg fusariosis in leatherback nests, an investigation of fungal burden

Friday, 1st August - 11:00: Pathogen Discovery (Saanich Room) - Oral

Samantha Kuschke [1]**, *Jeanette Wyneken*** [1]**, *Elizabeth Schultheis*** [1]**, *Tiffany Roberts Briggs*** [1]

1. *Florida Atlantic University, Boca Raton*

In recent years, there has been a significant rise in the prevalence of infectious diseases caused by fungi in marine ecosystems, presumably because of the rapid increase in ecological disturbances associated with anthropogenic climate change. Increasing temperatures and regional shifts in precipitation can foster fungal overgrowth within sea turtle nests, and reports of fungal infections of sea turtle eggs have increased around the globe. Fungal overgrowth by *Fusarium spp.* in sea turtle nests can cause sea turtle egg fusariosis (STEF). STEF causes embryo mortality and has been linked to decreased hatching success in all seven species of sea turtles. The leatherback sea turtle (*Dermochelys coriacea*), which has the lowest global average hatching success at 50%, 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 the sediment where leatherbacks nest, we are not aware of any published research on this topic in Palm Beach County, Florida and significant knowledge gaps persist. To fill these knowledge gaps, we obtained sediment samples from leatherback sea turtle nests at oviposition and excavation in Boca Raton, Juno Beach, and Jupiter Florida and used real-time polymerase chain reaction (qPCR) to measure the amount of *Fusarium spp.* present in nest sand. These quantitative data were used to determine whether the quantity of *Fusarium spp.* in the nest at each time point co-varies with emergence success, hatching success, and environmental factors. This molecular approach sheds light on key factors contributing to the occurrence and abundance of *Fusarium spp.* and whether it is associated with the low hatching success observed in crucial Florida nesting hotspots and therefore stifling population recovery. The knowledge gained from this research enhances our understanding of STEF and can help regulators plan mitigation strategies to improve hatching success.

Diverse and persistent impacts of West Nile virus on breeding bird populations in Pennsylvania

Friday, 1st August - 10:15: Ecology and Management (Oak Bay Room) - Oral

Brock Geary [1]***, Lisa Williams*** [2]***, Sean Murphy*** [2]***, Roderick Gagne*** [1]

1. *Wildlife Futures Program, University of Pennsylvania,* ***2.*** *Pennsylvania Game Commission*

Understanding disease impacts on wildlife health requires comparable and contemporaneous data on both pathogens and host populations, which are often challenging to collect. West Nile virus (WNV) caused declines in many North American bird populations upon its arrival in 1999, but more recent effects are less well-understood. Community-level responses to WNV have not been broadly assessed in over 15 years, and a better understanding of persistent effects from a landscape perspective is needed to improve future health outcomes for wildlife and humans.

We used Pennsylvania's mosquito surveillance database to model WNV occurrence at fine spatiotemporal scales, and estimated indices of said occurrence around Breeding Bird Survey routes over 19 years. WNV varied substantially in mosquitoes over space and time, and was correlated with factors such as temperature, elevation, and forest vs. urban land cover. Examination of annual WNV indices in relation to bird counts showed evidence of impacts to 20% of species (31/155). These findings suggest that WNV may play a substantial role in shaping bird population trends, with implications for the ecosystems and human settlements they inhabit. Current work seeks to assess commonalities in the traits of impacted bird species and the sites where impacts are most frequently seen, and future field-based studies will supplement model-based inferences to better understand how the virus shapes population trends relative to factors such as habitat degradation. This powerful new approach also shows promise for assessing other localized health threats, and demonstrates how community-sourced data sets can be leveraged for proactive management.

Five years of rabbit hemorrhagic disease virus 2 infections in wild lagomorphs in California, USA - tracking disease spread and mitigating impacts to an endangered species

Friday, 1st August - 10:30: Ecology and Management (Oak Bay Room) - Oral

Deana Clifford [1]***, Fumika Takahashi*** [2]***, Melinda Houtman*** [1]***, Jaime Rudd*** [3]***, Megan Moriarty*** [4]***, Mary Lou Berninger*** [5]***, Fawzi Mohamed*** [5]***, Thomas Connor*** [6]***, Cathleen Steinbeiser*** [6]***, Darren Minier*** [7]***, Robin Russell*** [8]***, Javier Asin Ros*** [9]***, Beate Crossley*** [9]

1. *Wildlife Health Laboratory, California Department of Fish and Wildlife,* ***2.*** *San Luis National Wildlife Refuge Complex, U.S. Fish and Wildlife Service,* ***3.*** *Endangered Species Recovery Program, California State University Stanislaus,* ***4.*** *University of California Santa Cruz,* ***5.*** *Foreign Animal Disease Diagnostic Laboratory, Plum Island Animal Disease Center,* ***6.*** *California Department of Fish and Wildlife,* ***7.*** *Department of Animal Care, Conservation and Research, Oakland Zoo,* ***8.*** *United States Fish and Wildlife Service,* ***9.*** *California Animal Health and Food Safety Laboratory, University of California*

Since rabbit hemorrhagic disease virus 2 (RHDV2) emerged in California (USA) in May 2020, geographic spread and temporal trends have been tracked via web-based reporting and follow up post-mortem PCR testing. To protect California's Central Valley endemic, endangered riparian brush rabbit (*Sylvilagus bachmani riparius*, RBR), an interagency/zoo/academia/non-profit team implemented emergency conservation actions. Applied research including diagnostic test validation and predictive modeling informed conservation efforts.

As of March 2025, 1,202 mortality reports were submitted and 290 carcasses subsequently tested. Mortality reports and RHDV2 case detections indicated rapid disease spread north-emergence, exhibited seasonal increases in winter-spring, and decreased yearly thereafter, with the exception of a notable resurgence in 2024. Seventy-seven infections have been confirmed in three species (*S. audubonii, S. bachmani, Lepus californicus*).

Prior to implementing vaccination of free-ranging RBRs, safety of the Felavac VHD K C+V® vaccine was assessed for 19 wild RBRs temporarily held in captivity. Predictive modeling coupled with camera-based population estimates were used to determine vaccination targets to minimize extinction risk. Vaccination of ~15% of the estimated RBR population began in September 2020. Approximately 1,221 RBRs have been vaccinated at least once since 2020. Spatially explicit mark-recapture-based density estimates using capture data from Fall 2020-Spring 2022 ranged from 2.66 - 62.52 RBRs/hectare. In Spring 2022, RHDV2-caused deaths of three unvaccinated RBRs confirmed species susceptibility. No mortalities of vaccinated RBRs were detected. Severe flooding in 2023 significantly reduced the RBR population, evidenced by decreased camera-trap detections and ~80% fewer RBR captures post-flood. Vaccination, disease surveillance, and population monitoring are ongoing to protect RBRs and monitor post-flood recovery. This emergency coalition of willing organizations meets monthly to guide efforts and has resulted in unique outreach opportunities through our zoological partners to raise awareness for conserving less well known, yet charismatic species inhabiting human-dominated landscapes.

A novel method of estimating badger population density for disease monitoring and vaccination delivery.

Friday, 1st August - 10:45: Ecology and Management (Oak Bay Room) - Oral

Ruth Cox [1]***, Verity Miles*** [2]***, Amy Griffiths*** [1]***, Richard (Dez) Delahay*** [1]

1. *Animal and Plant Health Agency,* ***2.*** *Institute of Zoology*

Reliable estimates of population density are essential for wildlife disease management. In the UK where badgers can be involved in transmission of bovine tuberculosis (bTB) to and from cattle, government policy has shifted from culling to vaccination. A better understanding of badger population density, particularly in post-cull locations, would support operational delivery and evaluation of the extent of vaccination coverage.

We tested a novel method of camera surveillance (the Random Encounter Model (REM)) as a non-intrusive means of estimating badger abundance and vaccination coverage in low density populations. We deployed up to 150 cameras at three sites (up to 5 km^2 each) for 6 weeks. These badger populations were subject to culling in recent years, while two of the populations were subsequently subject to vaccination. To determine vaccination coverage, we compared numbers of animals trapped and vaccinated with our REM estimates. We also assessed the resource requirements of the approach to determine its suitability for wider scale use.

Comparison of REM density estimates with mark-recapture data showed that reliable density estimates were achievable with reasonable survey effort. However, the small geographic scale of the vaccination sites resulted in high statistical uncertainty, limiting the ability to precisely estimate vaccination coverage. Uncertainty could be reduced by monitoring at larger temporal and spatial scales.

Camera surveillance was an effective, non-intrusive tool for estimating badger density in some scenarios. It was cost-effective relative to alternative methods, making it a practical tool for wildlife management strategies.

Guinea worm Disease Surveillance and Home range Analysis of Olive Baboons : Inform Programmatic Decisions for Eradication in Ethiopia.

Friday, 1st August - 11:00: Ecology and Management (Oak Bay Room) - Oral

ALEXANDRA SACK [1], ***Fitsum alemayehu Lemma*** [1], ***Misgana Amenu*** [2], ***Kassahun Demissie*** [3], ***Juhar Tesfaye*** [1], ***Yimer Mulugeta*** [4]

1. *The Carter Center,* ***2.*** *Ethiopian Wildlife Conservation Authority,* ***3.*** *Ethiopian Dracunculiasis Eradication Program at the Ethiopian Public Health Instutite,* ***4.*** *The Ethiopian Public Health Institute*

Guinea worm disease (GWD) was first detected in Olive baboons (*Papio anubis*) in 2013 in Ethiopia. Since then, questions have emerged about the role of Olive baboons in ongoing GWD transmission in Ethiopia. In support of eradication and to better understand transmission risks, the Ethiopia Dracunculiasis Eradication Program (EDEP) conducts surveillance activities among Olive baboon troops in the Gambella region considered high risk for GWD due to previous human or animal infections. Surveillance includes weekly tracking of baboon movement and water source use as well as trapping and sedation of baboons to physically check for emerged worms or signs of GWD three times a year. In 2024, we expanded trapping to include 15 troops, 241 baboons were sedated and screened for GWD, and we placed GPS collars on adult male baboons in all troops. GPS collars take hourly points for 17 hours a day. Home range was calculated using the minimum convex polygon method. Total area is used to cover all possible water sources used. This data is shared weekly with field teams and baboon trackers to directly address any programmatic gaps. An adult male baboon was confirmed with GWD in July, and definitive diagnosis is pending on a second adult male provisional infection detected in November. Each troop's home range varied from 2.5 to 25.0 square kilometers total. EDEP leverages findings from baboon surveillance activities and GPS collar data shared weekly to inform programmatic implementation strategies, including surveillance intensity, community mobilization, and water treatment to prevent GW transmission.

Posters

Histopathologic Lesions of Free-Ranging Rats in Hong Kong

Monday, 28th July - 15:00: (Salon A) - Poster

Lisa Lee [1]***, Jeanine Sandy*** [2]***, Theethawat Uea-Anuwong*** [2]***, Ioannis Magouras*** [2]***, Chelsea Himsworth*** [3]***, Kim Waggie*** [4]***, Bruce Wobeser*** [1]

1. *University of Saskatchewan,* ***2.*** *City University of Hong Kong,* ***3.*** *University of British Columbia,* ***4.*** *University of Washington*

Wild rats are globally distributed pests that can cause significant infrastructure damage and transmit pathogens infective to humans. Despite the cosmopolitan nature of rats, studies examining their diseases are limited to few geographic regions. Health assessments of wild rat populations are needed for a holistic view of their ecology, and to inform management strategies; sick animals may be more susceptible to carrying pathogens or affecting population dynamics. Our objective was to examine the spectrum of histopathologic lesions occurring in wild rats in Hong Kong. Two-hundred-twenty-one free-ranging rats (*Rattus norvegicus*, *n*=144; *Rattus tanezumi*, *n*=67; *Rattus andamanensis*, *n*=8; and *Niviventer huang*, *n*=2) were trapped in Hong Kong from 2020-2021 in urban residential sites and semi-rural areas including chicken and swine farms, and horse-riding schools. Lung, liver, kidney, spleen, skeletal muscle, and tissues with macroscopic abnormalities were examined histologically. Nematodes consistent with *Angiostrongylus cantonensis* (rat lungworm) were identified in 5.9% (13/221) of rats, frequently with granulomatous, eosinophilic pneumonia and pulmonary hemorrhage. *Rattus norvegicus* were exclusively infected and widely distributed. Rats rarely had significant disease, such as bacterial granulomas (1.4%, 3/221) or renal tubular loss with interstitial fibrosis (0.9%, 2/221). Incidental lesions included *Cysticercus fasciolaris* cestode larval cysts in the liver (5.1%, 11/216), and *Sarcocystis spp.* protozoal cysts without inflammation in skeletal muscle (4.8%, 10/207); *Sarcocystis spp.* were only detected in rats trapped in semi-rural areas. This study highlights lesions contributing to disease burdens in wild rats and provides surveillance for zoonotic parasites, like rat lungworm, in Hong Kong.

Spontaneous amyloidosis is associated with endoparasitism in wild rabbits (Sylvilagus spp.)

Monday, 28th July - 15:00: (Salon A) - Poster

Elliott Chiu [1], ***Arely Rosas*** [2]

1. City University of Hong Kong, 2. Disease Investigations, San Diego Zoo Wildlife Alliance

Current literature regarding spontaneous amyloidosis in rabbits undercuts the significance of this disease in rabbits. While it is by no means a novel disease, amyloidosis in rabbits exists primarily in the context of inducible disease with the most common manifestation as renal deposition. A previous survey of renal disease in rabbits identified a low prevalence (2 out of 312; 0.6%) leading others to conclude and report that amyloidosis is not a significant disease in rabbits. Here, we examine the presence and distribution of amyloid in wild rabbits (Sylvilagus spp.) including desert cottontails and brush rabbits found dead or euthanized on grounds of the San Diego Zoo Safari Park. Additionally, we statistically examine associations of co-morbidities with disease. Between August 1984 and April 2024, 157 rabbits were accessioned and full gross necropsies and histology was performed. Out of these cases, 29 rabbits were diagnosed with renal or systemic amyloidosis. Renal (interstitium, glomeruli, or both) amyloidosis was the most common manifestation. Vessels were the second most affected tissue disseminated throughout numerous organs. The spleen, heart, stomach, and adrenal gland were consistently but less affected, and sometimes inconspicuously so without the aid of Congo Red staining. Cestodiasis was significantly correlated with amyloidosis. Coccidiosis and trauma were negatively associated with disease. Our results provide a stark contrast to previous reports of amyloid in rabbits demonstrating that not only is spontaneous amyloidosis relatively common, but should be considered as a potential cause of death in wild rabbits.

Non-zoonotic disease systems and the One Health framework: Tiny ticks have big impacts to moose biology, management and culture

Monday, 28th July - 15:00: (Salon A) - Poster

Alaina Woods [1], ***Sandra De Urioste-Stone*** [1], ***Pauline Kamath*** [1]

1. *University of Maine*

The One Health (OH) framework has primarily been focused on zoonotic diseases with little attention to wildlife-specific diseases, even though these diseases can threaten ecosystem stability and culture surrounding the species they affect. For example, in Maine, moose are an ecological, economical, and culturally important species, and are experiencing high rates of mortality due to the winter tick. Here, we use the moose – winter tick system to showcase how the OH framework can be a tool in a large-scale project evaluating the social and biological implications of a non-zoonotic disease system. This project included stakeholder engagement to determine geographic extent and risk factors of infections; a content analysis of Maine news media to analyze how information regarding the system is being communicated; analysis of survival data to evaluate the role of parasites in over-wintering moose calf survival; and a host genomic study to explore the adaptive potential of an iconic species. While parasites are widespread geographically, and parasitic infection significantly decreases moose calf survival, news media messaging in the state surrounding the system is primarily risk-minimizing in nature with an emphasis on trust in managing agencies, but the future is still uncertain as it is too soon to discern how moose are responding to parasitic infection. Through this work, collaborations with state agencies were strengthened, and collaborations with tribal nations and stakeholders were created. This work highlights the strengths of using the OH framework analytically to evaluate a complex system by expanding the definition of health to include cultural connections.

HPAIV infection in peridomestic animals

Monday, 28th July - 15:00: (Salon A) - Poster

***Angela Bosco-Lauth* [1], *Stephanie Porter* [2], *Jeff Root* [2], *Jeremy Ellis* [2], *Kaytlin Bohr* [2], *Airn Hartwig* [1]**

***1.** Colorado State University, **2.** USDA National Wildlife Research Center*

Since its emergence in 2021, highly pathogenic avian influenza virus (HPAIV) clade 2.3.4.4b AIV (H5N1) has led to mass mortality events in numerous species of poultry, wild birds, and certain mammals worldwide. In 2024, the virus was first discovered in dairy cattle in the U.S. and has since impacted hundreds of dairies, with multiple instances of humans becoming infected by contact with infected cattle. Domestic cats are also highly susceptible to the currently circulating H5N1, and infection is often fatal. To better understand the host range, pathogenicity and transmission potential in different species of peridomestic animals, we tested the susceptibility of several wildlife species and domestic cats to replicate H5N1 HPAIV. Wildlife species included house sparrows (*Passer domesticus*), European starlings (*Sturnus vulgaris*), feral pigeons (*Columba livia*), striped skunks (*Mephitis mephitis*), Virginia opossums (*Didelphis virginiana*), and cottontails (*Sylvilagus* sp.), deer mice (*Peromyscus maniculatus)* and house mice (*Mus musculus),* All tested species replicated and shed virus, at least to some degree. Cats, striped skunks and Virginia opossums shed the highest viral titers, and cats and skunks also developed severe neurological disease. Overall, the results of this study indicate that certain peridomestic species could pose a biosecurity threat to poultry and/or cattle operations in some situations, and the risk of transmission to humans remains unclear. In addition, this study and field reports indicate that the HP AIVs circulating in the U.S. may have an extremely broad range of species that can be impacted by and/or replicate and shed these viruses.

Community partnership for successful eradication of African Swine Fever: Challenges and lessons learned from the 2023 outbreak in wild boar in Sweden

Monday, 28th July - 15:00: (Salon A) - Poster

Karin Olofsson-Sannö [1]***, Erik Ågren*** [1]***, Aleksija Neimanis*** [1]***, Erika Chenais*** [1]

1. *Swedish Veterinary Agency SVA*

In September 2023, Sweden detected its first outbreak of African swine fever (ASF) in free-living wild boar (*Sus scrofa*). Multiple dead wild boar were reported by local hunters to the wildlife disease surveillance programme. After evaluating the oldest cadaver found, the outbreak was estimated to have started in May -June 2023.

Containment of the outbreak required rapid coordination among authorities and hunters. The primary objective was to prevent further spread and secondly to eradicate ASF from the country. Key measures included systematic cadaver removal and effective, traceable sampling, as well as off-road access restrictions for humans and vehicles, all requiring well-coordinated community partnership. In the process, practical tools for search efforts and sampling, including digital mapping and reporting systems were developed. These systems needed to be applicable and user friendly, a challenging task during an outbreak. Almost 100 carcasses were located and sampled, with 62 positive for ASF, all within a 5 km zone. Cadaver removal, limiting wild boar entering the zone and culling of remaining wild boar in the area limited virus persistence and spread, while digital mapping and continuous communication between stakeholders streamlined the efforts. Transparent public communication and strong stakeholder collaboration ensured compliance and efficiency. One year after the first case, Sweden was officially declared free from ASF. The successful management of the outbreak highlights the importance of field adaptability, data-driven tools, and community engagement in ASF management when affecting free-living wild boar.

From surveillance to action – collaboration to manage Echinococcus hotspots in Sweden

Monday, 28th July - 15:00: (Salon A) - Poster

Erik Ågren [1]***, Kristina Busch*** [2]***, Heléne Duvgren*** [3]***, Gustav Averhed*** [1]***, Elina Thorsson*** [1]***, Eva Osterman Lind*** [1]

1. *Swedish Veterinary Agency SVA,* ***2.*** *Swedish Public Health Agency,* ***3.*** *Swedish Board of Agriculture*

Echinoccocus multilocularis was found in Sweden in 2011, after 10 years of surveillance in hunter-harvested red foxes (*Vulpes vulpes*). Two national surveillance programs, 2012 - 2014 and 2021 – 2024 both showed that the parasite is present very sporadically in the southern half of the country, with two known small areas with continuous infection since 2014. A third area with possible established infection was found in 2024 at the periphery of Uppsala, the first urban finding of this parasite. Human alveolar echinococcosis cases have usually acquired the infection abroad, but since 2012, nine cases have been identified as possible domestic infections. Several competent authorities are involved in this zoonotic disease and collaborate on how to move forward with the present surveillance results. Updating risk assessments regarding domestic dogs and activities such as gardening and growing vegetables are being done as an urban area implies many possibly exposed humans. Communicating risk management and recommendations for the public is an important task. As the parasite still appears to be limited to a few sporadic cases and very few localized established infected areas, the time for action is now. This is a window of opportunity to initiate a local campaign aiming at eradicating the parasite in an infected area by regularly deworming the foxes, before the infection spreads over larger areas, as in other parts of Europe. The result of the treatment would be done by regularly analyzing fox scats in the area. The overall objective is to lower the risk for human infection.

Occurrence and Genetic Characterization of Tick-borne Relapsing Fever Borrelia spp. in a Florida subspecies of soft ticks (Ornithodoros turicata americanus)

Monday, 28th July - 15:00: (Salon A) - Poster

Nicholas Canino [1]***, Kristen Wilson*** [1]***, Sebastian Botero-Cañola*** [1]***, Pacharapong Khrongsee*** [1]***, Kuttichantran Subramaniam*** [1]***, Samantha Wisely*** [1]

1. *University of Florida*

In Florida, the only recorded occurrence of the *Borrelia* pathogens that cause Tick-borne Relapsing Fever (TBRF) was in two domestic dogs (*Canis lupus familiaris*) in the 1990s. Florida boasts a substantial population of the soft tick vector, *Ornithodoros turicata americanus*, that is capable of transmitting *Borrelia*, yet this pathogen has never been recorded in these ticks. The goal of our study was to fill the knowledge gaps regarding this vector and its pathogens in the state. Our objectives were to 1) describe the distribution of *Borrelia* spp. in Florida ticks; 2) phylogenetically describe the pathogen species compared to the western *B. turicatae*. We pooled and extracted DNA from over 3,000 ticks systematically collected throughout the state. Conventional PCR was used with an IGS primer to detect any *Borrelia* spp. present in the ticks. We Sanger sequenced 4 pools (4/580; 0.69%) that were positive for *Borrelia* spp. Sequencing of the amplified IGS gene led to ambiguous results that did not provide a definitive conclusion on the *Borrelia* spp. present in these ticks. Two samples returned a 99.7% and 96.9% match for *B. turicatae* while the other two showed percent identity of 97% and 95.2% for *B. venezuelensis*. In order to fully understand the diversity of *Borrelia* spp. in the state, a modified whole-genome Multilocus Sequence Typing strategy will be employed. By uncovering the pathogens and their prevalence in the state, we can better understand and mitigate the risk of this vector-borne disease for humans and companion animals in Florida.

Evaluating the Ability of a Rapid, Field-Deployable, PCR Test to Screen Deceased Avian Wildlife for Influenza A Virus

Monday, 28th July - 15:00: (Salon A) - Poster

Lucie Pascarosa **[1]*, Roderick Gagne*** **[2]*, Michelle Gibison*** **[2]*, Erica Miller*** **[2]**

1. *University of Pennsylvania School of Veterinary Medicine,* ***2.*** *Wildlife Futures Program, University of Pennsylvania*

Highly pathogenic avian influenza (HPAI) encompasses a group of highly contagious and potentially zoonotic avian influenza A viruses. HPAI has high mortality rates in certain avian species and outbreaks have caused economic devastation in poultry. Waterfowl are reservoirs for avian influenza and facilitate the spread of the virus to domestic birds as they migrate. However, wild birds may also exhibit clinical signs or suffer mass fatalities. In January 2025, HPAI strain H5N1 killed over 5,000 snow geese in eastern Pennsylvania. The ability to effectively and rapidly screen for influenza A during similar avian mortality events would improve the speed of response decisions, advisories to properties or institutions that house poultry, and sample submissions to diagnostic facilities while protecting the health and safety of wildlife officials. Here, we assessed the ability of the Biomeme Franklin portable thermocycler with an Influenza A matrix rRT-PCR to detect the presence of influenza A virus in oropharyngeal swabs obtained from known positive and negative birds. We then evaluated the field-deployment capabilities of the device and found results could be obtained in several hours.

Electrocardiographic examination of 16 eastern grey kangaroos (Macropus giganteus) and a red kangaroo (Osphranter rufus)

Monday, 28th July - 15:00: (Salon A) - Poster

***Ann Carstens* [1], *Geoffrey Dutton* [1], *Hayley Stannard* [1], *Alice Birckhead* [1], *William Barkman* [1], *Joanne Connolly* [1]**

***1.** Charles Sturt University*

Kangaroos are macropod marsupials native to a variety of habitats in Australia and New Guinea. Habitat loss, trauma (roadkill, fence entrapment, predation), disease and natural disasters impact health and survival of macropods. Macropods are highly susceptible to exertional rhabdomyolysis (stress or capture myopathy), characterized by damage to skeletal or cardiac muscle following intense physical activity, which is more likely with elevated environmental temperatures. Cardiac disease reported in kangaroos includes hypertrophic cardiomyopathy (HCM), dilated cardiomyopathy (DCM), nutritional myodegeneration, valvular pathology, cardiovascular parasites, toxoplasmosis, and toxicities, but few echocardiographic evaluations have been published. The heart of macropods is approximately a third larger than size-matched eutherian mammals, almost as wide as it is long and is pointed at the apex.

The aim of this study was to echocardiographically evaluate sedated kangaroos in care opportunistically: 14 clinically normal eastern grey kangaroos (EGK - *Macropus giganteus*), two sick EGKs, and one sick red kangaroo (RK - *Osphranter rufus*). Standard B-mode images, M-mode mensuration, including relative wall thickness (RWT) and Doppler measurements were attained from healthy EGK. Normal kangaroo hearts showed thicker than expected left ventricular and interventricular septum walls, and RWTs of 0.5 and 0.6, whereas in humans an RWT >0.45 indicates HCM. Necropsy of three sick animals revealed HCM in one EGK (RWT of 1.02), myxomatous mitral valve degeneration and suspect DCM in the other two. Subclinical HCM may be present in apparently normal animals. These findings can be used for clinical health assessments and further research into macropod cardiac conditions.

Abdominal ultrasonographic evaluation of healthy juvenile eastern grey kangaroos (Macropus giganteus)

Monday, 28th July - 15:00: (Salon A) - Poster

***William Barkman* [1]*, Joanne Connolly* [1]*, Geoffrey Dutton* [1]*, Hayley Stannard* [1]*, Ann Carstens* [1]**

***1.** Charles Sturt University*

Kangaroos belong to the Macropodidae family, a diverse group of over 60 marsupial species native to a variety of habitats in Australia and New Guinea, including 24 species on the IUCN Red List. Wild macropods face challenges of urbanization, trauma (roadkill, fence entrapment, dog attack), disease, and climate change. During the Australian Black Summer Wildfires in 2019-2020, thousands of kangaroos were rescued and treated but many died from co-morbidities or pathologic sequelae. Ultrasonography may have detected underlying conditions such as blunt abdominal trauma, edema, smoke inhalational, pulmonary lesions, nephropathy, and myocarditis. Ultrasonography is a valuable imaging modality, providing a non-invasive, versatile, and accessible diagnostic tool for veterinarians, but literature on the ultrasonographic anatomy of macropods is minimal.

The aim of this study was to describe a systematic approach and document the normal ultrasonographic abdominal anatomy of the kangaroo (including liver, gall bladder, gastrointestinal tract, spleen, kidneys, adrenal glands, and urinary bladder). Ten macropod cadavers were used for initial dissections and preliminary ultrasonographic examinations. Seven healthy juvenile eastern grey kangaroos (*Macropus giganteus*) were ultrasonographically examined under heavy sedation in lateral recumbency. Compared to domestic species, ultrasonographic differences in anatomy included the forestomach, hindstomach, liver orientation, distinguishable adrenal glands, splenic branching and epipubic bones. The results of this study provided standardized ultrasonographic protocols and landmarks for the kangaroo developed to suit their unique anatomy and provides a foundation for the ultrasonographic diagnosis and interpretation of abdominal disease in this species.

Regional surveillance for Echinococcus species in wild canids in the Eastern United States

Monday, 28th July - 15:00: (Salon A) - Poster

Christopher Cleveland [1]***, Kayla Garrett*** [1]***, Casey Dukes*** [1]***, Justin Brown*** [2]***, Christine Casey*** [3]***, Richard Gerhold*** [4]***, Eliza Baker*** [4]***, Colleen Olfenbuttel*** [5]***, Kelly Douglass*** [6]***, Ethan Barton*** [7]***, Catherine Dennison*** [8]***, Kathryn Purple*** [9]***, Lauren Maxwell*** [10]***, Charlie Bahnson*** [11]***, Pablo Jimenez Castro*** [12]***, Michelle Evason*** [12]***, Christian Leutenegger*** [12]***, Samantha Loo*** [12]***, Kevin Niedringhaus*** [10]***, Michael Yabsley*** [1]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *Department of Veterinary and Biomedical Sciences, Penn State University,* ***3.*** *Kentucky Department of Fish and Wildlife Resources,* ***4.*** *University of Tennessee,* ***5.*** *North Carolina Wildlife Resources Commission,* ***6.*** *United States Department of Agriculture,* ***7.*** *West Virginia Division of Natural Resources,* ***8.*** *Ohio Department of Natural Resources,* ***9.*** *Lincoln Memorial University,* ***10.*** *Wildlife Futures Program, University of Pennsylvania,* ***11.*** *North Dakota Game and Fish Department,* ***12.*** *Antech Diagnostics*

Echinococcus species are zoonotic cestodes that can cause cystic and alveolar echinococcosis in wildlife, domestic animals, livestock, and humans. In North America, *E.* multilocularis, *E.* granulosus s.l. (*E.* canadensis), and *E.* granulosus s.s. use domestic dogs and wild canids (red fox [*Vulpes vulpes*], gray fox [*Urocyon* cinereoargenteus], coyotes [*Canis latrans*], and wolves [*C.* lupus]) as definitive hosts. While historically absent in the eastern US, these parasites have recently been detected in domestic animals and wildlife in this region.

Between 2021-2024, we examined gastrointestinal tracts from 1,188 wild canids across 14 states for adult cestodes, including red foxes (n=343), gray foxes (n=135), and coyotes (n=710). We detected *E.* multilocularis in 12 (1.7%) coyotes: seven from North Dakota, four from Pennsylvania, and one from Kentucky. We also found *E. canadensis* (G8) in three Pennsylvania animals: one red fox and two coyotes. Species identification was confirmed via cox1 PCR and sequencing.

Additionally, molecular testing of separate fecal samples using KeyScreen GI Parasite PCR (Antech Diagnostics, MARS Petcare, Science and Diagnostics) was done on 27,293 canids in Pennsylvania (262 wild canids, 52 domestic hunting dogs, and 26,979 pet dogs). *Echinococcus* multilocularis (haplotype European strain France E3, E4) was detected in two gray foxes (3.7%) and two coyotes (1.4%), while *E.* canadensis was found in one coyote (0.57%). No *Echinococcus* were detected in domestic dogs. These findings paired with the multistate surveillance data indicate broader *Echinococcus* distribution than previously recognized, warranting continued surveillance for public, veterinary and wildlife health.

Detection of Paranannizziopsis sp. in wild Swinhoe's japalure (Diploderma swinhonis) in Taiwan

Monday, 28th July - 15:00: (Salon A) - Poster

Chiao-Wen Chen [1]***, Pin-Huan Yu*** [2]***, Chun-Kai Yang*** [3]***, Pei-Lun Sun*** [4]***, Wen-Ta Li*** [5]

1. *Graduate Institute of Veterinary Clinical Sciences, National Taiwan University, Taipei, Taiwan,* ***2.*** *Institute of Veterinary Clinical Sciences, National Taiwan University, Taipei, Taiwan,* ***3.*** *Center for Interdisciplinary Research on Ecology and Sustainability, National Dong Hwa University, Hualien County, Taiwan,* ***4.*** *Department of Dermatology and Research Laboratory of Medical Mycology, Chang Gung Memorial Hospital, Linkou Branch, Taoyuan, Taiwan,* ***5.*** *Pangolin International Biomedical Consultant Ltd., Keelung, Taiwan*

Onygenalean dermatomycoses, caused by fungi in the order Onygenales, comprise some of the most prominent emerging pathogens in reptiles, including the genera *Nannizziopsis*, *Paranannizziopsis*, and *Ophidiomyces*. These fungal pathogens have gained increasing attention due to their high pathogenicity in reptiles and their potential threat to wild populations. To date, several large-scale investigations and ecological research studies have been conducted in Europe and the America, covering pet, captive, and wild reptiles, while reports from Asia are limited. In Taiwan, our research team confirmed *Nannizziopsis* infections in pet lizards, wild invasive green iguanas, and wild snakes. Therefore, we hypothesized that native wild lizards in Taiwan could also be at risk of *Nannizziopsis* infection. To investigate this, we conducted a study on wild native Swinhoe's japalure (*Diploderma swinhonis*) exhibiting skin lesions, performing skin biopsy, microscopic examination, fungal culture, molecular biology analysis, and histopathological examination. A total of 230 native Swinhoe's japalure (*Diploderma swinhonis*) were captured, 85 of which had skin lesions and were sampled. Among these, *Paranannizziopsis* sp., closely related to *P. australasiensis*, was isolated from five individuals, marking the first discovery of this pathogen in Asia. Additionally, *Nannizziopsis* sp. was isolated from one lizard. The skin lesions in all six affected lizards were mild, and phylogenetic analysis suggests that these pathogens may naturally exist in Taiwan. These findings highlight the potential presence of *Nannizziopsis* and *Paranannizziopsis* species in native reptile populations, warranting further research on the distribution, susceptible species, and population genetics of these possible novel pathogens.

Sarcoptic Mange in Rescued Raccoon Dogs (Nyctereutes procyonoides) of Chungcheongbuk-do, South Korea: Infection Prevalence, Mortality, and Urban Impact

Monday, 28th July - 15:00: (Salon A) - Poster

Kwon Mirim [1]***, Yujin Lee*** [1]***, Jongseung Kim*** [2]***, Nari Kim*** [1]***, Kiyoon Kim*** [1]***, Kyeongyeon Kim*** [2]***, Juyeong Park*** [2]***,***
Dong-Hyuk Jeong [1]

1. *Chungbuk National University,* ***2.*** *Wildlife Center of Chungbuk*

Wildlife-borne infectious diseases are an increasing public health concern, underscoring the need for zoonotic disease ecology research. The raccoon dog (*Nyctereutes procyonoides*), a key host of parasitic diseases, has growing contact with humans due to urbanization and the rising pet population. However, epidemiological data on *Sarcoptes scabiei*-induced mange in Korean raccoon dogs remain scarce despite its severity in this species. This study investigates *Sarcoptes scabiei* infections in rescued raccoon dogs and their association with urban environments, providing baseline data for future epidemiological modeling.

From 2012 to 2024, 719 rescued raccoon dogs were examined. Individuals were classified by age, sex, and rescue location to assess mange prevalence. An independent *t*-test compared group means, while Pearson correlation analyzed mortality-related variables. Data were analyzed using Excel and SPSS (v28.0).

Infected individuals had higher mortality (infected: 59%, non-infected: 49%), with adult infection rates at 76%. Urban infection rates (65.38%) exceeded non-urban rates (52.50%), showing a strong correlation with urban mortality. Cases declined from 65 (2014) to 41 (2019) but surged to 92 (2020), possibly due to an outbreak.

This retrospective study, based on wildlife center data, had limitations in environmental factor analysis. However, increasing urban infection rates and rescues highlight public health concerns. Further research should refine infection analyses, incorporate environmental factors, and establish long-term disease surveillance systems.

Clinical Management of H5N1 Avian Influenza in a Captive Flock of Red-Breasted Geese (Branta ruficollis)

Monday, 28th July - 15:00: (Salon A) - Poster

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Recent re-emergence of high pathogenicity avian influenza (HPAIV H5N1) has led to substantial global mortality across multiple host species.[1] Co-occurring infections in different species have demonstrated marked differences in morbidity and mortality.[1] A flock of 4.6 Red-breasted Geese (Branta ruficollis) and 1.1 Emperor geese (Anser canagnicus) were housed in an outdoor unsheltered aviary. A 4-month-old goose from the flock presented with right leg lameness and a superficial circular eschar along the right flank. Supportive care in the form of antibiotics and non-steroidal anti-inflammatory medication were initiated, but the goose was found deceased the next day. Because of reports of a regional increase in HPAI H5N1 cases in wild birds found in close proximity, the goose was tested post-mortem for HPAIV on PCR and was confirmed positive. 24 hours following death of the goose, an 11-year-old gander was found dead with no premonitory signs. This gander also tested positive for HPAIV. Key histopathologic findings on these geese included necrotizing pancreatitis, necrotizing myocarditis, lymphocytic hepatitis, and lymphocytic periganglioneuritis. A third case, a 12-year-old gander, presented 72 hours following the death of the first case and was confirmed positive. Clinical signs included lethargy, inappetence, bilateral oculonasal discharge, and increased respiratory sounds. Intensive supportive care in the form of fluids, antifungals, antibiotics, antivirals, pro-coagulants, mucolytics, and anti-inflammatory medication was initiated. This goose survived to convalescence and subsequently tested negative. All birds from the affected flock were isolated in indoor quarantine spaces. Two more Red-breasted Geese tested positive for HPAIV but never developed clinical signs. This outbreak would not have been managed successfully without close communication and coordination with multiple governmental and non-governmental agencies.

1. Plaza P, Gamarra-Toledo V, Eugui J, Lambertucci S (2019): Recent changes in patterns of mammal infection with highly pathogenic avian influenza A(H5N1) virus worldwide. Emerging Infectious Diseases 30, p. 444-452.

Improving the surveillance of canine and feline coronavirus in domestic and wild carnivores to understand the risk of cross-species transmission and the emergence of recombinant variants

Monday, 28th July - 15:00: (Salon A) - Poster

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Canine coronavirus (CCoV) and feline coronavirus (FCoV) belong to the *Alphacoronavirus-1* species. These alphacoronaviruses have a wide host range, encompassing both domestic and wild canids and felids, as well as humans. CCoV and FCoV each have two genotypes (1 and 2), and multiple recombinant variants between the genotypes have been reported. For example, FCoV type 2 (FCoV-2) is a recombinant between FCoV type 1 (FCoV-1) and canine coronavirus type 2 (CCoV-2). CCoV and FCoV commonly cause subclinical to mild signs, but specific mutant or recombinant variants can be highly pathogenic. In this study, we used archived samples collected in zoological institutions in the U.S. to perform retrospective epidemiological studies of FCoV and CCoV. Using different next-generation sequencing techniques, we show that (1) FCoV-1 can be transmitted between domestic and wild felids and (2) CCoV-2 can infect wild felids. Comparative genetic analyses of the receptor of FCoV-2 and CCoV-2 (the aminopeptidase N, APN) from wild felid species, including vulnerable and endangered species, revealed a high percentage of identity to the APN of the domestic cat (>95.7%). This close genetic relationship suggests that these species might also be vulnerable to FCoVs circulating in domestic cats. Furthermore, studies indicate that the APN of domestic cats allows the entry of FCoV-2, CCoV-2, and other alphacoronaviruses; thus, like domestic cats, wild felids could also serve as important mixing vessels for the emergence of recombinant alphacoronaviruses. Our findings underscore the importance of conducting surveillance of both FCoV and CCoVs in canids and felids to understand the risk of cross-species transmission and the emergence and spread of recombinant variants.

Emaciation and mortality in rough-skinned newts on the Olympic Peninsula, Washington State

Monday, 28th July - 15:00: (Salon A) - Poster

Daniel Trovillion [1], ***Katherine Haman*** [1], ***Betsy Howell*** [2], ***Max Lambert*** [3]

1. *Washington Department of Fish and Wildlife,* ***2.*** *United States Department of Agriculture Forest Service,* ***3.*** *The Nature Conservancy*

There is a substantial need for increased detection, identification and early response to amphibian declines. Common species are more likely to be observed and may serve as indicators of[RO1] [AM2] emerging issues such as new disease outbreaks or deteriorating habitat conditions. Here we report multiple years of observations of emaciated rough-skinned newts (*Taricha granulosa*) in five streams of the Satsop river basin and four lakes in the Olympic National Forest (ONF). Newts were frequently seen at these sites with a subset visibly displaying poor body condition with ribs, vertebra, and pelvic girdle protruding. Emaciated newts also demonstrated lethargy and erratic swimming, including twirling movements, and disorientation. Some newts also displayed abdominal swelling that restricted swimming and diving. Across three years of monitoring at one lake, newts appeared healthy early in the season, but die-offs and diseased animals became apparent in late summer as water levels receded. Research and testing are ongoing, but diagnostics from previously necropsied specimens tested negative for fungal pathogens *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal), but came back emaciated and dehydrated, with some displaying substantial liver damage. Previous newt swabbing efforts in the Olympic lakes have tested positive for Bd and one lake had a high prevalence of Bd. As with most amphibian die-offs and declines, the causes here remain enigmatic. Our goal here is to raise awareness of mortality and illness in common amphibians and encourage others to record and report field observations of sickly or emaciated amphibians to local fish and wildlife agencies.

THE EARLY BIRD CATCHES THE PARASITE: POTENTIAL INVERTEBRATE PATHWAY FOR BAYLISASCARIS PROCYONIS TO INFECT SONGBIRDS

Monday, 28th July - 15:00: (Salon A) - Poster

Scott Henke [1]

1. Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville, Kingsville

Baylisascaris larva migrans is a debilitating and potentially lethal zoonotic, parasitic condition that can infect a large variety of paratenic hosts, including birds and mammals and even humans. Typical pathway to become infected with baylisascariasis is to ingest *Baylisascaris* spp. eggs from contaminated feces or through contaminated soil where contaminated fecal matter decayed. I hypothesized that earthworms (*Lumbricus terrestris*) living in *Baylisascaris*-contaminated soils would incidentally ingest *Baylisascaris* spp. eggs, and in turn, if earthworms were consumed by songbirds, songbirds would become infected with baylisascariasis. I placed 100 earthworms in *Baylisascaris procyonis*-infused soil and determined that 92% of earthworms had, on average, 7.3 ± 0.4 *B. procyonis* eggs in their alimentary canals. When *B. procyonis*-infected earthworms were fed to European starlings (*Sturnus vulgaris*), 94% (17 of 18) of starlings displayed signs of ataxia, torticollis, and paralysis, of which 11 of 18 (61%) died within 22 days of first ingestion of *B. procyonis*-infected earthworms. White blood cell counts of starlings that ingested *B. procyonis*-infected earthworms increased by nearly 3-fold, % of eosinophils increased by 25-fold, and % of lymphocytes increased while % heterophils decreased from Day 0 to Day 12 post ingestion. Starlings within the control group remained healthy and displayed normal behaviors. This study highlights an overlooked pathway of baylisascariasis, which could be a major mortality factor of many species within terrestrial ecosystems.

The cetacean virome: Expanding the range of RNA viruses in cetaceans with disease presentation

Monday, 28th July - 15:00: (Salon A) - Poster

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Our understanding of viral infectious disease in cetaceans has advanced in recent years, however, due to the sampling restraints presented by this group of animals research into the breath of viruses that infect cetaceans is behind that of terrestrial animals. To address this, we employed a metatranscriptomic approach to screen tissue samples from 33 individual animals in Australia, comprising seven dolphin species and six whale species. A custom virus discovery pipeline was used to detect novel viruses from sequencing data and phylogenetic analysis to infer relationships within viral families.

Sequencing data revealed novel viruses from five families detected in animals with numerous disease presentations, including a novel pegivirus, pneumovirus, rhabdovirus, morbillivirus and hantavirus. A novel rhabdovirus was detected in a skin sample from a Rissos dolphin with severe skin lesions, while a novel hantavirus was detected in multiple tissues from a Common dolphin with severe myocarditis. In a pygmy sperm whale with congestion and tongue ulceration we identified in lung and oral tissue a novel pneumovirus of which constitutes a new genus within the *Pneumoviridae*. Interestingly, this is the first recording of a pneumovirus and hantavirus infecting marine mammals. Additionally, the morbillivirus detected in brain tissue from a pygmy killer whale suggests a new member of the cetacean morbilliviruses.

These results further our knowledge of viral infections in cetaceans and demonstrates that certain mammalian-associated viral families are not limited to land dwelling mammals. Furthermore, these finding could assist our understanding of the epidemiology and pathogenesis of previously uncharacterised viral families in cetaceans.

Serological investigation of livestock infectious diseases in Long-tailed goral(Naemorhedus caudatus) in the Republic of Korea

Monday, 28th July - 15:00: (Salon A) - Poster

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The long-tailed goral is an ungulate species belonging to the *Bovidae* family and *Caprinae* subfamily, susceptible to various diseases that can also affect livestock. Furthermore, wild animals can serve as reservoirs for various infectious diseases, posing a risk of transmission to domesticated livestock. Therefore, continuous monitoring of various diseases in wild animals is essential. This study aims to investigate the presence of antibodies against brucellosis, tuberculosis, Johne's disease, and leukosis in long-tailed goral in Korea.

A total of 23 long-tailed gorals were examined. All individuals were housed at the Korean Goral Restoration Center. Blood samples were collected from the jugular vein using heparinized tubes and centrifuged at 1500 g for 15 min to obtain plasma. The targeted diseases for antibody investigation included brucellosis, leukosis, tuberculosis, and Johne's disease. Enzyme-linked immunosorbent assay was performed for each disease.

Among 23 long-tailed gorals, the seroprevalence of three diseases including brucellosis, Johne's disease, tuberculosis and leukosis was 0%. Previous studies conducted on water deer and roe deer have identified seropositive for leukosis and brucellosis. However, in this study, all gorals tested negative for the diseases. In this study, the investigated gorals were not rescued from the wild, but were housed at the housed at the Korean Goral Restoration Center. The center implements strict measures to prevent contact with external wildlife, and the risk of disease transmission is likely lower than wild environment. Therefore, further studies for the investigation of gorals found in the wild are needed. The additional investigation would be beneficial to determine the actual prevalence of these diseases in Korea's wildlife animals, which could contribute to the prevention and control of disease transmission.

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Antibody response of endangered riparian brush rabbits to vaccination against rabbit hemorrhagic disease virus 2

Monday, 28th July - 15:00: (Salon A) - Poster

Megan Moriarty [1]***, Jaime Rudd*** [2]***, Fumika Takahashi*** [3]***, Eric Hopson*** [3]***, Colleen Kinzley*** [4]***, Darren Minier*** [4]***, Alex Herman*** [4]***, Mary Lou Berninger*** [5]***, Fawzi Mohamed*** [5]***, Muzafar Makhdoomi*** [5]***, Leslie Woods*** [6]***, Hon Ip*** [7]***, Deana Clifford*** [8]

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Rabbit hemorrhagic disease virus 2 (RHDV2), the cause of a highly transmissible and fatal lagomorph disease, has spread rapidly through the western United States and Mexico, resulting in substantial mortality in domestic and wild rabbits. The disease was first detected in California in May 2020, prompting a collaborative wildlife health team to implement emergency conservation actions to protect endangered riparian brush rabbits (*Sylvilagus bachmani riparius*). Prior to vaccinating wild rabbits, we conducted a vaccine safety trial by giving a single subcutaneous dose of Filavac VHD K C+V (Filavie) vaccine to 19 adult wild riparian brush rabbits captured and temporarily held in captivity. Rabbits were monitored for adverse effects, and serum was collected before vaccination, and at 7–10, 14–20, and 60 d post-vaccination. Sera were tested using an ELISA to determine antibody response and timing of seroconversion. Rectal swabs were tested using RT-qPCR to evaluate infection status. No adverse effects from the vaccine were observed. Before vaccination, 18 of 19 rabbits were seronegative, and RHDV2 was not detected by RT-qPCR on any rectal swabs. After vaccination, all rabbits developed an antibody response, with titers of 1:10–1:160. Seroconversion generally occurred at 7–10 d. The duration of antibody response was ≥60 d in 12 of 13 rabbits. Sixteen animals were released and 4 were recaptured several months later, offering a glimpse into longer duration immune response. Our study has informed vaccination strategies for this species and serves as a model for protecting other vulnerable lagomorphs against RHDV2.

Enterobacteriaceae and antibiotic resistance in howler monkeys (Alouatta palliata) from environments subject to high anthropogenic influence

Monday, 28th July - 15:00: (Salon A) - Poster

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Multidrug-resistant (MDR) bacteria are an emerging global threat that can only be addressed through a One Health approach. Among them, *Escherichia coli* and *Salmonella enterica*, capable of infecting multiple hosts, are often used as indicators of anthropogenic impact.

The howler monkey (*Alouatta palliata*), a vulnerable species, is adapted to living in human-modified environments, and its phylogenetic proximity to humans makes it an excellent sentinel species to assess the degree of environmental exposure to MDR bacteria. Here, we evaluated the carriage of MDR *E. coli* and *Salmonella* in 35 injured howler monkeys admitted in a veterinary hospital in Guanacaste, Costa Rica, to help characterizing the epidemiology of antimicrobial resistance in wildlife in the country

Primo isolation was performed by culture in selective media followed by PCR confirmation of the species identification and determination of the resistance phenotypes to 15 antimicrobials using broth microdilution.

Overall, *E. coli* was isolated in samples from 28 individuals and *Salmonella* (serovar Infantis) in one. All isolates were pansusceptible except two *E. coli* resistant to gentamycin and one with an extended-spectrum beta-lactamase (ESBL) producing phenotype. The single *Salmonella* isolate was retrieved from the same individual as the ESBL-EC and also had an ESBL phenotype.

Previous studies in howler monkeys found higher levels of resistance in *E. coli* compared with our findings that, while describing an overall low-level circulation of MDR isolates, also identified the presence of ESBL enterobacteria in howler monkeys in Guanacaste, highlighting the need to determine possible sources of infection.

Highly pathogenic avian influenza viruses in Mississippi Flyway dabbling ducks: a multi-season perspective

Monday, 28th July - 15:00: (Salon A) - Poster

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Since introduction to North America in 2021, highly pathogenic H5N1 (HP H5N1) influenza A virus (IAV) has been detected annually; it is unknown if this virus will follow the historic patterns observed with low pathogenic (LP) IAV in ducks. More than 6,000 *Anatidae* were sampled in the Mississippi flyway, prior to the detection of HP H5N1 through spring of 2025. Virologic results are consistent with historic seasonal and geographic patterns reported for LP IAV: peak HP H5N1 infections (53%) occurred in pre-migration staging areas in Minnesota during fall 2022 and HP H5N1 was detected, but at a lower prevalence (19%), on wintering areas in Louisiana/Texas during fall of that year. These high rates of infection were followed by an increase in estimated antibody prevalence. HP H5N1 has not been detected in our collections in Minnesota since fall 2022, and only from a single bird in Louisiana in fall 2023. An increase in antibody prevalence, similar to 2022/2023, was observed during the winter/spring period of 2023/2024; IAV antibody prevalence was high, especially in adult birds, in fall 2024. Prevalence of LP IAV from dabbling ducks at these long-term surveillance sites during collections from fall 2023/2024 approached historic averages. Results support an initial high infection rate of HP H5N1 in ducks in the Mississippi flyway followed by high prevalence of IAV, H5 and N1 subtype-specific antibodies, with limited detected infections since 2022. Observed patterns appear to be driven by population immunity during the migration cycle. Although HP H5N1 prevalence has been reduced following introduction, it is unknown if this pattern will persist or affect subtype diversity in this wild bird reservoir.

Wild turkey infectious disease prevalence across Pennsylvania landscapes

Monday, 28th July - 15:00: (Salon A) - Poster

Ryan Koch [1], ***Axel Hoarau*** [1], ***Tryssa de Ruyter*** [2], ***Caitlin Duffy*** [3], ***Lucie Pascarosa*** [3], ***Mary Jo Casalena*** [4], ***Erica Miller*** [1], ***Jay Armstrong*** [3], ***Carol Sobotyk*** [3], ***Brock Geary*** [1], ***Eman Anis*** [1], ***Roderick Gagne*** [1]

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Coinfections are extremely common in wildlife yet are often overlooked. Effects of coinfections can have significant impacts on host susceptibility, survival, fitness, and population dynamics, as a result of complex interactions between different pathogens. Research focusing on a single pathogen may, therefore, lead to a biased perspective of the host populations being managed. Recent work has found that wild turkeys (*Meleagris gallopavo*) are affected by various pathogens. For example, lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV), two retroviruses, negatively influence reproduction and survival, respectively. Population trends of Pennsylvania turkeys vary across landscapes, but it is unknown how pathogens are structured across landscapes or with each other. Here, we determined the associations and risk factors of LPDV, REV, and coinfections with parasites in Pennsylvania wild turkeys. Our results indicate varying infection rates in turkeys with LPDV (70%), REV (1%), and intestinal parasites (63%). LPDV was greater in adults but did not significantly differ with year, sex, region, or landscape type. Parasite load was greater in juveniles and males, and varied significantly by year and region. Coinfections with LPDV and parasites were the most common association (40%), compared to infections with only LPDV (27%) and only parasites (23%). Finally, infection with LPDV in turkeys was associated with a lower parasite load. These results reveal high rates of coinfections in turkeys, with each pathogen group displaying unique infection dynamics. Additional investigation will target specific landscape variables to gain a more holistic understanding of what shapes coinfections.

Validation of an Indirect Fluorescent Antibody Test for Sarcocystis neurona infection in California sea lions.

Monday, 28th July - 15:00: (Salon A) - Poster

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California sea lions (*Zalophus californianus*) (CSLs) are the most common pinniped to strand along the California coast. They have been significantly affected by infectious and non-infectious diseases and serve as indicators of ocean health. *Sarcocystis neurona*, a terrestrial-origin protozoan parasite, infects CSLs causing *Sarcocystis*-associated polyphasic rhabdomyositis (SAPR), which can lead to death. A large increase in SAPR cases in CSLs admitted to The Marine Mammal Center (Sausalito, CA) over the past decade has raised concerns. To provide a rapid, minimally invasive, low-cost diagnostic method, we aimed to validate an indirect fluorescent antibody test (IFAT) to detect *S. neurona*. Validation was conducted using a case-control study involving 50 cases and 103 controls. Cases were animals for which SAPR was a primary cause of death, while controls were CSLs that died from non-protozoal causes. The IFAT was compared to a gold standard approach that included histopathology and molecular detection of *S. neurona*. Sensitivity and specificity for 12 dilutions (1:40 to 1:81,920) were assessed using receiver operating characteristic (ROC) curves. The area under the ROC curve was 0.99 (95% CI: 0.99-1.00). The optimal Youden's index value was at a dilution of 1:320. At this cutoff, the *S. neurona* IFAT demonstrated highest combined sensitivity (1.00; 95% CI: 0.93-1.00) and specificity (0.92; 95% CI 0.85-0.97). The Kappa value for agreement between the combined gold standard and the IFAT was 0.89 (95% CI: 0.81-0.96), indicating excellent agreement. This suggests that the IFAT is a valuable diagnostic tool for detection of *Sarcocystis neurona* infection in CSLs.

Skua die-off from high pathogenicity avian influenza on Beak Island, Antarctica, 2023–2024

Monday, 28th July - 15:00: (Salon A) - Poster

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Over the last three decades, outbreaks of high pathogenicity avian influenza viruses (HPAIV) of the Goose/Guangdong lineage (Gs/Gd) have caused mass mortalities in a variety of wild and domestic bird species, but also mammals, almost worldwide. In February 2024, HPAIV of the currently dominating genetic clade 2.3.4.4b spread to Antarctica for the first time, raising concern on the potential impacts to endemic wildlife populations that aggregate in individual-dense colonies to breed during the Antarctic summer. In response to this, the Australis expedition was set up in March 2024 to explore the occurrence and spread of HPAIV in the Antarctic Peninsula. At Beak Island, part of the James Ross Island group off the northwestern Weddell Sea, we identified an unusual mortality event of brown and south polar skuas (*Stercorarius* spp.), with over 40 individuals found dead. We examined 10 carcasses, and detected HPAIV by RT-qPCR in multiple tissues, with high viral RNA levels in the brain, matching confirmations via immunohistochemical detections. These observations show that HPAIV Gs/Gd can also cause unusual mortality events in wildlife in Antarctica. We (i) conclude that HPAIV H5 represents a potential threat to conservation of skuas and (ii) highlight the role of skuas both as an early indicator for the local presence of HPAIV, and as possibly being involved in long-distance virus spread.

Understanding the health of Texas ocelots from their microbiome and virome.

Monday, 28th July - 15:00: (Salon A) - Poster

MAURICIO Rued [1]***, Alynn Martin*** [1]***, Ashley Reeves*** [2]***, Lisanne Petracca*** [1]***, Christopher Kozakiewicz*** [3]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***2.*** *East Foundation,* ***3.*** *W.K. Kellog Biological Station, Michigan State University*

The ocelot (*Leopardus pardalis*), a threatened mesocarnivore in South Texas, is confined to two relatively small and geographically isolated populations that are vulnerable to stochastic events, such as disease outbreaks. Understanding disease dynamics—by identifying key pathogens and factors affecting host susceptibility—is essential for the conservation of this species. Analyzing the microbiome (the diversity of microorganisms) and virome (the diversity of viruses) of ocelots can offer valuable insights into their health and resilience against disease. The gastrointestinal microbiome plays a crucial role in immunity, digestion, metabolism, and infection resistance. Disruptions to this microbiome—whether due to stress, environmental shifts, or pathogen exposure—can impact immune responses and infection susceptibility. The virome enables the detection of likely pathogenic viruses present in ocelot populations, such as Feline Immunodeficiency Virus, Feline Leukemia Virus, Distemper and Parvovirus. Characterizing the virome will help identify emerging diseases that could pose risks to ocelots currently existing in, and those being reintroduced to, this region. We propose using next-generation sequencing of blood, semen, and rectal samples from ocelots and sympatric species, including bobcats and coyotes, to analyze the gut microbiome and virome of mesocarnivores from South Texas. We will characterize the microbiome and virome in relation to host type and demographic factors. Our findings will enhance our understanding of host-pathogen interactions and sharing among South Texas mesocarnivores, informing management and conservation strategies to prevent infectious disease outbreaks.

Health assessment of snow leopards through non-invasive techniques in Nepal

Monday, 28th July - 15:00: (Salon A) - Poster

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The endangered snow leopard is sparsely distributed across the Himalayan region of Nepal. Among the numerous threats to its population, diseases remain a significant yet understudied concern. Limited information exists on the prevalence of diseases affecting snow leopards, particularly in the context of their depredation of livestock near human settlements. Their close proximity raises the potential risk of disease spillover from domestic animals to snow leopards, a critical knowledge gap that has yet to be explored in Nepal. Our study conducted the first non-invasive health survey of snow leopards in Nepal, investigating the presence of pathogens in snow leopards and livestock living near their habitat. We collected six snow leopard scat samples and 13 domestic animal scat samples from Lo Manthang in the Upper Mustang Region of Nepal. An additional 45 snow leopard samples from previous diet studies across the Annapurna Conservation Area were also included for analysis. Species identification of snow leopard samples was confirmed using DNA barcoding. Samples were analyzed for viral, bacterial, and parasitic pathogens using molecular and microscopic techniques. A brief questionnaire assessed community attitudes, and veterinary care availability. Samples are being processed, with results expected soon. Future plans aim to work with communities to continue sampling across Nepal and support interventions that minimize pathogens in domestic animals thus improving their health and welfare, as well as positively impacting snow leopard populations.

Thermal Geography of Sylon Disease in Commercially Important Prawns Under a Changing Climate

Monday, 28th July - 15:00: (Salon A) - Poster

Madeleine Abbott [1]***, Kyle Krumsick*** [2]***, Amanda Bates*** [1]

1. *University of Victoria,* ***2.*** *Fisheries and Oceans Canada*

Climate change is expected to alter the prevalence of many parasites, which could affect the sustainability of fisheries. However, long term datasets that include the presence of parasites are rare, making these changes difficult to evaluate. Spot prawns (*Pandalus platyceros*) are the subject of a multi-million dollar fisheries industry in British Columbia (BC), and are susceptible to the rhizocephalan parasite *Sylon* sp. which has been monitored since the 1970s. This parasite could have significant effects on populations due to its ability to castrate its host. In this study, we examine a 40 year time series (~1985-2024) of *Sylon* prevalence throughout BC collected by government research surveys and fisheries observers to determine whether prevalence is changing over time, and whether these changes are related to temperature patterns. *Sylon* was more commonly found in cooler areas of BC, less prevalent in warmer years, and had a declining trend over time. We also found rates of internal infection that suggest the spawner index (the average number of females and transitionals caught per trap, used to monitor the condition of the fishery) may be overestimating the number of potentially reproductive individuals in areas with *Sylon* present, which has implications for the timing of fisheries closures and spot prawn conservation. Our results suggest that the range of *Sylon* may contract in BC as sea surface temperatures warm, and indicates a need for increased surveillance in Alaska where temperatures may become closer to *Sylon's* optimum, and spot prawn stocks are already documented to be declining.

Comparison of two sampling protocols for the detection of Mycoplasma ovipneumoniae in hunter-harvested desert bighorn sheep

Monday, 28th July - 15:00: (Salon A) - Poster

Ann Fan ***[1], Anne-Justice Allen [1]***

1. *Arizona Game and Fish Dept.*

Bighorn sheep populations in Arizona have been impacted by pneumonia caused by *Mycoplasma ovipneumoniae*. The Department routinely includes testing for this disease during captures for research or translocation. Temporal spatial shifts in strain-types can significantly affect bighorn populations. Therefore, regular surveillance for *M. ovipneumoniae* is important for bighorn health management. Captures have been limited to a few select populations at irregular intervals. In order to assess populations that are not captured as well as to collect additional samples from monitored populations more frequently, the Department began collecting samples from hunter-harvested rams at check in 5 years ago. We wanted to determine whether or not collecting samples immediately after death would improve the detection of *M. ovipneumoniae*. Bighorn sheep hunters are concerned about the health of populations and frequently contribute to Department management activities. During the last two harvest seasons (2023 and 2024), we asked hunters to collect swabs at harvest in addition. In year one, 22 paired samples were collected. There were an additional 40 samples collected at check in and 28 samples collected by hunters. In year two, 68 paired samples were collected with an additional 20 samples collected by either the hunter or department. There was no difference in detection between paired samples in the first year. For all samples collected in year 1, *M. ovipneumoniae* was detected in 24 percent samples collected by the Department and 20 percent samples collected by hunters. Results are pending for the second year. Based on the first year, the sensitivity samples collected by hunters is equivalent to samples collected by the Department.

Tularemia in Utah beavers

Monday, 28th July - 15:00: (Salon A) - Poster

Virginia Stout [1]***, Jane Kelly*** [2]***, Carmen Lau*** [2]***, Arnaud Van Wettere*** [2]

1. *Utah Division of Wildlife Resources,* ***2.*** *Utah Veterinary Diagnostic Laboratory*

Tularemia is a bacterial disease caused by *Francisella tularensis*, which causes mortality in many wildlife species, most commonly in rabbits and other rodents. It is commonly found in the environment in the northern hemisphere, namely North America. Tularemia reservoirs in wild animals and can be transmitted through direct contact, aerosol, the environment, or through ticks, mosquitoes, and biting flies. Tularemia can affect over 250 wild species as well as domestic dogs, cats, and humans.

A recent mortality event, caused by Tularemia, occurred in Utah, killing over 7 beavers and a muskrat. Between April 1st and May 10th 2024, 2 male and 5 female beavers, and 1 male muskrat were necropsied at the Utah Veterinary Diagnostic Laboratory with lesions consistent of tularemia. Samples were confirmed for tularemia by qPCR in all 8 animals and by liver culture in 5 out of 8 animals at the Utah Public Health Laboratory. Three other beavers in contact with the original two were suspected to have Tularemia, but no necropsy was performed. An additional 3 beavers, 1 muskrat, and 1 mole were necropsied but found to have died from other causes.

It is unusual to have this many cases in Utah at one time and hasn't been seen in other states commonly. No link to the cases have been made, they were in separate watersheds and covering a fairly large distance. The last confirmed case of tularemia in Utah was in a cottontail rabbit from 2017. These cases affected UDWR's ability to translocate beavers last spring, but did not have a population level affect on beavers. Continued monitoring will occur in the future to ensure Utah's beaver populations aren't continuing to be affected.

Insights from a three-year observational study of High Arctic muskoxen (Ovibos moschatus) following an acute infectious disease epidemic

Monday, 28th July - 15:00: (Salon A) - Poster

McCaide Wooten **[1]**, ***Taya Forde*** **[2]**, ***Amélie Roberto-Charron*** **[3]**, ***Matthew Fredlund*** **[3]**, ***Sreejith Radhakrishnan*** **[2]**, ***Dayna Goldsmith*** **[4]**, ***Beverly Morrison*** **[1]**, ***Angela Schneider*** **[1]**, ***Frank van der Meer*** **[1]**, ***Ronan Donovan*** **[5]**, ***Susan Kutz*** **[1]**

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The muskox is an emblematic Arctic species that has been vital to the health of northern ecosystems and Indigenous Canadians for millennia. However, this ungulate now faces an infectious disease threat – Erysipelothrix rhusiopathiae – that has arisen in concert with regional population declines. Mortality events attributed to this pathogen have been observed in muskoxen across the Canadian Arctic Archipelago since 2010. Our research aims to identify the underlying factors that are promoting the success of this bacterium. From 2021-2024, we investigated a mortality event and its aftermath on Ellesmere and Axel Heiberg Islands, Nunavut, Canada. We collected samples for culture and PCR from 138 unique muskox carcass sites, including 46 sites re-visited over multiple years. Tissues from 17 muskoxen were analyzed histologically. Whole genome sequencing and phylogenetic analyses were performed on >200 bacterial isolates. Histological findings supported E. rhusiopathiae septicemia as a definitive cause of death for 2 muskoxen and presumptive cause for 29. Erysipelothrix rhusiopathiae was found in association with >80% of sampled carcasses. Most recovered isolates were of the same clonal lineage that has repeatedly been identified in outbreaks since first reported in 2009 (>1200km away). The bacterium remained viable at carcass sites for up to 3 years and was found in the feces of muskox predators and scavengers. Investigation of the roles of other candidate hosts, outbreak modelling, and detailed virulence profiling are priority areas for further research. Our results have contributed greatly to our understanding of pathogen-associated factors facilitating these impactful disease outbreaks.

Determinants of emerging disease at the global wildlife-human-livestock interface: a scoping review

Monday, 28th July - 15:00: (Salon A) - Poster

Alaina MacDonald [1], ***Manuel Perez Maldonado*** [1], ***Claire Jardine*** [2], ***Lauren Grant*** [1], ***Jane Parmley*** [1]

1. *Department of Population Medicine, University of Guelph,* **2.** *Department of Pathobiology, University of Guelph*

Infectious pathogens are emerging and re-emerging more frequently worldwide, often originating from wildlife and driven by changing ecological and socioeconomic factors. While current disease surveillance efforts are rapidly improving, most programs remain reactive in nature. To expand preventive actions and mitigate risk earlier, research is needed to identify drivers of emerging infectious disease worldwide.

We performed a scoping review which examined studies from four databases to identify events preceding disease emergence at the global human-wildlife-livestock interface.

One hundred fifty-one studies met the eligibility criteria. Most studies (n=101) involved emerging diseases caused by viral pathogens, followed by bacteria (n=41), helminths (n=3) and protozoa (n=3). Most studies focused on a zoonotic pathogen (n=123), many with significant economic consequences. The most common pathogens studied were highly pathogenic avian influenza virus H5N1 (n=29), followed by *Mycobacterium bovis* (n=16), and *Bacillus anthracis* (n=11). Wild birds were the most frequently studied wild species (n=48), followed by wild boar (n=5) and ungulates (n=3). Reported drivers of disease emergence included: 1) human activity including livestock management, 2) wildlife population characteristics, 3) changes in temperature and precipitation, 4) changes in pathogen characteristics, and 5) inequity. This presentation will also discuss potential wildlife data sources to represent drivers of disease emergence.

Understanding determinants of emerging disease and integrating representative data into surveillance may help future decision makers respond to cues before disease is detected. Recognizing the unequal distribution of resources for health will be a required step towards sustainable disease surveillance and health promotion.

PERFORMANCE DATA TRENDS FOR CANDIDATES TAKING THE AMERICAN COLLEGE OF ZOOLOGICAL MEDICINE BOARD EXAMINATION (2012-2024)

Monday, 28th July - 15:00: (Salon A) - Poster

Daniel Fredholm [1]

[1] *Disney's Animals, Science, and Environment*

To be certified as a diplomate of the American College of Zoological Medicine (ACZM), a credentialed veterinarian must pass the ACZM board examination. This exam is created, administered, and graded annually by the ACZM Examination Committee. First, candidates must pass the Qualifying Examination ("Day 1"), which is given in 5 sections, organized taxonomically. Subsequently, candidates must pass the Certifying Examination. This tests upon in-depth knowledge in a specific discipline of zoological medicine, which is chosen in advance by the examinee to reflect their experience and training. After the exam, a survey is sent to all candidates to collect data and feedback on their exam preparation and examination experience.

Since its inception in 1984, the ACZM exam's structure has evolved in response to various factors, including a rising number of candidates, the growing breadth of extant reference material, and feedback received both from examinees and diplomates. This presentation summarizes performance data of ACZM candidates over a span of 13 exams (2012-2024). Additionally, aggregate responses from post-examination surveys are included, highlighting trends in this feedback.

Over the evaluated time period, the pass rate has increased, especially for the Qualifying Examination. Pass rates for first-time candidates have also increased, while pass rates for those taking the exam on their 3rd+ attempt are comparatively lower. Factors that may have contributed to these trends include strategic alterations to the exam construction process, and the implementation of a peer-review process by subject matter experts.

Enterococcus faecalis and Enterococcus faecium from Wild Animals: Uncovering the Hidden Threat of Antimicrobial Resistance Pollution

Monday, 28th July - 15:00: (Salon A) - Poster

Elisa Massella [1], ***Simone Russo*** [1], ***Sara Castaldo*** [1], ***Caterina Siclari*** [1], ***Letizia Cirasella*** [1], ***Simona Perulli*** [1], ***Roberta Taddei*** [1], ***Camilla Torreggiani*** [1], ***Andrea Luppi*** [1]

1. *Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna*

Antimicrobial resistance (AMR) in wildlife indicates environmental contamination by resistant bacteria from human setting, with wild animals acting as AMR reservoir. Our study investigates enterococci as AMR indicators in wild mammals (WMs) and birds (WBs), focusing on resistance to Critically Important antimicrobials (CIAs).

Between January and December 2024, 102 *Enterococcus* strains were isolated from 58 WM and 44 WB faeces, collected in the Emilia Romagna region, Italy. Species was identified by MALDI-TOF. AMR profiles were assessed determining the Minimal Inhibitory Concentration, interpreted according to CLSI breakpoints.

We detected 60 *Enterococcus faecalis* and 42 *Enterococcus faecium* isolates. Sixty out of 102 (58.82%) strains were multidrug resistant (MDR) from 3 up to 8 different antimicrobial classes. *Enterococcus faecalis* was the species mostly associated with MDR (35/60, 58.33%).

Overall, the most common resistance frequencies were to quinupristin/dalfopristin (87/102, 85.29%), ciprofloxacin (56/102, 54.90%), erythromycin (51/102, 50.00%), followed by linezolid (34/102, 33.33%), daptomycin (32/102, 31.37%), chloramphenicol (30/102, 29.41%), tetracycline (20/102, 19.61%), tigecycline (9/102, 8.82%), high-dosage gentamycin (6/102, 5.88%) and ampicillin (3/102, 2.94%). Resistance to vancomycin and teicoplanin was not observed.

MDR was mostly associated with WMs (31/60, 51.67%) compared to WBs (29/60, 48.33%). Moreover, WMs showed the highest number of isolates resistant to more than 5 antimicrobials (14/24, 58.33%; WBs: 10/24, 41.67%).

Notably, a high percentage of enterococci isolated from wildlife were MDR and showed resistance to life-saving antimicrobials. Our data suggest wildlife could serve as a reservoir of AMR pathogens and a valuable indicator of AMR environmental pollution

TRICHINELLA SPP. IN WOLVES (CANIS LUPUS), RED FOXES (VULPES VULPES) AND WILD BOARS (SUS SCROFA) IN EMILIA-ROMAGNA REGION (ITALY) DURING 2020-2024.

Monday, 28th July - 15:00: (Salon A) - Poster

Camilla Torreggiani [1]***, Chiara Anna Garbarino*** [1]***, Matteo Ricchi*** [1]***, Elisa Massella*** [1]***, Alice Prosperi*** [1]***, Giovanni Pupillo*** [1]***, Gianluca Rugna*** [1]***, Giulia Maioli*** [1]***, Patrizia Bassi*** [1]***, Simona Perulli*** [1]***, Silva Rubini*** [1]***, Andrea Luppi*** [1]

1. *Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna*

Introduction

Trichinella spp. are widespread parasites that infect various hosts, with wildlife serving as the primary reservoir for these zoonotic nematodes. Red foxes (*Vulpes vulpes*) and wolves (*Canis lupus*) are notable because of their apex positions in the food chain in many European countries. In wild canids and wild boars (*Sus scrofa*), *Trichinella* infections are mainly caused by *T. britovi* and *T. nativa*, with *T. spiralis* and *T. pseudospiralis* contributing to a lesser extent.

This study reports on wild animal surveillance in the Emilia-Romagna (E-R) region of northern Italy over the past five years.

Materials and Methods

From 2020-2024, 358 found dead wolves, 3049 hunted or road-killed red foxes, along with 100419 wild boars were examined by Istituto Zooprofilattico Sperimentale of Lombardia and Emilia-Romagna (IZSLER) as part of the regional wildlife monitoring program. Five to ten grams of muscle from each animal were tested for parasite larvae using the magnetic stirrer method per Commission Regulation (EC) no. 1375/2015. Positive samples were sent to the European Union Reference Laboratory for Parasites for species identification via multiplex-PCR.

Results

Out of 358 wolves tested, seven resulted positive, along with five out of 3049 red foxes; all wild boars were negative. Multiplex-PCR identified *T. britovi* in 9 samples (three foxes and six wolves), *T. spiralis* in a red fox and a wolf; one fox sample was non-identifiable.

Discussion and Conclusion

Our findings confirm that *T.britovi* primarily but also *T.spiralis* circulate among wild carnivores in Italy, posing a threat to humans due to its adaptability and high larval production.

Gut Inflammatory Consequences of Gastrointestinal Parasitism in Bighorn Sheep in SE Oregon

Monday, 28th July - 15:00: (Salon A) - Poster

Marci Witczak [1], ***Brianna Beechler*** [2], ***Anna Jolles*** [2], ***Alex Morris*** [3], ***Jo Lello*** [3], ***Rob Spaan*** [2], ***Clinton W. Epps*** [2], ***Holly Arnold*** [2], ***Justin Sanders*** [2], ***Sara Carpenter*** [2], ***Alejandra Ortega*** [2]

1. *Carlson College of Veterinary Medicine, Oregon State University,* ***2.*** *Oregon State University,* ***3.*** *Cardiff University*

Consequences of gastrointestinal (GI) nematodes and coccidia are often measured through fitness costs, such as decreased body condition and fecundity. However, fitness costs due to gastrointestinal parasitism can be challenging to identify in wild animals, with further complexity introduced by host responses, including resistance and tolerance. Furthermore, common techniques identifying GI nematodes and coccidia provide poor detection of parasite abundance, adding to the challenges of understanding the host-parasite relationship in wildlife. Assays evaluating gut inflammatory proteins offer a unique, non-invasive, fecal-based approach to evaluate wildlife health. We adapted a commercial ELISA kit measuring lactoferrin, an iron-binding protein released by neutrophils in the gut as a result of inflammation, to wild bighorn sheep feces as a proxy of gut health in response to parasitism and other environmental factors. We evaluated the direct effects of nematodes on bighorn sheep health and secondary effects of nematode-removal, including coccidia prevalence and fecal lactoferrin concentration. A treatment-control, randomized experiment was carried out in a population of wild bighorn sheep in SE Oregon with a long-acting anthelmintic. In fecal samples collected from initial treatment to 7 months post anthelmintic administration, nematode and coccidia presence were identified through fecal egg/oocyst counts and molecular techniques. Lactoferrin concentration was independent from treatment and taxonomically course nematode burden did not influence lactoferrin concentration, though species-dependent interactions were revealed. Month of sample also influenced lactoferrin concentration across study individuals. This is a unique first investigation at how fecal inflammatory parameters may directly assess health consequences of parasites and other environmental parameters.

INVESTIGATING THE CAUSE OF ELEVATED MORTALITIES OF GREATER ONE-HORNED RHINOCEROS (RHINOCEROS UNICORNIS) IN CHITWAN NATIONAL PARK IN NEPAL, 2004-2024

Monday, 28th July - 15:00: (Salon A) - Poster

Carmen Smith **[1]*, Amir Sadaula* [2]*, Bijaya Kumar Shrestha* [3]*, Pradeepa Silwal* [2]*, Kiran Raj Rijal* [2]*, Carol Meteyer* [4]*, Emily Mitchell* [5]*, Tina Morgan* [6]*, Prakriti Kandel* [7]*, Jessica Bodgener* [8]*, Ram Chandra Kandel* [9]*, Naresh Subedi* [2]*, Martin Gilbert* [1]**

1. *Cornell K. Lisa Yang Center for Wildlife Health,* ***2.*** *National Trust for Nature Conservation,* ***3.*** *Chitwan National Park Office, Kasara, Chitwan,* ***4.*** *Wildlife Pathologist,* ***5.*** *University of Pretoria,* ***6.*** *International Zoo Veterinary Group,* ***7.*** *Department of Biological Sciences, University of Denver,* ***8.*** *University of Kent,* ***9.*** *Department of National Parks and Wildlife Conservation*

Nepal is home to one fifth of the world's greater one-horned rhinoceroses (*Rhinoceros unicornis*), of which 92% (694/752), reside in Chitwan National Park. Mortalities from 2004 to 2024 (n=332) were classified within broad categories: fighting (25.6%, 95% CI: 25.1–26.1, n=332), anthropogenic causes (16.2%, 95% CI: 15.9–16.6, n=332), and predation (8.1%, 95% CI: 7.9–8.4, n=332). The remainder (50.0%, 95% CI: 49.0-51.0, n=332) were considered "open." Mortalities increased from an average of 7.2 cases/year (95% CI: 4.0–10.3 n=11) between 2004 and 2014, to 25.3 cases/year (95% CI: 19.9–30.7, n=10) between 2015 and 2024. This increase was mostly attributable to a rise in "open" cases. Epidemiologic data was supplemented with postmortem examinations and histopathologic review of 48 cases. To address constraints in the movement of samples, we focused on developing in-country facilities and expertise to prepare histological sections, which were digitized using a portable slide scanner (Ocus® 20, Grundium Ltd., Tampere Finland) for remote consultation. Major histopathologic findings included chronic liver disease (35.4%; 95% CI: 35.1–35.7, n=48) with acute hepatic necrosis (4.2%; 95% CI: 4.0–4.3, n=48) and kidney disease with glomerulopathy and proteinosis (40%; 95% CI: 38.9–41.1, n=20). These changes included histopathologic features that are non-specific but can be seen in a short list of differential diagnoses including sinusoidal obstruction syndrome, chronic toxicities, and chronic anemia. Some of these features are similar to those seen with veno-occlusive disease in cheetahs (*Acinonyx jubatus*) and with bush tea (pyrrolizidine alkaloid) toxicity in people.

Validating portable X-ray fluorescence for bone lead measurements of Virginia opossums (Didelphis Virginiana)

Monday, 28th July - 15:00: (Salon A) - Poster

Amanda Rappaport [1] ***, Renee Schott*** [1] ***, Alison Demir*** [1]

1. *Wildlife Rehabilitation Center of Minnesota*

Lead (Pb) Toxicity threatens wildlife species, especially scavenging species, worldwide. An inexpensive and non-invasive measurement of long-term lead exposure, portable X-ray fluorescence (XRF) devices have been previously used and validated in bone samples in avian species. In this study, we assessed the portable XRF for bones lead measurements in Virginia Opossums (*Didelphis virginiana*). Using 20 deceased animals we obtained lead measurements from five different sites (skull, right and left lateral tibia, right and left medial tibia) with skin-over-bone and without skin using the portable XRF. Our results suggest that portable XRF is an useful technology that can allow for non-invasive measurements of long-term lead exposure in Virginia Opossums.

Malagasy flea microbiota results from a combination of vertically transmitted and environmentally acquired microbes

Monday, 28th July - 15:00: (Salon A) - Poster

victoria carcauzon [1]

1. *Reunion island university*

Fleas (Insecta, Siphonaptera) are the known vectors of serious bacterial pathogens, such as *Yersinia pestis* and *Rickettsia typhi*. The microbiota of fleas has been poorly investigated although it has a known influence on vector competence. Here, we report and analyse the microbiota of 577 flea specimens from Madagascar, a hotspot of plague transmission. Importantly, endemic Malagasy fleas show low host specificity, allowing addressing the importance of vertebrate host species in microbiota composition, as well as that of abiotic variables. We describe through Illumina sequencing of 2 hypervariable regions of 16S rDNA the bacterial composition of 577 flea specimens of Madagascar. We address the importance of biotic (mammalian host and flea species) and abiotic (season and sampling site) variables on bacterial community composition. Bacterial composition appears driven by flea species and season, but interestingly not by the flea's vertebrate hosts. These results suggest that the flea microbiota is at least in part acquired before they become adult, possibly in the immature off-host stages. Taken together, our results suggest that the microbiota of sampled fleas are composed of bacterial taxa with vertical transmission, such as *Wolbachia* which are prevalent in the present dataset, together with several bacterial taxa for which the occurrence is driven by environment factors, especially season and habitat. Given the importance of the microbiota in vector competence, we discuss the epidemiological consequences of environmentally-driven acquisition of microbiota in fleas on plague transmission in Madagascar.

Whole Genome Sequence Analysis of Brucella spp. from Human, Livestock, and Wildlife in South Africa

Monday, 28th July - 15:00: (Salon A) - Poster

Koketso Desiree Mazwi [1], ***Kgaugelo Edward Lekota*** [2], ***Barbara A Glover*** [1], ***Henriette van Heerden*** [1]

1. *University of Pretoria*, **2.** *Unit for Environmental Sciences and Management, North-West University*

Brucellosis is a zoonotic disease affecting humans, livestock, and wildlife health globally. *Brucella abortus* and *B. melitensis* have been isolated from human, livestock (cattle and goat), and wildlife (sable) in South Africa (SA) but with little knowledge of the population genomic structure of this pathogen in SA. As whole genome sequencing can assist to differentiate and trace the origin of outbreaks of *Brucella* spp. strains, the whole genomes of retrospective isolates (n = 19) from previous studies were sequenced. Sequences were analysed using average nucleotide identity (ANI), pangenomics, and whole genome single nucleotide polymorphism (wgSNP) to trace the geographical origin of cases of brucellosis circulating in human, cattle, goats, and sable from different provinces in SA. Pangenomics analysis of *B. melitensis* (n = 69) and *B. abortus* (n = 56) was conducted with 19 strains that included *B. abortus* from cattle (n = 3) and *B. melitensis* from a human (n = 1), cattle (n = 1), goat (n = 1), Rev1 vaccine strain (n = 1), and sable (n = 12). The wgSNP analysis confirmed the *B. melitensis* isolated from human was more closely related to the goat from the Western Cape Province from the same outbreak than the *B. melitensis* cattle sample from different cases in the Gauteng Province. The *B. melitensis* sable strains could be distinguished from the African lineage, constituting their own African sub-clade. The sequenced *B. abortus* strains clustered in the C2 lineage that is closely related to the isolates from Mozambique and Zimbabwe. This study identified genetically diverse *Brucella* spp. among various hosts in SA. This study expands the limited known knowledge regarding the presence of *B. melitensis* in livestock and humans in SA, further building a foundation for future research on the distribution of the *Brucella* spp. worldwide and its evolutionary background.

Geographic Distribution and Neuropathology of Elaeophora schneideri in Shiras Moose (Alces alces shirasi) in Idaho, USA

Monday, 28th July - 15:00: (Salon A) - Poster

Christine Haake [1]***, Kyle Taylor*** [1]***, Logan Weyand*** [2]***, Eric Van Beek*** [3]***, Chrissy Eckstrand*** [1]***, Laura Williams*** [1]***,***
Stacey Dauwalter [4]***, Nicole Walrath*** [4]***, Hollie Miyasaki*** [4]***, Shane Roberts*** [4]***, Mark Hurley*** [4]***, Janet Rachlow*** [3]

1. *Washington State University,* ***2.*** *Nebraska Game and Parks Commision,* ***3.*** *University of Idaho,* ***4.*** *Idaho Department of Fish and Game*

Elaeophorosis, infection by the filarial worm Elaeophora schneideri, is a parasitic disease of wild ungulates in North America; however, our understanding of the relevance of E. schneideri to moose (Alces alces) morbidity and mortality is incomplete. Between March 2020 and July 2022, necropsy and histopathology were performed on 61 Shiras moose (Alces alces shirasi) in Idaho, US. Among the 41 adults (greater than 1 yr old), 21 moose were from northern Idaho, and 20 were from southeastern Idaho. Elaeophorosis was diagnosed in 24% (10 of 41). All 10 infected moose were from southeastern Idaho; none of the 21 moose from northern Idaho were infected. No juvenile moose (nine from northern and 11 from southeastern Idaho) were infected. Microfilariae were detected histologically in 9 of 10 infected moose, most consistently in brain tissue associated with lesions indicative of ischemic injury to the neuroparenchyma attributed to occlusion of arterioles and capillaries by microfilariae or fibrin thrombi, including edema, necrosis, and glial nodules. Microfilariae found in other tissues of the head, including the eye, tongue, and pinnae of some animals, as well as in lung, heart, liver, and kidney, typically were associated with inflammation. Three of the 10 infected moose had cropped ears attributed to elaeophorosis, and four exhibited abnormal behavior, which may have been due to neuropathology associated with E. schneideri microfilariae in the brain.

Tick distribution, phenology and hosts across altitudinal gradients in the central Pyrenees, Spain. Preliminary results

Monday, 28th July - 15:00: (Salon A) - Poster

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Tick-borne diseases pose a significant global public health challenge. Despite their relevance, data on tick distribution, ecology, and pathogen prevalence in the Pyrenean region—an endemic area for Lyme disease—remain scarce. To address this gap, the PyrTick project coordinates Spanish and French researchers to study Pyrenean ticks in a harmonized manner. Systematic field sampling was conducted from May 2024 to January 2025. Standardized vegetation flagging was performed to collect questing ticks across forest and pasture habitats. Sampling sites were distributed at 200-meter elevation intervals across five valleys in Aragón (Northern Spain), ranging from 600–800 to 1600–1800 m.a.s.l. A total of 1,782 ticks were collected, including 973 larvae, 709 nymphs, 57 adult males, and 43 adult females. *Ixodes ricinus* was the dominant species, with peak abundance recorded at intermediate altitudes (1000–1200 m). Seasonal variations were observed across life stages: larvae peaked in August, nymphs in May, and adults in May–June. Other tick species identified included *Ixodes acuminatus, Haemaphysalis inermis, H. punctata, Dermacentor marginatus,* and *Hyalomma* sp. Micromammals (n = 86) were trapped in spring using Sherman traps at low, intermediate, and high altitudes in three valleys. The captured species included *Apodemus sylvaticus, Apodemus flavicollis, Clethrionomys glareolus, Eliomys quercinus, Mus spretus,* and *Crocidura russula.* Of these, 71 individuals (82.5%) harbored ticks, primarily immature stages of *I. ricinus* and *D. marginatus.* Ticks were also collected from 46 hunted wild ungulates (*Capreolus capreolus, Cervus elaphus, Rupicapra pyrenaica,* and *Sus scrofa*) by hunters and environmental agents, mainly comprising adults of *I. ricinus* and *D. marginatus.* Additionally, viviparous lizards (*Zootoca vivipara*, n = 146) were captured in one valley, with 99% parasitized by immature *I. ricinus* (88% had larvae, 44% had nymphs). These preliminary findings provide the first insights into the distribution and tick population dynamics across altitudinal gradients and habitat types in the Pyrenees.

Rabies in Early Life: A Case Report of a 10-week-old Aardwolf (Proteles cristatus)

Monday, 28th July - 15:00: (Salon A) - Poster

Giovana Martins Miranda [1], ***Katja Koeppel*** [1], ***Jennie Hewlett*** [1], ***Jacques O Dell*** [1], ***Francis Cameron-ellis*** [1]

1. *University of Pretoria*

Rabies is a zoonotic viral disease transmitted in various settings, from strains predominantly found in wildlife to those primarily recorded in domestic species. Although rabies has been documented in a wide range of hosts, it is rarely described in young animals, particularly in wildlife species. This report presents a case of rabies in a 10-week-old aardwolf (*Proteles cristatus*) that was being transferred between facilities. The animal was housed with a conspecific of the same age, which remained asymptomatic. Initial clinical signs included inappetence, hypersalivation, and an unusual degree of docility compared to its previously wild behavior. These symptoms are commonly associated with the paralytic (dumb) form of rabies, typically observed in herbivores, whereas carnivores more frequently exhibit the furious form.

Upon presentation with neurological signs, rabies was considered a differential diagnosis alongside other infectious diseases. Diagnostic testing ruled out snake bite venom, canine distemper virus and parvovirus infection. Supportive care, including intravenous fluid therapy and empirical antibiotic treatment for possible bacterial encephalitis, was initiated. However, the animal showed no improvement over 24 hours, and euthanasia was elected. Post-mortem examination revealed no macroscopic abnormalities, but Negri bodies (cytoplasmic inclusion) were observed histopathologically. In accordance with South African legislation, the direct fluorescent antibody (DFA) test is the gold standard for rabies diagnosis. Refrigerated brain samples were submitted to the ARC-Onderstepoort Veterinary Research Institute, where rabies virus infection was confirmed using the DFA technique.

This report highlights the occurrence of rabies in very young animals and underscores the critical need for strict precautionary measures when handling animals with neurological signs, given the disease's near 100% fatality rate in humans. Further testing is underway to determine the specific rabies strain involved in this case and to identify the potential source of infection.

Arrival and Expansion of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) in the Western United States and Mexico.

Monday, 28th July - 15:00: (Salon A) - Poster

Cole Wzientek [1], ***Hannah Shapiro*** [2], ***Dana Karelus*** [3], ***Sandra Rideout-Hanzak*** [1], ***Scott Henke*** [1], ***Alynn Martin*** [4]

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Rabbit Hemorrhagic Disease Virus (RHDV) is a fatal virus that first emerged in Europe in the 1970s-1980s. Since its discovery, RHDV spread to nearly global distribution, killing 250 million domestic and wild rabbits by 2007. In 2010, a new serotype of the virus, RHDV2, emerged in France and was later discovered in domestic North American rabbits in 2016. RHDV2 was determined to be more virulent than RHDV, as it can infect younger rabbits (<6-8 weeks) and a wider array of species. First detected in wild New World lagomorphs in New Mexico, United States (US), in March 2020, RHDV2 rapidly spread into neighboring US states and Mexico. Using five years of RHDV2 case data from the Wildlife Health Information Sharing Partnership (WHISPers; US Geological Survey), we analyzed spatiotemporal patterns of disease spread. We document more than 5,000 reported mortalities and identify several counties in the US states of Texas and New Mexico that experienced multiple, temporally-distinct outbreaks. The virulence and persistence of RHDV2 raises concerns for wild lagomorph populations in North America, particularly vulnerable or threatened species, such as the Davis Mountain cottontail rabbit (*Sylvilagus robustus*). An effective RHDV2 management strategy would provide options to protect wild rabbits and hares in this region. Future research will test the immune response of eastern cottontail rabbits (*Sylvilagus floridanus*) to an emergency-use recombinant RHDV2 vaccine, with inference for application in similar species.

Community pathogen surveillance in Chicagoland aquatic turtles

Monday, 28th July - 15:00: (Salon A) - Poster

Laura Adamovicz [1], ***Madison Kasbaum*** [1], ***Samantha Johnson*** [1], ***Varun Seth*** [1], ***Marguerite Bednarek*** [1], ***Javelis Marin Castro*** [1], ***Nick Liszka*** [1], ***Surina Birk*** [1], ***Carly Etter*** [1], ***Kamila Grochowski*** [1], ***Katelyn Deppe*** [1], ***Jaime Lyke*** [1], ***Kaitlin Moorhead*** [1], ***John Winter*** [1], ***Rose Arnold*** [2], ***Joey Cannizzaro*** [2], ***Amber Simmons*** [1], ***Crystal Moreno-Garcia*** [1], ***Maris Daleo*** [1], ***Matthew Allender*** [1]

1. *Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign,* ***2.*** *Illinois Natural History Survey - Prairie Research Institute*

Pathogen surveillance is commonly performed in wildlife to characterize threats to endangered species, game species, food animals, and humans. This approach creates knowledge gaps about pathogen occurrence and effects for commonly-occurring and non-game species, which is problematic when pathogens are shared between these animals and those threatened with extinction. Aquatic turtle communities in Illinois comprise common and endangered species, however pathogen surveillance has historically been limited to species of conservation concern. The purpose of this study was to characterize the epidemiology of 34 pathogens at the community level in Chicagoland aquatic turtles. Turtles (N = 2,140) representing eight species from six Northern Illinois counties were evaluated using physical examination, hematology, and molecular testing of oral/cloacal/shell swabs in 2023 – 2024. Overall, 13.6% of turtles tested positive for at least one pathogen and eight pathogen groups were detected including multiple herpesviruses and adenoviruses, frog virus 3, *Mycoplasmopsis* spp., *Leptospira* spp., *Salmonella* spp., intranuclear coccidiosis of Testudines, and *Emydomyces testavorans*. Pathogen prevalence was greatest in invasive red-eared sliders (*Trachemys scripta elegans*; 23.6%) followed by most native common species, then state-endangered species including Blanding's turtles (*Emydoidea blandingii*; 4/2%) and spotted turtles (*Clemmys guttata*; 3.5%). Prevalences also varied by year, location, season, age class, sex, and the presence of physical examination abnormalities ($p < 0.05$). Importantly, many pathogens were detected in more than one host species. These data provide a valuable baseline for understanding pathogen impacts on aquatic turtle communities and can be used to support the wellness of both threatened and common species.

Thyroid Hyperplasia in Wild Brook Trout (Salvelinus fontinalis) from Lake Florentien (Quebec, Canada)

Monday, 28th July - 15:00: (Salon A) - Poster

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As part of the restoration of a brook trout (*Salvelinus fontinalis*) population, the Florentien Lake was restocked with farmed brook trout following its full depopulation using rotenone. Anglers reported the presence of protruding masses in the ventral isthmus in ≈1% of the fish. These masses were diagnosed as thyroid hyperplasia (goiter). To better characterize this condition, 213 brook trout were sampled from the affected lake. Nineteen brook trout from a nearby lesion-free control lake were also examined for comparison. Follicular thyroid hyperplasia of mild intensity was documented in 46.5% of the fish from the affected lake. Thyroid hyperplasia is a non-tumoral proliferative change resulting from excessive stimulation of the thyroid tissue to produce hormones. This condition has rarely been documented in wild fish, with the only known reports dating back to the 1970s in landlocked Atlantic salmon from the Great Lakes. Potential causes of goiter include iodine-deficient water, insufficient dietary iodine and exposure to goitrogenic substances. Levels of water iodine in the two lakes were similar, but the level of iodine in the gastric contents of the brook trout from the affected lake was three times lower than the level detected in trout from the lesion-free control lake. This observation suggests that this hyperplastic condition is caused by an iodine-poor diet. It could be hypothetised that the rotenone treatment might have decreased prey diversities, which could have led to an iodine deficient diet. High fish density, associated with increased competition for food resources, could also have played a role.

HEPATIC LIPIDOSIS IN BATS IN PENNSYLVANIA, USA

Monday, 28th July - 15:00: (Salon A) - Poster

Taylor Chan [1]***, Stephanie Stronsick*** [2]***, Greg Turner*** [3]***, Madeline Vile*** [1]***, Kevin Niedringhaus*** [1]

1. *Wildlife Futures Program, University of Pennsylvania,* ***2.*** *Pennsylvania Bat Conservation and Rehabilitation,* ***3.*** *Pennsylvania Game Commission*

Bats play an important ecological role in arthropod suppression and pollination, with 9 species commonly found in Pennsylvania, USA. There are few publications describing spontaneous, non-infectious disease in bats. Hepatic lipidosis is a well-described disease in many animals, following abrupt negative energy balance. The resulting hepatocyte dysfunction can cause significant metabolic dysregulation and death. It has been rarely reported as a cause of mortality in captive bats, without definitive etiology. We describe the clinical presentation and pathologic findings of presumably fatal hepatic lipidosis in multiple bat species in Pennsylvania and discuss possible underlying causes in context of current literature of fatal lipidosis in mammalian species. Hepatic lipidosis was diagnosed by postmortem examination in nine wild and rehabilitated bats from three species (1 evening bat, 7 big brown bats, 1 eastern red bat) from 2022-2025. Seven bats were cared for by rehabilitation centers for 1 day to 2 years and found dead without prior known disease, while two were found dead in the wild. All bats had abundant visceral fat and 6/9 bats had minimal gastrointestinal contents. The liver in 5/9 bats was enlarged and discolored yellow to red-orange, tan, and pale pink. The microscopic findings of all nine bats include diffuse accumulation of discrete lipid vacuoles, effacing the normal hepatocellular cytoplasm. Well-conditioned bats may have increased susceptibility to developing fatal hepatic lipidosis in response to external stressors. In the absence of other findings, fatal hepatic lipidosis should be considered a potential cause of sudden death in bats.

Fatal bronchopneumonia cases in California mountain lions with concomitant feline leukemia virus and Mycoplasma sp. infection

Monday, 28th July - 15:00: (Salon A) - Poster

***Jane Riner* [1], *Omar Gonzales-Viera* [2], *Heather Fritz* [2], *Steven Kubiski* [3], *Quinton Martins* [4], *Graham Crawford* [4], *Fernando Najera* [5], *Deana Clifford* [1]**

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In California (USA), mountain lions (*Puma concolor*) are a specially protected species and a high priority for conservation. Multiple mountain lion population monitoring studies collaborate to conduct mortality investigations to assess disease prevalence and identify factors that may limit individual and population health. Here we report a cluster of five mountain lion mortalities due to bacterial bronchopneumonia, all with concomitant infection with exogenous feline leukemia virus (FeLV) and four with *Mycoplasma* sp. We review necropsy findings, histopathology, and ancillary pathogen testing (bacterial culture, PCR, immunohistochemistry, serology, and in-situ hybridization) and highlight important patterns among cases. Mortalities occurred in individuals from two distinct geographic populations (three from Sonoma and two from Tehachapi) during February to October 2024. Four mortalities were adult individuals collared for research purposes. Quantitative PCR revealed progressive FeLV infection in four animals, and antigen testing was positive in all five cases. At least two of the deceased mountain lions were known to have interacted with domestic cats, which may represent a possible spillover source. DNA sequencing of the *Mycoplasma* sp. isolated from two animals confirmed *M. felifaucium*. The clinical significance of *M. felifaucium* in mountain lions should be further explored, as it may play an important role in pathogenesis of pneumonia similar to other *Mycoplasma* spp. described in felids. Feline retrovirus infections are known to cause systemic immunosuppression and progressive disease, with most felids succumbing to associated conditions. Compounding existing threats to mountain lion conservation in California, highly virulent and pathogenic FeLV strains may pose significant morbidity and mortality risks to this species. Understanding factors related to susceptibility, virus strain, exposure source, comorbidities, and clinical outcomes will help predict impacts and guide future research efforts.

Effect of prairie dog burrow density on tick abundance on small mammals in South Dakota

Monday, 28th July - 15:00: (Salon A) - Poster

***Zack Wilson* [1], *Madisen Hartlaub* [1], *Travis Livieri* [2], *Shelli Dubay* [1], *Ben Sedinger* [1]**

***1.** University of Wisconsin-Stevens Point, **2.** Prairie Wildlife Research*

Grasshopper mice (*Onychomys leucogaster*) and deer mice (*Peromyscus maniculatus*) co-occur on grasslands in South Dakota and may be parasitized by *Ixodes sculptus* and *I. kingi* tick species. These ticks could serve as bridging vectors for tularemia (*Francisella tularensis*), a zoonotic bacterial disease, in the grassland ecosystem. Tularemia has caused mortality in deer mice and grasshopper mice and can cause localized mortality in prairie dogs (*Cynomys* spp.). Small mammal abundance has been shown to increase on prairie dog complexes. We aimed to identify relationships between small mammal densities, prairie dog burrow densities, and tick abundance on small mammals in Conata Basin/Badlands National Park, South Dakota. We hypothesized that the number of small mammals trapped and the presence of ticks parasitizing them would be positively correlated with prairie dog burrow density. We captured 615 individual small mammals on eighteen 150m x 150m plots using Sherman traps. Ticks were found on 111 of them. We found that grasshopper mice had a 47% chance of having at least one tick, whereas all other small mammals had a 13% chance of harboring a tick. We found no significant relationship between the number of small mammals captured or the number of ticks on small mammals and prairie dog burrow density. Grasshopper mice are the most likely small mammal host to transport *Ixodes* spp. ticks around the grassland.

Resource sharing of wallows by feral swine and native wildlife and the potential for interspecies disease transmission at Anahuac and Aransas national wildlife refuges, Texas, USA

Monday, 28th July - 15:00: (Salon A) - Poster

Rachel Maison [1]**, *Samuel Golon*** [1]**, *Ian McMillan*** [2]**, *Jeffrey Marano*** [1]**, *Bruce Leland*** [3]**, *Vienna Brown*** [4]**,**
Bradley Borlee [1]**, *Angela Bosco-Lauth*** [1]

1. *Colorado State University,* ***2.*** *University of Hawaii,* ***3.*** *USDA-APHIS-WS,* ***4.*** *USDA-APHIS-VS*

Understanding the ecological processes that drive disease transmission is vital to mitigate risk to vulnerable populations. Increasingly, shared water sources have been shown to accumulate pathogens and foster cross-species transmission events. Concurrently, feral swine are an invasive mammal present throughout North America and capable of vectoring pathogens that threaten human and animal health. To investigate the role of feral swine in interspecific transmission, we monitored three wallows from March to September 2024 in Texas, USA. Wallows were monitored with game cameras to document site use, and environmental samples tested for organisms vectored by feral swine. To evaluate how likely pigs were the source of any environmental detections, we collected biological samples from pigs removed nearby and examined them for the same pathogens. Feral swine were observed at all sites, along with various avian species, with one currently classified by the IUCN as near threatened. Other taxa detected included white-tailed deer, coyote, and domestic cattle; activities of these species coincided closely with that of feral swine, demonstrating sufficient temporal overlap necessary for transmission events to occur. *Bacillus anthracis* bacteria were isolated environmentally from one wallow, and corresponded with high seroprevalence (59.2%, n=27) in swine sampled nearby, implying the site may be a source of anthrax exposure. Additionally, antibodies against *Brucella suis, Coxiella burnetii*, *Leptospira*, and pseudorabies virus, as well as *Ehrlichia chaffeensis* DNA were detected in subsets of swine. These results emphasize the need for research into the potential for interspecies disease transmission, particularly in areas with high levels of biodiversity.

Tracking Tularemia: Insights into Ferret Exposure and Tick Dynamics in South Dakota

Monday, 28th July - 15:00: (Salon A) - Poster

Madisen Hartlaub [1]***, Travis Livieri*** [2]***, Zack Wilson*** [3]***, Shelli Dubay*** [1]

1. *University of Wisconsin-Stevens Point,* ***2.*** *Prairie Wildlife Research,* ***3.*** *Univeristy of Wisconsin-Stevens Point*

Tularemia (*Francisella* tularensis) can be fatal to prairie dogs (*Cynom*ys spp.), the primary prey of endangered black-footed ferrets (*Mustela nigripes*; ferret). Ferrets survive tularemia exposure and seroconvert, but the infection route is unknown. Ticks commonly parasitize ferrets and may transmit tularemia but are prone to desiccation in arid environments. We aimed to explain ferret exposure to tularemia and to determine where ferrets acquire *Ixodes* spp. ticks. We hypothesized that: 1) Ferret exposure would be influenced by environmental moisture (Palmer Drought Severity Index [PDSI] averaged 3 months prior to sampling), and 2) Ticks would commonly parasitize small mammals but would rarely quest in the environment. We tested 1,356 ferret sera from 2002-2024 via microagglutination inhibition (positive titer ≥1:128) to determine if sex, age, season, or PDSI explain tularemia exposure. In summer 2024, we trapped 1,207 small mammals on eighteen 150m x 150m plots on prairie dog colonies. We recorded species, sex, age, and tick abundance on trapped animals. We sampled ticks from the environment by dragging vegetation, swabbing prairie dog burrows, and scraping soil at burrow entrances. Juvenile male ferrets captured in spring when PDSI was higher (wetter) were more likely to be exposed to tularemia. Ticks were common on small mammals (57.7%) with the highest abundance on grasshopper mice. We only collected 5 ticks from the environment using traditional sampling methods. We recommend trapping small mammals to sample ticks in grasslands. Other mechanisms of transmission, including soil, should be considered.

Prevalence, Diversity, and Intensity of Trichinella spp. in Wildlife from Northern Canada and Alaska: New Geographic and Host Records for Trichinella chanchalensis

Tuesday, 29th July - 10:00: (Salon A) - Poster

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

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

A new species of the zoonotic nematode *Trichinella—T. chanchalensis* (T13)—was recently discovered in wolverines and an American marten in the Northwest Territories (NWT) and in wolverines from the Yukon, Canada. It is not currently known if T13 can infect wildlife species other than mustelids. This study aimed to further investigate the ecology of T13 to determine geographic and host ranges. We worked with northern partners to sample terrestrial carnivores and omnivores from Alaska, USA, and the three northern Canadian territories. The double separatory funnel method was used to recover larvae from tissues and all recovered larvae were genotyped using deep amplicon next-generation sequencing on the Illumina MiSeq. Animals positive for *Trichinella* spp were found in the Yukon (158/213 (74%)), Alaska (53/157 (33.8%)), the NWT (53/157 (33.8%)), and from Nunavut (41/50 (82%)). Co-infections with *Trichinella nativa* and *Trichinella* T6 (169/281, 60%) were most common, but the number of co-infections ranged significantly from 33% (Alaska) to 87% (NWT). T13 was detected in 41/158 (25.9%) animals in the Yukon, 2/31 (6.5%) in NWT, 9/41 (22%) in Nunavut, and 1/51 (2%) in Alaska. T13 was predominantly found in mixed infections 50/53 (94.3%) with one or more additional taxa. T13 was found in two lynx (*Lynx canadensis*), two wolves (*Canis lupus*), and one coyote (*Canis latrans*), all of which are new host records for T13. Moreover, T13 was also detected for the first time in Nunavut and Alaska. This study provides new geographic and host records for T13 and also contributes meaningful updates to *Trichinella* prevalence, diversity, and intensity in four geographic regions while using a novel metabarcoding. Research into host-specific differences in prevalence, intensity, and diversity of *Trichinella* spp. is essential to assess the risk for food safety and to support food sovereignty.

Egyptian fruit bats (Rousettus aegyptiacus) present functionally distinct proteomic profiles in serum during pregnancy

Tuesday, 29th July - 10:00: (Salon A) - Poster

Brooke Genovese [1], ***Nistara Randhawa*** [2], ***Benjamin Neely*** [3], ***Gabriela Grigorean*** [4], ***Brian Bird*** [1], ***Jonna Mazet*** [2]

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Egyptian fruit bats (*Rousettus aegyptiacus*; ERB) play an important role as seed dispersers, pollinators, and nutrient recyclers across Africa; however, evidence supports that they are natural hosts for several zoonotic viruses. Previous ecological studies suggest that temporal patterns of virus shedding and pathogen spillover from bats to humans are correlated with seasonal bat reproductive cycles; yet, important questions remain regarding the complex interplay between ERB virus dynamics and the energetically demanding periods of pregnancy and lactation.

In this work, we used data-independent, LC-MS/MS proteomics to perform a quantitative analysis of blood samples collected from seven captive-reared dams and characterized maternal serum proteomic profiles with advancing gestational age. Pairwise differential expression analysis between pre-mating and longitudinal time points revealed 46 biologically significant proteins ($\log2(FC) \geq 1.5$; q-value < 0.05) associated with mid-and-late gestation. Biological relevance of key up-and-down regulated proteins were interpreted with GO analysis and linked to a variety of physiological processes, including cell mediated immunity, lipid metabolism, and organogenesis. Our subsequent and ongoing analysis will compare these proteomic signatures to the serum profiles of wild, free-ranging fruit bats (n=22) where we expect to detect departures from non-reproductive and/or non-infected baselines.

At the time of writing, this study is the first of its kind to employ a high-throughput and multi-system analyses of bat physiology in the context of reproductive cycle changes. These results can be used to inform proactive human-wildlife contact interventions meant to reduce zoonotic disease risk and promote the coexistence of bats and humans.

Impacts of agricultural disturbances on small mammal population and Sin Nombre Virus temporal dynamics

Tuesday, 29th July - 10:00: (Salon A) - Poster

Laura Budd **[1], *Mathieu Pruvot*** **[1]**

1. *University of Calgary, Faculty of Veterinary Medicine*

Sin Nombre Virus (SNV) is a rodent-borne, zoonotic, North American Hantavirus that causes Hantavirus cardiopulmonary syndrome (HCPS). Deer mice (*Peromyscus maniculatus)*, the primary reservoir, are found across many habitats, including many anthropogenically disturbed habitats. In natural habitats, deer mouse abundance, SNV prevalence, and outbreaks of HCPS can sometimes be predicted from changes in vegetation cover and climatic events. It is unknown if these relationships hold in agricultural or peridomestic settings, where most cases of HCPS are acquired. Agricultural disturbances that disrupt vegetation cover, such as harvesting and grazing, impact small mammal community structure, population dynamics, and movement. How these responses might alter SNV dynamics across types of agricultural land-use is unknown. Using a multi-season capture-mark-recapture study, we compare the community, population, and SNV dynamics of small mammals in cereal crop, hay, and cattle pasture fields in Alberta, Canada. The differences in type and timing of disturbance are expected to impact rodent community composition, timing of peak abundance, and in turn fluctuations of SNV prevalence. Initial results indicate deer mice and meadow voles are the dominant species, but disturbance impacts who dominates in which fields. Deer mouse abundance consistently peaks with peak vegetation cover while meadow vole abundance increases seasonally in pastures. Initial SNV results will be presented at the time of the conference. This study is one of the first to compare the fine-scale impacts of different agricultural practices on both small mammal populations and SNV dynamics and will help predict and mitigate SNV spillover risk in agricultural settings.

RETROSPECTIVE AND PROSPECTIVE EVALUATION OF MEDIASTINAL AND PULMONARY MINERALIZATION IN PENINSULAR PRONGHORN (Antilocapra americana peninsularis): DIAGNOSTIC IMAGING, CLINICAL, AND PATHOLOGICAL FINDINGS

Tuesday, 29th July - 10:00: (Salon A) - Poster

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There are less than 150 free-ranging peninsular pronghorn (*Antilocapra americana peninsularis*) in Baja California, Mexico.[1] Understanding the health status of animals under managed care is imperative to support in situ and ex situ populations for this endangered subspecies.

Intrathoracic mineralization was identified in a population of peninsular pronghorn under managed care. This study determined the causes, prevalence, and outcomes of thoracic lymph node or pulmonary mineralization in peninsular pronghorn at the San Diego Zoo Wildlife Alliance (SDZWA).

A combined prospective cross-sectional imaging study and a retrospective review of medical and necropsy records of pronghorn at SDZWA (2013 – 2024) was performed. Pronghorn with antemortem thoracic imaging and/or complete necropsy were included (n=32). Pulmonary or mediastinal/tracheobronchial mineralization were identified in four individuals (prevalence 12.5%). Euthanasia was performed in three cases, due to declining health. *Cryptococcus* sp. (n=1) and atypical, non-tuberculosis *Mycobacterium* spp. (n=2) were diagnosed by histopathology, mycobacteriosis confirmed via culture and PCR. A single animal diagnosed with mediastinal mineralization is alive one year after diagnosis with no clinical concerns. Due to the difficulty of collecting antemortem samples at the lesion location, direct sampling has not been performed and the etiologic agent in this case remains unknown. This investigation suggests intrathoracic granulomatous lymphadenitis and pneumonia with dystrophic mineralization are relatively common in this carefully managed population, can be caused by a variety of etiologic agents, and may be manageable conditions. Additionally, this study highlights the importance of thoracic imaging during illness and preventative medical examinations in this species of increasing conservation importance.

Examination of pathogen shedding patterns, based on variation in temperature and housing groups, in confiscated eastern box turtles (Terrapene carolina carolina)

Tuesday, 29th July - 10:00: (Salon A) - Poster

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Eastern box turtles (*Terrapene carolina carolina*) have experienced population declines due to the illegal wildlife trade and its association with the spread of infectious diseases. Managing live animals confiscated from the trade can be critical for conservation, and best practices are needed to determine how to manage confiscated turtles. Fifteen confiscated eastern box turtles were sampled during 8-week trials with different housing groups and environmental temperatures within a temperature-controlled chamber: 1) group housed at cold temperatures, 2) group housed within a temperature gradient, 3) group housed at warm temperatures, and 4) individually housed at warm temperatures. Turtles were sampled weekly for *Terrapene* herpesvirus 1 (TerHV1), *Terrapene* adenovirus (TerAdv), and box turtle *Mycoplasma* sp. (BTMyco). A sensitivity analysis was conducted to determine optimal sampling methods based on the housing environment for the group. Pathogen prevalence varied weekly but was highest when housed together at a temperature gradient (BTMyco=100%, TerAdv=100%, TerHV1=46%). More co-infections and deaths (n=2) occurred when the environmental temperature was warm, and weekly pathogen shedding was lowest when the turtles were individually housed. The best detection rate for two swabs includes weekly sampling for each pathogen, but if turtles are housed longer than two weeks, it is most optimal to sample every third week. This study provides evidence-based sampling strategies to maximize the detection of individuals infected with common box turtle pathogens. These findings have implications for the clinical management of box turtles in managed care and can inform placement and release decisions during confiscation events.

Investigating Bartonella spp. in Fleas Parasitizing Voles from Interior Alaska

Tuesday, 29th July - 10:00: (Salon A) - Poster

Tabitha Page [1]***, Cristina Hansen*** [1]***, Shawn Crimmins*** [2]

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Bartonella spp. are gram-negative bacteria capable of causing numerous zoonotic diseases in humans, domestic animals, and wildlife worldwide. Rodents serve as important reservoirs for several *Bartonella* species, as well as their associated ectoparasites, particularly fleas.

In Alaska, several *Bartonella* spp. have recently been detected in voles (*Clethrionomys rutilus, Microtus pennsylvanicus*) across the Interior region. Prevalence of *Bartonella* ranged from 0-45%, and voles with fleas were more likely to be infected by *Bartonella*. However, *Bartonella* prevalence in fleas from Alaska remains unknown.

The study aims to identify flea species infesting 40 voles from Interior Alaska and detect *Bartonella* spp. using PCR targeting the 16S rRNA gene. If detected, this would be the first documented presence of *Bartonella* in fleas from Alaska.

While the analysis is ongoing, finding the presence of *Bartonella* in fleas in Alaska will contribute to the understanding of the relationship and interactions between Bartonella spp., voles, and their vectors. With climate change expected to facilitate the northward expansion of arthropods, research on vector-borne pathogens will become increasingly important for human and wildlife health, particularly in northern ecosystems.

Presence of Infectious Agents in Free-Ranging Urban Mice from the Metro Vancouver Regional District in British Columbia, Canada

Tuesday, 29th July - 10:00: (Salon A) - Poster

***Lisa Lee* [1], *Chelsea Himsworth* [2], *Theresa Albers* [3], *Rajeev Dhawan* [3], *Ken Henderson* [3], *Guy Mulder* [3], *Kim Waggie* [4], *Harveen Atwal* [1], *Imara Beattie* [1], *Bruce Wobeser* [1], *Kaylee Byers* [5]**

1. *University of Saskatchewan,* **2.** *University of British Columbia,* **3.** *Charles River Laboratories,* **4.** *University of Washington,* **5.** *Simon Fraser University*

Wild mice live in close association with people in cities. Mice can carry several microbial pathogens that pose serious health risk such as lymphocytic choriomeningitis virus, Hantavirus, *Leptospira spp.,* and *Salmonella spp.* Despite significant public health concern, little is known about how widely these pathogens are carried by free-ranging mice in buildings where people regularly reside or work. Our objective was to survey for a panel of bacteria, viruses, and protozoa in free-ranging mice within the Metro Vancouver Regional District of British Columbia, Canada. We collaborated with pest management professionals to collect wild mice that were lethally trapped in residential and commercial premises from April–June 2021. Two deer mice (*Peromyscus maniculatus*) and 122 house mice (*Mus musculus*) were collected. Polymerase chain reactions (PCR) were performed using kidneys and/or feces to detect the nucleic acid of infectious agents, while Multiplexed Fluorescent ImmunoAssays (MFIA) were performed on heart blood to detect antibodies. Lymphocytic choriomeningitis virus, Hantavirus, *Leptospira spp.*, and *Salmonella spp.* were not detected in any mice. The most prevalent pathogens by PCR were *Helicobacter spp.* (18/106; 83%), mouse adenovirus (26/86; 30%), and *Rodentibacter heylii* (31/106; 29%). Mouse rotavirus (19/89; 21%) and mouse cytomegalovirus (17/89; 19%) were most often identified by MFIA. While pathogens of significant public health concern were not detected, this may be due to limited sample sizes and heterogenous distribution of pathogens in wild rodents geographically. Given how closely mice interact with people in urban settings, continued surveillance is needed to mitigate potential risk to human health.

Prevalence of Leptospira spp. in mesocarnivores from North Carolina

Tuesday, 29th July - 10:00: (Salon A) - Poster

Adam Rose [1]***, Seth Lattner*** [1]***, Kelly Douglass*** [2]***, Colleen Olfenbuttel*** [3]***, Michael Yabsley*** [1]***, Christopher Cleveland*** [1]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *United States Department of Agriculture,* ***3.*** *North Carolina Wildlife Resources Commission*

Leptospirosis, a zoonotic disease caused by bacteria in the genus *Leptospira*, is transmitted through the urine of infected animals and poses significant risks to wildlife, domestic animals, and humans. While mesocarnivores such as raccoons (*Procyon lotor*), coyotes *(Canis latrans*), and red foxes (*Vulpes vulpes*) serve as important maintenance hosts that facilitate the spread of *Leptospira* spp., research on the prevalence of *Leptospira* spp. in North Carolina's mesocarnivore population remains limited. This study seeks to determine the prevalence of *Leptospira* spp. in mesocarnivores in North Carolina and examine its relationship with host demographics, geographic location, and environmental factors. To address this question, 600 kidney tissue samples were obtained through collaborations between the Southeastern Cooperative Wildlife Disease Study, the North Carolina Wildlife Resources Commission, and the United States Department of Agriculture. Samples were collected from depredation and damage control trapping, hunter harvest, roadkill, and clinical cases. DNA was extracted and analyzed using real-time polymerase chain reaction targeting the LipL32 gene of pathogenic *Leptospira* spp. Generalized linear models will assess relationships between *Leptospira* prevalence, species, age class, sex, and location. Our preliminary results indicate *Leptospira* spp. are present in 3.6% (7/191) of mesocarnivore samples. Additional testing is ongoing. Our results will enhance the understanding of *Leptospira* spp. epidemiology in mesocarnivores and contribute to wildlife disease surveillance efforts, while providing valuable insights for public health, wildlife management, and disease mitigation strategies.

A ‘Purr-sistent’ Problem: How Interactions Between Domestic Cats and Wildlife Contribute to the Spread of Canine Distemper Virus in an Urban Setting

Tuesday, 29th July - 10:00: (Salon A) - Poster

Shayna Orens [1]***, Laura Plimpton*** [2]***, Neeti Patel*** [3]***, Xiyu Wang*** [3]***, Jessica Noll*** [4]***, Benjamin Kaza*** [5]***, Marie Lilly*** [6]***, Maria Diuk-Wasser*** [7]***, Sally Slavinski*** [8]***, Amandine Gamble*** [5]***, Gary Whittaker*** [4]***, Laura Goodman*** [3]***, Ximena Olarte-Castillo*** [4]

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Since 2022, New York City (NYC) has experienced subsequent outbreaks of Canine Distemper Virus (CDV). Unlike other viruses in its family, CDV can infect an astonishing variety of species with varying degrees of pathogenicity. Urban environments, where many carnivore species (both domestic and wild) interact, may offer an ideal setting for maintaining CDV in an enzootic state. Our study seeks to better characterize the multi-species “metareservoir” of interconnected carnivore populations that enables the ongoing circulation of CDV in NYC. We screened samples from free-ranging domestic cats (Felis catus) and raccoons (Procyon lotor) from two collection activities. One includes the brains from suspected rabies cases collected from the five boroughs of NYC between 2022 and 2024. The other includes samples collected in Brooklyn from 2021 to 2023, during which animals were captured and anesthetized to collect samples and attach radio collars for tracking movement patterns. We have screened 303 brain samples and 89 saliva/rectal swabs for CDV using qRT-PCR. Interestingly, we detected CDV in the saliva samples from two cats and in the brain of one cat. While several CDV epidemic events in wild felids have been reported, to date, there are no reports of naturally occurring CDV infections in domestic cats. Whole genome sequencing and phylogenetic analyses revealed that the CDVs detected in cats are closely related to those circulating in raccoons. Our study provides new insight into the role free-ranging domestic cats play in the complex epidemiology of CDV in an urban environment through their interactions with wildlife.

FATAL VERMINOUS PNEUMONIA AND AIRSACCULITIS RESULTING FROM DIPLOTRIAENA SP. INFECTION IN A PILEATED WOODPECKER (DRYOCOPUS PILEATUS)

Tuesday, 29th July - 10:00: (Salon A) - Poster

Jay Muir **[1]** ***, Stéphane Lair*** **[1]** ***, Manigandan Lejeune*** **[2]**

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The pileated woodpecker (Dryocopus pileatus) is a key bird species of mature North American deciduous and boreal forests. Very few reports of causes of mortality for this species are available in the literature. We report a fatal case of respiratory infection with the nematode Diplotriaena sp. in an adult male pileated woodpecker found dead in Quebec, Canada in 2022. This bird was in poor nutritional condition and displayed a diffuse thickening and opacification of the air sacs associated with the presence of numerous white nematodes usually embedded in the air sac walls. Histologically, extensive fibrinous, heterophilic/histiocytic inflammatory changes associated with numerous sections of often degenerate nematodes were observed in the air sacs and lungs. Nematodes, associated with hyperplasia of the bronchial glands, were also observed in the lumen of the secondary bronchi. These approximately 700 µm in diameter adult nematodes had a thick cuticle and a coelomyarian musculature separated by two prominent lateral chords. The gross morphology of these nematodes was characteristic of the genus Diplotriaena sp. Molecular identification was unsuccessful. A focal fungal airsacculitis was also observed and believed to be a complication of the parasitic infection. Based on the severity of the lesions and of the poor nutritional condition, the cause of death of this bird was attributed to this parasitic infection. This parasite was not documented in the other 29 pileated woodpeckers examined by our network of laboratories (CWHC) over the years. The mode of transmission and occurrence of this parasite in this species of woodpecker are unknown.

Ocular Plague (Yersinia pestis) in a Mule Deer (Odocoileus hemionus) from Idaho, USA

Tuesday, 29th July - 10:00: (Salon A) - Poster

Tiffany Lin [1] ***, Elis Fisk*** [1] ***, Kyle Taylor*** [2]

1. *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University,* ***2.*** *Washington State University*

Yersinia pestis, the causative agent of plague, is rare in wild and domestic ungulates. Of the few reported cases of plaque in deer, ocular lesions are the predominant manifestation. This report describes the first reported case of ocular plague in a free-ranging mule deer (*Odocoileus hemionus*) from Idaho, USA. The deer was observed to be bilaterally blind and emaciated. The animal was euthanized via cervical gunshot and a field necropsy was performed. Histopathological analysis of the eyes revealed bilateral chronic fibrinosuppurative and necrotizing endophthalmitis. Additional lesions in other organs included chronic fibrinous pericarditis with intralesional plant material, moderate pulmonary vascular intimal proliferation with perivascular lymphoplasmacytic infiltrates and focal lymphocytic vasculitis, and generalized severe fat atrophy. *Yersinia pestis* was detected in ocular tissues using real-time PCR but was not detected in the heart, lungs, or liver. While the underlying cause of the unique ocular presentation in deer is not known, it is possible that ocular immune privilege may impede bacterial clearance even after sepsis has resolved. This is the third report of ocular plague in free-ranging deer in the United States. Due to serious public health implications, plague should be considered a differential diagnosis in deer with ocular lesions and appropriate precautions should be taken by wildlife disease professionals.

Investigating the top-down disease control of a recolonizing predator

Tuesday, 29th July - 10:00: (Salon A) - Poster

Ishana Shukla [1]***, Justine Smith*** [1]

1. *University of California Davis*

One Health states that the health of animals, the ecosystem, and humans are inextricably connected. However, ecosystem health has historically been underexplored in a One Health Framework, despite its large functional importance in providing ecosystem services. Similarly, many One Health approaches towards maintaining ecosystem services, like disease mitigation, have rarely been examined through a zoology and community ecology lens. Via the natural recolonization of wolves into California, we examine the potential top-down control of one of the most common vector-borne illnesses: Lyme disease. The risk instilled by the possibility of predation by carnivores can alter the behavior and activity of lower trophic levels, with implications for disease ecology. Here, we monitored changes in activity at the apex, mesopredator, small mammal, and tick community levels via GPS collars, camera traps, and mark-capture release methods.

Our results suggest that through a behavioral-mediated cascade, wolves indirectly suppress Peromyscus spp, the primary reservoir host for Lyme disease. We found that wolf-induced changes in spatiotemporal behavior in subordinate mesopredator carnivores (e.g., coyote, fox, marten) cause subsequent cascading changes in mouse exploratory behavior, with implications for tick exposure. Furthermore, by monitoring wolf activity since entering the state, we found that counties without wolves were likely to have significantly more cases of Lyme disease as compared to counties with wolves. Our results help to inform potential disease networks as rewilded-predator restoration efforts become more common, while simultaneously highlighting the importance of incorporating zoology and community ecology in accomplishing One Health goals.

Metabolic chemistry and hematology parameters as a proxy for body condition in Columbia River Sea lions

Tuesday, 29th July - 10:00: (Salon A) - Poster

Louise Bishop [1], ***Brianna Beechler*** [1], ***Julia Burco*** [2]

1. *Oregon State University,* ***2.*** *Oregon Department of Fish and Wildlife*

Fat stores in the form of blubber in marine mammals are important for the survival of individuals. In marine mammals, average blubber depths exceed the fat stores in most terrestrial animals, making traditional body condition scoring (BCS) schemas, like palpation and visual assessment, difficult to impossible. This poses a challenge for researchers and caregivers in accurately assessing body condition in marine mammals. Ultrasound techniques can be used to assess BCS, but require someone trained for ultrasound, and may produce variable results among practitioners (Castrillon et al, 2020). Necropsy provides the most accurate assessment of blubber thickness and therefore body condition, but is not feasible for live animal studies. Hematology and metabolic chemistry parameters have been shown to be reliable predictors of body condition in other mammals (Ezenwa et al, 2009, Santos et al, 2020). Here, we assessed post-mortem blubber thickness in 19 adult male Steller sea lions (Eumetopias jubatus) and 29 adult male California sea lions (Zalophus californianus) that were lethally removed for conservation of endangered migrating fish populations from the Columbia River in Oregon, USA. We used a generalized linear model to assess the correlation between blubber thickness and hematology and metabolic chemistry using whole blood. We found that packed cell volume (PCV) and total protein (TP) were positively correlated with blubber depth ($p < 0.05$) while cholesterol was negatively correlated ($p<0.05$).These results may be useful for live animal research purposes where ultrasound is not available, as well as wildlife rehabilitators for monitoring of body condition using a more objective standard than physical palpation.

Comparing the utility of nasal and conjunctival swabs to tissue samples for the detection of canine distemper virus in wild carnivores using real-time RT-PCR

Tuesday, 29th July - 10:00: (Salon A) - Poster

Seth Lattner [1], ***Colleen Olfenbuttel*** [2], ***Kelly Douglass*** [3], ***Rebecca Pelc*** [4], ***John Bunting*** [4], ***Ellen Haynes*** [1], ***Michael Yabsley*** [1], ***Christopher Cleveland*** [1]

1. *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***2.*** *North Carolina Wildlife Resources Commission,* ***3.*** *United States Department of Agriculture,* ***4.*** *North Carolina State Laboratory of Public Health, Department of Health and Human Services*

Canine distemper virus (CDV) is a highly infectious morbillivirus (Family Paramyxoviridae) that causes morbidity and mortality in numerous mammalian species, especially carnivores. Virus is shed from all bodily secretions during acute infection and shedding may persist for weeks. Currently, CDV diagnosis in wild carnivores is through post-mortem detection of CDV in tissue samples. Here, we examined the suitability of testing nasal and conjunctival swab samples for CDV detection as compared to brain samples. In collaboration with the North Carolina State Laboratory of Public Health, paired brain tissue samples and swabs (nasal and conjunctival) were collected from wild carnivores and tested for CDV using real-time RT-PCR. Results between sampling types were compared using Cohen's kappa statistic (κ), and Spearman's correlation coefficient (ρ) was used to determine the correlation between swab and tissue sample cycle threshold (Ct) values. In total, CDV has been detected in 44% (79/178) of brain samples, 41% (74/181) of nasal swabs, and 39% (69/179) of conjunctival swabs. High agreement was found between CDV results from both swab types and brain samples (κ=0.87 for both swab types). There was also a strong correlation between Ct values of both nasal (ρ=0.86) and conjunctival (ρ=0.84) swabs and brain tissue samples. Alternative sampling methods that are less invasive compared to traditional brain tissue collection are important to evaluate. Swabs are safer to collect from rabies suspects and they are easily implemented in field settings and allow for nonlethal sampling, which can be used for rare, endangered, or captive wild carnivores.

Silent sentinels ?: reptiles and birds as alternative host reservoirs in Trypanosoma cruzi ecology

Tuesday, 29th July - 15:00: (Salon A) - Poster

Mycha Van Allen [1]***, Lisa Aukland*** [1]***, Heather Prestridge*** [1]***, Gary Voelker*** [1]***, Sarah Hamer*** [1]

1. *Texas A&M University*

Trypanosoma cruzi is a protozoan parasite that causes Chagas disease, a neglected tropical disease. Endemic from the southern United States to South America, transmission primarily occurs through mammalian hosts. Yet, evidence suggests that reptiles and birds, thought to be refractory, may serve as alternative reservoir hosts. Past experimental studies show that immunosuppression enables T. cruzi infection in lizards while recent studies have detected T. cruzi DNA in wild lizards in Chile. Studies of chickens have shown natural resistance to T. cruzi infection, historically leading researchers to assume all birds are immune. However, recently, an owl carcass tested positive for T. cruzi infection challenging this dogma. Habitat disruption and environmental changes could lead to immunosuppression in wildlife populations, potentially increasing their susceptibility to T. cruzi infection. There is a lack of knowledge regarding the role of reptiles and birds in T. cruzi disease ecology. This study aims to investigate the prevalence of T. cruzi in birds and reptiles while examining how environmental stressors affect immunity and susceptibility to infection. Our findings will enhance our understanding of T. cruzi ecology in the US and contribute to reptile and bird conservation efforts. To do this, we are testing invasive house geckos (Hemidactylus tursicus), that cohabitate with triatomines, and owl tissue from Texas A&M's Biodiversity Collections. We have tested 24 geckos and 36 owls for T. cruzi by qPCR thus far, with no infection detected. Sampling will continue across different seasons and study sites to acquire the sample size necessary to determine prevalence.

Bridging the gap: multi-sector perspectives on wildlife, domestic animal and human leptospirosis in Ontario, Canada.

Tuesday, 29th July - 15:00: (Salon A) - Poster

Kellie Libera [1]***, Jane Parmley*** [2]***, Katie Clow*** [2]***, J. Scott Weese*** [1]***, Lauren Grant*** [2]***, Claire Jardine*** [1]

1. *Department of Pathobiology, University of Guelph,* ***2.*** *Department of Population Medicine, University of Guelph*

Although leptospirosis is one of the most common zoonoses worldwide, our understanding of the occurrence and distribution of this disease in humans and animals is limited and would benefit from a One Health integrated surveillance approach. As an initial step to engage key participating actors, we used a web-based survey of experts from human, domestic animal, wildlife, and environmental health fields, to investigate awareness and risk perception of leptospirosis and views on leptospirosis surveillance in Ontario, Canada. Multiple choice and qualitative based responses also identified factors perceived to affect disease occurrence, such as *Leptospira* distribution, human activities, and weather conditions. Most experts perceived leptospirosis as a health risk to domestic animals (87%; 69/79) and human health (85%; 62/73), however negative impacts to wildlife were only recognized by 54% (43/79). In general, experts viewed wildlife as a risk factor for human and domestic animal disease opposed to considering health impacts to wildlife, although participants also reported a comparative lack of knowledge of leptospirosis with respect to wildlife. A higher proportion of respondents with animal health training identified leptospirosis as a public and animal health threat in Ontario compared to respondents from the public health sector. Finally, 91% (70/77) of respondents indicated that current surveillance of leptospirosis in Ontario is inadequate, and all participants acknowledged that integrated surveillance systems have benefits over current methods. These findings demonstrate the interest and perceived potential for developing an integrated framework for leptospirosis surveillance in Ontario.

Who infected whom? Inferring transmission dynamics of foot-and-mouth disease virus in African buffalo (Syncerus caffer)

Tuesday, 29th July - 15:00: (Salon A) - Poster

Cambrey Knapp [1], ***Richard Orton*** [2], ***Eva Perez-Martin*** [3], ***Roman Biek*** [4], ***Brianna Beechler*** [1], ***Anna Jolles*** [1]

1. *Oregon State University,* ***2.*** *Center for Viral Research, University of Glasgow,* ***3.*** *Pirbright Institute,* ***4.*** *University of Glasgow*

The transmission of highly contagious viruses is dependent on a multitude of factors, from host immunity and behavior to carrier individuals to competition among genotypic lineages. Although foot-and-mouth disease virus (FMDV) is one of the most infectious diseases in the world, persistence of viral lineages nearly necessitates the presence of carrier individuals in African buffalo (*Syncerus caffer*), which serve as the wildlife reservoir for the virus. However, identifying which carrier animals are responsible for transmission events requires examining a combination of host immune parameters and genotypic parameters. Phylogenomic methods can be used to create inferences on viral transmission patterns between individuals and determine which lineages are most likely to persist in populations. From 2014-2018, we placed contact collars on and sampled all individuals in a closed buffalo herd of 108 unique individuals in Kruger National Park every 2 months. FMDV sequences were obtained from probang and tonsillar swab samples and ancestral state reconstruction was used to visualize the persistence of dominant strains and determine which individuals were more likely to transmit to others. We then asked if animals that were more likely to transmit had altered contact patterns in the herd or altered physiological states prior to transmitting virus. This study provides a phylogenomic framework for comparing the viral genotypes transmitted with the behaviors and immune parameters to identify variability in transmission competence across potential carrier individuals.

Disease Considerations in Beaver Translocation

Tuesday, 29th July - 15:00: (Salon A) - Poster

Reid Ballard [1], ***Dan Preston*** [1]

1. *Colorado State University*

With beaver translocations becoming more common in Western states for a variety of reasons, there is a subsequent need for heightened awareness among wildlife management entities regarding diseases that could be carried by translocated beavers. These diseases could cause harm to the ecosystem they are being moved to, pose a risk to public health, as well as lower relocation success rates.

In collaboration with Colorado Parks & Wildlife (CPW) in order to assist in their creation of a statewide beaver management plan, a document has been created to better elucidate diseases of importance for wildlife management. This document consists of two parts: the first is a general overview of infectious agents and resulting diseases relevant to beaver translocation, including: Tularemia, Leptospirosis, Rabies, Yersiniosis, Giardiasis, Chytridiomycosis, Whirling Disease, and invasive aquatic species. The included infectious agents are organized into those relevant to public health and those relevant to wildlife health. Relevant aquatic invasive species are also included briefly.

The second section of the document is a summary of a survey sent to the Western Association of Fish & Wildlife Agencies which sought to elicit policies currently in place in other jurisdictions regarding disease management in translocated beavers. The survey resulted in 12 responses from 11 states and provinces. 5 responding jurisdictions reported that they undergo disease testing when translocating beaver; some report testing based on clinical signs only, while others report testing each beaver for a panel of diseases. At the end of the section, additional state-specific beaver translocation policy information that was found from online searches is provided with relevant references.

Retrospective Serological Study of Toxoplasma gondii in Bighorn Sheep

Tuesday, 29th July - 15:00: (Salon A) - Poster

Laurel Hossler [1], ***Frances Cassirer*** [2], ***Hollie Miyasaki*** [2], ***Stacey Dauwalter*** [2], ***Kate Huyvaert*** [1]

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Toxoplasma gondii is a protozoan parasite that infects a diversity of vertebrates, including bighorn sheep. Felidae, the definitive hosts, spread the parasite by releasing oocysts, leading to exposure in intermediate hosts. Vertical transmission from mother to fetus can cause abortion and neonate loss. Infection in wildlife may be associated with higher human and domestic cat density, which increase with urbanization, possibly creating environments where *T. gondii* transmission is more likely. Seroprevalence may increase with age, potentially due to age-related immunosuppression or more exposure, a pattern observed in domestic sheep. Our goal was to explore whether age and distance to human communities are associated with *T. gondii* seroprevalence in Idaho bighorn sheep. Antibodies to *T. gondii* were detected using the Indirect Fluorescent Antibody test, and distance to human settlements (≥5,000 people) was measured in ArcGIS using the Near tool from each sheep's capture coordinates. Of 179 samples from eight populations, 18 (10%), from two populations were seropositive. 12 of 12 (100%) sheep from a population within 10 miles of an urban area were seropositive, whereas 4 of 20 (20%) sheep tested in a population 45 miles away from the nearest urban area were seropositive. Negative sheep were found, on average, 62 miles from the nearest urban area. These results suggest herds near urban areas may have a greater risk of *T. gondii* exposure, but no association was found with age. We will explore additional metrics of exposure risk to felids such as proximity to farms and finer-scale measures of human settlements.

What can microbiomes tell us about the health of wild birds?

Tuesday, 29th July - 15:00: (Salon A) - Poster

Carolina Gutierrez [1], ***Karla Vargas*** [1], ***John Winter*** [2], ***Matthew Allender*** [2], ***Evan Tanner*** [3], ***Alexis Rickert*** [1], ***Javan Bauder*** [1], ***Leigh Combrink*** [1]

1. *University of Arizona,* ***2.*** *Wildlife Epidemiology Laboratory, University of Illinois Urbana-Champaign,* ***3.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville*

Avian species in the United States are facing significant declines, predominantly due to habitat loss, urbanization, and climate change. The spread of infectious diseases, such as avian influenza, malaria, and hepatitis, further exacerbates the challenges our wild populations face, underscoring the need for improved conservation strategies and effective disease monitoring. In humans, microbiomes have become valuable diagnostic tools for both chronic and infectious diseases, but their use in wildlife health monitoring remains nascent. Our investigation aims to examine the potential use of avian microbiomes as biomarkers or indicators of disease presence, overall avian health, and habitat quality. We collected oral and cloacal/fecal samples from three avian species - wood ducks (Aix sponsa), northern bobwhite quail (Colinus virginianus), and Gambel's quail (Callipepla gambelii) - across distinct habitat types and regions in the mid- and southwestern United States. Our primary objectives were to address these two key questions: (1) Can avian microbiomes and their respective health biomarkers reliably diagnose the presence of diseases? and (2) How do host factors and habitat characteristics influence avian microbiome composition across species? By linking microbiome data with disease profiles and habitat quality, we explore the potential for non-invasive microbiome sampling as a tool for wildlife health surveillance. Our findings contribute to the expanding field of wildlife microbiome research and provide insights that could inform future conservation, habitat preservation, and disease management strategies for wild avian populations.

Marine Birds as Early Sentinels of Harmful Algal Blooms: Identifying Key Indicator Species

Tuesday, 29th July - 15:00: (Salon A) - Poster

Carmen Ross [1]***, Terra Kelly*** [2]***, Devin Dombrowski*** [3]***, Rachel Avilla*** [3]***, Emma Hagen*** [2]***, Pranav Pandit*** [1]

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Harmful algal blooms (HAB) affect a wide range of taxa, including marine birds. Brevetoxin, produced by Karenia brevis, is the primary driver of HAB-related morbidity in marine birds off the Florida coast. A recent HAB event revealed that Laughing gulls admitted to wildlife rehabilitation organizations exhibited clinical signs of brevetoxin exposure before environmental testing detected K. brevis, suggesting that some marine bird species may serve as early indicators of HABs, but it remains unclear which species have this ability This study identifies species that can signal HABs earlier than current detection methods.

Marine bird stranding data of 108 species from WildAlert, an early warning wildlife surveillance system, and K. brevis count data from the Florida Fish and Wildlife Conservation Commission (2016-2024) were analyzed using cross-correlations to assess the relationship between the timing of strandings and presence of K. brevis.

Preliminary results revealed a statistically significant number of strandings before K. brevis detection in the environment among Great egrets (r=0.04, 15 and 36-day lags), Royal terns (r=0.05, 3, 6, and 7-day lags), and Laughing gulls (r=0.04, 10-day lag and r=0.02, 4). Our research suggests that these three species may serve as early indicators for K. brevis blooms and need to be investigated further. The relationship between the timing of strandings in key species presenting with signs of neurological and nutritional disease (commonly observed with brevetoxin exposure in marine birds) and the detection of K. brevis in the environment will also be explored.

Monitoring of Viral Agents in Wild Mammals from an Urban Center in Brazil

Tuesday, 29th July - 15:00: (Salon A) - Poster

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The survival of wildlife in fragmented environments depends on environmental challenges and anthropogenic pressures, favoring generalist species with high ecological plasticity. In urban ecosystems, these mammals act as strategic sentinels for pathogen surveillance. Belo Horizonte, located in Brazil's most economically developed region, contains approximately 86 forest fragments composed of Cerrado and Atlantic Forest, where previous studies have detected respiratory viruses such as Influenza A and SARS-CoV-2 in asymptomatic coatis. In this context, viral agents were monitored in *Didelphis* sp., *Callithrix penicillata*, and *Nasua nasua* within urban parks in the city. Specimens were captured using distributed traps, restrained, and anesthetized following protocols approved by the necessary ethical and environmental licenses. Non-lethal biological sample collection (whole blood, oral, and rectal swabs) was performed by a trained team using personal protective equipment. All animals received a subcutaneous microchip implant and underwent clinical evaluation. Carcasses found near the study areas were collected for pathological examination. DNA and RNA extraction and purification were conducted using magnetic beads. Molecular analyses involved the detection of viral agents within a respiratory panel, including pathogens relevant to human health, zoonotic transmission, and biodiversity conservation. Respiratory agents were detected in all three species studied, alongside outbreaks of canine distemper and herpesvirus in primates. These findings highlight the need for integrated epidemiological surveillance, considering that viruses capable of successful spillover among wildlife species have a higher potential for zoonotic emergence.

Wild Pig-Livestock Interactions and their Consequences for Disease Transmission

Tuesday, 29th July - 15:00: (Salon A) - Poster

Luis Salazar [1]

1. *University of Calgary, Faculty of Veterinary Medicine*

Introduction: Wild pigs (*Sus scrofa*) are invasive in Canada, causing severe damage to agriculture and ecosystems. Importantly, they may alter the risk of infectious disease transmission, with potentially devastating consequences for wildlife, public health, and veterinary systems. Because data on wild pigs is frequently unavailable, estimating disease transmission is often difficult. Accurate measurements of wild pig-livestock and wild pig-carcasses (conspecific) contact patterns can provide key parameters to model infectious disease transmission such as African Swine Fever (ASF) and explore control strategies. ASF is a highly contagious and devastating disease that can be spread by wild pigs, posing a serious threat to the domestic pigs.

Objective: This study aims to estimate the risk of African Swine Fever (ASF) transmission between wild and domestic pigs in Alberta by measuring contact patterns and modeling disease spread.

Methods: Contact rates were measured using camera trap studies, surveys, and interviews. These data were used to estimate key parameters for constructing a mathematical model of ASF transmission between wild pigs and livestock.

Results: The model identifies potential spillover events and explores various control measures to determine the optimal response. This is the first study to describe wildlife-livestock interactions (i.e., wild-domestic pigs) and simulate ASF transmission in Alberta.

Conclusion: Results will support decision-making to control ASF and prevent spillover events in the event of an introduction in the province.

Genetic Epidemiology of North Dakota Deer: Identifying Polymorphisms Influencing Epizootic Hemorrhagic Disease

Tuesday, 29th July - 15:00: (Salon A) - Poster

Ethan Baker [1]***, Sarah Daman*** [2]***, Charlie Bahnson*** [3]***, William Jensen*** [3]***, Turk Rhen*** [1]***, Susan Ellis-Felege*** [1]***, Brian Darby*** [1]

1. *University of North Dakota,* ***2.*** *University of Victoria,* ***3.*** *North Dakota Game and Fish Department*

Genetic epidemiology examines how genetic variation within a species interacts with environmental factors, providing valuable insights into disease dynamics and can be helpful at informing wildlife management strategies. Epizootic Hemorrhagic Disease (EHD) is a viral disease that can have high mortality rates in white-tailed deer (*Odocoileus virginianus)*. EHD is transmitted by an adult biting midge within the genus *Culiciodes*, whose emergence can be influenced by suitable temperatures for its life cycle completion. Thus, changing climate conditions has led to an increase in EHD outbreaks across northern states. In North Dakota (ND), white-tailed deer can experience high-mortality outbreaks that can directly impact population health and recreational opportunity. Recent research from Illinois examined polymorphisms at codons 59 and 116 in Toll-like receptor 3 (TLR3) that were linked to reduced EHD susceptibility. We collected and sequenced 1,030 white-tailed and 218 mule deer (*Odocoileus* hemionus) tissue samples from across ND to identify and quantify these previously documented EHD susceptibility polymorphisms. We found no genetic variation at codons 59 or 116 throughout all samples. Our results point to less haplotype variation across the TLR3 gene compared to the previous study with only one nonsynonymous mutation and four synonymous mutations found in ND. Our study highlights the need for additional research with the TLR3 gene to better understand haplotype diversity and TLR3's association with EHD susceptibility.

Comparison of Canadian Wildlife Health Cooperative wildlife disease surveillance data streams in Ontario

Tuesday, 29th July - 15:00: (Salon A) - Poster

Kaytlyn Wise **[1]**, ***David L. Pearl*** **[2]**, ***Jenna Matsuba*** **[3]**, ***Leonard Shirose*** **[1]**, ***Brian Stevens*** **[3]**, ***Jolene A. Giacinti*** **[4]**, ***Claire Jardine*** **[1]**

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Wildlife disease surveillance is critical for generating knowledge about wildlife health, and informing actions to protect wildlife, domestic animal, and human health. Passive surveillance via opportunistic carcass submission and necropsy is a major component of the Canadian Wildlife Health Cooperative's (CWHC) wildlife disease surveillance program. Recently, the CWHC has introduced an online wildlife health reporting tool, however the value of this additional method for generating surveillance data has not been assessed. Our objective was to describe and compare the information obtained from carcass submissions and online reports to the CWHC in 2022. Using descriptive methods, we categorized and compared submissions and online reports by vertebrate class, species categories, reporting month, and location. A total of 1373 carcass submissions and 1069 online reports were received. For both data streams, birds were the predominant vertebrate class represented, followed by mammals. However, the species categories within those classes differed (e.g., 24% of online reports about mammals were ungulates, compared to only 10% of mammalian carcass submissions). A greater richness of species and species categories were seen in carcass submissions. The number of carcass submissions peaked prior to the peak in online reports (April and June, respectively). The geographic distribution was similar between the data streams. These findings demonstrate differences in timing, species breadth and species categories captured by these two components of the CWHC's wildlife disease surveillance program. Using online reports will allow us to direct carcass submissions and increase the amount of wildlife health information generated through the program.

The influence of baiting on the prevalence of avian influenza virus (AIV) in Ontario dabbling ducks

Tuesday, 29th July - 15:00: (Salon A) - Poster

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Dabbling ducks have been implicated as a major carrier for H5N1 (clade 2.3.4.4b) highly pathogenic avian influenza virus (HPAIV) since its introduction to Canada in 2021, as they typically remain asymptomatic and migrate long distances. It has been proposed that congregation of ducks may promote HPAIV transmission locally. Consequently, we compared the prevalence of AIV and H5Nx in ducks at baited banding sites to ducks at sites without bait influence in fall 2023. Oropharyngeal and cloacal swabs for AIV matrix gene and H5-genotype PCR testing were obtained from live dabbling ducks at 3 banding sites where bait trapping is used (Group 1, n=173) and 3 bait authorization sites (Group 2, n=336) across Ontario. Hunter-harvested ducks were similarly sampled at 4 sites near bait authorization sites (Group 3, n=262) and 5 sites without bait influence (Group 4, n=402). There was a higher prevalence of AIV detected in Group 1 ducks than all others. Similarly, a higher prevalence of the H5-genotype was detected in both Group 1 and Group 2 ducks as opposed to all other groups. This suggests that congregation resulting from bait trapping facilitates HPAIV transmission at the site level. However, Group 3 ducks demonstrated a similar prevalence of the H5-genotype to ducks within Group 4, suggesting that despite increased prevalence of the H5-genotype at the site level, this does not appear to impact prevalence in the local flock. The results of this study will be used to inform management practices related to baiting and banding of ducks in Ontario.

Efficacy of the “pouring over feed” oral administration method for the commercially available Bacillus anthracis Sterne strain 34F2 vaccine in white-tailed deer (Odocoileus virginianus)

Tuesday, 29th July - 15:00: (Salon A) - Poster

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Bacillus anthracis, also known as Anthrax, is a soil-borne pathogen that poses a significant threat to both wildlife and domestic livestock. In its spore form, *B. anthracis* exhibits resistance to environmental extremes and decontamination strategies, complicating disease management efforts. To avoid further spread of infection, animal carcasses need to be disposed of properly, however the conventional disposal methods are both labor-intensive and expensive. The commercially available Sterne strain 34F2 vaccine has been successfully employed for subcutaneous administration however its application in wildlife populations remains challenging. In Texas, one common mitigation strategy has involved the incorporation of antibiotics into wildlife feed. However regulatory changes under the Veterinary Feed Directive, implemented in January 2017, now prohibit the use of antibiotics in feed for any purpose other than those specifically approved on the label. Another mitigation strategy involves pouring the commercially available vaccine over feed, despite subcutaneous injection being its recommended administration method. While development of an effective oral vaccine is critical for sustainable anthrax management in wildlife, this study evaluated the effectiveness of the “pouring over feed” method compared to subcutaneous administration in white-tailed deer (WTD; *Odocoileus virginianus*, n=9). We assessed the immune response in WTD serum collected over six weeks using enzyme-linked immunosorbent assays. Results demonstrated that pouring the commercially available vaccine over feed oral administration failed to elicit an immune response even with the addition of a scarifying agent, highlighting the necessity for further research and development of an effective oral vaccine for wildlife populations.

Pathogen Detection of Wild Turkeys Across North Dakota

Tuesday, 29th July - 15:00: (Salon A) - Poster

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Wild turkey (*Meleagris gallopavo*) populations are declining in much of the contiguous United States. One suspected reason for these declines is poor reproductive success which may be influenced by pathogen exposure. Pathogen exposure rates are unknown but may be important, given the frequent contact turkeys have with livestock and wildlife, as well as their adaptability to peridomestic settings. The University of North Dakota and North Dakota Game and Fish Department captured 227 turkeys and screened for infection or antibodies to eight pathogens using cloacal swabs, oral swabs, and serum. All capture and data collection was done between 1 January to 31 March in 2023 and 2024. Birds were captured at eight locations across North Dakota and samples were sent to referral labs. Our most notable results include 39.7% positive for Lymphoproliferative disease virus (LPDV), 32.3% positive for *Toxoplasma gondii,* and 15.7% positive for *Mycoplasma meleagridis*. Avian Influenza, *Mycoplasma gallisepticum*, and *Mycoplasma synoviae* were not detected. Co-infections were found in 46 individuals. LPDV was found to be the most common pathogen associated with co-infections across both years of sampling. Our results open the door to discuss how North Dakota wild turkeys fit into the One Health approach. Turkey-human and turkey-livestock interactions are common (and increasing) in North Dakota. In some cases, they are even considered a nuisance as they consume sileage or defecate in livestock feedlots, particularly in the winter months. As wild turkey conflicts continue and expand, there is an increased risk of pathogen transmission between turkeys and livestock.

Spatial Dynamics of Zoonotic Pathogens in Bank Vole (Myodes glareolus) Populations from Northern Sweden

Tuesday, 29th July - 15:00: (Salon A) - Poster

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This study examines spatial patterns of zoonotic pathogens in two bank vole populations near Umeå, northern Sweden. Our aim is to assess how landscape and community structure influence pathogen occurrence and distribution. One of our focuses is on the Puumala orthohantavirus (PUUV) associated with bank voles (*Myodes glareolus*) as a reservoir which can cause a mild to moderate form of hemorrhagic fever with renal syndrome (HFRS), also called nephropathia epidemica, in humans.

Bank voles from a full generation cycle from coastal- and inland-forest sites were analyzed for pathogen occurrence and prevalence. Randomized subsets out of 1303 samples were determined using FreeCalc by EpiTools to test for disease absence in these populations based on published pathogen prevalences. The lowest reported prevalence for each pathogen guided sample size calculations to confirm disease absence, with additional testing conducted upon positive results to establish true prevalence.

PUUV S-segment RNA in lung tissue was detected using an established conventional reverse transcription-polymerase chain reaction (RT-PCR) protocol with subsequent DNA sequencing. PUUV RNA was detected in 27.5% (11/40) of inland-forest voles and 12.5% (5/40)[URG1] of coastal-forest voles. Furthermore, DNA from subsets of samples was tested negative for other zoonotic pathogens using established quantitative PCR-protocols, including *Toxoplasma gondii*, *Francisella tularensis* and pathogenic *Leptospira* spp., while 0.4% (1/234; Ct:34.22) of coastal-forest voles tested positive of *Yersinia pseudotuberculosis*.

These findings suggest potential spatial variability in pathogen presence and prevalence, contributing to our understanding of small mammals' role in zoonotic pathogen transmission.

This research is part of the BEPREP project (HORIZON-CL6-2021-BIODIV-01).

Wildlife Rehabilitation: The Unseen Partner in Wildlife Health

Thursday, 31st July - 10:00: (Salon A) - Poster

William Funk [1]

1. *Oklahoma State University*

Wildlife rehabilitation is a budding branch in the field of wildlife conservation, and one that is often overlooked by members of the wildlife health community. Traditionally viewed as an animal welfare venture, the profession of wildlife rehabilitation started out as individuals working to save injured and orphaned animals. However, as the vocation has grown, so too has our potential to aid in wildlife conservation and health sectors, furthering the One Health Initiative while holding true to the ethics of rehabilitation and release. In this presentation, I expand on the potential that wildlife rehabilitators have to contribute to the various fields of wildlife science and improve their captive management simultaneously, as well as some of the difficulties associated with this partnership.

Collaboration, Communication, Education, and disease surveillance

Thursday, 31st July - 10:00: (Salon A) - Poster

Shelley Spanswick [1]

1. *Center for Wildlife*

The field of wildlife rehabilitation has evolved immensely over the past 30 years. This presentation will utilize Center for Wildlife (CFW) in Cape Neddick, Maine as an example of how wildlife rehabilitators can, and do, play a significant role in education, conservation, and disease surveillance.

CFW's mission is focused on long-term systemic change, sustainability, and a One health approach and mentality. By focusing on a larger picture the center has prioritized and created working relationships with state organizations, universities, and other non-profit organizations which has aided in disease surveillance (Covid, HPAI), data collection utilized to support legislation efforts (loon mortality data/lead fishing tackle), and contributions to baseline data (raptor research).

Along with contributing to research efforts nationwide the center collaborates and works with many areas of state and federal government. By sitting on steering committees with Maine IF&W helping to update policy and standards within the field of wildlife rehabilitation, to hosting training sessions for Wildlife Conflict Agents with the Maine Warden Service to gain hands on experience transporting and handling wildlife, to organizing meetings with new dispatch staff to educate and collaborate to provide consistent messaging to the public.

Our efforts in collaboration and communication are working towards building more consistency with messaging to the public regarding wildlife conflicts and disease information. Creating more consistency in messaging and education will have a greater impact on all areas of our work. Our community learns about present threats wildlife face in their backyard, the animals in need will get to the closest, qualified licensed rehabilitator, the public will be informed and protected from injury/disease, there will be higher trust from the public in the ability of all parties and be more likely to follow regulations, and any needed human and/or wildlife health concerns will be reported in the proper manners.

Deep dive on cetacean health from New South Wales, Australia

Thursday, 31st July - 10:00: (Salon A) - Poster

Heather Fenton **[1]**, ***Jane Hall*** **[1]**, ***Yi-Jou Chen*** **[2]**, ***Jan Slepta*** **[2]**, ***Jianning Wang*** **[3]**, ***Karrie Rose*** **[1]**

1. *Australian Registry of Wildlife Health,* **2.** *The University of Sydney,* **3.** *Australian Centre for Disease Preparedness*

This project aimed to take a deeper dive into archived free-ranging cetacean data and samples collected from coastal New South Wales (NSW). Records from the Australian Registry of Wildlife Health, a 40-year-old wildlife health program of the Taronga Conservation Society were searched for cetacean cases. The Registry database reports 175 individual animals from 26 species spanning the period of 1999-2024. Specific pathogens of interest that were targeted for additional analyses included influenza A viruses, cetacean morbilliviruses, *Brucella* sp., *Coxiella burnettii*, and *Toxoplasma gondii*. Frozen archived samples were available from 103 individual cetaceans collected with Influenza A viruses, *Brucella* sp., and *Coxiella burnetti* not being detected in any of the samples tested. A single pygmy killer whale from 2011 with multiple comorbidities tested positive for cetacean morbillivirus. *Toxoplasma gondii* testing was done on a subsample of individuals examined between 2019 and 2023 (n = 14) and interpreted to have contributed to mortality in at least four dolphins. Additional genetic characterisation of the protozoa parasite suggests that *T. gondii* of the same genotype has been circulating in terrestrial animals in New South Wales. Notable increases in rainfall seem to be associated with detection of cases of toxoplasmosis highlighting interconnectedness among human, animal, and environmental health. Overall, the project summarizes notable findings from the dataset and emphasizes the importance of maintaining standardized records and tissue archives for future analyses to better inform conservation management.

Less Lethal Wildlife Deterrent Round Impacts on Simulated Tissue

Thursday, 31st July - 10:00: (Salon A) - Poster

Owen Slater [1]***, Gordon Stenhouse*** [2]

1. *University of Calgary,* ***2.*** *GBS Wildlife Consulting*

Deterrent rounds are used throughout North America for aversive conditioning or hazing of polar, grizzly and black bears due to human, animal and property concerns. Previously referred to as “non-lethal,” these rounds are now more accurately defined as “less lethal” due to their potential to cause significant injury and death. While deterrent rounds are routinely used on bears, the impact characteristics of these rounds has not been well documented in the scientific literature. This study tested commonly available deterrent rounds used in typical field conditions when bears are encountered. Rounds were tested at set distances (5-20m) and temperatures (+20-40°C), with impact characteristics measured after rounds contacted standardized gelatin blocks that replicated tissue. Velocity, mass and kinetic energy of each round were measured as well as the depth and width of penetration. Results showed that the kinetic energy, shape and consistency of deterrent rounds were the most important factors responsible for depth of penetration. With decreasing temperature, firm rubber rounds had greater penetration and as distance increased, the accuracy of rounds decreased. The use of deterrent rounds with lower kinetic energy and/or that deform or break apart on impact showed the least amount of impact penetration and whenever feasible, these rounds are recommended as the first deterrent round option at close distances to reduce the chance of significant injury. Testing of and practice with deterrent rounds in simulated field conditions is recommended prior to use to determine if, or under what conditions less lethal rounds are suitable for deployment on wildlife.

Disease Outbreaks & Vaccine Efficacy in Raccoons in Rehabilitation: A Pilot Study

Thursday, 31st July - 10:00: (Salon A) - Poster

William Funk **[1]*****, Mackenzie Thomas*** **[2]*****, Mattingly Yates*** **[2]*****, Alexandra Ford*** **[1]*****, Sunil More*** **[1]*****, Kyle Abbott*** **[2]**

1. *Oklahoma State University,* **2.** *WildCare Oklahoma*

The Northern raccoon (Procyon lotor) is a common patient admitted to rehabilitation throughout the United States. These animals are prone to a multitude of diseases, including rabies, canine distemper, and parvoviruses. A high-volume rehabilitation center in Oklahoma has noticed an increased in neurologic and gastrointestinal disease in their raccoon patients, despite following current best practice standards. Historic diagnostics has isolated an unspecified parvovirus as the causative agent, despite many of the affected patients having received three rounds of vaccinations against both canine and feline parvoviruses. As such, the aim of this study was to evaluate the efficacy of vaccines in preventing disease in raccoons in a rehabilitation setting. While initial findings suggest that the age a patient is admitted to care may have a larger effect on survival of disease as opposed to the vaccination status, further research in needed to evaluate differences in the symptomatic presentation between vaccination groups.

Addressing the global gaps in wildlife health data management through a community-of-practice-supported database

Thursday, 31st July - 10:00: (Salon A) - Poster

Diego Montecino-Latorre [1]***, Sarah H Olson*** [1]***, Mathieu Pruvot*** [1]***, Paloma H F Shimabukuro*** [2]***, Christopher M Barker*** [3]***, Liz P Noguera*** [4]***, Susan Kutz*** [4]***, Fernanda Dorea*** [5]***, Claire Cayol*** [6]***, Damien Joly*** [7]***, Emily Denstedt*** [1]***, Sreyem Sours*** [1]***, Santi Choun*** [1]***, Steve Gallo*** [1]***, Jonathan Palmer*** [1]

1. *Wildlife Conservation Society,* ***2.*** *Global Biodiversity and Information Facility,* ***3.*** *University of California Davis,* ***4.*** *University of Calgary,* ***5.*** *Food And Agriculture Organisation of the United Nations,* ***6.*** *World Organisation for Animal Health,* ***7.*** *Canadian Wildlife Health Cooperative*

Wildlife health surveillance (WHS) is critical for addressing health hazards in wild populations. WHS relies on diverse data generated by many parties through various methodologies. Databases facilitate structuring, centralizing, accessing, understanding, sharing, analyzing, communicating, and responding to these data, supporting the implementation and operation of WHS. However, information systems in WHS are rare and there is no comprehensive, accessible, purpose-built database for wildlife health. As a result of this gap, relevant data are often lost, incomplete, and lack harmonization and standardization. Data archiving and sharing are hindered and the performance of WHS systems is compromised.

To address this gap, Wildlife Conservation Society (WCS) is developing a community-of-practice-based database designed to support WHS operation: the WildHealth Database (WHeDB). WHeDB supports data security and safety and it can uniquely accommodate the diverse data types and levels of multi-sourced WHS information under one structure. WHeDB is based on the expertise of a global community of practice that includes WCS' Health Program, the Canadian Wildlife Health Cooperative, VectorSurv, the Global Biodiversity Information Facility, members of the World Organization for Animal Health and Food, Agriculture Organization of the United Nations, and other experts in animal health. WHeDB is the first platform of its type that will be offered in multiple languages and provided as a common good for conservation professionals, researchers, and the global community of wildlife health practitioners. In this presentation, we will share the database structure, functions, and examples of its usage with the community of potential users at the conference.

Improving Wildlife Disease Surveillance through Rehabilitation Center Partnerships: Focus on HPAI

Thursday, 31st July - 10:00: (Salon A) - Poster

Amanda Rappaport [1]

1. *Wildlife Rehabilitation Center of Minnesota*

Wildlife rehabilitation centers admit and treat injured and sick wildlife with the goal of returning them to the wild. The abundance of animals admitted annually to rehabilitation centers provides a unique opportunity to investigate pathogens that impact not only wildlife species but also domestic animals and humans. Rehabilitation centers can act as sentinels for disease pandemics and contribute significantly to One Health initiatives. Collaboration with rehabilitation centers enables surveillance of pathogens and investigations of mortality events. This can result in datasets that address critical questions about host-pathogen-environment interactions.

Highly pathogenic avian influenza (HPAI) virus is an emerging and ongoing disease threat to the health of wildlife, poultry, livestock, and humans. The Wildlife Rehabilitation Center of Minnesota (WRCMN) is collaborating with the University of Minnesota Veterinary Diagnostic Lab (VDL) to better understand which wildlife species serve as reservoirs for HPAI virus. It also seeks to establish a wildlife virus surveillance program with a reference library of HPAI virus isolates. This will enable future characterization of the virus, with the goal of identifying specific mutations. Understanding viral diversity is critical for guiding mitigation strategies for wildlife and for formulating warnings to the public, particularly the agricultural and public health communities.

Wildlife rehabilitation centers offer a valuable opportunity for researchers to collect samples from animals already under care. These facilities provide access to diverse species with minimal additional effort. Utilizing this resource enhances studies on health and disease while benefiting both individual animal recovery and broader wildlife conservation and management efforts.

Characterizing Wildlife Rehabilitation Centres in the British Isles: an Antimicrobial Use Perspective

Thursday, 31st July - 10:00: (Salon A) - Poster

Daniela Losada-Medina [1]***, Nicola J Rooney*** [1]***, Fernando Sánchez-Vizcaíno*** [1]***, Irene Bueno Padilla*** [1]

1. *Bristol Veterinary School, University of Bristol*

Wild animals in rehabilitation centres often receive antimicrobial treatments, which may contribute to the selection of antimicrobial resistant microorganisms in their microbiota and surrounding environment. Despite this, antimicrobial use in wild animals undergoing rehabilitation remains poorly understood. In the British Isles, wildlife rehabilitation centres range from large, well-equipped hospitals, to small, home-based settings. However, little is known about the functioning of these centres and how this relates to antimicrobial use. Studying antimicrobial use in wild animals in this context is increasingly relevant as regulations limit antimicrobial prescribing to veterinarians. Therefore, this study aims to characterize wildlife rehabilitation centres in the British Isles, focusing on antimicrobial use.

Wildlife rehabilitators and veterinarians from rehabilitation centres of varying sizes in the British Isles were interviewed online or in person. Interviews explored rehabilitation centre functioning and were recorded, transcribed, and thematically analyzed using NVivo software.

Preliminary results indicate that wildlife rehabilitation centres differ in the species they admit and animal transfer between centres may occur. Animals are brought into the centres from the public, veterinary practices, other rehabilitation centres, governmental services, and animal welfare organizations. Some centres rely on veterinary practices in the area, while others have their own veterinary team. Frequently, wildlife rehabilitators or other staff initiate antimicrobial treatments with guidance from veterinarians or pre-established protocols.

This study provides a foundational insight into the context in which antimicrobial prescribing occurs in wildlife rehabilitation. Understanding this is crucial for identifying potential exposure routes to antimicrobial resistant microorganisms in wild animals in the British Isles.

Detection of Leptospira in Oregon Wildlife: groundwork for investigating prevalence and diversity across a range of small mammals in contact with humans

Thursday, 31st July - 10:00: (Salon A) - Poster

Kacy Hayes [1], ***Celia Noel*** [2], ***Alejandra Ortega*** [1], ***Justin Sanders*** [1], ***Brianna Beechler*** [1]

1. *Oregon State University,* ***2.*** *École Nationale Vétérinaire de Toulouse*

Leptospirosis is a neglected bacterial zoonotic disease that has diverse effects on human and animal health, is responsible for around 60,000 human deaths annually and severe impacts in livestock and companion animals. Leptospira bacteria spread primarily through water sources contaminated with urine from wildlife maintenance hosts. In an effort to investigate the rise in leptospira cases in Oregon veterinary cases (Grayzel and DeBess, 2016, Oregon Health Authority), potential exposure to humans, locally significant wildlife hosts, and to better understand the pathogen's diversity across the landscape, 577 wildlife carcasses were collected as donations from wildlife rehabilitation facilities, a pest control company, the USDA, and private individuals in western and central Oregon. Samples of kidney tissue were extracted and screened for leptospirosis using a rtPCR with primers that amplify the 16s region (n=577), then samples with a lot of high quality DNA (n=23) were amplified at seven loci using an MLST protocol to identify species and serovar of Leptospira. Target DNA was detected in 46 individuals (8%) via rtPCR across all the samples, and within 16 species. Four samples fully amplified across MLST (Scheme II) identified Leptospira interrogans and Leptospira kirschneri species, both of which have zoonotic potential. Further sequence analysis is pending. Animals were much more likely to test positive for leptospirosis if their life history was associated closely with aquatic nesting and foraging. This was driven primarily by high prevalence in beavers and nutria, and low prevalence in arboreal species like tree squirrels. Interestingly, one vole tested positive, and voles have been found to be important in transmission in Europe. Future work will investigate the role of an agricultural pest, gray- tailed voles in transmission of leptospirosis locally.

Causes of Mortality in Captive, Captive-release and Wild Vancouver Island Marmots (Marmota vancouverensis)

Thursday, 31st July - 10:00: (Salon A) - Poster

Malcolm McAdie [1]***, Adam Taylor*** [1]***, Kevin Gourlay*** [1]***, Craig Stephen*** [2]***, Stephen Raverty*** [3]***, Karl Larsen*** [4]***, Douglas Whiteside*** [5]

1. *Marmot Recovery Foundation,* ***2.*** *McEachran Institute,* ***3.*** *Animal Health Centre,* ***4.*** *Thompson Rivers University,* ***5.*** *Wilder Institute / Calgary Zoo*

The Vancouver Island marmot (*Marmota vancouverensis*, VIM) is a critically endangered sciurid endemic to the mountains of Vancouver Island, BC. In response to precipitous declines in the 1980s and 1990s, an intensive captive breeding and reintroduction program was initiated. This recovery effort has generated significant, health-related data from the captive, captive-release, and wild VIM populations, including the results of postmortem examinations and field mortality investigations. This presentation summarizes these findings and compares mortality causes between the three management groups. Captives exhibited greater longevity, were monitored with greater intensity, and were safeguarded against the threat of predation. This allowed for the prompt recognition, recovery, and evaluation of mortalities. Cardiomyopathy and neoplasia represented the most significant cause of mortality in captive marmots. These findings were not observed in the *in-situ* population, possibly due to reduced longevity, dissimilar risk patterns, or limited opportunities to evaluate intact carcasses. In many instances, mortalities of free-ranging VIM presented with incomplete remains or were inaccessible belowground, and these situations were evaluated according to evidence collected during on-site, field investigations. The first wild hibernation was a time of significant mortality for captive-releases. However, individuals that survived their first winter post-release displayed a low incidence of hibernation mortality in subsequent winters. Predators represented the most common cause of mortality for both captive-release and wild marmots. Obesity in captive marmots, reduced hibernation survival of first-year, captive-release marmots, and predation of free-ranging marmots, particularly from cougars, appear to represent important factors influencing the health and recovery of this critically endangered species.

Wildlife Health Communications – A Walk through (Jurassic) Park

Thursday, 31st July - 10:00: (Salon A) - Poster

Brooke Ezzo [1]

1. *Wildlife Futures Program, University of Pennsylvania*

Communicating wildlife health is challenging, especially in today's political climate. With so much distrust surrounding health research and recommendations, conveying messages meant to keep domestic animals, wildlife, and humans safe can be difficult.

The Wildlife Futures Program, a wildlife health partnership between the Pennsylvania Game Commission and the University of Pennsylvania School of Veterinary Medicine, strives to communicate these difficult yet necessary conversations with our stakeholders, ranging from hunters and trappers to bird watchers to urban residents who interact with wildlife more than they think. With research projects spanning West Nile virus impacts on bird populations, chronic wasting disease diagnostics and the effects of rodenticides on mesocarnivores, we've done our fair share of discussing wildlife health data and recommendations to our diverse audiences. In this presentation, our Communications Coordinator, Brooke Ezzo, will review tips on connecting with, engaging, and inspiring audiences to not only be open to science communication but also digest it and enact positive behavioral changes.

The wild sea lion gut ecosystem: characterizing host-microbe-parasite interactions and assessing links to health

Thursday, 31st July - 10:00: (Salon A) - Poster

Emma Little [1]***, Justin Sanders*** [2]***, Julia Burco*** [3]***, Katie Prager*** [4]***, Holly Arnold*** [2]***, Brianna Beechler*** [2]

1. *Carlson College of Veterinary Medicine, Oregon State University,* ***2.*** *Oregon State University,* ***3.*** *Oregon Department of Fish and Wildlife,* ***4.*** *University of California Los Angeles*

Marine sentinel species (e.g. pinnipeds) offer a unique perspective into wildlife and ocean function in an era of intensifying anthropogenic stressors and environmental change. Although health assessments of pinnipeds pose challenges, extensive evidence supports the intricate association between the ecosystem of gastrointestinal microbiota and parasites within a host and wildlife physiology, fitness, and ecology. Here, we characterize gut microbial and parasite communities in California sea lions (*Zalophus californianus)* and Steller sea lions *(Eumetopias jubatus)* sampled lethally and nonlethally in Astoria, Oregon and the Columbia River Basin, Oregon and assess links to metrics of host health and disease. Preliminary results suggest sampling location, and therefore diet, explains variation in microbial communities, while species differences do not. Initial characterization shows core microbiomes are dominated by phyla belonging to Firmicutes, Fusobacteriota, Bacteroidota, Actinobacteriota, and Proteobacteria. Putative parasitic presence is variable between individuals: Digenea, Filaroididae, Myxosporea, Eucestoda, and Anisakidae are found present in 98.3%, 75.8%, 75.4%, 45.9%, and 16.1% of California and Steller sea lions respectively. While this gut microbial and parasite community reflects that of other pinnipeds, the relationship between host health, community composition, and function remains to be explored. Our health investigation has the potential to strengthen marine mammal conservation and disease monitoring efforts.

Increasing awareness of collaboration opportunities with your partners in wildlife rehabilitation

Thursday, 31st July - 10:00: (Salon A) - Poster

Sarah Sirica [1]

1. *City Wildlife*

There are many opportunities for collaboration on wildlife health initiatives between wildlife rehabilitators and public or private institutions. While there may be differences in belief regarding wildlife management or other issues, there is a shared goal of wildlife health, and partnership can be achieved. Wildlife rehabilitation has rapidly professionalized, and there are many rehabilitators with backgrounds in biology, ecology, animal behavior, and veterinary medicine. There are multiple examples of rehabilitation being done at academic institutions, where there has been inspiring and useful collaboration over decades, but the collaboration does not need to be limited to these higher institutions. City Wildlife is located in Washington, DC, and has been open for wildlife rehabilitation since 2013, with between 1,500-2000 patients annually. Work from City Wildlife can exemplify effective collaboration in the wildlife health sector between rehabilitators and departments of health and natural resources, among others. Examples over the last decade include partnership on toxin and disease surveillance, response and professional expertise with avian influenza and other wildlife health events, and public advocacy for migratory bird conservation.

Management and short-term monitoring of leishmaniosis (Leishmania infantum) in a European Mink (Mustela lutreola)

Thursday, 31st July - 10:00: (Salon A) - Poster

Jacobo Giner [1], Rafael Guerra [2], José Villora [1], Diana Marteles [1], Pablo Quílez [1], Cristina Riera [3], Magdalena Alcover [3], Roser Fisa [3], Javier Millán [4], Sergio Villanueva-Saz [1]

1. *Universidad de Zaragoza,* ***2.*** *Córdoba Zoo Conservation Center,* ***3.*** *Universidad de Barcelona,* ***4.*** *Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA)*

Leishmania infantum causes an endemic disease in the Mediterranean Basin, affecting humans and various mammals, including domestic, captive, and wild mammals such as mustelids. Clinical leishmaniosis has been reported in mustelids, with recent documented cases in domestic ferrets (*Mustela putorius furo*) and a captive Eurasian otter (*Lutra lutra*). The European mink (*Mustela lutreola*), one of the world's most endangered mammals, has experienced a significant population decline. Factors such as habitat degradation, climate change, the impact of invasive species, and various diseases may contribute to this decline. This communication presents the first case report of clinical leishmaniosis in a captive European mink in an endemic area of leishmaniosis (Spain), including treatment with anti-*Leishmania* therapy and follow-up. The affected mink exhibited weight loss, pyogranulomatous blepharitis, and an enlarged popliteal lymph node. Blood tests revealed anemia, hypergammaglobulinemia, and elevated serum renal values. The diagnosis was based on clinical signs, pathological findings including moderate antibody levels against *L. infantum*, which was confirmed through cytological examination, where amastigotes were detected in macrophages from a skin lesion sample, as well as parasite culture. Oral administration of miltefosine resulted in poor clinical response due to inadequate drug intake. However, a combination treatment using meglumine antimoniate and allopurinol led to clinical improvement. The potential impact of this disease on the critically endangered European mink should be considered when developing new conservation strategies, including captive breeding programs in endemic areas.

Bobcat population health in New York state

Thursday, 31st July - 10:00: (Salon A) - Poster

Jennifer Bloodgood [1], ***Haley Turner*** [2], ***Josh Twining*** [2], ***Krysten Schuler*** [1], ***Gavin Hitchener*** [1], ***Melissa Fadden*** [1], ***David Stallknecht*** [3], ***Deborah Carter*** [3], ***Rebecca Poulson*** [3], ***Kevin Hynes*** [4], ***Angela Fuller*** [5]

1. *Cornell Wildlife Health Lab,* ***2.*** *New York Cooperative Fish and Wildlife Research Unit, Department of Natural Resources and the Environment, Cornell University,* ***3.*** *Southeastern Cooperative Wildlife Disease Study, University of Georgia,* ***4.*** *New York State Department of Environmental Conservation,* ***5.*** *U.S. Geological Survey, New York Cooperative Fish and Wildlife Research Unit, Department of Natural Resources and the Environment, Cornell University*

Monitoring wildlife health is important for species conservation and management. Bobcats (*Lynx rufus*) occur throughout upstate NY and currently have hunting and trapping seasons. As a complement to ongoing research to estimate population density and movement to inform management decisions surrounding these seasons, we evaluated population health to investigate potential impediments to population growth. Bobcats in NY (12 males, 4 females; 14 adults, 2 juveniles) were live-captured and anesthetized for GPS collar placement and collection of biological samples including blood, feces, and ectoparasites. We tested blood for hematological and biochemical analyses, blood type, *Cytauxzoon felis*, feline leukemia virus, and antibodies to *Toxoplasma*, canine distemper virus, feline parvovirus (panleukopenia), and influenza A virus (IAV). We found bobcats hosted a diverse assemblage of endoparasites and all hosted *Ixodes scapularis* ticks which are potential vectors for multiple pathogens. All individuals were blood type A. All individuals tested negative for *C. felis* (16/16) and feline leukemia virus (15/15). There was antibody evidence of exposure to *Toxoplasma* (13/14), canine distemper virus (13/15), feline parvovirus (13/15), and IAV (9/16). Four bobcats that tested positive for antibodies to IAV tested positive for antibodies to both H5 and N1. Five weeks post-capture, an adult male was found dead from H5N1 infection; it did not have previous exposure to the virus. We demonstrate that NY bobcats face a variety of health challenges, including a newly introduced highly pathogenic avian influenza (H5N1), which can be considered as part of the species' vulnerability to threats in future management decisions.

A Community-Driven Sperm Whale Health Assessment Program in Dominica

Thursday, 31st July - 10:00: (Salon A) - Poster

O. Alejandro Aleuy [1], *Annie Page* [2]

1. *Florida Atlantic University,* ***2.*** *Florida Atlantic University, Harbor Branch Oceanographic Institute*

Sperm whales (Physeter macrocephalus) are listed as endangered under the Endangered Species Act, but research and conservation efforts are challenged by complex and costly data collection in difficult-to-access offshore areas. Dominica, an island nation in the West Indies, hosts one of the few year-round nearshore sperm whale populations and is working toward establishing the world's first sperm whale marine reserve. Unfortunately, whale populations in Dominica and the Caribbean have steadily declined over the past 20 years due to poorly understood drivers. Our objective is to present our community-driven sperm whale health assessment program, which we aim to establish in Dominica, and gather feedback to enhance its impact. Wildlife health assessments provide essential baseline data to identify and mitigate conservation threats. Integrating these initiatives within local communities ensures conservation efforts are effective and inclusive. The overreaching goal is to develop sustainable decision-support tools for wildlife management while strengthening the community's connection to whales. The program consists of three objectives: i) Community knowledge - compile and organize local and traditional knowledge on sperm whales and marine mammals through participatory epidemiology and collaborative workshops; ii) Sperm whale research - determine and monitor health indicators using scientific approaches and data collection in collaboration with local tourism operators; and iii) Marine mammal stranding response - work with Dominican authorities to establish response protocols and decision trees, based on FAU's Stranding and Population Assessment team's expertise. Sperm whales hold ecological and cultural significance for Dominica, and their population decline raises concerns about their survival and the sustainability of whale-based tourism, a key economic activity on the island. Engaging and training local community members will empower local stakeholders, foster a deeper understanding of whale health, and ensure conservation practices benefit both the community and the ecosystem.

Collaboration in Wildlife Health Research & Surveillance

Thursday, 31st July - 10:00: (Salon A) - Poster

Michelle Benavidez Westrich [1]

1. *Indiana Department of Natural Resources*

Wildlife health programs often face challenges in funding and capacity; therefore, developing innovative methods for increasing capacity is crucial to continued growth and development. One method of increasing capacity is developing and improving relationships with external partners, such as wildlife rehabilitators. Wildlife rehabilitators frequently interact with sick or injured native wildlife and potentially possess valuable information regarding trends in wildlife health issues. Furthermore, members of the public will often choose to alert wildlife rehabilitators of wildlife health issues prior to contacting state government. Knowing this, over the past two years, the Indiana DNR Fish & Wildlife Health Program has aimed to foster better relationships with the state's wildlife rehabilitators. Initiatives include a free PPE distribution program, increased communication regarding wildlife health events, and opportunities to engage in research. These collaborative approaches have only begun to open windows of opportunity to foster trust and engagement between our state agency and wildlife rehabilitators. This poster will outline the potential benefits of working with wildlife rehabilitators and the strategies we have used to build trust with the community. Overall, developing partnerships to increase capacity within wildlife health programs not only provides additional benefits for monitoring wildlife health, it also increases community engagement to better educate the public about how we can work together to foster a healthier environment.

Development of an Optimized Capture and Anesthesia Protocol for Formosan Sika Deer (Cervus nippon taiouanus) in South Korea

Thursday, 31st July - 10:00: (Salon A) - Poster

***Nari Kim*[1], *Seong-Hoon Kim*[1], *Kiyoon Kim*[1], *Yujin Lee*[1], *Ockju Im*[1], *Eui-Kyeong Kim*[2], *Dong-Hyuk Jeong*[1]**

1. Chungbuk National University, 2. Research Institute of Korea National Service

Effective and humane capture methods are essential for managing wildlife populations, particularly invasive species that may impact native ecosystems and serve as potential disease reservoirs. Formosan sika deer (*Cervus nippon taiouanus*), an invasive species in South Korea, requires systematic management, yet comprehensive anesthesia protocols tailored for their physiological responses remain lacking. This study aimed to optimize a capture and anesthesia protocol while assessing its implications for animal welfare and wildlife health monitoring.

Fieldwork was conducted in Songnisan National Park on 11 deer (8 males, 3 females; 1–6 years old; 15–40 kg). Immobilization was performed using intramuscular ketamine (3 mg/kg) and medetomidine (90 μg/kg) via dart gun, with atipamezole (450 μg/kg) administered for reversal. Physiological parameters, including rectal temperature, heart rate, respiratory rate, blood pressure, and SpO$_2$, were monitored every five minutes. Blood samples were collected for hematology, biochemistry, cortisol, and creatine phosphokinase (CPK) analysis, providing insights into stress physiology and muscle damage.

Results indicated rapid anesthesia induction (ataxia: 9.3 ± 7.2 min, sternal recumbency: 12.6 ± 8.6 min, lateral recumbency: 16.8 ± 9.2 min) and swift recovery (<1 min). Compared to previous studies, lower cortisol (2.77 μg/dl vs. 4.25 μg/dl) and CPK (1,515 IU/L vs. 2,894 IU/L) levels indicate reduced stress and muscle trauma, supporting the protocol's physiological safety and welfare benefits. Post-release tracking confirmed normal home range movement (2–3 km^2). These findings provide a reliable approach for invasive species management while enabling wildlife health assessments in the field, with potential applications in disease surveillance.

Interagency Collaboration for Increase Capacity and Response Time to HPAI

Thursday, 31st July - 10:00: (Salon A) - Poster

Anne Justice-Allen [1] ***, Ann Fan*** [1]

1. *Arizona Game and Fish Dept.*

The recent outbreaks of Highly Pathogenic Avian Influenza (HPAI) have raised substantial concerns among wildlife practitioners, poultry farms, and public health officials. Arizona has experienced an increase in detections since December 2024. As wildlife veterinarians at the Arizona Game and Fish Department (AZGFD), our primary objectives are to minimize human exposure by providing accurate information and to identify locations where HPAI is circulating in wild birds to inform partners.

We focused on building strong relationships and having open, direct communications between governmental agencies, wildlife rehabilitators, and the public. In response to the first detections, we coordinated with 3 largest wildlife rehabilitators in Arizona to test birds with signs of infection. The rehabilitators submit samples directly or provide us with specimens to necropsy and submit for testing. The cost of testing was covered by a zoonotic disease grant from USFWS. We hold bi-weekly updates and discussions regarding the response, and actively coordinate for public communications and sample testing with Arizona Department of Health Services and Agriculture, and USDA APHIS and Wildlife Services. Participation in HPAI study with Arizona State University has increased our surveillance capacity. In addition to the USDA annual targeted HPAI surveillance along the Colorado River, we received support for testing captured waterfowl and turkeys in other areas of the state (n = 15). We have tested 48 clinical birds from October 2024 to February 2025. Through proactive communication and partnerships, we are minimizing the negative impacts of HPAI, and other diseases, on wildlife, livestock, and people.

Gut microbiome as an indicator of Florida Manatee (Trichechus manatus latirostris) health across diverse ecosystems contaminated by microplastics

Thursday, 31st July - 10:00: (Salon A) - Poster

Tracie Baker [1]***, Emily Kintzele*** [1]***, Maite De Maria*** [2]***, Margaret Hunter*** [2]***, Nolan Lyons*** [3]***, Mallory Llewellyn*** [1]***,***
BRIDGET BAKER [1]

1. *University of Florida,* ***2.*** *USGS,* ***3.*** *Univerity of Florida*

The Everglades, one of the most extensive wetland ecosystems globally, has seen significant changes in size and health over 200 years due to anthropogenic activities. The 2022 Willoughby Expedition retraced a historic 1897 journey across the Everglades and assessed emerging contaminants, including microplastics, revealing impacts to even the most remote areas of the Everglades with implications for wildlife health across freshwater and marine, and urban to remote habitats. Microplastics, when ingested, can cause mechanical damage to the digestive tract by causing abrasions or perforations in the mucosal lining, the first line of defense against pathogens and bacterial translocation. Microplastics can also influence the type or amount of food ingested, leading to potential changes in gut microbiome by depriving symbionts of crucial nutrients and substrates. We paired investigation of microplastic presence and gut microbiome changes in Florida manatees (*Trichechus manatus latirostris)* by examining their fecal matter. Studies on other species have used fecal samples as a proxy for gut microbiome, but this approach introduces microplastic accumulation as a possible explanation for microbiome changes in a novel species. Fresh and archived fecal samples, and water samples were collected from free-ranging manatees across diverse ecosystems, including parts of the Everglades, Indian River Lagoon (Brevard County, FL), and Crystal River National Wildlife Refuge. Initial analysis suggests that microplastics were present in manatee fecal samples dating back to 2011. Analysis to evaluate for statistically significant temporal, spatial, and sex differences is ongoing, while also considering unusual mortality events (UMEs) as a factor. This study will provide insights into the health of manatees affected by microplastic ingestion across diverse ecosystem, urging enhanced conservation strategies tailored at mitigating environmental contaminants.

“NEMATOES” – IDENTIFICATION OF MASERIA VESPERTILIONIS ASSOCIATED WITH SWOLLEN TOES IN REHABILITATED BIG BROWN BATS (EPTESICUS FUSCUS)

Thursday, 31st July - 10:00: (Salon A) - Poster

Paige Fino [1], Stephanie Stronsick [2], Michael Yabsley [3], Greg Turner [4], Justin Brown [1]

***1.** Department of Veterinary and Biomedical Sciences, Penn State University, **2.** Pennsylvania Bat Conservation and Rehabilitation, **3.** Southeastern Cooperative Wildlife Disease Study, University of Georgia, **4.** Pennsylvania Game Commission*

During March, 2024, an adult, female, big brown bat (*Eptesicus fuscus*) was admitted to the Pennsylvania Bat Conservation and Rehabilitation (PBCR) due to traumatic injuries, including bruising and lacerations on the right wing and periocular swelling around the left eye. The bat was emaciated, dehydrated, and unable to fly, but was alert and responsive. Over the subsequent weeks, the traumatic injuries healed, and the bat's overall condition improved; however, multiple toes on both feet became markedly swollen and painful. The swollen toes were gently squeezed by the rehabilitator and small nematodes were expressed from the tissues. The nematodes were morphologically consistent with *Maseria vespertilionis*. Genetic analysis of partial cytochrome c oxidase subunit I sequence (679bp) confirmed the placement of the worm in the Family Muspiceidae and was genetically most similar to *Riouxgolvania kapapkamui*, another intradermal parasite reported from bats in Japan. After expression of the nematodes, the swollen toes gradually resolved until they appeared grossly normal. The bat recovered from the initial injuries and was released in June. Based on a review of PBCR records, nematode-associated swollen toes are relatively common. During 2023-2024, six cases of nematode-associated swollen toes were identified, all in big brown bats. Clinical presentations were consistent between bats with the dominant sign being painful, non-ulcerated swellings of multiple toes on both feet. None of the six cases had swollen digits on admission; rather, all were identified several weeks post-admission. In all cases, the swellings in the toes resolved after manual expression of the nematodes and a short course of an anthelmintic (Fenbendazole). Five of the six bats were successfully released. Although this appears to be a relatively common syndrome in big brown bats in rehabilitation centers, there is little known about the biology, transmission mechanism, or virulence of this nematode, and further research is needed.

Leveraging Clinical Wildlife Data for Enhancing Wildlife Health Monitoring and Research

Thursday, 31st July - 10:00: (Salon A) - Poster

Rachel Avilla **[1]**, ***Devin Dombrowski*** **[1]**, ***Pranav Pandit*** **[2]**, ***Terra Kelly*** **[3]**

1. *The Wild Neighbors Database Project, Middletown, CA, USA,* ***2.*** *Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, CA, USA,* ***3.*** *EpiEcos, Flagstaff, AZ, USA*

Wildlife rehabilitation organizations admit thousands of animals annually, providing a critical yet underutilized data source for understanding wildlife health trends, emerging disease threats, and conservation challenges. Through The Wild Neighbors Database Project's (WNDP) Wildlife Rehabilitation Medical Database (WRMD), rehabilitators systematically collect standardized data on injured and sick wild animals, including species, age class, location found, reasons for admission, and physical exam findings—offering invaluable insight into wildlife health. WRMD data is actively used in research on wildlife population health, including national studies assessing how rehabilitated species contribute to conservation. It also enhances wildlife disease surveillance by supporting early detection of unusual health events. WNDP's WildAlert tool, powered by WRMD data, provides real-time anomaly detection, alerting agencies and researchers to potential outbreaks, novel diseases, and other concerning patterns. Research has shown that rehabilitators often detect shifts in wildlife health weeks to months before traditional monitoring systems. Early warnings from WRMD data have prompted agency investigations, leading to definitive diagnoses and timely management actions. By strengthening collaboration between rehabilitators, researchers, and management agencies, WRMD is becoming an essential tool for wildlife health monitoring and research. Expanding outreach and investment in data-sharing frameworks is increasing access to this valuable resource, helping to answer key questions in wildlife health, conservation, and disease ecology.

A Thousand Pelicans: California Brown Pelican Mass Stranding Event 2024

Thursday, 31st July - 10:00: (Salon A) - Poster

Rebecca Duerr [1], ***Corrine Gibble*** [2]

1. *International Bird Rescue,* ***2.*** *Marine Wildlife Veterinary Care and Research Center, California Department of Fish and Wildlife, Santa Cruz, CA, USA*

California Brown Pelicans periodically strand in large numbers on the California coast, and live birds are typically admitted for wildlife rehabilitation. These events are known to have occurred in 2009, 2010, 2011, 2012, 2022, and again in 2024. The 2024 event brought 1,067 live pelicans into care at 12 coastal wildlife rehabilitation centers, with the bulk of birds admitted during April and May, from San Diego to Marin Counties, California. Affected birds were largely 1-3-year-old sub-adults or after-third-year adults, and included small numbers of young-of-the-year. No pathogens or toxins were identified by diagnostic testing as the cause of the event. Severe emaciation and hypothermia suggestive of starvation were the primary life-threatening problems found in live birds: 41.7% of captured birds died within the first 24 hours; 44% were significantly injured, 18.5% from recreational fishing gear and 15.1% showed fractured bones. Approximately 40% survived to be released. Most released birds were federally leg banded, some also received color auxiliary bands and/or Motus bands. Necropsies were performed on 131 deceased birds by numerous collaborators including International Bird Rescue, California Department of Fish and Wildlife, Los Angeles County Veterinary Public Health, the National Wildlife Health Center, and the California Animal Health and Food Safety Laboratory. Significant findings reflected live bird findings of emaciation +/- traumatic injuries. Many birds showed plumage problems that included bleaching, excessive wear, and fault bars on multiple generations of flight and contour feathers, suggestive of nutritional stress in excess of a single annual molt cycle. In care, birds commonly began molting flight feathers once nutritional health was restored, which suggests molt had been delayed due to energetic deficiencies. Further work examining the causes of these stranding events is ongoing.

Detection of European haplotype of Echinococcus multilocularis in coyotes in Washington state and implications for global surveillance strategies

Thursday, 31st July - 10:00: (Salon A) - Poster

Yasmine Hentati [1]***, Ellie Reese*** [1]***, Claire Curran*** [2]***, Erika M. Miller*** [3]***, Dakeishla Díaz-Morales*** [4]***, Samantha E.S. Kreling*** [1]***, Laura R. Prugh*** [1]***, Christopher J. Schell*** [5]***, Chelsea Wood*** [1]

1. *University of Washington,* **2.** *College of William & Mary,* **3.** *Sound Data Management LLC,* **4.** *DePaul University,* **5.** *University of California Berkeley*

Echinococcus multilocularis is a zoonotic cestode with canids as definitive hosts and rodents as intermediate hosts. In humans, this parasite is the causative agent of alveolar echinococcosis, a severe disease. Historically, *E. multilocularis* was considered rare in North America outside of two core zones: the north central region (the Great Plains region) and the north tundra zone (Alaska and northern Canada). Recently, haplotypes of European and Asian origin have been reported across North America. We confirmed the presence of a non-native haplotype of *E. multilocularis* in wild canids in western Washington state, USA, using a combination of morphological and molecular techniques across carcasses and field-collected scats of coyotes (*Canis latrans*). Morphological identification of adult worms was supported by next-generation sequencing using a custom primer as well as Sanger sequencing. We found that DNA amplified more reliably from intestinal swabs than from extracted fecal samples, with fecal samples showing a 50% false-negative rate. We identified a non-native haplotype of *E. multilocularis* that matched populations in British Columbia. Our study provides the first genetic confirmation of *E. multilocularis* in a wild host in the region, and our results reveal methodological insights for detecting *E. multilocularis* in wildlife and pets. The difference in amplification success between sample types presents significant implications for surveillance programs, as non-invasive fecal sampling may lead to underestimation of parasite prevalence. *E. multilocularis* is a parasite of nearly all wild canid species in the Northern Hemisphere as well as a major public health concern. Reliance on fecal-based surveys of canids may contribute to underreporting of *E. multilocularis*, hindering control measures and increasing the risk of undetected transmission to humans. This study highlights the urgent need for improved diagnostic strategies and reinforces the importance of proactive surveillance in wild canids, particularly in regions with significant human-wildlife interfacing.

Serosurvey of California mountain lions and implications for management and conservation

Thursday, 31st July - 10:00: (Salon A) - Poster

Jessica N. Sanchez [1]***, Jaime Rudd*** [2]***, Mathias W. Tobler*** [3]***, T. Winston Vickers*** [4]***, Deana Clifford*** [5]***, David Garcelon*** [6]***, Christopher C. Wilmers*** [7]***, Quinton Martins*** [8]***, Elisha Frye*** [9]***, Patricia M. Gaffney*** [10]

1. *Utah State University,* ***2.*** *Wildlife Health Lab, California Department of Fish and Wildlife,* ***3.*** *Conservation Science and Wildlife Health, San Diego Zoo Wildlife Alliance,* ***4.*** *Karen C. Drayer Wildlife Health Center, University of California, Davis,* ***5.*** *California Department of Fish and Wildlife,* ***6.*** *Institute for Wildlife Studies,* ***7.*** *Environmental Studies Department, University of California, Santa Cruz,* ***8.*** *Audubon Canyon Ranch, True Wild LLC,* ***9.*** *Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University,* ***10.*** *Disease Investigations, San Diego Zoo Wildlife Alliance*

California, U.S.A. is a complex landscape, ranging from remote wilderness to megalopolises with surrounding urban sprawl. Habitat fragmentation due to human development has resulted in spatially isolated subpopulations, providing opportunity to explore geographic differences in pathogen exposure.

Mountain lions are host to several pathogens which are shared among domestic and wild animals, including humans. Impacts of infectious disease on mountain lion population health is an area of active research, with some pathogens already known to cause morbidity/mortality and vary in prevalence with different levels of urbanization. We collected 395 serum samples from 254 individuals from six study sites across California from 2001 – 2024, representing six of ten previously identified genetically-distinct mountain lion populations. Prevalence estimates were weighted for resampling of individuals, and compared between age (kitten, subadult, adult), sex, and study site.

Exposure to *Toxoplasma gondii* (86.1%, 338/395) increased at higher latitudes, especially in study sites nearer the coast, and kittens had higher titer values than adults. Feline panleukopenia virus exposure was common across all sites (76.3%, 304/395), with highest prevalence in adults. *Leptospira* spp. prevalence varied widely by serovar (pomona 49.3% [198/395], icterohaemorrhagiae 43.5% [175/395], hardjo 23.3% [86/395], grippotyphosa 3.8% [12/395], canicola 0.9% [5/395]). For serovar pomona, prevalence increased with latitude for all sites except the furthest north, with adults and males having highest prevalence.

Detection of feline leukemia virus antigens was rare (1.7%, 7/388). We found no evidence of exposure to SARS-CoV-2 (0/95 samples) or avian influenza virus H5N1 (0/65 samples), despite six H5N1 infections confirmed in California mountain lions (three from one of our study sites).

Differences in exposure prevalence and antibody titer levels provide context for interpreting mortalities and can inform management actions (e.g., translocations). People working with California mountain lions should wear appropriate PPE due to the high prevalence of leptospirosis in the population.

An Overview of Prion Protein Gene Diversity in European wild Cervids

Thursday, 31st July - 12:45: (Salon A) - Poster

Sonja Ernst [1]***, Katayoun Goudarzi*** [2]***, Jörn Gethmann*** [1]***, Dolores Gavier-Widén*** [3]***, Agata Pietrzynska-Kajtoch*** [4]***, Johann Laubier*** [2]***, Jaana Kekkonen*** [5]***, Erik Ågren*** [3]***, Gustav Averhed*** [3]***, Aurélie Baroiron*** [6]***, Vincent Bourret*** [7]***, Martin H. Groschup*** [1]***, Miroslaw Polak*** [8]***, Maryline Pellerin*** [6]***, Christine Saint-Andrieux*** [6]***, Agnieszka Szumiec*** [4]***, Anne Van De Wiele*** [6]***, Michael Tranulis*** [9]***, Fiona Houston*** [10]***, Christine Fast*** [1]

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Susceptibility to Chronic Wasting Disease (CWD), a prion disease of cervids, depends on the genetic structure of the cellular prion-protein, encoded in the Prion-Protein Gene (*PRNP*). Since the ongoing CWD-epidemic and the CWD-emergence in Fennoscandia in novel contagious and sporadic forms, the risk for CWD spread within Europe must be considered. We therefore aim to compare *PRNP*-alleles in cervids to estimate a potential impact of CWD on population dynamics.

PRNP-sequencing data of cervid species from several European countries were collected for geographical and statistical analysis. These data include over 4,000 sequences of red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*), sika deer (*Cervus nippon*), white-tailed deer (*Odocoileus virginianus*) and moose (*Alces alces*) among others from France, Germany, UK, Poland, Norway, Denmark, Finland, Czech Republic and Sweden.

Most roe and sika deer samples were monomorphic, with only a small prevalence of polymorphisms. However, red deer revealed a broad *PRNP*-variability with geographically clustered allele-occurrence, suggesting “*PRNP*-linages”. Despite suffering from a severe founder effect in the past, Finnish white-tailed deer showed moderate *PRNP*-variability. Polish moose were monomorphic for a single genotype, but Swedish and Norwegian moose showed *PRNP*-variability.

This is the first geographical and statistical European-wide analysis of cervid *PRNP*-variation. Based on data from North American and European CWD-studies, we would predict that the majority of European cervids are probably CWD-susceptible. However, for a more detailed risk assessment, *in vitro* testing of the identified alleles is required to predict their impact CWD-susceptibility. Nevertheless, these results contribute to improve European risk assessment and control measures.

Wildlife disease research in Texas: Trends over the past three decades

Thursday, 31st July - 12:45: (Salon A) - Poster

Norelia Solis [1]***, Scott Henke*** [2]***, Jamie Benn*** [1]***, Alynn Martin*** [1]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***2.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville, Kingsville*

Texas encompasses a unique geographical region that spans ten ecoregions and hosts a diversity of wildlife. It is also a central point for major bird migratory flyways, hosts > 1930 km of international border with high movement of people and animals, and is situated in a climatic region expected to warm significantly in the next few decades. These factors make Texas a region of interest for understanding wildlife disease emergence and zoonotic disease risk. Here, we reviewed three decades of literature reporting wildlife diseases in Texas to understand regional and temporal trends. We utilized the Web of Science platform to perform a literature review using the following search terms and Boolean operators: “disease” AND “wildlife” AND “Texas”, which returned 772 primary research articles as of September 2023. These were filtered by a strict set of criteria to identify 87 primary articles. We noted a gradual increase in disease research in Texas with most studies focused on cervids, feral species (e.g., feral swine [*Sus scrofa*]), and species at the urban-wild interface (e.g., coyotes [*Canis latrans*] and raccoons [*Procyon lotor*]). Pathogens that were most prevalent in the literature were vector-borne, including *Trypanosoma cruzi* (Chagas disease) and *Borrelia burgdorferi* (Lyme disease). Zoonotic diseases comprised >50% of the literature reviewed. We acknowledge that, in part, this trend reflects researcher interests and funding opportunities; however, it should not diminish the importance of Texas as a geographically important region with species distributions shifting northward (e.g., the northward movement of vampire bats) and vectors experiencing less seasonality with climate change.

WHAT'S THE SCOOP ON VULTURE POOP: INVESTIGATING THE ROLE OF AVIAN OBLIGATE SCAVENGERS IN THE SPREAD OF CHRONIC WASTING DISEASE (CWD) INFECTIOUS PRIONS

Thursday, 31st July - 12:45: (Salon A) - Poster

Ashlyn Halseth-Ellis [1], ***Levi Heffelfinger*** [2], ***Michael Cherry*** [3], ***Evan Tanner*** [3], ***Ashley Tanner*** [3], ***Rodrigo Moreales*** [4], ***Alynn Martin*** [3]

1. *Ceasar Kleberg Wildlife Research Institute,* ***2.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University- Kingsville,* ***3.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***4.*** *The University of Texas Medical School at Houston*

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy impacting free-roaming and captive cervids across North America. Not only are CWD infections invariably fatal, increases in CWD cases jeopardize economic activity across a wide diversity of stakeholders. Transmission of CWD is thought to be predominantly horizontal through direct contact with excreta of infected hosts and contact with contaminated environments; however, sympatric species that frequently and functionally interact with cervids, such as predators and scavengers, may play a role in CWD spread. While non-obligate scavengers can shed infectious prions in feces, this has not been assessed in obligate avian scavengers, which have unique microbiomes and high potential for long-distance movements prion dispersal. North American vultures, specifically turkey vultures (*Cathartes aura*) and black vultures (*Coragyps atratus*), are obligate scavengers with known diets of CWD susceptible cervid species. This study aims to understand the potential role of turkey and black vultures in the spread of infectious CWD prions. Specifically, we will (1) screen for CWD prions in vulture fecal material in geographic regions with high CWD prevalence in cervids, and (2) assess seeding activity of CWD prions in avian scavenger's fecal material. Our findings will enhance our understanding of scavengers' roles in CWD transmission and infer potential spread into regions where surveillance is limited. Results will also inform current spread mitigation strategies in the context of avian scavenger presence and justifies additional surveillance across vulture ranges where the disease has not yet been documented.

Population genomics of white-tailed deer reveals major rivers and highways as potential barriers to chronic wasting disease spread in Kentucky and Tennessee, USA.

Thursday, 31st July - 12:45: (Salon A) - Poster

Sarah Tomke [1]***, Noelle Thompson*** [2]***, Roderick Gagne*** [1]***, A. S. Apostolopoulos*** [3]***, Matthew Springer*** [4]***, Steven Price*** [4]***, John Cox*** [4]

1. *Wildlife Futures Program, University of Pennsylvania,* ***2.*** *Western Association of Fish and Wildlife Agencies,* ***3.*** *Kentucky Department of Fish and Wildlife Resources,* ***4.*** *University of Kentucky*

White-tailed deer (*Odocoileus virginianus*) positive for chronic wasting disease (CWD) were detected in northwestern Tennessee near the border of Kentucky (USA) in summer of 2021. Because CWD had not yet been detected in Kentucky, a CWD surveillance zone was established. Yet, population parameters that could help inform CWD management was lacking within this now high-risk region. To delineate potential CWD transmission pathways to inform adequate risk-based surveillance and appropriate management actions, we genotyped 3,278 SNPs to investigate the population genetic structure and genetic connectivity of deer in the region. We also assessed the diversity and spatial heterogeneity of polymorphisms in the *PRNP* prion protein gene of 695 deer to determine how high-susceptibility genotypes are distributed across the landscape and to identify populations that are high-risk for CWD transmission. We found that deer were clustered into four admixed genetic clusters generally delineated longitudinally by the Tennessee River and latitudinally by Interstate-69. Admixture clustering models and estimates of genetic differentiation indicated that gene flow is occurring across these barriers; however, the Tennessee River is a stronger barrier to gene flow than I-69. High-susceptibility *PRNP* variants were common in both states, but were generally higher in the eastern Tennessee region. Protective *PRNP* variants were more prevalent in Kentucky, specifically in the eastern Kentucky region. We recommend that management strategies account for these barriers to deer movement and take the necessary actions to deter transportation of deer across these landscape features to mitigate the spread of CWD throughout western Kentucky.

Contact Networks of White-tailed Deer and Their Scrapes: Implications for the Spread of CWD

Thursday, 31st July - 12:45: (Salon A) - Poster

Ian Burke [1]***, Miranda Huang*** [2]***, Steve Demarais*** [1]***, Bronson Strickland*** [3]***, Eric Michel*** [1]***, Gino D'Angelo*** [4]***, Marcelo Jorge*** [4]***, Lisa Jorge*** [4]***, Richard Chandler*** [4]***, Michael Chamberlain*** [4]***, Mark Ruder*** [5]

1. *Department of Wildlife, Fisheries and Aquaculture, Mississippi State University,* ***2.*** *Department of Fisheries, Wildlife and Conservation Biology, University of Minnesota,* ***3.*** *Mississippi State University,* ***4.*** *Warnell School of Forestry and Natural Resources, University of Georgia,* ***5.*** *Southeastern Cooperative Wildlife Disease Study, University of Georgia*

Cervids across North America are threatened by the continuing spread of chronic wasting disease (CWD). As the first prion disease affecting wildlife, creative management and tool implementation is imperative. Natural sites of congregation could be used for environmental sampling. During the breeding season, white-tailed deer (Odocoileus virginianus; WTD), a North American cervid, create communal signposts called scrapes. Scraping behaviors deposit urine, saliva, and nasal secretions, all fluids that shed prions. Real-time quaking-induced conversion (RT-QuIC) testing has identified prions in scrapes. There can be upwards of 211 scrapes per km^2, providing many options for WTD engagement. Popular scrapes, those with higher visitation and more behavioral interactions, may serve as hubs for prion accumulation. During the 2023-2024 breeding season, we ran camera traps at 29 scrapes in Gene Rush Wildlife Management Area, Arkansas. Using data from 1272 WTD scrape interactions we built contact networks of both deer and scrapes. Contact networks show there are hub scrapes, $p < 0.001$, observing greater rates of deer interactions. Likewise, there are WTD that move between an area's scrapes at a high visitation rate compared to their peers, with betweenness scores averaging 38.3 and ranging 0 - 356. Mobile "scrape-happy" deer interact with both hub scrapes and less popular scrapes, increasing connectivity and, if they are shedding prions, exposure potential to all deer, including those not frequenting community hubs. This knowledge increases the understanding of WTD behavioral interactions, with management implications for potentially informing selected removal decisions and highlighting priority areas suited for CWD environmental testing.

Population stability for Davis Mountain Cottontails (S. robustus) post-Rabbit Hemorrhagic Disease Virus 2 (RHDV2) outbreak in western Texas.

Thursday, 31st July - 12:45: (Salon A) - Poster

Hannah Shapiro [1]***, Cole Wzientek*** [1]***, Alynn Martin*** [1]***, Sandra Rideout-Hanzak*** [1]***, Dana Karelus*** [2]***, John Mclaughlin*** [2]***, Scott Henke*** [1]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville, Kingsville,* ***2.*** *Texas Parks and Wildlife Department*

Rabbit Hemorrhagic Disease Virus (RHDV) first emerged in China in 1984 from imported domestic rabbits. The virus quickly spread to the rest of the world through the sale of domesticated rabbits and rabbit products. In 2010, a new variant of RHDV - designated RHDV2 - appeared in France that was genetically distinct from previous variants. RHDV2 has a much wider range of lagomorph hosts and spread through native cottontails and hares in the western United States. The virus spreads quickly and can decimate a rabbit population. There have been several RHDV2 outbreaks in wild rabbit populations across 14 states in the western United States. The recent documentation of RHDV2 in western Texas in 2020 spurred concern about the potential impact on the Davis Mountain Cottontail Rabbits (DMCR), a species of greatest conservation need. Using 50 years of standardized roadside small mammal survey data collected by the Texas Parks and Wildlife Department, we have investigated lagomorph abundance trends across Texas, specifically assessing population trends pre- and post- RHDV2 emergence in western Texas. We documented cyclical peaks that occurred every 5 – 7 years with substantial variability in abundance from 1977 – 2011. There were two noticeable reductions in abundance with the first in 2012 possibly corresponding to the extreme drought conditions and the second reduction in abundance following the RHDV2 outbreak in 2020. Future research will be focused on serosurveillance of DMCR to assess past exposure of RHDV2 and the potential threat the virus poses to this at-risk population.

The Influence of Vegetation Structure on the Prevalence and Intensity of Strongyloid Nematodes Infecting Native Rodents in an African Savanna.

Thursday, 31st July - 12:45: (Salon A) - Poster

***Thaleia Roda* [1], *Minenhle Ngcobo* [2], *Sandra Romao* [3], *Logan Davis* [1], *Gugu Gcinile Simelane* [3], *Sebastian Botero-Cañola* [1], *Robert Fletcher* [4], *Robert McCleery* [1], *Laurence Kruger* [5], *Ara Monadjem* [3], *Samantha Wisely* [1]**

1. *University of Florida,* **2.** *University of Witwatersrand,* **3.** *University of Eswatini,* **4.** *University of Cambridge,* **5.** *University of Cape Town*

The structure and complexity of vegetation cover influence a broad range of ecological processes. One of these processes is pathogen transmission, for which the influence of vegetation structure on host abundance and abiotic conditions can have important effects. Savannas, characterized by a heterogeneous vegetation structure of trees and grasses, are ideal systems to explore the mechanisms relating to disease and habitat structure. Furthermore, as regional defaunation and land management regimes influence the structure of savannas, an understanding of the effects of vegetation structure on pathogen transmission becomes an issue of applied relevance. Here, we assessed the cascading influence of vegetation structure, through host abundance and abiotic conditions, on the prevalence and intensity of Strongyloid nematodes infecting native rodents in a Southern African savanna. We hypothesized that increased vegetation cover will increase nematode prevalence and intensity and host abundance due to protection from sun exposure and host predation. We tested our hypotheses at the Mlawula Nature Reserve in Eswatini with plots simulating different techniques of vegetation management. Sherman traps were used to capture rodents and collect fecal samples inspected for nematode egg counts. Using data collected in 2023 and 2024, we found that canopy diversity had a positive relationship with nematode prevalence while grass and shrub cover had significant relationships with nematode intensity that varied depending on host species. These results will advance our understanding of parasite transmission and host ecology in response to changing landscapes for the improvement of land management in Southern African savannas.

Are white-tailed deer in Pennsylvania dying with or of chronic wasting disease?

Thursday, 31st July - 12:45: (Salon A) - Poster

Jennifer Høy-Petersen [1]***, Justin Brown*** [2]***, Roderick Gagne*** [1]***, W. David Walter*** [3]***, Kevin Niedringhaus*** [1]

1. *Wildlife Futures Program, University of Pennsylvania,* ***2.*** *Department of Veterinary and Biomedical Sciences, Penn State University,* ***3.*** *U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University*

Chronic wasting disease (CWD) is a geographically widespread fatal neurodegenerative disease in cervids. While several pathologies are associated with CWD it is difficult to identify morbidities or lesions caused by CWD in free-ranging deer due to carcass decomposition and scavenging. The aim of this study is to explore associated pathological lesions in white-tailed deer with CWD to define direct and indirect impacts in a CWD endemic area. We outfitted white-tailed deer in Pennsylvania with GPS-collars programmed to emit a mortality signal to promptly retrieve carcasses for a full necropsy with associated ancillary tests to determine the cause of death. Of the 45 white-tailed deer that we have investigated, 69% tested CWD-positive (31/45). All of the deer that died of infectious causes (e.g. pneumonia, sepsis) likely not associated with CWD infection tested positive for CWD (6/6). Additionally, 3/4 (75%) deer that died from vehicle-strike and 7/9 (78%) by predation were CWD-positive. Each deer that had characteristic CWD lesions (e.g. aspiration pneumonia or emaciation) were CWD-positive (4/4 and 3/3, respectively). The only group that had a larger proportion of CWD-negative deer were those shot by hunters (9/15, 60%). These results support previous associations found between lesions and CWD-positive status but also sheds light on other causes of death in a deer population with high CWD prevalence. Moreover, deer in a CWD-endemic region are regularly dying with end-stage CWD which results in carcasses highly concentrated with infectious prions and considered a risk for disease transmission on the landscape.

A landscape of disease: metapopulation dynamics structure the history of disease exposure in desert bighorn sheep

Thursday, 31st July - 12:45: (Salon A) - Poster

Sara Carpenter [1]***, Nicholas Shirkey*** [2]***, Paige Prentice*** [2]***, Brandon Munk*** [2]***, Clinton W. Epps*** [1]***, Brianna Beechler*** [1]***, Anna Jolles*** [1]

1. *Oregon State University,* **2.** *California Department of Fish and Wildlife*

Dynamics of infectious disease in natural populations result from processes across biological scales: pathogens must successfully establish in individual animals, transmit between hosts to establish within a population, and rely on dispersing hosts to move between populations, generating exposure patterns at the landscape scale. However, multi-scale datasets of pathogen exposure patterns in natural populations are rare, limiting opportunities to explore the interplay of factors shaping the occurrence of infectious disease in space and time. We leveraged serological data from 18 populations of desert bighorn sheep (*Ovis canadensis nelsoni)* in southern California to investigate drivers of exposure to ten viral and bacterial pathogens, from individual to landscape factors. Across those pathogens, we found high diversity in patterns of temporal dynamics, spatial distribution, and local abundances when detected. While our analysis showed limited effects of host age, sex, and co-exposed pathogens on seroprevalence patterns, we found significant variation in pathogen presence and seroprevalence between populations. At the population scale, proximity to cattle grazing allotments emerged as the most consistent predictor of pathogen exposure. Presence of neighboring cattle allotments were positively associated with pathogens that were temporally and spatially patchy, suggesting that detection in bighorn may represent spillover from domestic cattle. Population connectivity also correlated with the distribution and abundances of some of the pathogens studied, structuring the landscape into regions that shared similar seroprevalence patterns. Altogether, our study illustrates how population location and network position define the landscape of disease exposure in a natural metapopulation of wild mammals.

Mapping the Host Community of Leptospira in the Eastern Pacific Coastal Ecosystsem Using Novel Genomic Approaches

Thursday, 31st July - 12:45: (Salon A) - Poster

Katie Prager [1], ***Niesa Kettler*** [2], ***Rinosh Mani*** [2], ***Jason Sahl*** [3], ***Nate Stone*** [3], ***David Wagner*** [3], ***James Lloyd-Smith*** [1]

__1.__ University of California Los Angeles, __2.__ Michigan State University, __3.__ Northern Arizona University

Leptospira causes regular outbreaks in California sea lions (*Zalophus californianus;* CSL). Infection has been detected in other marine mammals, but their involvement in transmission and maintenance is unknown. Pathogen genotyping can illuminate epidemiological linkages, but historically has required culture from a fresh sample. We leveraged newly available genomic techniques, applicable to archived or fresh samples, to genotype *Leptospira* from many host species across expanded temporal and spatial ranges. We sought to determine whether infecting genotypes are similar (representing a common source, or circulation of a shared genotype) or distinct (representing separate sources and transmission cycles) across marine mammal species.

Using PCR, we screened 367 samples from 7 pinniped species, harbor porpoises (*Phocoena phocoena*), and southern sea otters (*Enhydra lutris;* SSO). Forty-eight samples were positive, from CSL, SSO, northern elephant seals (*Mirounga angustirostris;* NES), Pacific harbor seals (*Phoca vitulina;* HS), and Steller sea lions (*Eumetopias jubatus;* SSL). PCR and amplicon sequencing of LigB confirmed, for the first time, *L. interrogans* serovar Pomona in NES, HS, SSL, and SSO.

To gain resolution, we conducted DNA enrichment and whole genome sequencing (6 CSL, 3 HS, 7 NES, 1 SSL, 5 SSO). Phylogenetic analyses of whole genome sequences indicated that genotypes infecting non-CSL marine mammals are closely related to isolates from CSL, but are found both within CSL clusters and in distinct clades, suggesting that infection sometimes occurs via spillover from CSL but can also originate from other sources. Our recent detection of closely-related genotypes in terrestrial mesocarnivores in coastal California suggests terrestrial-to-marine spillover.

Evidence of Novel Gastric Helicobacter Species in Stranded Pygmy (Kogia breviceps) and Dwarf (Kogia sima) Sperm Whales on the East Coast of Florida

Thursday, 31st July - 12:45: (Salon A) - Poster

Wendy Marks **[1], *Jessy Castellanos-Gell*** **[2], *Nicole Pegg*** **[1], *David Rotstein*** **[3], *Steve Burton*** **[1], *April Childress*** **[2], *Annie Page*** **[1], *Sushan Han*** **[4]**

1. *Florida Atlantic University, Harbor Branch Oceanographic Institute,* ***2.*** *University of Florida,* ***3.*** *Marine Mammal Pathology Services,* ***4.*** *Denver Zoo*

Gastric spirochetes consistent with Helicobacter spp. were identified in four pygmy sperm whales (Kogia breviceps) and one dwarf sperm whale (Kogia sima) that stranded along the east coast of Florida during 2017–2021. Experimental polymerase chain reaction (PCR) targeting conserved 16S rRNA gene sequences within the Helicobacter genus produced amplification in at least one gastric tissue sample (e.g., forestomach, fundus, pylorus) from all five cases. All PCR-positive samples also contained histologically visualized spiral bacteria. Two different, novel Helicobacter-like sequences were identified in four samples from three whales, although there was not enough sequence alignment to any known Helicobacter spp. sequences to be accurately classified as a known member of this genus. Metabarcoding analysis of gastric tissue samples from three whales resulted in 835 Helicobacter spp. gene hit counts spanning 27 different Helicobacter species, with H. pylori being the most frequent hit. All five whales in this study were infested with gastric nematodes; in four whales, there was one or more of the following histopathologic findings: gastritis, gastric ulceration and gastric fibrosis. These lesions were not attributed as a cause of death in the whales but may have contributed to stranding via reduced fitness. This study represents the first report of Helicobacter spp. bacteria identified in Kogia spp. whales and expands the known host range of this organism. Further studies into these potentially novel Helicobacter spp. should include additional morphological and molecular characterization of the spirochete bacteria and any associated lesions.

Development of Passive Viral eDNA Detection Methods for Mule Deerpox Virus

Thursday, 31st July - 12:45: (Salon A) - Poster

Lillan Maxwell [1], ***Braxton Sizemore*** [1], ***Thien Nguyen*** [1], ***Samantha Wisely*** [2], ***Kuttichantran Subramaniam*** [2], ***Juan Campos-Krauer*** [1]

1. *University of Florida College of Veterinary Medicine,* ***2.*** *University of Florida*

Florida is home of numerous emerging pathogens especially in livestock. These new emerging infections are often associated with high morbidity, mortality, and economic loss. Florida deer farms are at a special risk from these pathogens due to the lack of research and logistical constraints of dealing with cervids such as white-tailed deer (*Odocoileus virginianus*). Of particular concern, Mule Deerpox Virus (DPV) is one of the most common viruses on Florida deer farms and displays a high mortality in fawns up to 3 months. While recently characterized, little about the disease including transmission is unknown and current detection methods are unreliable. To address these research gaps, we first developed a quantitative PCR assay to detect DPV. Second, we addressed the role of insects in the transmission of the virus. Other poxviruses typically transmit mechanically through vectors. With this information, we collected 195 *Muscoid* and 389 *Tabanus* flies from three Florida white-tailed deer farms and tested them for DPV DNA to understand preliminary vector competency. In addition to vector transmission, we developed a passive method of DPV in the environment by testing environmental DNA (eDNA) in 70 soil and 38 fecal samples. These neoteric methods will allow us to diversify our detection of viral pathogens using non-invasive techniques. With this broader understanding of the environment's role in disease transmission we will be able to identify disease presence faster. A greater understanding of poxvirus transmission is extremely important to protect the health of both farmed and wild cervids.

California’s Chronic Wasting Disease Educational Outreach and Surveillance

Thursday, 31st July - 12:45: (Salon A) - Poster

***Liberty Wood* [1], *Linell Hansen* [1], *Alex Heeren* [1], *Brandon Munk* [1]**

1. *California Department of Fish and Wildlife*

Chronic Wasting Disease (CWD) is a fatal neurologic disease of cervids and one of the most important diseases of management concern. In May 2024, CWD was confirmed for the first time in two California deer, one from Madera and the other Inyo County. Following these initial detections, regulations established CWD Management Zones (CMZs) and mandatory testing of hunter harvested deer within those zones. This resulted in a four-fold increase in CWD samples statewide and a 10-fold increase within CMZs. Prior to these detections, the California Department of Fish and Wildlife designed and implemented an educational outreach campaign aimed at deer and elk hunters, meat processors, taxidermists and other agency partners to increase CWD awareness, encourage best practices and improve statewide surveillance. The initial campaign (2022-2024) included surveys, direct mailers, branding, a website redesign and trainings. We saw an increase in overall concern, awareness, and participation among partners but no increase in statewide sampling from year to year until after initial detections. However, successful hunters that received a direct mailer - sampling kit, cover letter, and how-to-guide - were approximately 2x more likely to submit a sample before and after initial detections. These were the top 2% of successful hunters as determined by 8 years of harvest reports and may be a good subset of hunters to focus outreach efforts to increase surveillance participation. Active outreach and engagement activities helped raise awareness of CWD before it was detected and allowed for rapid response to understand the outbreak and mitigate potential risks.

From Theory to Action: Insights from a Systematic Review of Chronic Wasting Disease Management Strategies

Thursday, 31st July - 12:45: (Salon A) - Poster

Sarah Robinson [1]***, Erica Dong*** [1]***, Cait Nelson*** [2]***, Caeley Thacker*** [3]***, Kaylee Byers*** [1]

1. *Simon Fraser University,* ***2.*** *BC Ministry of Forests, Lands and Natural Resource Operations,* ***3.*** *Government of British Columbia*

Chronic Wasting Disease (CWD) is a highly contagious and fatal prion disease affecting cervids (deer, elk, moose, and caribou). Its emergence in British Columbia in January 2024 underscores the urgent need for evidence-informed management strategies to mitigate its negative impacts on wildlife and communities. We conducted a systematic literature review to identify management strategies that have been implemented or recommended and to describe evidence of their success. We searched the peer-reviewed literature across three databases (PubMed, Web of Science, and Scopus) using the terms “CWD” or “chronic wasting disease,” combined with “management,” “human dimensions,” “risk,” “risk perception,” “perceive* risk,” or “perception.” This search yielded 4,354 manuscripts. After removing duplicates, 3,180 were screened for relevance. Based on our inclusion criteria, 194 were included. Most studies were theoretical (175), with few evaluating implemented management measures. For example, several studies used mathematical models to project disease spread under different cervid reduction strategies to inform management decisions. Applied studies were limited in scope, focusing almost exclusively on culling and harvest. To address the complexity of CWD, experts suggested implementing multiple concurrent measures, such as population reductions and regulations on carcass transport. There was strong consensus on the need to engage rightsholders, hunters, and other collaborators in management, with community support recognized as essential for program sustainability. This review highlights the importance of tailoring management strategies to local biological, environmental, and social contexts to enhance their relevance and effectiveness. Future research should engage a broader range of rightsholders and collaborators, mapping groups affected by and involved in CWD responses to identify priority populations and document potential impacts. Leveraging Implementation Science, evaluating the application and effectiveness of these context-specific approaches will be essential for developing sustainable and responsive management solutions.

A One Health Risk Framework Towards CWD Management in Saskatchewan

Thursday, 31st July - 12:45: (Salon A) - Poster

Iga Stasiak [1]***, Daphne Murphy*** [1]***, Graeme Mansfield*** [2]***, Wendy Wilkins*** [2]***, Julie Kryzanowski*** [3]***, Nicole White*** [3]***,***
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1. *Saskatchewan Ministry of Environment,* ***2.*** *Saskatchewan Ministry of Agriculture,* ***3.*** *Saskatchewan Ministry of Health*

Chronic wasting disease (CWD), an infectious fatal prion disease affecting mule deer, white-tailed deer, elk, moose, and caribou, is considered to be the most important disease threatening North American cervids (Association of Fish and Wildlife Agencies, 2018). It represents a significant threat to the health and sustainability of free-ranging wildlife populations in Saskatchewan. The prion that causes CWD in cervids has not been identified as causing disease in humans, however, potential for transmission to humans cannot be excluded. As a precaution, Health Canada and the World Health Organization recommend that people not eat meat or other parts of a CWD-infected animal. The disease poses a risk to hunting recreation as well as food security for Indigenous communities, whose diet depends on traditional foods such as wild game meat. In 2023-24, the Ministries of Health, Agriculture, and Environment collectively developed a new One Health risk assessment framework to assess the risks of CWD to stakeholders, rights-holders, and the province; to assess both costs and benefits of a suite of potential management actions to minimize disease impacts; and to evaluate residual risk to the province under various management regimes. Concurrently, Indigenous engagement was undertaken to better understand the significance of CWD to Indigenous communities and ensure their perspectives are considered in management planning.

Wild Cats and Wiggly Critters: Parasitic Insights from the Scat of Ocelots (Leopardus pardalis) and Bobcats (Lynx rufus) of the Southern United States

Thursday, 31st July - 12:45: (Salon A) - Poster

Tiffany Pope [1]***, Alynn Martin*** [2]***, Ashley Reeves*** [3]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville,* ***2.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***3.*** *East Foundation*

Parasites have varying physiological effects on their hosts including reduced nutrient absorption, decreased blood cell activity, and damage to host tissues. These impacts from parasite presence can be compounded by other internal (e.g., genetic inbreeding) and external (e.g., environmental) factors, which may increase morbidity. 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 endoparasite profiles and identify parasites of greatest concern for these two wild felid species. Further, we aim to understand the overlap of parasite communities between bobcats and ocelots. Fecal flotation was conducted on 48 felids (ocelots, n=17; bobcats, n=31) spanning four years (2019-2022). Helminths were observed in 100% of ocelots and 94% of bobcats, while protozoa were observed in 59% of ocelots and 55% of bobcats sampled. The most common intestinal parasites observed were the helminths *Toxascaris leonina* (ocelots) and *Ancylostoma* spp. (bobcats), both of which are considered pathogenic in felines. These findings provide a better understanding of the felid population's susceptibility to parasitism and assist in planning strategies that aid in reducing or preventing transmission of parasites.

New Techniques to Optimize Real-Time Quaking Induced Conversion for Chronic Wasting Disease Detection in White-Tailed Deer Feces

Thursday, 31st July - 12:45: (Salon A) - Poster

Madison Davis [1]***, Jennifer Høy-Petersen*** [1]***, Roderick Gagne*** [1]***, Michelle Gibison*** [1]

1. *Wildlife Futures Program, University of Pennsylvania*

A concerning disease of North American cervids is caused by an infectious protein that results in a fatal, neurodegenerative disease known as Chronic Wasting Disease (CWD). As CWD continues to spread rapidly across North America, new detection methods are needed more than ever to assess the prevalence of CWD in live animals and across the landscape. Detecting CWD prions in the excreta of cervids remains difficult, as inhibitors within feces and intermittent prion shedding result in lower sensitivity and specificity with the amplification assay real-time quaking induced conversion (RT-QuIC) compared to its use with other tissue types. To overcome these barriers, we propose a modification to previous fecal homogenization methods to enhance sensitivity and specificity by scraping the outer surface region from white-tailed deer fecal pellets. As feces pass through the intestinal tract, they will contact the intestinal mucosa, where prions are likely shed, therefore allowing more intestinal mucosal cells to be incorporated into the fecal homogenate. This homogenization method may also reduce fecal inhibitors that whole pellet homogenization may have with the RT-QuIC assay. Our results show improved sensitivity and specificity using this method. Using this approach fecal RT-QuIC is possible without prior use of protein cyclic amplification assay (PMCA). By effectively detecting CWD prions in feces, testing methods using feces in a non-invasive antemortem manner or from the environment could be implemented along with CWD diagnostics to enhance surveillance and improve management decisions.

Phthalate esters (plasticizers) in dead southern right whales (Eubalaena australis) at Península Valdes, Argentina.

Thursday, 31st July - 12:45: (Salon A) - Poster

Luciana Gallo [1], Melina Paola Michlig [2], María Rosa Repetti [2], Agustina Donini [3], Mariano Sironi [4], Marcela Uhart [5]

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Southern right whales (SRW, *Eubalaena australis*) use the waters off Peninsula Valdés (PV), Argentina, mainly as a winter breeding area, yet feeding events during spring are increasingly recorded. Although the ingestion of plastic debris has been documented in this population, the transfer and accumulation of plastic additives has not been studied to date.Here, three phthalate esters (PAEs), dimethyl phthalate (DMP), dibuthyl phthalate (DBP), and diethylhexyl phthalate (DEHP), were quantified in the blubber of 13 whales (three calves, three juveniles and seven adults, one of these a male) stranded dead in 2021 at PV. Gas chromatography coupled with tandem mass spectrometry was used for its determination, with quantification limits (LOQs) at 10 ng/g dw for DMP and 50 ng/g dw for DBP and DEHP. Our results indicate that DMP was detected in six (46.2%) whales (one calf, three adult females, one adult male, and one juvenile; all at levels <LOQ). DBP was detected in four (30.8%) whales (two calves, one adult female, and one juvenile; 23.1% at quantifiable levels and 7.7% at levels <LOQ), with median concentrations at 213.3 ng/g dw (range=LOQ-438). DEHP was detected in eight (61.5%) whales (three calves, three female adults, and two juveniles; 46.1% at quantifiable levels and 15.4% at levels <LOQ), with median concentrations of 304.0 ng/g dw (range=LOQ-2605). At least one PAE was above the LOQ in 6/13 samples, and the simultaneous occurrence of all PAEs was observed in one calf. These findings reveal exposure and potential for accumulation of plasticizers in SRW, providing relevant context for understanding sources of plastic pollution and potential health effects from exposure. More samples are available to evaluate PAEs transfer between mothers and calves, assess exposure by age/sex, identify trends over time and compare with other mysticetes worldwide. This is the first report of PAEs in blubber of SRW.

Epidemiological Features, Genome Characteristics, and Antimicrobial Resistance of Trueperella pyogenes Isolated from Farmed White-tailed Deer (Odocoileus virginianus) in Florida

Thursday, 31st July - 12:45: (Salon A) - Poster

***An-Chi Cheng* [1], *Austin Surphlis* [1], *Kuttichantran Subramaniam* [1], *John Lednicky* [1], *KwangCheol Jeong* [1], *Samantha Wisely* [1], *Juan Campos-Krauer* [2]**

***1.** University of Florida, **2.** University of Florida College of Veterinary Medicine*

Trueperella pyogenes is a gram-positive, facultatively anaerobic bacterium known to cause infections in both domestic and wild animals, including white-tailed deer (WTD; *Odocoileus virginianus*). However, limited studies have focused on its impact on farmed WTD. In this study, we aimed to explore the epidemiological features, antimicrobial resistance (AMR) profiles, and virulence factors of *T. pyogenes* isolated from farmed WTD in Florida. Between 2016 and 2023, we managed 831 cases involving deceased farmed WTD. Specimens from 715 animals were subjected to bacterial culture. *T. pyogenes* was isolated from 147 (20.6%) animals, ranking as the second most commonly isolated bacterial pathogen after *Escherichia coli*. All *T. pyogenes*-infected animals exhibited pneumonia. *T. pyogenes* infection cases were notably more prevalent during summer and fall. Between September 2020 and May 2022, a total of 37 isolates from various specimen types, collected from 30 diseased deer, were analyzed using whole-genome sequencing and phylogenetic analyses. The results revealed significant genetic diversity among the *T. pyogenes* strains. Antimicrobial resistance profiling identified a predominance of genes conferring resistance to tetracyclines. Notably, 32.4% of the strains lacked any detectable AMR genes. Genes for several virulence factors were also identified, including pyolysin (plo), collagen-binding protein (cbpA), and various adhesion molecules. This study emphasizes the importance of developing comprehensive disease management strategies that include routine surveillance, targeted antimicrobial use, and enhanced farm management practices to mitigate the risk of *T. pyogenes* transmission in the population.

Mycoplasma ovipneumoniae strain types in Arizona, USA: Spatiotemporal trends inform risk assessments

Thursday, 31st July - 12:45: (Salon A) - Poster

Anne-Justice Allen [1]

1. *Arizona Game and Fish Dept.*

Bighorn sheep pneumonia has caused periodic all age mortality events and low lamb recruitment in several regions of Arizona. Since 2009, the Department has used strain-typing of *Mycoplasma ovipneumoniae* bacteria as part of routine herd health assessments and to guide translocation plans. In an all age mortality event in 2015 in the Black mountains of northwestern Arizona, we identified the incursion of strain originally detected in the Marble Mountains, California and Spring Range, Nevada in 2013. This strain was then replaced by another strain of unknown origin in 2017. In the early 2000s, the Kofa mountain population experienced a population decline of 50 percent accompanied by an increase in the seroprevalence to *M. ovipneumoniae*. Since then, we have detected 3 different strains of *M. ovipneumoniae*. These strains appear to possess a low level of pathogenicity as the population has recovered to pre-decline numbers. In the early 2000s, disease was also detected in the Kanab Creek region of the north rim of the Grand Canyon. Several strains have been detected in subsequent years; these strains appear to have a significant level of pathogenicity as this population continues to under perform with low levels of recruitment. In all, 19 strains with distinct geographic distributions have been identified in Arizona bighorns managed by the Department. Collar data has demonstrated that many Arizona bighorn sheep populations are connected to populations managed by other agencies. In order to effectively manage disease in bighorn sheep, we should establish regional data-sharing agreements and management objectives.

Exploring Toxoplasma gondii prevalence and impact on survival and fawn quality of a popular game species

Thursday, 31st July - 12:45: (Salon A) - Poster

Kendall Bancroft [1]***, Alynn Martin*** [1]***, Tyler Campbell*** [2]***, Randy DeYoung*** [1]***, Aaron Foley*** [1]***, David Hewitt*** [1]***,***
Miranda Hopper [1]***, Kevin Lovasik*** [1]***, Alfonso Ortega*** [1]***, Landon Schofield*** [2]***, Bryan Spencer*** [1]***, Jason Sawyer*** [2]***,***
Michael Cherry [1]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***2.*** *East Foundation*

Toxoplasmosis (*Toxoplasma gondii*) is a zoonotic disease, causing significant but often overlooked morbidity worldwide. In wildlife, *T. gondii* infection may influence reproduction and behavior, including increased risk of abortion, tendency for aggression, and abnormal movement. Less understood is whether *T. gondii* impacts host survival or influences population dynamics. We captured and radiomarked white-tailed deer (*Odocoileus virginianus*) on rangelands in South Texas, USA and assessed survival of does and offspring based on doe serostatus during 2020–2023. Serology revealed 29 of 59 (49%) radiomarked does had a titer ≥1:25 on a modified agglutination test and were considered seropositive. Annual survival of seropositive and seronegative does ranged from 70-100% and 85-100%, respectively. Adult survival was high except during 2022, a year with harsh winter and drought, when survival of seropositive does was lower (70% vs. 85%). Across all years, fawn survival did not significantly differ. However, in 2021, a year with above-average rainfall, fawns from seropositive does had lower survival (20% vs. 46%). Birth weight and hindfoot length, proxies for fawn quality and condition, were not influenced by doe serostatus. These trends suggest *T. gondii* may compound external stressors on adult deer in poor conditions but more noticeably when range conditions were favorable during fawning, survival of fawns from seronegative does increased while fawn survival from seropositive does remained low. Further research is needed to understand *T. gondii's* impact on survival, recruitment, and behavior in wildlife and its potential risk to human health.

PARASITISM IN QUAIL: WHAT WE KNOW AND SHOULD WE BE CONCERNED?

Thursday, 31st July - 12:45: (Salon A) - Poster

Liza Soliz [1], Andrea Montalvo [2], Stephanie Shea [3], Andrew Olsen [4], Stacie Villarreal [5], Nicole Traub [6], Maedean Cardenas [1], Alan Fedynich [7], Dale Rollins [8], Ryan Luna [9], Fidel Hernandez [1], Alynn Martin [1]

1. Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville, 2. East Foundation, 3. The University of Maine, 4. Intermountain West Joint Venture, 5. Texas A&M University-AgriLife, 6. Huntington Learning Center of Georgetown, 7. Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, 8. Rolling Plains Quail Research Foundation, 9. Borderlands Research Institute, Sul Ross State University

North American quail have been experiencing population declines, attributed to habitat loss and shifting climatic conditions. However, even in areas with ample habitat and years of above-average precipitation, quail populations still exhibit below-expected abundance. Parasitic helminths, such as eyeworms (*Oxyspirura* petrowi) and cecal worms (*Aulonocephalus* pennula), have been hypothesized as potential contributors to these declines. A general trend arising from over a decade of research suggests that a spatial gradient exists in eyeworm prevalence, with prevalence decreasing from North Texas to South Texas, and no such gradient observed for cecal worms. Beyond this spatial gradient, little is known about factors driving differences in prevalences observed between North and South Texas. We conducted a meta-analysis to explore quail parasitism trends between northern and southern Texas. We collated a 10-year dataset (2007−2019) of hunter-harvested and live-trapped northern bobwhites and scaled quail using raw data from past studies. Histograms of prevalence (% infected) and intensity (no. worms/infected bird) were generated by region and through time. Our data supported the spatial gradient in eyeworm prevalence between northern (54%) and southern (4%) Texas; however, intensity was low in both regions (most birds infected with <10 worms). Prevalence of cecal worms was relatively high in both regions (65% northern Texas and 81% southern Texas), as well as intensity (few birds possessing low worm burdens <10). These data raise the question whether cecal worms should be of greater concern than eyeworms.

Identifying and Diagnosing Two Distinct Species of Carotid Worms Infecting Wild Cervids in Wyoming, USA

Thursday, 31st July - 12:45: (Salon A) - Poster

***Kara Robbins* [1], *Samantha Allen* [1]**

1. *Wyoming Game and Fish Department*

Elaeophora schneideri (the carotid worm) is a filarial nematode that parasitizes moose (*Alces alces)*, deer (*Odicoileus* spp.), elk (*Cervus canadensis*), and other wild ruminants in North America. Heavy parasite loads in the carotid arteries along with larvae migrating through the bloodstream can restrict blood flow to tissues of the head and neck and contribute or directly lead to mortality in moose. Because our ability to detect and track these infections is limited to finding adult worms grossly post-mortem, our objective was to develop a qPCR test to detect carotid worm infections from both ante- and post-mortem tissues to establish surveillance in Wyoming cervids.

Adult carotid worms were collected from across Wyoming from free-ranging moose, mule and white-tailed deer during post-mortem examination. Samples were analyzed using both DNA barcoding with Sanger Sequencing analysis and Next Generation Sequencing with variant comparison analysis. Two distinct species of *Elaeophora* sp. were identified and a multiplex qPCR was developed to detect and differentiate between the two species. From there, this qPCR test was run on carotid worms from deer and moose as well as tissues (brain, 3rd eyelid, or facial tissue) collected from moose post-mortem. All deer samples (n=7) were identified as *E. schneideri*, however out of the moose samples (n=19), 3 were *E. schneideri* and 16 were *Elaeophora* sp.

This research has identified the complexity of a rarely studied species of parasite and more work is needed to determine the potential pathogenesis of each species in individual hosts.

Pathologic, serologic, molecular and preliminary epidemiologic characterization of leptospirosis in southern sea otters (Enhydra lutris nereis)

Thursday, 31st July - 12:45: (Salon A) - Poster

Padraig Duignan [1]***, Margaret Martinez*** [1]***, Mike Murray*** [2]***, Cara Field*** [1]***, Mani Rinosh*** [3]***, Katie Prager*** [4]***, James Lloyd-Smith*** [4]***, Mary Gomes*** [5]***, Melissa Miller*** [5]

1. *The Marine Mammal Center,* ***2.*** *Montery Bay Aquarium,* ***3.*** *Michigan State University,* ***4.*** *University of California Los Angeles,* ***5.*** *Marine Wildlife Veterinary Care and Research Center, California Department of Fish and Wildlife, Santa Cruz, CA, USA*

Leptospirosis causes periodic outbreaks among California sea lions (CSLs) and sporadic phocid deaths, but it is unknown among sympatric southern sea otters (SSOs). As sentinels of California estuarine and coastal health, the goal was to determine whether leptospirosis contributes to SSO mortality. A retrospective search (2005-'23) for cases with renal or hepatic pathology found 17 candidates. Gross lesions were generally unremarkable and only 4/16 had tubulointerstitial nephritis and necrosis consistent with leptospirosis. Other lesions were non-specific nephritis (septicemia, 2), chronic infarction (1), bile nephropathy (microcystin toxicosis, 2), incidental non-specific mild interstitial nephritis (4), and mild age-related glomerulopathies (3). Immunohistochemistry (IHC) for leptospiral antigen was positive for the 4 suspecs. Livers had incidental lymphoplasmacytic and neutrophilic portal hepatitis (6), random hepatitis (septicemia, 3), or centrilobular necrosis (microcystin toxicosis, 6). IHC was negative for all livers. The four suspect cases had high antibody titers against *L. interrogans* serovar Pomona, the common serovar in CSLs, four others were weakly positive against either *L. interrogans* serovar Icterohemorrhagiae or *L. interrogans* serovar Hardjo. The latter cases are likely serologic cross-reactivity. PCR was positive for pathogenic *Leptospira* spp. on 12/17 and most (10/12) were adults without sex bias. Cases were mostly clustered from January to June (wet season) and most (10/12) were from the greater Monterey Bay region. In conclusion, leptospirosis causes mortality in SSOs and based on PCR, they can, like CSLs, be asymptomatic carriers. *L. interrogans* serovar Pomona is found in both hosts suggesting that further investigation is needed to understand disease transmission dynamics.

LACK OF EVIDENCE FOR EYEWORM AND CECAL WORM DRIVING QUAIL CONDITION AND POPULATION DYNAMICS

Thursday, 31st July - 12:45: (Salon A) - Poster

Maedean Cardenas [1] ***, Fidel Hernandez*** [1] ***, Liza Soliz*** [1] ***, Andrea Montalvo*** [2] ***, Stephanie Shea*** [3] ***, Andrew Olsen*** [4] ***, Stacie Villarreal*** [5] ***, Nicole Traub*** [1] ***, Alan Fedynich*** [6] ***, Dale Rollins*** [7] ***, Ryan Luna*** [8] ***, Alynn Martin*** [1]

1. *Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville,* ***2.*** *East Foundation,* ***3.*** *The University of Maine,* ***4.*** *Intermountain West Joint Venture,* ***5.*** *Texas A&M University-AgriLife,* ***6.*** *Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville,* ***7.*** *Rolling Plains Quail Research Foundation,* ***8.*** *Borderlands Research Institute, Sul Ross State University*

Over the last decade, northern bobwhite (*Colinus virginianus*) populations across Texas have experienced perceived declines despite favorable climatic conditions. The lack of response of quail populations to favorable environmental drivers, such as precipitation, has led to speculation that other factors may be driving quail population dynamics. Rising concerns surrounding quail species' stability in Texas have fueled research efforts focused on identifying the cause of declines, and two parasitic helminths— eyeworms (*Oxyspirura petrowi*) and cecal worms (*Aulonocephalus pennula*)—have been implicated. However, no data exist linking helminth presence to population declines or condition decline in individual quail. We investigated the impact of worm burden on quail at both the population and individual scale. We leveraged 12 years of quail abundance data and ten years of quail body mass data from Texas to assess the impact of helminth burden on each. Body mass is an indicator of individual condition and can be used as a proxy for health status. We documented 1) weak and inconsistent correlations between helminth burden and quail abundance in various regions of the state at the population scale, and 2) no relationship between helminth burden and body mass at the individual scale. These results will represent a foundation on which to build our understanding of the impact of helminths on quail and their role in driving population dynamics.

Acute multisystemic sarcocystosis due to Sarcocystis alceslatrans in a wild elk calf (Cervus canadensis) in Washington State, USA

Thursday, 31st July - 12:45: (Salon A) - Poster

Emmalina Wineland [1], ***Holly Drankhan*** [1], ***William Moore*** [2], ***Mark Vekasy*** [2], ***Paul Wik*** [2], ***Kristin Mansfield*** [2], ***Kyle Taylor*** [3]

1. *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University,* ***2.*** *Washington Department of Fish and Wildlife,* ***3.*** *Washington State University*

As part of a surveillance study on survival and mortality of juvenile elk, a 3.5-month-old female elk (*Cervus canadensis*) calf was submitted for necropsy in September 2021, having died while under radio-collar monitoring with no outward evidence of predation. Histopathological examination revealed severe suppurative and histiocytic interstitial pneumonia, mild necrotizing encephalitis, and mild glossitis, each associated with intraendothelial schizonts, as well as multisystemic hemorrhage. The schizonts were determined to be over 99% similar to *Sarcocystis alceslatrans* based on PCR and DNA sequencing of the 18S ribosomal RNA gene utilizing universal *Sarcocystis* primers. PCR performed for *Toxoplasma* and *Neospora* spp. were negative. Mortalities attributed to sarcocystosis have rarely been reported in other cervids, including a captive white-tailed deer from an unknown species of sarcocyst and a wild moose calf due also to *Sarcocystis alceslatrans* . In both cases, environmental exposure to large infective doses was hypothesized as the cause of overwhelming infection; however, the age of this animal also warrants consideration of immunodeficiency.

Effects of parasite co-infection on disease dynamics of Sin Nombre hantavirus in deer mice (Peromyscus maniculatus)

Thursday, 31st July - 12:45: (Salon A) - Poster

Madeline Rowland [1], ***Angela Luis*** [1]

1. *Population and Disease Ecology Lab, University of Montana*

Wildlife populations are exposed to diverse communities of interacting parasites, where co-infection is the rule rather than the exception. As human activities continue to alter parasite distributions and expose wildlife to new combinations of parasites and pathogens, it is increasingly important to understand the mechanistic effects of co-infection on disease dynamics in wildlife populations. This requires moving beyond the traditional focus on single pathogen - single host systems. For this study, we use infection of Sin Nombre hantavirus (SNV) in deer mice (*Peromyscus maniculatus*) in Montana as a model system to determine mechanistic effects of parasite co-infection on disease dynamics of SNV in its reservoir host. First, we assess direct effects of helminth-only infection and SNV-only infection on deer mouse condition and immune response. Then, we estimate indirect effects of helminth infection on SNV infection in deer mice with host condition and immune response as mediators. Methods include small mammal capture-mark-recapture in Montana, removal of deer mice for dissection to identify and quantify adult helminth infection, serological assays to determine SNV serostatus, cytological assays of blood smears to assess immune response, and structural equation modeling of weight and size measurements to estimate condition. Data collection and analyses are currently in progress, and preliminary results will be presented at the conference. Results from this study will improve our understanding of ecological drivers and within-host interactions of co-infecting parasites in the deer mouse – SNV model system. Additionally, it will advance our knowledge of the mechanistic effects of co-infection on disease dynamics in wildlife populations.

Portrait of viral communities in deer upper respiratory tracts across the United States

Thursday, 31st July - 12:45: (Salon A) - Poster

Axel Hoarau [1], ***George Wittemyer*** [2], ***Guillaume Bastille-Rousseau*** [3], ***Travis Gallo*** [4], ***Jennifer Mullinax*** [4], ***Meggan Craft*** [5], ***Jennifer Malmberg*** [6], ***Todd Nordeen*** [7], ***Georgia Titcomb*** [2], ***Maria Diuk-Wasser*** [8], ***W. David Walter*** [9], ***Daniel Grove*** [10], ***Lisa Muller*** [10], ***Mark Wilber*** [10], ***Kezia Manlove*** [11], ***Kim Pepin*** [6], ***Roderick Gagne*** [1]

1. *Wildlife Futures Program, University of Pennsylvania,* ***2.*** *Colorado State University,* ***3.*** *Southern Illinois University,* ***4.*** *University of Maryland,* ***5.*** *University of Minnesota,* ***6.*** *USDA National Wildlife Research Center,* ***7.*** *Nebraska Game and Parks Commission, Alliance,* ***8.*** *Columbia University,* ***9.*** *U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University,* ***10.*** *University of Tennessee,* ***11.*** *Utah State University*

North American deer have an increasing number of pathogens, some that threaten deer populations and others that are zoonotic. For instance, a growing number of pneumonias with unknown etiology have been reported as well as evidence that deer are a reservoir for SARS-CoV-2. In this study, we use a metagenomic approach to characterizing viral communities in white-tailed deer (*Odocoileus virginianus*) and mule deer (*O. hemionus*) upper respiratory tracts across the United Sates. We tested a total of 210 nasopharyngeal swabs collected in nine states and 14 locations representing a variety of geographical contexts (*e.g.*, rural *versus* urban populations, different environments, interaction with humans *versus* interaction with domestic animals). Our aims were to (1) identify known and unknown/rare pathogens, (2) understand how geography shapes viral communities, and (3) compare results among species. Our preliminary results reveal the presence of expected (*e.g.*, SARS-CoV-2) and less expected viruses (*e.g.*, an Aphthovirus). They also indicate variations in viral communities based on the species and on the location where deer were sampled. Our findings contribute to a better understanding of deer pathogens within the United States and ultimately will inform management of pathogens for the health of deer and humans.

Sex-Ratio of Dioecious Acanthocephalan Endoparasites In Harbor Seal (Phoca Vitulina) Hosts

Thursday, 31st July - 12:45: (Salon A) - Poster

***Jasper Nevis* [1], *Hannah Tucker* [1]**

***1.** University of Washington*

The Acanthocephala are a phylum of parasitic worms commonly found in the gastrointestinal tracts of mammals and birds. They are dioecious, having distinct male and female sexes. Despite their frequent occurrence, there is little research describing the ratio of sexes in acanthocephalans infecting marine mammals. Understanding the life cycles and life history traits of parasites is important to understanding the ecosystem as a whole. This study aims to determine the sex ratio of Corynosoma spp. infecting harbor seals, which will increase knowledge of transmission and reproduction within harbor seals and potential intraspecific competition between acanthocephalans. The results from this study will be used within a larger project to calculate the energetic burden that endoparasites have on their hosts and help inform seal and parasite conservation efforts. To do this, we will first determine key morphological differences (size, weight, body shape, and number of spines) between the sexes, then count the numbers of males and females present in each seal's gastrointestinal tract. We will calculate the ratio of male to female acanthocephalans within each individual harbor seal and use those values to generate an average sex ratio for acanthocephalans across all sampled harbor seals. Finally, average weights will be determined for each sex to help confirm if there is a size difference between sexes and determine relative biomass differences across the sexes within harbor seal hosts.

The science behind the scent – An interdisciplinary approach to understanding how chronic wasting disease influences feces from white-tailed deer leading to discrimination of disease status by canines.

Thursday, 31st July - 12:45: (Salon A) - Poster

Michelle Gibison [1]***, Amalia Berna Perez*** [2]***, Dawei Dong*** [3]***, Amritha Mallikarjun*** [4]***, Casey Maynard*** [5]***, Brenna Aizen*** [1]***, Anna Kashina*** [6]***, Cynthia Otto*** [4]***, Audrey John*** [2]***, Julie Ellis*** [5]

1. *Wildlife Futures Program, University of Pennsylvania, PennVet,* ***2.*** *Division of Infectious Diseases - Children's Hospital of Pennsylvania,* ***3.*** *Penn Institute for Biomedical Informatics - Perelman School of Medicine,* ***4.*** *Penn Vet Working Dog Center, University of Pennsylvania, PennVet,* ***5.*** *Wildlife Futures Program, University of Pennsylvania,* ***6.*** *Department of Clinical Sciences and Advanced Medicine, University of Pennsylvania*

Chronic wasting disease (CWD) is an ever-expanding threat to both wild and captive cervids. Management of the disease is compounded by its ability to spread directly and indirectly, be shed and persist in the environment, and cause the invariable fatal outcome of infected individuals. Agencies are challenged to sample significant numbers of individuals to detect the disease, but these efforts are hampered by the costs, sample numbers, test turnaround times, and the fact that only post-mortem sampling is currently approved for testing. Developing antemortem and landscape-scale detection methods could become a critical game changer in CWD diagnostics and management. In collaboration with multiple state and federal agencies along with departments across the University of Pennsylvania, we are addressing this need by studying how CWD affects its host and leads to systemic changes in white-tailed deer, including changes in their fecal microbiome and associated volatile organic compound (VOC) profiles. Our team discovered that CWD leads to significant changes in the fecal microbiome and VOC profiles, and that canines can discriminate between feces from CWD positive and negative animals. Changes to the microbiome and VOC profiles occurred gradually with disease progression but remained distinct enough for molecular detection and canine discrimination. Interestingly, the VOC fingerprints and fecal microbiome changes differ significantly between captive and wild cervids, suggesting that factors such as diet and ecology may play additional roles in disease progression. The long-term goal of this collaborative project is to develop new, potentially rapid, antemortem or environmental diagnostics for CWD detection in the field.

Dogs and Cats Infected with Bat Rabies Virus Variants—United States, 2012–2021

Thursday, 31st July - 15:00: (Salon A) - Poster

Natalie Bauer [1], ***Samir Koirala*** [2]

1. University of Pennsylvania School of Veterinary Medicine, 2. Nebraska Department of Health and Human Services

Investigating broad impacts of a public health concern often requires multi-institutional collaboration and communication across local, state, and federal agencies. The number of rabid US dogs and cats infected with bat rabies virus variants (RVVs) is unknown. We collaborated with the CDC Rabies Team and state and local health departments to advance our epidemiologic understanding of this zoonotic disease through a One Health approach.

Using 2012–2021 US National Rabies Surveillance System (NRSS) data, we identified 30 dogs (n = 7) and cats (n = 23) from 15 states infected with eight distinct bat RVV strains. Twenty cases were reported to NRSS, with 10 additional cat cases discovered during validation with state officials. Just 10% (3/30) were ever-vaccinated for rabies but not current; 90% (27/30) were never-vaccinated or unknown. Of 99 subsequently exposed animals, only 13 were ever-vaccinated and the remaining 86 unvaccinated animals were either euthanized (54/86), required lengthy quarantine (22/86), or were lost to follow-up (10/86). With 83% (25/30) of cases exposing people, 92 humans required post-exposure prophylaxis, costing an estimated $747,891.

We demonstrate dogs and cats are infected with bat RVVs more than previously recognized. Given the importance of bats in our shared ecosystem and ever-growing wildlife interaction, failure to vaccinate pets constitutes a considerable public health threat. Collaboration among partners across the nation helped elicit findings that can be leveraged to raise community awareness for risks of this deadly yet preventable zoonotic disease through communication and education to help promote increased rabies vaccination compliance in clinical practice.

A summary of investigations of Pasteurella multocida in bighorn sheep respiratory disease

Thursday, 31st July - 15:00: (Salon A) - Poster

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The bighorn sheep respiratory disease complex, like all diseases, involves interactions between the host, environment, and pathogens. One of the bacterial components of the disease, *Pasteurella multocida*, is commonly detected in respiratory tissues from affected animals, but is often dismissed as normal flora. However, *P. multocida* possesses numerous virulence factors, is considered a primary pathogen for diseases among a wide range of hosts, and may be important in at least some instances of bighorn sheep respiratory disease. Over the past decade, we have examined the role of *P. multocida* in bighorn sheep respiratory disease in Colorado. Using retrospective PCR-based methods we found a strong association between the detection of *P. multocida* and the presence of upper respiratory lesions. To investigate a possible causative role for *P. multocida* in the development of upper respiratory lesions, we conducted an experimental inoculation study in captive bighorn sheep, with equivocal results. To investigate a possible association between specific strains of *P. multocida* (and/or other bacterial pathogens) and disease patterns, we developed a multilocus strain typing (MLST) assay. We are using that assay to examine respiratory samples from free-ranging Colorado bighorns, collected over the past 15 years. The interpretation of findings to date indicate that *P. multocida* is likely present, perhaps at undetectable levels, in the normal flora of bighorn sheep, but that *P. multocida* is more readily detectable in cases of chronic respiratory disease and may be useful as a diagnostic indicator of chronic respiratory disease.

Retrospective Study of Causes of Mortality of Chelonians Submitted to the Southeastern Cooperative Wildlife Disease Study, 1981-2018

Thursday, 31st July - 15:00: (Salon A) - Poster

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Chelonians are a diverse reptilian order that serve as indicators of ecosystem health, yet are underrepresented in wildlife health surveillance. Chelonian population declines are often attributed to pathogens and contaminants. Understanding these threats to wild turtle health is critical to inform conservation and management efforts. The objective of this retrospective study was to explore causes of morbidity and mortality in free-living chelonians based on 37 years of diagnostic data at the Southeastern Cooperative Wildlife Disease Study (SCWDS). Specifically, we aimed to determine and categorize causes of mortality to analyze potential demographic, spatial, and temporal associations. We reviewed all chelonid case submissions to SCWDS from August 1981-2018. Turtles underwent post-mortem evaluation, including gross and histopathology and ancillary testing to determine causes and contributors to death. Diagnoses were categorized as infectious, non-infectious, other, and undetermined. Among 222 cases, including 15 species of aquatic (n= 151) and 3 species of terrestrial (n=71) chelonians, infectious disease was most commonly diagnosed (39% and 65% of aquatic and terrestrial chelonians, respectively). Non-infectious causes encompassed 20% (aquatic) and 29% (terrestrial) of cases, followed by ulcerative shell disease of unknown cause (23% of aquatic; and 6% of terrestrial). Seasonal and demographic trends varied by cause of mortality; spatial distribution was biased by larger mortality events. While these data are limited by submission bias, they provide important insights into potential chelonian health issues, informing evaluations of current and future causes of mortality to formulate targeted surveillance efforts in chelonian species.

Defining Population Health in Rewilding Projects by Stakeholder Engagement

Thursday, 31st July - 15:00: (Salon A) - Poster

Stuart Patterson [1]

1. *Royal Veterinary College*

An individual's health may be considered as its ability to carry out normal physical and mental functions. Population health can either be expressed as an aggregate of the health of all members, or, more usefully for management, can instead be considered as the population's ability to carry out its expected functionality. For any population, a range of stakeholders will have views on expected functions; some may be things that the population is expected to do, some may be defined by not doing what it is expected not to do (eg disease transmission). Population health definitions are therefore context-specific and ought to be determined by stakeholder agreement of "ideal population" characteristics.

Domestic cattle are regularly used in rewilding projects as proxies for absent megaherbivores. Guidance on assessing population health have not been developed in the UK, nor have stakeholders been consulted on what would constitute good health. This study set out to address that, taking a survey-based approach in February – March 2024, following an initial pilot. This elicited 189 responses from a range of stakeholder groups including farmers, ecologists, and the general public.

Preconceptions around the word "health" were highlighted by the pilot, leading to this being omitted from the final study. Responses varied widely in terms of familiarity with the subject, and with attitudes ranging from enthusiastic support to extreme negativity. Further workshops are planned with a cross-section of respondents, but lessons from this first study include the value of a pilot to optimise wording, and also the range of traits which may be considered under "health" with an open-minded approach. These included environmental impacts, behavioural traits, and disease resilience. Outputs from both survey and workshop can be used to build health plans for these animals, of benefit both to their welfare and the success of rewilding projects themselves.

Susceptibility and transmission potential of ectotherms and house sparrows to Japanese encephalitis virus (JEV)

Thursday, 31st July - 15:00: (Salon A) - Poster

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1. *Colorado State University*

Japanese encephalitis virus (JEV) is a vector-borne flavivirus that is maintained in an enzootic lifecycle between wading birds, mosquitos and pigs. An estimated 75,000 human cases are reported annually, and symptoms in humans can range from a mild fever to severe neurological complications. Arboviral diseases are spreading to new areas at alarming rates secondary to increases in global trade and travel, climate change and migration of animals and vectors. Although JEV is currently only endemic in Asia, concerns for the spread of JEV into new areas are rising. JEV holds high potential to become established in the U.S. based on the recent emergence of a closely related flavivirus, West Nile virus, in the U.S. and similarly poses a risk to wildlife health. However, little is known about what animal reservoirs, particularly wildlife inhabiting mosquito-dense locales, could contribute to JEV ecology in the U.S. Therefore, we performed experimental infections of ectotherms and house sparrows to determine their susceptibility to the four most prevalent genotypes of JEV. Here our data shows that ball pythons, garter snakes, and house sparrows are susceptible to JEV genotypes I and III, but not to JEV genotypes II and IV. Meanwhile, frogs, toads, alligators and green anoles were not susceptible to any of the four genotypes. No clinical signs were seen in any of the animals. Our results expand upon the knowledge base of susceptible species and provide evidence that domestic wildlife species could play a role in the introduction or maintenance of JEV within the U.S.

Collaborative Approaches to Addressing Health Risks from Wildlife Trade in Guatemala and the Andes-Amazon-Orinoco region

Thursday, 31st July - 15:00: (Salon A) - Poster

Lucy Keatts [1]***, Yovana Murillo*** [1]***, Mariana Da Silva*** [1]***, Fabiola Suarez*** [1]***, Paulo Colchao*** [1]***, Kiara Acurio*** [1]***, Luis Guerra*** [1]***, Kurt Duchez*** [1]***, Ana Solares Escobar Solares Escobar*** [1]***, Rosa Vento*** [1]***, Chris Walzer*** [1]

1. *Wildlife Conservation Society*

Commercial wildlife trade, legal and illegal, is a recognized driver of disease emergence. Infection cycles along live wildlife trade chains, on farms, and in markets, are very different to those in natural, free-ranging wildlife populations, and facilitate cross-species transmission of pathogens.

Policy change, legislation and capacity strengthening, and successful enforcement of the law facilitate long-term risk reduction for spillover and spread of pathogens via wildlife trade. However, trade chains and management bodies involve complex networks of actors and stakeholders at multiple social, political, and institutional levels that must be considered for effective policies to be developed and sustained.

Co-creation of needs-assessments by wildlife trade and One Health experts and subsequent consultations across diverse stakeholders from multiple government sectors, civil society organizations, communities, and others, can identify key knowledge gaps, critical control points, and legislative and capacity needs that must be addressed to reduce health risks from wildlife trade, benefitting conservation, human, and animal health.

Application of this approach across 53 stakeholder groups in Guatemala, Peru, and Bolivia, through support from the International Alliance against Health Risks in Wildlife Trade, enabled characterization of legal and illegal wildlife trade chains, elevated understanding of current perceptions regarding health risks, and the challenges and needs to address these risks.

Findings enabled targeted, evidence-driven research, policy, capacity and infrastructure interventions to mitigate health risks from wildlife in resource-challenged settings e.g., risk analyses of high-risk wildlife trade chains; surveillance planning at critical control points; protocols and legislation to define responsibilities for and strengthen wildlife health and wildlife trade enforcement; provision of PPE; and relevant training curricula development for government and students to support sustainability.

A molecular survey of zoonotic pathogens of public health importance in rodents/shrews and their ectoparasites trapped in Puducherry, India

Thursday, 31st July - 15:00: (Salon A) - Poster

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The increasing overlap between human populations and wildlife habitats heightens the risk of zoonotic spillover. Synanthropic rodents and shrews, which thrive in human-dominated landscapes, serve as reservoirs for pathogens that can impact both human and wildlife health. However, surveillance in India remains limited, restricting our ability to detect and mitigate emerging disease threats.

This study aimed to assess the prevalence of *Orientia tsutsugamushi* (scrub typhus), *Leptospira* spp., *Cryptosporidium* spp., *Coxiella burnetii*, *Rickettsia* spp., and methicillin-resistant *Staphylococcus aureus* (MRSA) in rodents, shrews, and their ectoparasites in peri-domestic areas of Puducherry, India. By investigating these pathogens in wildlife, we sought to improve our understanding of disease ecology and potential transmission at the human-wildlife interface.

Rodents and shrews were trapped in 11 villages with a history of zoonotic disease cases. Ectoparasites and tissue samples were collected and screened using molecular techniques, including conventional and real-time PCR. Phylogenetic analysis was performed to characterize detected strains.

Among 58 captured rodents and shrews, *O. tsutsugamushi* was detected in 3.45% of host tissues and 7.41% of ectoparasite pools, with a Gilliam-related strain identified. MRSA was found in 3.13% of shrews. No *Leptospira* spp., *Cryptosporidium* spp., *Coxiella burnetii*, or *Rickettsia* spp. were detected.

These findings underscore the importance of zoonotic pathogen surveillance in wildlife to prevent human outbreaks, promote awareness amongst local stakeholders, improve diagnostic and treatment options, and inform on vector control strategies. Understanding pathogen circulation in synanthropic species helps identify emerging threats, protect ecosystem health, and strengthen One Health interventions.

Collaborative Infectious Disease Notification Networks?

Thursday, 31st July - 15:00: (Salon A) - Poster

Diana Boon [1], ***Ryan Michalesko*** [1]

1. *International Crane Foundation*

How can we create a global network? During the current avian influenza global bird pandemic, the limitations in finding accurate and timely data on the internet or through state or federal type websites remain apparent. Data transparency, testing result lag time, impacts of published results on agricultural trade, funding, and differing governmental philosophies all impact how the wildlife community can communicate about diseases in real time and have a detrimental impact on effective response. The knowledge that HPAI is moved around the world by waterfowl along the global migration routes provides a geographical and seasonal focus to develop a non-governmental reporting network. At the International Crane Foundation (ICF), we are building local and international networks anchored by wetland researchers in areas where cranes, and myriad waterfowl, live. ICF also integrates into other avian and disease networks around the world. Building a larger network is dependent on inclusion of all established connections and resources, and how to best utilize those networks to efficiently incorporate animal and environmental testing, funding, and other research needed globally to protect wildlife flyways and people.

Ecological Patterns of Chigger Mites and Small Mammals in Korea: Implications for Public Health

Thursday, 31st July - 15:00: (Salon A) - Poster

Kiyoon Kim [1]**, *Jusun Hwang*** [2]**, *Kyungmin Kim*** [3]**, *Daehyun Oh*** [4]**, *Yungchul Park*** [5]**, *Donghyeok Jeong*** [1]

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Scrub typhus in Korea is primarily transmitted by chigger mites, which use small mammals as key hosts. This study investigates small mammal assemblages and ectoparasite communities across four habitats—grassland, ecotone, forest, and agricultural land—during fall and spring. Small mammals were more abundant in fall (133 individuals) than in spring (52 individuals), with the highest captures in grasslands (84 individuals), followed by ecotone (55), forest (34), and farmland (6). *Apodemus agrarius* was the dominant species (142 individuals).

Ectoparasites were classified into four families and one order. Cluster analysis revealed that most chigger mites appeared in October, parasitizing small mammals in grasslands and ecotones. *Leptotrombidium pallidum*, the dominant chigger mite species, increased in density with higher *A. agrarius* populations. Habitat simplification reduced host diversity, leading to an increase in dominant host populations and, consequently, higher ectoparasite loads. These findings suggest that small mammal-borne diseases peak in October, particularly in grasslands and ecotones where *A. agrarius* is dominant.

Given these results, targeted surveillance and vector control efforts should be intensified in these habitats during peak periods to mitigate disease risks. Understanding host dynamics and habitat-specific risks will enhance disease prevention strategies, reducing the public health burden of mite-borne diseases.

Managing Shared Resources: Using Workshops to Increase Resources for Detecting and Responding to Wildlife Disease Events

Thursday, 31st July - 15:00: (Salon A) - Poster

***Anne-Justice Allen* [1], *Ann Fan* [1], *Katie Schwartz* [2], *Jaclyn Cubillas* [3]**

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The SARS-CoV-2 epidemic and subsequent detections of the virus in captive and free-ranging wildlife demonstrated the need for coordinated disease outbreak detection and response networks in wildlife. Arizona is unique among western states with 22 Federally recognized tribal nations managing over 43,000 square miles of land and natural resources, and nearly 58,000 square miles of public land together accounting for more than 75% of the land in the state. The veterinarians at the Arizona Game and Fish Department provided a series of workshops to develop outbreak detection and response skills in the natural resource departments of Arizona tribal agencies. The first two-day workshop was held in May 2023 and was attended by seventeen biologists. The workshop consisted of lectures, a “live” outbreak investigation scenario, and necropsies. The initial workshop will be followed by several smaller workshops in 2024 at locations throughout the state. Each attendee receives an outbreak investigation kit and electronic and print versions of the material. This effort has increased coordination and communication between agencies during the avian influenza outbreak. Presentations have been provided to the Arizona Intertribal Council and the Southwest Chapter of the Native American Fish and Wildlife Society. We will provide an update on lessons learned and our communication and coordination efforts to address wildlife health issues.

A retrospective summary of pronghorn (Antilocapra americana) morbidity and mortality in Wyoming, USA (2015-2023)

Thursday, 31st July - 15:00: (Salon A) - Poster

Samantha Allen [1]***, Kelsey Rayment*** [2]***, Lee Knox*** [1]***, Peach Van Wick*** [1]***, Jessica Jennings*** [1]

1. *Wyoming Game and Fish Department,* ***2.*** *The Raptor Center*

The pronghorn (*Antilocapra americana*) is an iconic member of western North American wildlife communities, and Wyoming is home to approximately 40% of the rangewide population. Free-ranging pronghorn are faced with both natural and anthropogenic challenges that can limit survival and reproduction. Key among these are climate change, habitat loss, barriers limiting seasonal movements, and pathogens. All of which we currently have a limited understanding of their impact in regards to the health of the individual and population. Our objective was to identify and characterize causes of morbidity and mortality in free-ranging Wyoming pronghorn opportunistically submitted by field staff for diagnostic evaluation over a 9-yr period (2015-2023). Submissions included carcasses submitted for full postmortem examination (gross and histopathological; *n*=115) and field-collected post-mortem tissues (*n*=140). Ancillary tests were performed on a case-by-case basis.

A total of 255 cases submitted to the Wildlife Health Laboratory (Wyoming Game and Fish, Veterinary Services) were included in this study. There were more females than males, most were adults, and the majority of cases were submitted in autumn. Infectious disease was the most common general cause of morbidity and mortality (61.1%; 156/255) and was most often bacterial in etiology (61.0%; 95/156). The most common primary bacterial infectious diseases diagnosed in pronghorn was *Mycoplasma bovis* (56.2%; 54/96), followed by *Truperella pyogenes* (18.8%; 18/96). Deaths attributed to noninfectious causes (20.0%; 51/255) were most commonly attributed to trauma (54.9%; 28/51). Eighteen fawns were submitted; noninfectious disease (50.0%; 9/18) was the most common cause of morbidity and mortality.

These results reveal that infectious, environmental, and anthropogenic-associated causes of morbidity and mortality are commonly diagnosed in pronghorn in Wyoming, USA, and represent potential population threats that should continue to be monitored.

RATical - Re-envisioning Rat-Management

Thursday, 31st July - 15:00: (Salon A) - Poster

Kaylee Byers [1]***, Chelsea Himsworth*** [2]

1. *Simon Fraser University,* ***2.*** *University of British Columbia*

Urban rats are notorious for their ability to carry numerous zoonotic pathogens that can be transmitted among animals and to people. Because of the health risks and infrastructural damage associated with rat infestations, municipalities have waged war on rats for as long as there have been cities. Yet rats continue to thrive due to increased urbanization and densification. To manage rats now and in the future, we need to approach rat-associated issues differently, and we argue that this must start with a fundamental shift in how we think about rats and their associated risks. Drawing on systems thinking, socio-ecological frameworks and ecological management practice, we propose the development of a Rat Risk Index comprised of metrics related to rat infestation magnitudes and the consequences of infestations. We discuss the need to consider rat-associated impacts holistically (e.g., physical and mental health outcomes) as well as the importance of grounding these approaches in equity so that they prioritize those most vulnerable to rat-associated harms. The Rat Risk Index would leverage diverse data sources depending on the settings and resources available to promote more adaptive and responsive management in cities that address local contexts and needs.

Identifying One Health Priorities and Collaborations in California using Cognitive Maps of Mental Models

Thursday, 31st July - 15:00: (Salon A) - Poster

Hannah Shapiro [1]***, Mark Lubell*** [1]***, Deana Clifford*** [2]***, Brandon Munk*** [2]***, Alex Heeren*** [2]***, Will Schmelter*** [2]***,***
Kirsten Gilardi [1]

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Operationalizing a One Health framework requires interdisciplinary collaboration, an understanding of the complex system surrounding the emergence of wildlife disease, and a common vision for prioritizing management actions and policies. Mental models, or organized, simplified knowledge structures that people form to make sense of complex issues, provide a way to generate common understandings of complex social-ecological systems, which enables cooperation, learning, and policy interventions. We conducted a mental model exercise with One Health practitioners at a workshop to graphically map the relationships of key factors that influence the emergence and occurrence of disease in California wildlife. We found that experts had similar vision about what determinants of health should be included in the models, but low agreement on how these determinants connect, signaling the need for more systems-level research and communication among scientists and decision makers. Participants also identified human dimensions components of the system (e.g., policy, collaboration, agency capacity) as important elements for a wildlife health cooperative to focus on despite the fact that these components were not as well connected to the system as ecological components. Our research design and analysis demonstrates how mental models can be used to chart a course from common understanding to policy impact in complex One Health systems where cooperation is the key to effective management and governance.

Assessing health and feasibility of releasing confiscated eastern box turtles (Terrapene carolina carolina): A quantitative framework for informed conservation decisions

Thursday, 31st July - 15:00: (Salon A) - Poster

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The global commerce of wild turtles significantly contributes to the decline in chelonian populations. Among these, the eastern box turtle (*Terrapene carolina carolina*) is classified as vulnerable by the IUCN and is currently among the most numerous North American turtles in the illegal trade. The major dilemma arising from the illegal wildlife trade is deciding the fate of confiscated animals, particularly regarding their potential release of pathogen-positive individuals into suitable habitats with existing turtles. This study simulated the change in the health of a population of 778 free-ranging turtles after the release of 17 confiscated eastern box turtles. Using an online application, we built a quantitative health score framework (0-1, with higher scores meaning more pathogen impact) built on occupancy and survival modeling that incorporated pathogen prevalence into a random binomial probability distribution. When simulating these populations, the health score of the free-ranging population (0.262) prior to repatriation was in a higher plane of health than the confiscated population (0.405). After repatriating this confiscated population, the free-ranging health score increased to 0.34 over 25 years, demonstrating a lower plane of health in the long term. The application provides a simplified and reproducible user-friendly framework that allows users to change their pathogen prevalence values, the impact of the pathogen prevalence, population size, and simulation length. The findings of this study underscore the importance of quantitative health assessments derived from real-world data woven into statistical approaches that inform conservation decision-making to protect turtle populations.

Molt induction Using Levothyroxine in Five Captive Spheniscus Penguins

Thursday, 31st July - 15:00: (Salon A) - Poster

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Annual molt in penguins, occurring post-breeding, is crucial for waterproofing and temperature regulation. Irregular molting commonly occurs and can lead to health issues when they persist. Though the complete mechanisms driving avian molt remain to be fully understood, researchers have investigated how thyroid and sex hormones influence penguin molting patterns. Prior research on hormone-based forced molting has produced inconsistent outcomes, particularly noting poor success with synthetic thyroxine (levothyroxine). This research evaluated commercial levothyroxine's effectiveness in inducing molt in five captive penguins (one Humboldt penguin, *Spheniscus humboldti*, and four African penguins, *Spheniscus demersus*) with inadequate molting patterns. The five-week treatment protocol involved weekly dose adjustments with gradual increases and reductions. Three penguins received the standard protocol; two molted during treatment, while one molted three months after treatment completion. A fourth penguin required an extra week at maximum dosage and began molting in the final week. The fifth penguin, showing insufficient drug absorption, needed an alternative delivery method in week five and two additional treatment weeks before molting commenced. The successful molt induction in all five penguins through oral levothyroxine administration suggests this method could effectively address abnormal molting in *Spheniscus* penguins.

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20 years of research on SpayVac-equid, a multi-year, single-dose vaccine to control fertility of free-roaming horses

Thursday, 31st July - 15:00: (Salon A) - Poster

Ursula Bechert [1]

1. *SpayVac for Wildlife, Inc.*

Free-roaming horse populations can grow at rates of 15-20% annually, negatively impacting native flora and fauna. Populations are challenging to manage: their habitats are diverse, stakeholders have different objectives, and people hold strong views about how free-roaming horses should be managed (if at all). Controlling fertility, together with removals, is the best way to rapidly stabilize numbers for the long-term. Porcine zona pellucida (pZP) vaccines are safe to use, block fertilization with antibodies that bind to ovarian tissue, and are favored by some horse advocacy and animal-welfare groups. However, ZonaStat-H, the only commercially available pZP vaccine for equids, requires boosters 3-4 weeks after initial vaccination and then annually thereafter, rendering it impractical in most field situations. SpayVac®-equid is a unique pZP vaccine that results in *multi-year, single-dose*

efficacy. Over the past 20 years, several collaborative trials have been conducted to demonstrate SpayVac's contraceptive efficacy in horses and learn more about how the immune and reproductive systems respond to vaccination. A 4-year trial, initiated in 2003, demonstrated that one dose of SpayVac significantly lowered foaling rates. Another study identified for the first time, a second mechanism of action for pZP vaccines through direct effects on the ovaries. To learn more about immune responses to SpayVac, a fluorescent bead-based assay distinguished mare IgG isotype responses against pZP. An ongoing study has demonstrated significant differences in both immune response and contraceptive efficacy based on neck versus rump injection sites. These research results suggest that SpayVac can help managers effectively manage free-roaming horse populations.

Predicting Avian Hotspots of Potential West Nile Virus Outbreaks: A case study in Arizona

Thursday, 31st July - 15:00: (Salon A) - Poster

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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 150 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 and predict their spatiotemporal shifts in the future, we used MaxEnt species niche distribution modeling and ArcGIS Pro to model the habitat distribution of one high-competency amplifying host (American Robin [T. migratorius]), two low-competency hosts (American Crow [C. brachyrhynchos]; Woodhouse's Scrub-Jay [Aphelocoma woodhouseii]), and one supersuppressor host (Northern Cardinal [C. cardinalis]) of WNV in Arizona. We included variables influencing habitat use and distribution, such as temperature, rainfall, normalized difference vegetation index, and elevation. Different climate change scenarios were then projected onto these environmental variables to understand how climate change is likely to affect them, and in turn, the habitat distribution of the aforementioned host species. 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 in human and avian communities.

A first glimpse into the fungal microbiota on the skin of leatherback sea turtles

Thursday, 31st July - 15:00: (Salon A) - Poster

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1. *Florida Atlantic University,* ***2.*** *Florida Atlantic University, Boca Raton,* ***3.*** *The University of Tennessee*

Due to the increased understanding of its importance and advances in high throughput sequencing, the amount of literature available on the microbiome of humans, non-human animals, and plants has increased in recent years. Unfortunately, research investigating fungi as a part of the microbiome is lagging far behind bacterial research and large data gaps persist. However, the emergence of significant fungal diseases over the past few decades highlights the importance of understanding the fungal microbiota and the role it plays in host health and disease. Filling these knowledge gaps is critical for understanding and preventing diseases caused by fungi, especially for threatened and imperiled species. The leatherback sea turtle is one such imperiled species and recent work has revealed that neonatal leatherbacks appear to be especially susceptible to fungal infections such as sea turtle egg fusariosis and mycotic dermatitis. As such, understanding of their fungal microbiota will add to our understanding of the pathogenesis of these diseases. Here we present the first baseline fungal skin microbiota data from leatherbacks sea turtles at emergence, 3-4 weeks of age, and in nesting females. We identified large shifts in the most predominant fungal phyla, families, and genera between age groups. Additionally, significant differences in beta diversity suggest that the fungal communities on the skin of leatherbacks are significantly different between age groups. These data not only provide novel baseline fungal microbiota data for leatherbacks but may also be used to elucidate the source of fungal infections in leatherback neonates.

“What is this thing?” How Sample Management Plays a Pivotal Role in Ongoing and Future Research

Thursday, 31st July - 15:00: (Salon A) - Poster

Casey Maynard [1], ***Julie Ellis*** [1], ***R. Scott Larsen*** [1], ***Erica Miller*** [1], ***Michelle Gibison*** [1]

1. *Wildlife Futures Program, University of Pennsylvania*

Wildlife faces threats such as habitat destruction, disease, and climate change. As populations adapt or decline, biorepositories have never been more critical. They have the potential to answer future questions about these imperiled species and can provide biological, evolutionary, and ecological history about them. Biorepositories require several main hallmarks: samples should maintain integrity, be easily retrievable, and have accurate and traceable management to facilitate solid scientific research. To achieve these criteria, samples should be numerous and of the best possible quality. Oftentimes, there is a struggle to maintain the organization of specimens due to numerous challenges such as space and budget limitations, accurate record keeping, concurrent projects, multiple people involved with samples, and staff turnover. The Wildlife Futures Program has worked with input from experts in the field to devise a biorepository to ensure best practices for specimen collection, inventory management, optimization of storage containers and subsampling protocols, proper labeling, freezer monitoring systems, detailed specimen collection and required sample metadata protocols, species-specific sampling needs, and use of remote storage for long term large-volume sample collections. In just 2 years, we have been able to store ~17,500 samples from ~40 species, doubled our storage capacity, and been able to detect freezer issues before equipment failure. Our biorepository can serve as a framework for other groups or agencies, using lessons learned from our own development. It is more critical than ever, with the threats facing our wildlife, to preserve representative samples with appropriate historical data for the future. Remember, “garbage in is garbage out.”

Absence of Antimicrobial Resistance in Elasmobranchs (Elasmobranchii) in a Marine Management Area of the North Pacific Coast of Costa Rica

Thursday, 31st July - 15:00: (Salon A) - Poster

Gianmarco Bettoni [1], ***Elías Barquero-Calvo*** [2], ***Diego Fallas-Madrigal*** [3], ***Paola Chavarría Quiros*** [4], ***Sergio Madrigal Mora*** [5], ***Mario Espinoza*** [3]

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Antimicrobial resistance (AMR) is emerging as a global health issue from a One Health perspective, threatening wildlife populations, the environment and public health. Due to its rapid spread in terrestrial and marine environments, particularly in urban and anthropogenized areas, AMR surveillance in wildlife has intensified in recent years. However, there have been few studies in protected and relatively pristine areas of the planet, raising concerns about the impact of AMR on wildlife in these areas. Elasmobranchs have the potential to act as indicators of ecosystem health due to their high trophic positions, complex movement ecology and inter-specific interactions, making them ideal sentinel taxa for antimicrobial resistance surveillance in a wide range of aquatic environments. In August 2024, 17 elasmobranchs (Elasmobranchii) were sampled with cloacal swabs, cultured and tested for antimicrobial susceptibility in a relatively undisturbed, protected area of the Pacific coast of Costa Rica. A total of 10 bacterial species from different families were successfully isolated from 16 of the 17 sampled individuals. Overall, isolated bacteria in the captured elasmobranchs had high susceptibility, with only some isolates showing intrinsic antimicrobial resistance not related to selective pressure. Using elasmobranchs as model taxon, this study suggests that protected areas act as a barrier against anthropogenic pollution, particularly against the spread of AMR. This conclusion could be part of the evidence to support future plans to create networks of marine protected areas that can increase the conservation benefits of wide-ranging elasmobranchs, while reducing the impact of AMR on wildlife.

INVESTIGATING A MYSTERIOUS NECROTIZING AND ULCERATIVE DERMATOLOGIC SYNDROME IN BULL ELK (CERVUS CANADENSIS)

Thursday, 31st July - 15:00: (Salon A) - Poster

***Taylor Chan* [1], *Justin Brown* [2], *Natalie Bauer* [3], *Joseph Yarkovich* [4], *Jeremiah Banfield* [5], *Lisa Murphy* [1], *Elizabeth Mauldin* [6], *Charles Bradley* [6], *Nicole Nemeth* [7], *Laurie Baeten* [3], *Kevin Niedringhaus* [1]**

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Describing the etiology, pathogenesis, and clinical effects of novel diseases in free-ranging wildlife often requires multi-institutional collaboration. These partnerships are particularly valuable when suspected cases are poorly-defined and uncommon but affect a visible, high-profile species. We attempt to establish a case definition for a mysterious necrotizing and ulcerative dermatologic syndrome in elk (*Cervus canadensis*) and describe the investigative process, highlighting the collaboration of multiple disciplines across several universities and government agencies.

From 2014 to 2020, skin biopsies or full necropsies were performed on nine elk in the Great Smoky Mountain National Park and northcentral Pennsylvania. Affected elk were adult bulls that displayed lesions throughout the year but predominantly in October through January. Bulls had large areas of affected skin over the dorsal midline, shoulders, withers and hindquarters that ranged from patchy to regional alopecia, to crusting, ulceration and sloughed necrotic skin. Microscopically, there was epidermal and superficial dermal necrosis, granulation tissue with fibrosis, and marked secondary inflammation. Possible causes considered include photosensitization, ectoparasitism, and hereditary collagen dysplasia. Future directions for the project are to obtain more samples to evaluate for possible phototoxins, perform electron microscopy on dermal collagen, and analyze DNA for genetic mutations.

By incorporating observations of field personnel and public observers, species-specific knowledge of biologists and wildlife veterinarians, and expertise in interpreting pathologic and other changes by laboratory diagnosticians, this project utilizes each collaborator’s strengths, emphasizing the importance of holistic investigations to determine the underlying cause of an undefined, uncommon, and highly visible disease.

Linking population modeling with a health assessment to determine the impact of an invasive acanthocephalan parasite in an island fox population

Thursday, 31st July - 15:00: (Salon A) - Poster

O. Alejandro Aleuy [1], Benjamin J Padilla [2], Victoria Bakker [3], Daniel Doak [4], Stacey Baker [5], Juliann Schamel [5], Jason Rohr [6], Kevin Lafferty [7]

1. Florida Atlantic University, 2. Oregon Department of Fish and Wildlife, 3. Montana State University, 4. University of Colorado Boulder, 5. Channel Islands National Park, 6. University of Notre Dame, 7. U.S. Geological Survey

The island endemic San Miguel Island fox (*Urocyon littoralis littoralis*, SMIF) nearly went extinct in the late 1990s due to hyperpredation by invasive golden eagles. An intensive recovery program, including the capture of the few remaining foxes, an in-situ captive breeding program, and the removal of non-native species, enabled successful reintroduction and recovery in the early 2000s. The SMIF population grew rapidly until 2012 when the parasite *Pachysentis canicola* was first detected. Recently, observed increases in fox mortality and poor body condition coupled with apparent population fluctuations raised concerns about the long-term future of the population. To understand the influence of environmental/spatial variables and the emergence of *P. canicola* in SMIF population trends, we analyzed capture-recapture data (2006–2022) using spatially explicit capture-recapture and Bayesian multi-state Cormack-Jolly-Seber models to estimate SMIF population trends. The SMIF population peaked at an average of 551 individuals (SE: 80) between 2011–2013, then declined to 156 (SE: 34) individuals by 2018, coinciding with the emergence of *P. canicola* and low annual precipitation (2012–2015). From 2019–2022, the SMIF population recovered with increased rainfall but remained below pre-2013 levels (range: 229–367 individuals). The decline was driven by a sharp reduction in pup survival from 2013–2017, a subtle but sustained increase in non-pup mortality from 2013–2022, and a decrease in average body condition. The additive effects of low precipitation and the parasite's impact on SMIF condition likely drove the 2013–2018 population decline. Our analyses suggest that SMIF is relatively resilient to either stressor alone but that simultaneous exposure drives declines. With drought intensity rising in California and *P. canicola* established on the island, proactive monitoring is critical for timely management if declines recur.

Analysis of Stress Factors in Formosan Macaques: A Comparison Between Shoushan and Other Populations

Thursday, 31st July - 15:00: (Salon A) - Poster

AiMei Chang [1], ***Chen-Chih Chen*** [1], ***Wan-Jhen Chen*** [1]

1. *National Pingtung University of Science and Technology*

Since the establishment of Shoushan National Nature Park, human activities have increasingly overlapped with the habitat of Formosan macaques (*Macaca cyclopis*), influencing their populations and behaviors. Since 2013, macaques in Shoushan have exhibited bilateral symmetrical alopecia, a condition linked to chronic stress. Key stressors include high population density and competition for resources.

This study analyzed stress hormone metabolites in fresh fecal samples and conducted a year-round population survey to assess the relationship between stress levels, population density, and seasonal plant growth. Comparisons with macaque populations in areas with lower human interference showed significantly higher stress levels in Shoushan, particularly in high-density areas and non-plant growth seasons.

Wildlife studies confirm that increased population density heightens stress, intensifying competition when food declines. Elevated stress can trigger disease outbreaks, mortality, reduced birth rates, and zoonotic disease risks. Given that human feeding sustains high macaque densities in Shoushan, the study recommends strict regulation of feeding practices and considers contraception—leveraging recent contraceptive vaccine developments—as a population control strategy.

A One Health Response to the Eagle Gold Heap Leach Failure in the Yukon, Canada

Thursday, 31st July - 15:00: (Salon A) - Poster

Jane Harms [1], ***Benton Foster*** [1], ***Sudit Ranade*** [1], ***Judy Booth*** [1], ***Erin Dowd*** [1], ***Tyler Williams*** [1], ***Brendan Mulligan*** [1], ***Michelle Thompson*** [1], ***Maud Henaff*** [1], ***Myles Brown*** [1], ***Cameron Sinclair*** [1], ***Michelle Anderson*** [2], ***Celine Totman*** [2], ***Kathryn Matheson*** [2]

1. *Yukon Government,* ***2.*** *SLR Consulting*

On June 24, 2024, a landslide at the heap leach facility of the Eagle Gold Mine in northeastern Yukon released an estimated 4 million tonnes of cyanide-contaminated heap leach material. This incident has the potential for significant impacts on the health of the environment, animals, and humans in the surrounding area and downstream. Despite ongoing efforts to contain the heap leach material, manage water balances and treat contaminated water, the failure has resulted in movement of contaminants including cyanide, mercury and cobalt into surrounding surface and ground water. The public has expressed concern about fish and wildlife health and human use of surrounding watercourses and lands for fishing, hunting, recreational purposes, traditional cultural usage and drinking water. This environmental accident is a pertinent example of a complex issue that demonstrates the interconnectedness of animal, human and environmental health.

Response to the heap leach failure and subsequent environmental contamination has involved multidisciplinary collaborations between government agencies, First Nations and technical consultants. Analysis and modelling of surface and ground water quality near and downstream of the mine site are key to informing health and environmental risk assessments. Ongoing monitoring and response projects include: fish health monitoring, assessing changes in fish populations and testing fish tissues for contamination levels; testing tissues from harvested wildlife for contaminants; and human health risk assessments based on contaminant threshold monitoring in water and development of human health-based adaptive management plans.

Work to understand the full impacts of the heap leach failure and to monitor and mitigate health risks will require innovative approaches and continued collaboration and communication between all agencies and groups involved. Here we describe early monitoring and assessment activities following the heap leach failure, lessons learned, and use this as a case study to describe a rapid, collaborative One Health approach.

Modelling human-rat interactions: A One Health investigation into the ecosocial determinants of rat-associated risks in urban neighbourhoods

Thursday, 31st July - 15:00: (Salon A) - Poster

Christine Yanagawa [1]

1. *Simon Fraser University*

Cities worldwide face complex challenges managing human-rat interactions (HRIs) and associated health risks. Although rats are known vectors of zoonotic diseases, they are not inherently harmful; rather, the risks arise from interactions at the interface of rats, humans, and the urban environment. Increased rat activity is consistently linked to high population density, substandard housing, and inadequate waste management—conditions often stemming from neighbourhood neglect. Despite this complexity, many cities continue to rely on conventional pest control measures that can have deleterious knock-on effects on other wildlife and frequently fail to address the underlying social-ecological drivers of HRIs. Within the context of rapid global urbanization, the complex human-rat relationship is an increasingly relevant One Health issue that requires more holistic consideration of the health of all urban residents, including humans, pets, rats, and other wildlife. My doctoral research asks: “How do ecosocial factors promote distributions of human-rat interactions and associated health risks across urban neighbourhoods in the City of Vancouver?”

My mixed-methods study integrates a systematic literature review on urban social, ecological, and infrastructural factors associated with urban HRIs and geospatial modelling and analyses using combined pest control data, 311 complaints, a citizen science platform, and public survey responses linked to census and open data sources. The study will identify if significant clustering exists by neighbourhood and determine significant indicators of HRIs. An area-based equity index will assess how neighbourhood advantage/disadvantage correlates with HRIs. If funding permits, rat leptospirosis data will serve to create new hypotheses on leptospirosis risks and HRIs at the neighbourhood level. Findings will support the development of an HRI Risk Index to guide urban planning and public health interventions in Vancouver.

Expanding the plague-control toolbox: Edible flea-control baits show promise for plague mitigation

Thursday, 31st July - 15:00: (Salon A) - Poster

***Jason Fly** [1], **Travis Livieri** [2], **Randy Matchett** [3], **Eddie Childers** [4], **Magnus McCafferey** [5]*

***1.** University of Wisconsin-Stevens Point, **2.** Prairie Wildlife Research, **3.** U.S. Fish and Wildlife Service, **4.** Badlands National Park, National Park Service, **5.** Turner Institute of Ecoagriculture*

Sylvatic plague (a flea-borne disease) poses a significant problem for conservation managers across western North America. Black-tailed prairie dogs (*Cynomys* ludovicianus; prairie dogs*)* experience extreme mortality (>95%) during plague epizootics. The critically endangered black-footed ferret (*Mustela nigripes*) is prairie dog reliant, and ferret populations can be extirpated by plague epizootics. Managers apply deltamethrin dust into prairie dog burrows to control flea populations, which is a timely and costly procedure. We aimed to test the efficacy of inexpensive pulicides (flea-killing agents) in black-tailed prairie dogs at Badlands National Park, South Dakota. We tested five edible pellet baits: 4.0 mg Afoxolaner, 40.0 mg Fluralaner, 60.0 mg Spinosad, 0.4 mg Fipronil (low dose), and 1.3 mg Fipronil (high dose) replicated across two prairie dog colonies on plots ranging in size from 2-5 ac. We followed a before-after-control-impact (BACI) statistical design to assess flea loads: we combed prairie dogs before treatments, then 1- and 12-months post-treatments. Transects were used to apply 125 baits per hectare. We used a negative binomial linear model to compare flea abundance between treatments and time periods. We detected >1,000 fleas and combed 321 prairie dogs before and 275 prairie dogs after treatments. All pulicides proved to lower prairie dog flea loads. However, flea loads were lower with both Fipronil baits when compared to the other treatments and the higher fipronil dose was most effective. Fipronil bait pellets show considerable promise for plague mitigation in the context of conservation and One Health objectives; they are effective, inexpensive, and easily distributed.

The Role of Hookworm-Specific IgG and Antimicrobial Peptides on the Survival of South American Fur Seal Pup

Thursday, 31st July - 15:00: (Salon A) - Poster

Juntian Bu [1]***, Diego Joaquin Perez Venegas*** [2]***, Jason McAlister*** [3]***, Jennifer Geddes-McAlister*** [3]***, Mauricio Sequel*** [4]

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Infectious diseases are major drivers of wildlife mortality paralleling global health threats such as antimicrobial resistance. Understanding the immune strategies that enable animals to resist infection is vital for both conservation and medicine. South American fur seals (Arctocephalus australis) on Guafo Island in northern Chilean Patagonia suffer high early-life mortality due to hookworm (Uncinaria spp.) infection. These parasites cause severe anemia and intestinal mucosal damage, increasing susceptibility to secondary bacterial infections.

Previous studies suggest that pups who survive often mount strong adaptive immune responses, particularly through hookworm-specific IgG. However, pups must also resist secondary bacterial infections, with antimicrobial peptides (AMP) potentially playing a key role in this defense. We asked: which immune mechanism – adaptive (IgG) or innate (antimicrobial peptides, AMPs) – better predicts survival in this pathogen-rich environment? We hypothesized that hookworm-specific IgG is a stronger predictor of pup survival than AMPs, due to its dual role in limiting both parasitic damage and secondary infections.

To test this, we collected longitudinal plasma samples from 24 pups across five capture events between December and February of 2023 and 2024 breeding seasons. Hookworm-specific IgG levels were quantified via ELISA, and AMP abundance in plasma was obtained using proteomics through liquid chromatography-mass spectrometry. Generalized linear mixed models and multi-model inference were used to assess which immune markers best predicted survival outcomes.

This study offers new insight into the comparative strength of innate versus adaptive immunity in a wild mammal facing intense parasitic pressure. By identifying reliable immunological predictors of survival, our findings will inform targeted conservation strategies for pinniped populations. More broadly, this work highlights host-derived immune defenses as potential models for developing alternatives to antibiotics in medicine – contributing to global efforts to combat antimicrobial resistance.

Authors Index

Unprecedented co-circulation of bluetongue and epizootic haemorrhagic disease viruses in wild ruminants in Northeast Spain

Monday, 28th July - 15:00: (Salon A) - Poster

Velarde, Roser[1]; Sanz, Albert[2]; Estruch, Josep[1], Marco, Ignasi[3], Aguilar, Xavier F[4,5].

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Climate and ecological changes are altering the dynamics of vector-borne diseases, expanding their distribution, and increasing disease prevalence in Mediterranean and temperate regions. In Europe, the emergence of *Culicoides*-vectored orbiviruses is particularly notable. Bluetongue (BT) is becoming endemic in some parts of the Mediterranean biome, with an increasing diversity of serotypes and sporadic emergences in temperate biomes. Additionally, epizootic hemorrhagic disease (EHD) emerged in the Mediterranean biome in fall 2022 and is spreading towards new regions.

After more than a decade free from orbiviruses, Catalonia (Northeast Spain) experienced outbreaks of both BT and EHD in summer and fall 2024, affecting livestock and wild ruminants. In wildlife, passive surveillance confirmed BT virus (BTV) in a dead mouflon (BTV-8, n=1) and in a diseased Pyrenean chamois (BTV, n=1), and EHD virus serotype 8 (EHDV-8) in red deer (n=2), with characteristic orbiviral lesions including moderate to severe non-suppurative encephalitis. Additionally, qPCR detected EHDV-8 in found-dead roe deer (n=1) and red deer (n=1) with encephalic siderocalcinosis. Targeted sampling on hunted wild ruminants further confirmed both BTV-8 and EHDV-8 in the spleens of apparently healthy red deer, including several cases of coinfections.

These findings represent the first historical detection of EHDV in wildlife in Catalonia and records of BTV-EHDV co-infections in European wildlife. They highlight an exceptional circulation of orbiviruses in Northeast Spain and underscore the growing significance of these viruses in Europe. Further research is needed to better understand the role of wildlife in the spread and maintenance of orbiviruses within Europe's evolving vector-host dynamics.

Vitreous Humor as an Alternative to Blood Serum for Postmortem Urea Analysis in Red Deer (Cervus elaphus)

Monday, 28th July - 15:00: (Salon A) - Poster

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Vitreous humor is widely used in human forensic pathology as a stable alternative to blood for postmortem biochemical investigations, particularly in cases where advanced decomposition compromises blood analysis. In wildlife forensics, carcasses with unknown clinical histories and significant autolysis present challenges in assessing ante-mortem metabolic conditions. This study evaluated the potential of vitreous humor as a substitute for blood serum in post-mortem urea analysis by comparing urea concentrations in both sample types from freshly euthanized red deer (Cervus elaphus).

Nineteen semi-captive healthy adult female red deer were humanely euthanized for reasons unrelated to this study in September 2022 (n=10) and February 2023 (n=9). Immediately postmortem, vitreous humor was collected into plain Eppendorf tubes using an 18-gauge needle and blood was collected into serum tubes from the jugular vein. Samples were stored at -80°C until analysis via spectrophotometric methods using the same analyzer for both sample types. Statistical analysis included Pearson correlations and OLS regression models.

Findings revealed a positive linear relationship between urea concentrations in the vitreous humor and blood serum (r=0.73, B=0.84, p<0.00047), suggesting that vitreous humor may serve as a reliable proxy for blood urea measurements. Further analysis is required to assess the relationship between additional biochemical markers, such as creatinine, phosphate, or beta hydroxybutyrate, in these sample types. These findings have significant implications for wildlife post mortem investigations, where vitreous humor may provide a viable alternative when blood samples are unavailable or degraded.