



Joint virtual conference

CUENCA 2021

August 31 to September 2



69th WDA
14th EWDA





Joint virtual conference



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August 31 to September 2





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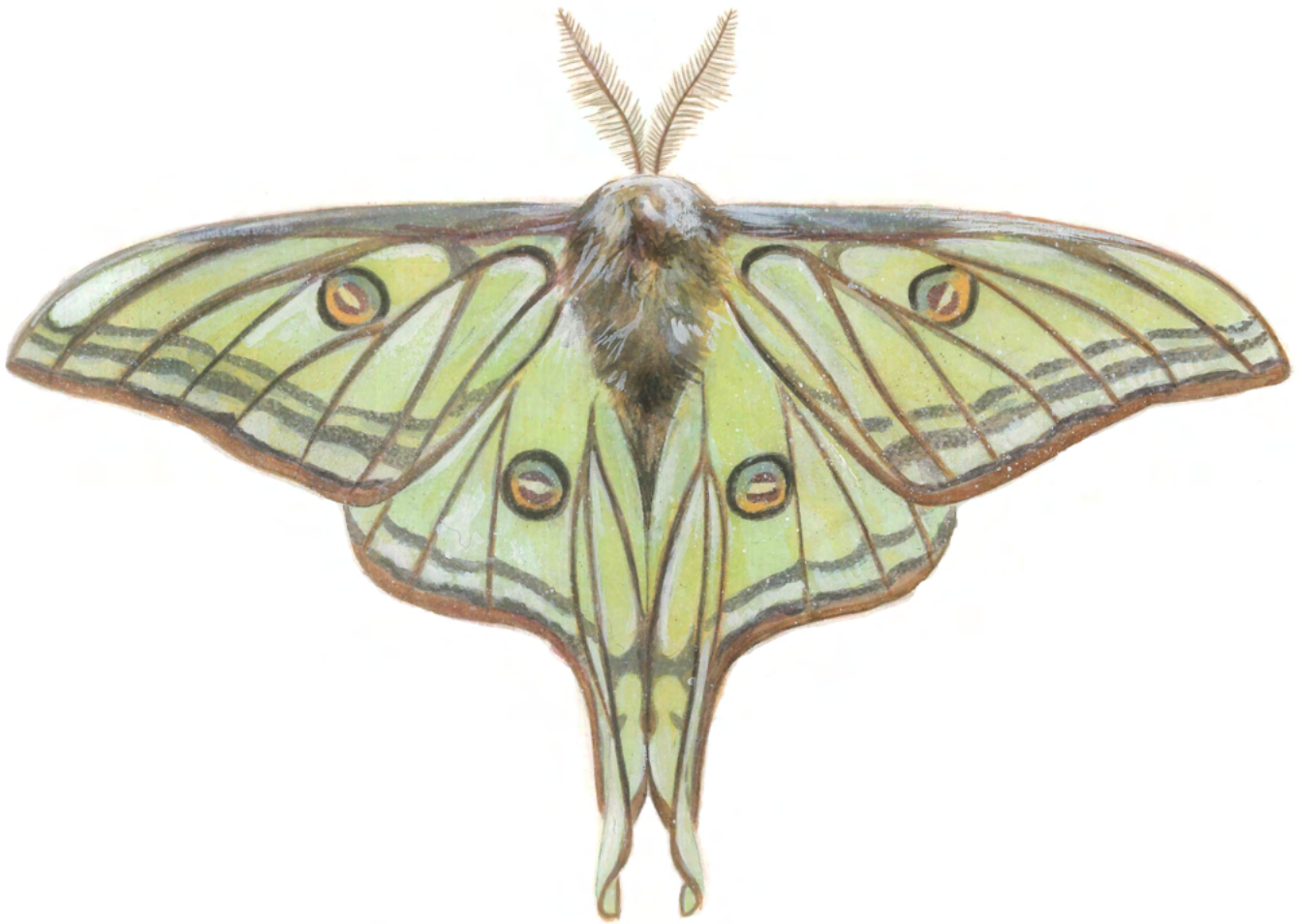
Managing Wildlife Diseases for Sustainable Ecosystems



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GRAELLSIA ISABELLAE

Spanish moon moth



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197	General E - Posters



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GENERAL INFORMATION

DATES

August 31 to September 2, 2021

LOCATION

Virtual

ORGANIZES AND CONVENES

Wildlife Disease Association WDA - European Wildlife Disease Association EWDA.

SCIENTIFIC-TECHNICAL SECRETARIAT

Viajes El Corte Inglés, S.A.
Scientific-Medical Congresses
Cuenca2020@viajeseci.es

VIRTUAL PLATFORM

The congress will start on Tuesday, August 31 at 9.00 am CEST, but you will be able to access on Monday, from 8:00 pm CEST in order to familiarize yourself with the platform.

The congress platform will give you the possibility to attend the scientific sessions, interact with the participants of the round tables by sending questions to the speakers and moderators, visit the electronic poster area and also the exhibition area, where you will be able to interact with the companies through written chat and/or live video calls.

You will have at your disposal the virtual bag, where you will find the congress program and your certificates and you will also be able to save in it all the information about the stands.

Conference contents will be available for recorded viewing until September 16th at 21:15 CEST.

UTC Summer 2021	Time diff. w/ Cuenca	15	16	17	18	19	20	21	22	23	24	1	2	3	4	5	6	7	8	9	10	11	12	13	14
UTC -8 Anchorage	-10																								
UTC -7 Los Angeles	-9																								
UTC -6 Calgary	-8																								
UTC -5 Chicago	-7																								
UTC -4 New York, Santiago (CH)	-6																								
UTC -3 Buenos Aires	-5																								
UTC +1 London	-1																								
UTC +2 CUENCA, Cairo	0																								
UTC +5.30 Dehli	3:30																								
UTC +8 Beijin, Perth	6																								
UTC +10 Sidney	8																								
UTC +12 Wellington	10																								



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SPONSORS

Platinum



Animal and Plant Health Inspection Service
U.S. DEPARTMENT OF AGRICULTURE

Gold



Silver



Bronze





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SCHEDULE

All times are in CEST (Central European Summer Time)

TUESDAY AUG. 31st - 69th WDA / 14th EWDA - Joint Virtual Conference			
Time	ROOM 1	Time	ROOM 2
9:00 - 13:00 Morning Sessions			
9:00 - 9:15	President welcome		
9:20 - 10:05	Plenary talk. Dr. Oliver Restif		
10:10 - 11:00	Scientific Session 1. Ecosystem health, global change and diseases	10:10 - 11:00	Scientific Session 2. Emerging and re-emerging wildlife diseases
10:10 - 10:25	S 1.1 (ID139)	10:10 - 10:25	S 2.1 (ID271)
10:25 - 10:40	S 1.2 (ID368)	10:25 - 10:40	S 2.2 (ID284)
10:40 - 10:55	S 1.3 (ID223)	10:40 - 10:55	S 2.3 (ID187)
11:00 - 11:30	Break / Networking / E-posters		
11:30 - 13:00	Scientific Session 3. Ecosystem health, global change and diseases	11:45 - 13:00	Scientific Session 4. Emerging/Neglected diseases
11:30 - 11:45	S 3.1 (ID 331)		
11:45 - 12:00	S 3.2 (ID 235)	11:45 - 12:00	S 4.2 (ID 85)
12:00 - 12:15	S 3.3 (ID 162)	12:00 - 12:15	S 4.3 (ID 143)
12:15 - 12:30	S 3.4 (ID 377)	12:15 - 12:30	S 4.4 (ID 119)
12:30 - 12:45	S 3.5 (ID 362)	12:30 - 12:45	S 4.5 (ID 160)
12:45 - 13:00	S 3.6 (ID267)	12:45 - 13:00	S 4.6 (ID 50)
17:00 - 21:00 Evening Sessions			
17:00 - 17:15	President welcome		
17:20 - 18:05	Plenary talk. Prof. A. Alonso Aguirre		
18:10 - 19:00	Scientific Session 5. Ecosystem health, global change and diseases	18:10 - 19:00	Scientific Session 6. New technological insights into wildlife disease surveillance
18:10 - 18:25	S 5.1 (ID 36)	18:10 - 18:25	S 6.1 (ID 345)
18:25 - 18:40	S 5.2 (ID 156)	18:25 - 18:40	S 6.2 (ID 358)
18:40 - 18:55	S 5.3 (ID 369)	18:40 - 18:55	S 6.3 (ID 332)
19:00 - 19:30	Break / Networking / E-posters		
19:30 - 21:00	Scientific Session 7. Impact of diseases on wildlife conservation	19:30 - 21:00	Scientific Session 8. Infection transmission at the wildlife-livestock-human interface
19:30 - 19:45	S 7.1 (ID 370)	19:30 - 19:45	S 8.1 (ID 339)
19:45 - 20:00	S 7.2 (ID 298)	19:45 - 20:00	S 8.2 (ID 229)
20:00 - 20:15	S 7.3 (ID 276)	20:00 - 20:15	S 8.3 (ID 261)
20:15 - 20:30	S 7.4 (ID 87)	20:15 - 20:30	S 8.4 (ID 206)
20:30 - 20:45	S 7.5 (ID 354)	20:30 - 20:45	S 8.5 (ID 253)
20:45 - 21:00	S 7.6 (ID 289)	20:45 - 21:00	S 8.6 (ID 164)
21:30 - 23:30 Student-Mentor Mixer			



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WEDNESDAY SEPT. 1 - 69th WDA / 14th EWDA - Joint Virtual Conference			
Time	ROOM 1	Time	ROOM 2
9:00 - 13:00 Morning Sessions			
9:00 - 9:45	Plenary talk. Prof. Anita Michel		
9:50 - 11:05	Student Session 1. Integrated monitoring of wildlife populations and disease	9:50 - 11:05	Student Session 2. Wildlife disease control, global change and ecosystem health
9:50 - 10:05	Student Scientific Session 1.1 (ID94)	10:10 - 10:25	Student Scientific Session 2.1 (ID274)
10:05 - 10:20	Student Scientific Session 1.2 (ID88)	10:25 - 10:40	Student Scientific zSession 2.2 (ID316)
10:20 - 10:35	Student Scientific Session 1.3 (ID322)	10:40 - 10:55	Student Scientific Session 2.3 (ID131)
10:35 - 10:50	Student Scientific Session 1.4 (ID61)	10:35 - 10:50	Student Scientific Session 2.4 (ID118)
10:35 - 10:50	Student Scientific Session 1.5 (ID236)	10:35 - 10:50	Student Scientific Session 2.5 (ID239)
11:05 - 11:30	Break / Networking / E-posters		
11:30 - 12:00	2020 Student Research Award Presentation		
12:00 - 12:30	2021 Student Research Award Presentation		
12:35 - 13:05	Student Session 3. Emerging and re-emerging wildlife diseases	12:35 - 13:05	Student Session 4. Host-pathogen interactions in wildlife
12:35 - 12:50	Student Scientific Session 3.1 (ID142)	12:35 - 12:50	Student Scientific Session 4.1 (ID67)
12:50 - 13:05	Student Scientific Session 3.2 (ID336)	12:50 - 13:05	Student Scientific Session 4.2 (ID384)
15:00 - 17:00	WDA Business meeting		
17:00 - 21:05 Evening Sessions			
17:00 - 17:45	Plenary talk. Prof. Meggan Craft		
17:50 - 19:00	Student Session 5. Integrated monitoring of wildlife populations and disease & Molecular Epidemiology	17:50 - 19:00	Student Session 6. Wildlife disease dynamics
17:50 - 18:05	Student Scientific Session 5.1 (ID268)	17:50 - 18:05	Student Scientific Session 6.1 (ID181)
18:05 - 18:20	Student Scientific Session 5.2 (ID277)	18:05 - 18:20	Student Scientific Session 6.2 (ID145)
18:20 - 18:35	Student Scientific Session 5.3 (ID182)	18:20 - 18:35	Student Scientific Session 6.3 (ID209)
18:35 - 18:50	Student Scientific Session 5.4 (ID215)	18:35 - 18:50	Student Scientific Session 6.4 (ID193)
18:50 - 19:05	Student Scientific Session 5.5 (ID48)	18:50 - 19:05	Student Scientific Session 6.5 (ID93)
19:05 - 19:30	Break / Networking / E-posters		
19:30 - 20:00	WDA-IAAAM Winner Presentation		
20:05 - 20:50	Student Session 7. Wildlife Disease Dynamics	20:05 - 20:50	Student Session 8. Emerging and re-emerging wildlife diseases
20:05 - 20:20	Student Scientific Session 7.1 (ID202)	20:05 - 20:20	Student Scientific Session 8.1 (ID133)
20:20 - 20:35	Student Scientific Session 7.2 (ID203)	20:20 - 20:35	Student Scientific Session 8.2 (ID152)
20:35 - 20:50	Student Scientific Session 7.3 (ID344)	20:35 - 20:50	Student Scientific Session 8.3 (ID204)



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THURSDAY SEPT. 2 - 69th WDA / 14th EWDA - Joint Virtual Conference			
Time	ROOM 1	Time	ROOM 2
9:00 - 11:00 Morning Sessions			
9:00 - 10:15	Scientific Session 9. Host-pathogen interactions in wildlife	9:00 - 10:15	Scientific Session 10. Integrated monitoring of wildlife populations and disease
9:00 - 9:15	S 9.1 (ID 319)	9:00 - 9:15	S 10.1 (ID 170)
9:15 - 9:30	S 9.2 (ID 337)	9:15 - 9:30	S 10.2 (ID 353)
9:30 - 9:45	S 9.3 (ID 255)	9:30 - 9:45	S 10.3 (ID 64)
9:45 - 10:00	S 9.4 (ID 186)	9:45 - 10:00	S 10.4 (ID 272)
10:00 - 10:15	S 9.5 (ID 74)	10:00 - 10:15	S 10.5 (ID 309)
10:15 - 10:45	Break / Networking / E-posters		
10:45 - 11:30	Plenary talk. Prof. Andrew P. Dobson		
11:30 - 13:00	Scientific Session 11. Infection transmission at the wildlife-livestock-human interface	11:30 - 13:00	Scientific Session 12. Integrated monitoring of wildlife populations and disease
11:30 - 11:45	S 11.1 (ID 183)	11:30 - 11:45	S 12.1 (ID 318)
11:45 - 12:00	S 11.2 (ID 103)	11:45 - 12:00	S 12.2 (ID 320)
12:00 - 12:15	S 11.3 (ID 275)	12:00 - 12:15	S 12.3 (ID 314)
12:15 - 12:30	S 11.4 (ID 127)	12:15 - 12:30	S 12.4 (ID 375)
12:30 - 12:45	S 11.5 (ID 234)	12:30 - 12:45	S 12.5 (ID 361)
12:45 - 13:00	S 11.6 (ID 222)	12:45 - 13:00	S 12.6 (ID 365)
15:00 - 16:30	Awards' Ceremony		
17:00 - 21:15 Evening Sessions			
17:00 - 17:45	Plenary Talk. AAWV Al Franzmann Speaker. Daniel J. O'Brien		
17:50 - 19:05	Scientific Session 13. Wildlife disease control	17:50 - 19:05	Scientific Session 14. Host-pathogen interactions in wildlife
17:50 - 18:05	S 13.1 (ID 256)	17:50 - 18:05	S 14.1 (ID 144)
18:05 - 18:20	S 13.2 (ID 60)	18:05 - 18:20	S 14.2 (ID 376)
18:20 - 18:35	S 13.3 (ID 201)	18:20 - 18:35	S 14.3 (ID 299)
18:35 - 18:50	S 13.4 (ID 111)	18:35 - 18:50	S 14.4 (ID 325)
18:50 - 19:05	S 13.5 (ID 150)	18:50 - 19:05	S 14.5 (ID 211)
19:05 - 19:30	Break / Networking / E-posters		
19:30 - 21:00	Scientific Session 15. Molecular epidemiology of wildlife pathogens	19:30 - 21:00	Scientific Session 16. Mixed thematic areas
19:30 - 19:45	S 15.1 (ID 185)	19:30 - 19:45	S 16.1 (ID 224)
19:45 - 20:00	S 15.2 (ID 265)	19:45 - 20:00	S 16.2 (ID 329)
20:00 - 20:15	S 15.3 (ID 269)	20:00 - 20:15	S 16.3 (ID 287)
20:15 - 20:30	S 15.4 (ID 290)	20:15 - 20:30	S 16.4 (ID 54)
20:30 - 20:45	S 15.5 (ID 191)	20:30 - 20:45	S 16.5 (ID 123)
20:45 - 21:00	S 15.6 (ID 310)		
21:00 - 21:15	Closure		



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August 31, Tuesday

MORNING SESSIONS

- 09:20 - 10:05 Plenary Talk**
Reservoirs Sans Frontières: can ecology help us predict viral spillover risk from bats?
Chair: Marie-Pierre Ryser-Degiorgis
Speaker: Dr. Olivier Restif
- 10:10 - 11:00 Session 1. Ecosystem health, global change and diseases.**
Chair: Marie-Pierre Ryser-Degiorgis
- 10:10 - 10:25 ID 139. *Thinking about transformative changes in wildlife health activities***
Thijs Kuiken, Lineke Begeman, Jorge R. Lopez-Olvera, Beatriz Rubio Alonso, Graham Smith, Ana P. Vale, Barbara R. Vogler
Chair: Karin Lemberger
- 10:25 - 10:40 ID 368. *Can we reduce the risk to ecosystems from conservation translocations through use of disease risk analysis?***
Anthony W. Sainsbury
- 10:40 - 10:55 ID 223 *Cavers care deeply about bats – but there are some important gaps in knowledge and biosecurity habits regarding White Nose Syndrome. A survey of delegates to an international caving conference (SPELEO 2017).***
Jasmin Hufschmid, Soraya Salleh, Keren Cox-Witton
- 10:10 - 11:00 Session 2. Emerging and re-emerging wildlife diseases.**
- 10:10 - 10:25 ID 271. *Ecology of West Caucasian Bat Lyssavirus (WCBV) in a group of Schreibers' bent-winged bats (Miniopterus schreibersii) from Italy and its spillover to a domestic cat***
Stefania Leopardi, Dino Scaravelli, Petra Drzewniokova, Pamela Priori, Giuseppe Manna, Andrea Lombardo, Celogero Terregino, Paola De Benedictis
- 10:25 - 10:40 ID 284. *Surveillance of West Nile Virus (WNV) in living wild birds from Peloponnese Region in Southern Greece***
Marina Sofia, Alexios Giannakopoulos, Antonia Touloudi, Zoi Athanasakopoulou, Dimitris C. Chatzopoulos, Vassiliki Spyrou, Maria Satra, Dimitrios Galamatis, Vassilis Diamantopoulos, Spyridoula Mpellou, Charalambos Billinis
- 10:40 - 10:55 ID 187. *A novel approach to a novel pathogen: student-powered surveillance of Batrachochytrium salamandrivorans***
Olga Milenkaya, Brittany A. Mosher, Jenifer B. Walke, Oliver Hyman, Sasha E. Greenspan, Michelle S. Koo, Daniel A. Grear, Michael J. Adams
- 11:30 - 13:00 Session 3. Ecosystem health, global change and diseases.**
Chairs: Andrew Peters & Ursula Höfle
- 11:30 - 11:45 ID 331. *Effects of heat stress on the response of wild captive birds of prey and owls to handling and immunization against West Nile virus***
Ursula Höfle, Juan Manuel Blanco, Pilar Alberdi
- 11:45 - 12:00 ID 235. *Prevalence of hantavirus in bank voles and humans: the effect of wildlife and environmental factors***
Yingying Wang, Liina Voutilainen, Mahdi Aminikhah, Heikki Helle, Otso Huitu, Juha Laakkonen, Jukka Niemimaa, Jussi Sane, Tarja Sironen, Olli Vapalahti, Heikki Henttonen, Eva Kallio
- 12:00 - 12:15 ID 162. *Carriage of antibiotic resistant bacteria in endangered and declining Australian pinniped pups***
Mariel Fulham, Rachael Gray, Rebecca McIntosh, Fiona Mcdougall, Michelle Power
- 12:15 - 12:30 ID377. *Exposure to low salinity waters identified as cause of the 2019 Northern Gulf of Mexico bottlenose dolphin unusual mortality event***
Alissa C. Deming, Debra Moore, Tim Morgan, Mackenzie Russell, Gabriella Vasquez, Lauren Albrittain, Brittany Baldrice, Blair Mase, Erin Fougères, Kathleen Colegrove, Alex Costidis, Brian Dzwonkowskj, Steve Dykstra, Teri Rowles, Lance Garrison, Jenny Litz, Deborah Fauquier



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- 12:30 - 12:45 *ID 362. Demographic trends and skin lesion prevalence of stranded bottlenose dolphins following a freshwater event*
Jennifer Bloodgood, Cristina Díaz Clark, Mackenzie Russell, Ruth Carmichael, Alissa Deming
- 12:45 - 13:00 *ID 267. Linking zoonotic disease prevalence to human and livestock exposure risk across a gradient of anthropogenic land use in Madagascar*
Kayla M. Kauffman, Jérémy Dubrulle, Fiona Baudino, Victoria Carcauzon, Camille Lebarbenchon, Toky M. Randriamoria, Tamby N. Ranaivoson, Jean Yves Rabezara, Courtney Werner, Georgia Titcomb, Michelle Pender, Julie T. Shapiro, Shai Pilosof, Peter J. Mucha, James Moody, Voahangy Soarimalala, Steven M. Goodman, Pablo Tortosa, Charles L. Nunn
- 11:45 - 13:00 **Session 4. Emerging & neglected wildlife diseases.**
Chairs: Graham Smith & Dolores Gavier-Widén
- 11:45 - 12:00 *ID 85. Rabies, Lyssaviruses and 'small mammals': reservoirs, vectors, victims, phantasms, or ...?*
Charles E. Rupprecht, Ryan Wallace, Thomas Mueller
- 12:00 - 12:15 *ID 143. Retrospective study on avian paramyxoviruses in wild birds in the United States identifies several putative new species*
Kelsey T. Young, Jazz Q. Stephens, Rebecca L. Poulson, David E. Stallknecht, Kiril M. Dimitrov, Salman L. Butt, James B. Stanton
- 12:15 - 12:30 *ID 119. Domestic dogs as bridges for disease between wildlife and indigenous Waiwai in Guyana, South America*
Marissa Milstein, Christopher Shaffer, Philip Suse, Aron Marawanaru, Daniel Heinrich, Peter Larsen, Tiffany Wolf
- 12:30 - 12:45 *ID 160. RT-QuIC detection of CWD prion seeding activity in white-tailed deer muscle tissues*
Manci Li, Marc D. Schwabenlander, Gage R. Rowden, Jeremy M. Schefers, Chris S. Janelle, Michelle Carstensen, Davis Seelig, Peter A. Larsen
- 12:45 - 13:00 *ID 50. The implementation gap in managing emerging disease risks in the wildlife trade*
Craig Stephen, Luís Pedro Carmo, Damarys De Las Nieves Montano Valle, Brian Fricker, Filipe Maximiano Sousac, Beatriz Vidondoc

AFTERNOON SESSIONS

- 17:20 - 18:05 **Plenary Talk.**
Illegal wildlife trade and emerging infectious diseases: pervasive impacts to species, ecosystems and human health
Chair: Jonna Mazet
Speaker: Prof. A. Alonso Aguirre
- 18:10 - 19:00 **Session 5. Ecosystem health, global change and diseases.**
Chair: Jonna Mazet
- 18:10 - 18:25 *ID 36. Combined effects of land use practices and weather on the abundance and presence of mosquito-borne disease vectors and mosquito diversity in Eastern Ontario*
Rindra Miarisoa Rakotoarinia, David Lapen, Patrick Leighton, Nicholas Ogden, Antoinette Ludwig
- 18:25 - 18:40 *ID 156. Climate and long term trends in pathogen seroprevalence in polar bears (Ursus maritimus) in the western Canadian Arctic*
Emily Jenkins, Nicholas Pilfold, Evan Richardson, John Ellis, Brad Scandrett, Adrián Hernández-Ortiz, Kayla Buhler, David Mcgeachy, Batol Al-Adhami, Kelly Konecsni, Vladislav Lobanov, Megan Owen, Bruce Rideout, Nicholas Lunn
- 18:40 - 18:55 *ID 369. Are introduced rodents involved in disease outbreaks threatening subantarctic wildlife?*
Amandine Gamble, Baudouin Des Monstiers, Lorien Boujot, Romain Dedet, Augustin Clessin, Marine Bely, Romain Garnier, Jérémy Tornos, Hubert Gantelet, Nicolas Keck, Thierry Boulinier



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- 18:10 - 19:00** **Session 6. New technological insights into wildlife disease surveillance.**
Chair: Thijs Kuiken
- 18:10 - 18:25** *ID 345. Population connectivity protects desert bighorn sheep from infectious pneumonia*
Brian Dugovich, Brianna Beechler, Brian Dolan, Rachel Crowhurst, Ben Gonzales, Jenny Powers, Debra Hughson, Regina Vu, Clinton Epps, Anna Jolles
- 18:25 - 18:40** *ID 358. New diagnostic techniques to characterize fetal, placental, and maternal health in bottlenose dolphins following the deepwater horizon oil spill*
Forrest M. Gomez, Cynthia R. Smith, Kathleen M. Colegrove, Whitney Musser, Jennifer M. Meegan, Ashley Barratclough, Jeanine S. Morey, Ryan Takeshita, Marina Ivancic, Abraham Cardenas Llerenas, Teri K. Rowles, Veronica Cendejas, Eric Zolman, Lori Schwacke
- 18:40 - 18:55** *ID 332. Re-evaluating ideal release weight for rehabilitated harbor seal (Phoca vitulina) pups*
Sarah J. Teman, Denise J. Greig, Sarah Wilkin, Joseph K. Gaydos
- 19:30 - 21:00** **Session 7. Impact of diseases on wildlife conservation.**
Chairs: Francisco Ruiz-Fons & Isabel G. Fenandez de Mera
- 19:30 - 19:45** *ID 370. Structured decision-making: a tool for disease risk analysis and management planning in the face of uncertainty*
Katie Beckmann, Peter Cranswick, Geoff Hilton, Nigel Jarrett, Andrew Routh, Natacha Rasolozaka, Michelle O' Brien, Anthony Sainsbury, Ruth Cromie, Björn Beckmann, Taiana Costa, Daniel Calvo-Carrasco, Andrew Bamford, Richard Kock, Stefano Canessa, John Ewen
- 19:45 - 20:00** *ID 298. Investigating the risk from disease in a proposed assisted colonization of an extinct in the wild species, the sihek (Guam kingfisher, Todiramphus cinnamominus)*
Claudia Carraro, Stefano Canessa, Suzanne Medina, Anthony Sainsbury, Amanda Trask, John Ewen, Deidre K. Fontenot, Scott Newland
- 20:00 - 20:15** *ID 276. Setting the terms for zoonotic diseases: effective communication for research, conservation, and public policy*
Julie Teresa Shapiro, Luis Viquez-R, Stefania Leopardi, Amanda Vicente-Santos, Ian H. Mendenhall, Winifred F. Frick, Rebekah C. Kading, Rodrigo A. Medellín, Paul Racey, Tigga Kingston
- 20:15 - 20:30** *ID 87. Protect people, protect bats, avoid rabies!*
Mark L. Drew, Rita D. Dixon, David MCGowan, Leslie Tengelsen
- 20:30 - 20:45** *ID 354. What are the effects of pathogens in pregnancy and body condition of tundra caribou?*
Xavier Fernandez Aguilar, Lisa Marie Leclerc, Kugluktuk Angoniatit Association, Emmanuel Serrano, Niroshan Thantrige-Don, Om Surujballi, Gabriela Mastromonaco, Susan Kutz
- 20:45 - 21:00** *ID 289. Host exposure history alters pathogen transmission and virulence in a wild songbird*
Ariel E. Leon, Arietta E. Fleming-Davies, James S. Aldeman, Dana M. Hawley
- 19:30 - 21:00** **Session 8. Infection transmission at the wildlife-livestock-human interface.**
Chairs: Sonia Hernández & Jorge López-Olvera
- 19:30 - 19:45** *ID 339. Wildlife surveillance at mink farms in the US following SARS-CoV-2 outbreaks*
Susan A. Shriner, Thomas J. Deliberto
- 19:45 - 20:00** *ID 229. Sensitivity of international notification system of wildlife diseases: a case study using WAHIS data on tularemia*
Angela Fanelli, Paula Caceres-Soto, François Diaz, Keith Hamilton, Peter Melens, Roberta Morales, Lina Mur, Sophie Muset, Lorenz Nake, Lesa Thompson, Tiggy Grillo, Chadia Wannous, Paolo Tizzani
- 20:00 - 20:15** *ID 261. Assessing the animal and public health hazard of urban wild boars using an Agent-Based Model approach*
Carlos Gonzalez-Crespo, Beatriz Martinez-Lopez, Carles Conejero, Raquel Castillo-Contreras, Emmanuel Serrano, Josep Maria Lopez-Martin, Santiago Lavin, Jorge Ramon Lopez-Olvera
- 20:15 - 20:30** *ID 206. Search and find: zoonoses of urban wild boar in Barcelona, Spain*
Raquel Castillo-Contreras, Gregorio Mentaberre, Carles Conejero, Marta Valdeperes, Xavier Fernández Aguilar, Jordi Serra-Cobo, Richard Birtles, Marta Cerdà-Cuellar, Gustavo Del Real, Abir Monastiri, Marc López-Roig, Andreu Colom-Cadena, Jessica L. Hall, Paloma Encinas, Stefania Tampach, Santiago Lavín, Jorge Ramón López-Olvera



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- 20:30 - 20:45 *ID 253. Evaluating interspecific transmission of ticks, fleas and canine vector-borne pathogens between dogs and foxes in a human-dominated landscape*
Aitor Cevidanes, Sophia Di Cataldo, Claudia ulloa, Irene Sacristán, Nicole Sallaberry, Sebastián Klarian, Fernando Esperón, Javier Millán
- 20:45 - 21:00 *ID 164. Occurrence and significance of psittacosis caused by Chlamydia psittaci in garden birds in Sweden.*
Ellinor Spörndly-Nees, Henrik Uhlhorn, Tomas Jinnerot, Aleksija Neimanis



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September 1, Wednesday

MORNING SESSIONS

- 09:00 - 09:45 **Plenary Talk.**
Wildlife through the lens of One Health: An African perspective
Chair: Tiggy Grillo
Speaker: Prof. Anita Michel
- 09:50 - 11:05 **Student scientific session 1. Integrated monitoring of wildlife populations and disease.**
Chairs: Lineke Begeman & Gabor Czirjak
- 09:50 - 10:05 *ID 94. A One Health Approach to the Impact of Trace Metal Contamination from Derelict Lead Mines in Wales*
Andrea Isabel Sartorius, Scott Young, Malcolm Bennett, Matthew Johnson, Kerstin Baiker, Paul Edwards, Lisa Yon
- 10:05 - 10:20 *ID 88. The shedding of paramyxovirus RNA in the urine of straw-coloured fruit bats (*Eidolon helvum*)*
Elli Rosa Jolma, Louise Gibson, Grace Fleischer, Samuel Asumah, Richard Suu-Ire, Olivier Restif, James L. N. Wood, Andrew A. Cunningham
- 10:20 - 10:35 *ID 322. Patterns of gammaherpesvirus reactivation in genital tract linked to stressors in European badgers (*Meles meles*)*
Ming-Shan Tsai, Sarah François, Chris Newman, David W Macdonald, Christina D Buesching
- 10:35 - 10:50 *ID 61. Fate of Lynx orphans in Switzerland: A retrospective study*
Stéphanie Borel, Andreas Ryser, Anja Molinari-Jobin, Mainity Batista Linhares, Iris Marti, Francesco Origi, Christine Breitenmoser, Marie-Pierre Ryser-Degiorgis
- 10:50 - 11:05 *ID 236. Capture and transport of white rhinoceroses (*Ceratotherium simum*) cause shifts in their gut bacterial microbiota composition more towards potential pathogens*
Carolin Frei, Friederike Pohlin, Leith Meyer, Narciso Martin Quijada, Beate Conrady, Franz-Ferdinand Roch, Cameron Strachan, Markus Hofmeyr, Gabrielle Stalder, Stefanie Urimare Wetzels
- 09:50 - 11:05 **Student scientific session 2. Wildlife disease control, global change and ecosystem health.**
Chairs: Stuart Patterson & Miriam Maas
- 09:50 - 10:05 *ID 274. Modelling the effect of climate change on spatiotemporal transmission of parasitic disease in reindeer*
Anna Ciezarek, Rebecca K. Davidson, Torill Mork, Geir Rune Rauset, Diana J. Williams, Hannah Rose Vineer
- 10:05 - 10:20 *ID 316. Investigating the transmission of gastro-intestinal nematodes between livestock and roe deer using deep-sequencing analyses*
Camille Beaumelle, Hélène Verheyden, Libby Redman, Jill De Rijke, Florence Veyssière, Noémie Bégoc, Slimania Benabed, Bruno Cargnelutti, Bruno Lourtet, Marie-Thérèse Poirel, Glenn Yannic, Philippe Jacquiet, John S Gilleard, Gilles Bourgoin
- 10:20 - 10:35 *ID 131. Toxoplasma gondii infection in the protected Eurasian lynx (*Lynx lynx*) in Switzerland*
Patrick Scherrer, Marie-Pierre Ryser-Degiorgis, Stéphanie Borel, Caroline F. Frey, Walter U. Basso
- 10:35 - 10:50 *ID 118. Evaluating the application of a novel serological assay in wild red deer for a tuberculosis surveillance program in Spain*
Elisa Ferreras-Colino, María Ángeles Risalde, Inmaculada Moreno, María De La Cruz Arnal, Ana Balseiro, Mercedes Domínguez, Daniel Fernández De Luco, Christian Gortázar
- 10:50 - 11:05 *ID 239. Ivermectin plasma concentration in Iberian Ibex (*Capra pyrenaica hispanica*) following oral administration*
Barbara Moroni, José Enrique Granados, Jorge ramón López-Olvera, Arián Ráez-Bravo, José espinosa Cerrato, Gregorio Mentaberre, Paulino Fandos, Marco Pazzi, Monica Romagnoli, Giulia Gardini, Luca Rossi, Marta Valldeperes, Emmanuel Serrano, Blanca Ramos, Rosangela Odore



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September 1, Wednesday

- 11:30 - 12:00** **2020 Student Research Recognition Award. Feline leukemia virus (felv): an emerging threat to wild felids without protection from endogenous feline leukemia virus (enfelv)**
Chair: Tiggy Grillo
Spaker: Elliott Chiu
- 12:00 - 12:30** **2021 Student Research Recognition Award. An apathogenic virus predicts transmission dynamics of a pathogen and reveals paradoxes and synergies in pathogen management in the florida panther (*puma concolor coryi*)**
Chair: Tiggy Grillo
Spaker: Marie Gilbertson
- 12:35 - 13:05** **Student scientific session 3. Emerging and re-emerging wildlife diseases.**
Chair: Lineke Begeman
- 12:35 - 12:50** *ID 142. Epidemiology and molecular characterization of canine bufavirus and cachavirus in grey wolves (*Canis lupus*) of the Northwest Territories*
Kelsi Fry, Marta Canuti, H. Dean Cluff, Heather Fenton, Andrew Lang
- 12:50 - 13:05** *ID 36. Evaluating black bear (*Ursus americanus*) survival and recovery from sarcoptic mange*
Hannah S. Tiffin, Justin D. Brown, Mark Ternent, Jennifer M. Mullinax, Erika T. Machtinger
- 12:35 - 13:05** **Student scientific session 4. Host-pathogen interactions in wildlife.**
Chair: Stuart Patterson
- 12:35 - 12:50** *ID 67. Semi-quantitative serology unveils the epidemiology of Myxoma and Rabbit Haemorrhagic Disease viruses in the European rabbit*
Joana Coelho, Henrique Pacheco, Paulo Célio Alves, Nuno Santos
- 12:50 - 13:05** *ID 384. Pathological changes and viral antigen distribution in tissues of Iberian hare (*Lepus granatensis*) infected with myxoma virus*
Irene Agulló-Ros, Ignacio García-bocanegra, Débora Jiménez-Martín, Leonor Camacho-Sillero, Christian Gortázar, Lorenzo Capucci, David Cano-Terriza, Félix Gómez-Guillamón, Irene Zorrilla, Antonio Lavazza, Maria A. Risalde

AFTERNOON SESSIONS

- 17:00 - 17:45** **Plenary Talk.**
Understanding pathogen transmission in a solitary, secretive carnivore (*Puma concolor*)
Chair: Justin Brown
Speaker: Prof. Meggan Craft t
- 17:50 - 19:05** **Student scientific session 5. Integrated monitoring of wildlife populations and disease & molecular epidemiology.**
Chairs: Anne-Justice Allen & Justin Brown
- 17:50 - 18:05** *ID 268. Metagenomic detection of tick-borne pathogens using nanopore adaptive sequencing*
Evan J. Kipp, Laramie L. Lindsey, Benedict Khoo, Christopher Faulk, Jonathan D. Oliver, Peter A. Larsen
- 18:05 - 18:20** *ID 277. Using metabarcoding to study effective contact for brainworm transmission between moose and gastropods*
Tyler J. Garwood, Seth A. Moore, Nicholas M. Fountain-Jones, Peter A. Larsen, Tiffany M. Wolf
- 18:20 - 18:35** *ID 182. Coccidian parasites in harvested Beluga whale (*Delphinapterus leucas*) and Caribou (*Rangifer tarandus*) in the Canadian North*
Adrián Hernández Ortiz, Émilie Bouchard, Rajnish Sharma, Sonja K. Ostertag, Lisa L. Loseto, Ellen Avard, Patrick Leighton, Emily J. Jenkins
- 18:35 - 18:50** *ID 215. Population impacts of domoic acid exposure in Southern Sea otters: an increasing threat in a changing climate*
Megan E. Moriarty, M. Tim Tinker, John L. Largier, Melissa A. Miller, Christine K. Johnson



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- 18:50 - 19:05 *ID 48. Exploring the use of the erythrocyte sedimentation rate as an inflammatory marker for free ranging wildlife - a case study in African buffalo (*Syncerus caffer*)*
Eberle Elizabeth Yarborough, Brianna Beechler, Caroline Glidden, Jennifer Johns, Courtney Coon, Claire Couch, Danielle Sisson, Anna Jolles
- 17:50 - 19:09 **Student scientific session 6. Wildlife disease dynamics**
Chairs: Laurie Baeten & Heather Fenton.
- 17:50 - 18:05 *ID 181. Using whole-genome sequencing and a One Health approach to understand the epidemiology of Salmonella and associated antimicrobial resistance at the human, wildlife, environmental, and livestock interface in southern Ontario*
Nadine A. Vogt, Benjamin M. Hetman, David L. Pearl, Richard J. Reid-Smith, Adam A. Vogt, E. Jane Parmley, Stefanie Kadykalo, Kim Ziebell, James Robertson, John H. E. Nash, Amrita Bharat, Michael R. Mulvey, Vanessa Allen, Nicole Ricker, Kristin J. Bondo, Samantha E. Allen, Claire M. Jardine
- 18:05 - 18:20 *ID 145. Differential response to anthropogenic disturbance by cave-dwelling bats: an eco-immunological approach*
Amanda Vicente-Santos, Bernal Rodriguez-Herrera, Eugenia Corrales Aguilar, David J. Civitello, Gábor Á. Czirják, Thomas R. Gillespie
- 18:20 - 18:35 *ID 209. Evaluating associations between environmental parameters and *Ophidiomyces ophidiicola*, the causative agent of ophidiomycosis (snake fungal disease)*
Michelle Waligora, Csaba Varga, Ellen Haynes, Matthew Allender
- 18:35 - 18:50 *ID 193. Opposing mechanisms lead to non-monotonic patterns between competitors and disease: A theoretical investigation with a directly-transmitted zoonosis*
Andreas Eleftheriou, Angela D. Luis
- 18:50 - 19:05 *ID 93. Experimental susceptibility of North American raccoons (*Procyon lotor*) and striped skunks (*Mephitis mephitis*) to SARS-CoV-2*
Raquel Francisco, Sonia M. Hernandez, Daniel G. Mead, Kayla G. Adcock, Sydney C. Burke, Nicole M. Nemeth, Michael J. Yabsley
- 19:30 - 20:00 **WDA-IAAAM winner presentation. Esophageal measurement of core body temperature in the Florida manatee (*Trichechus manatus latirostris*)**
Chair: Julie Melotti
Speaker: Molly Martony
- 20:05 - 20:50 **Student scientific session 7. Wildlife Disease Dynamics.**
Chair: Julie Melotti
- 20:05 - 20:20 *ID 202. Epidemiology of ophidiomycosis in Lake Erie watersnakes (*Nerodia sipedon insularum*)*
Ellen Haynes, Kristin Stanford, Kathryn Vivirito, Kennymac Durante, Allison Wright, Csaba Varga, Matthew C. Allender
- 20:20 - 20:35 *ID 203. Causes of bald eagle morbidity and mortality in the Eastern United States from 1989 to 2021*
Aidan M. O'Reilly, Mark G. Ruder, M. Kevin Keel, Heather Fenton, Nicole M. Nemeth
- 20:35 - 20:50 *ID 344. Temporal and spatial patterns in Canine Distemper Virus cases in wildlife diagnosed at the Southeastern Cooperative Wildlife Disease Study (SCWDS), 1975-2019*
Jonathan Wilson, Kishana Taylor, Andrew Park, Nicole Nemeth, Michael Yabsley, Heather Fenton, Kevin Keel, Nicole Gottdenker
- 20:05 - 20:50 **Student scientific session 8. Emerging and re-emerging wildlife diseases.**
Chair: Heather Fenton
- 20:05 - 20:20 *ID 133. Domestic Turkeys as an Experimental Model for Lymphoproliferative Disease Virus in Wild Turkeys*
Chloe Chan Goodwin, Kayla Guinn Adcock, Charbel Elie Gerges, Sydney Burke, Mark Gregory Ruder, Rebecca Lynne Poulson, Nicole Marie Nemeth
- 20:20 - 20:35 *ID 152. Susceptibility of wild turkeys (*Meleagris gallopavo*) to experimental West Nile virus infection*
Melanie R. Kunkel, Daniel G. Mead, Mary Jo Casalena, Mitchell Blake, Mark G. Ruder, Nicole M. Nemeth



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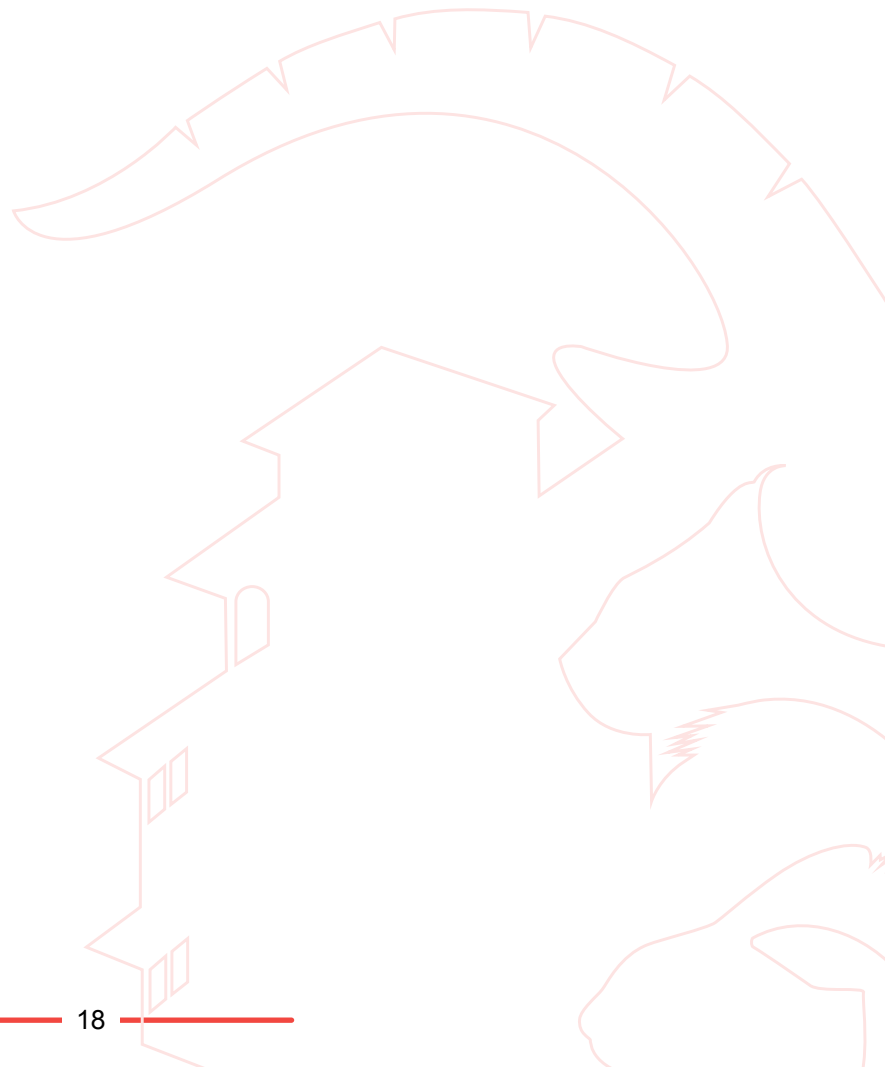


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20:35 - 20:50

ID 204. What is Blackhead Disease in Free-Ranging Wild Turkeys (Meleagris gallopavo)?: Comparison of Tetratrichomonas gallinarum, Simplicimonas sp., and Tritrichomonas sp. infections with Histomonas meleagridis

Rowan E. Back, Michael J. Yabsley, Kayla Buck Garrett, Melanie R. Kunkel, Charlie Bahnson, Rebecca Radisic, Elizabeth Elsmo, Nicole M. Nemeth





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09:00 - 13:00 **Morning Session**

09:00 - 10:15 **Session 9. Host-pathogen interactions in wildlife.**

Chairs: Emmanuelle Gilot-Fromont & Céline Richomme

09:00 - 09:15 *ID 319. A century of co-infection research: a review*

Cristina Garrido-Amaro, Roser Velarde, Anna E. Jolles, Nicholas M. Fountain-Jones, Konstans Wells, Alison Peel, Jorge R. López-Olvera, Emmanuel Serrano

09:15 - 09:30 *ID 337. Spatial modelling of Hyalomma lusitanicum ticks shape Crimean-Congo haemorrhagic fever virus exposure in Doñana National Park, Spain*

Alfonso Peralbo-Moreno, Raúl Cuadrado-Matías, Sara Baz-Flores, Patricia Barroso, Roxana Triguero-Ocaña, Saúl Jiménez-Ruiz, Pelayo Acevedo, Francisco Ruiz-Fons

09:30 - 09:45 *ID 255. Previous Usutu virus infection induces clinical protection against West Nile virus infection in grey partridges (Perdix perdix)*

Elisa Pérez-Ramírez, Francisco Llorente, Cristina Cano-Gómez, Pilar Aguilera-Sepúlveda, María Del Carmen Barbero, Mathieu Sarasa, Jovita Fernández-Pinero, Miguel Ángel Jiménez-Clavero

09:45 - 10:00 *ID 186. Gut microbiota diversity and composition is associated with infection and coinfection status and individual pathogens in wild bank voles (Myodes glareolus)*

Ilze Brila, Anton Lavrinienko, Eugene Tukalenko, Eva Riikka Kallio, Tapio Mappes, Phillip Charles Watts

10:00 - 10:15 *ID 74. The roles of mammalian predators in the epidemiology of Francisella tularensis in north west Spain*

Francois Mougeot, Raquel Escudero, Xavier Lambin, Fernando Jubete, María Dolores Vidal Roig, Silvia Herrero Cofreces, Rosa Gonzales, Veronica Merino, Isabel Jado, Juan José Luque Larena

ROOM 2

09:00 - 13:00 **Morning Session**

09:00 - 10:15 **Session 10. Integrated monitoring of wildlife populations and disease.**

Chairs: Becki Lawson & Joaquín Vicente

09:00 - 09:15 *ID 170. Mallards on the leash: Why don't they bark for HPAIV intruders?*

Anja Globig, Anne Günther, Timm Harder, Angele Breithaupt, Christian Grund, Klaus Depner, Laura Zani, Frank Busch, Anne Pohlmann, Martin Beer, Thomas C. Mettenleiter

09:15 - 09:30 *ID 353. Descriptive epidemiology and genetic characterisation of Trichomonas gallinae infections in ornithophilous birds of prey from North-Western France (2012-2015)*

Carole Godin, Maggy Jouglin, Laurence Malandrin, Philippe Gourlay

09:30 - 09:45 *ID 64. Implementing environmental DNA detection method in the surveillance of amphibian pathogen Batrachochytrium salamandrivorans*

David Lastra González, Vojtech Baláž, Jirí Vojar, Petr Chajma

09:45 - 10:00 *ID 272. Investigation about mortality in a hedgehog's population in Northern Italy*

Tiziana Trogu, Sabrina Canziani, Sara Salvato, Clara Tolini, Anna Castelli, Silva Rubini, Martina Munari, Davide Tartari, Lorenzo Borghi, Enrica Sozzi, Davide Lelli, Antonio Lavazza, Ana Moreno

10:00 - 10:15 *ID 309. ENETWILD project: towards harmonising mammal integrated monitoring in Europe*

Ezio Ferroglio, Pelayo Acevedo, Marco Apollonio, Jose Antonio Blanco, Francesca Brivio, Jim Casaer, Guillaume Body, Patrick Jansen, Sonia Illanas, Oliver Keuling, Kamila Pliš, Tomasz Podgorsky, Massimo Scandura, Graham Smith, Rachele Vada, Stefania Zanet, Joaquín Vicente

10:15 - 10:45 **Break / networking / e-posters**



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- 10:45 - 11:30 Plenary talk**
The Ecology, Economics and Evolution of Emerging Pathogens
Chair: Christian Gortázar
Speaker: Prof. Andrew P. Dobson
- 11:30 - 13:00 Session 11. Infection transmission at the wildlife-livestock-human interface.**
Chairs: Ana Balseiro & Christian Gortázar
- 11:30 - 11:45 ID 183. Investigation on the role of red fox in TB maintenance community – second opus: experimental infection with a virulent field Mycobacterium bovis strain**
Céline Richomme, Sandrine Lesellier, Francisco Javier Salguero, Jacques Laurent Barrat, Jean-Marc Boucher, Jennifer Reys-Reys, Sylvie Hénault, Kristel De Cruz, Lorraine Michelet, Konstantin Lyashchenko, Conor O'Halloran, Ana Balseiro, Maria Laura Boschioli
- 11:45 - 12:00 ID 103. Interaction patterns between wildlife and cattle assessed by camera traps reveal chances for mycobacteria transmission in Atlantic habitats**
Lucía Varela-Castro, Iker A. Sevilla, Ariane Payne, Emmanuelle Gilot-Fromont, Marta Barral
- 12:00 - 12:15 ID 275. Spatial epidemiology of animal tuberculosis at the wildlife-livestock interface at national scale**
César Herráiz, Joaquín Vicente, Christian Gortázar, Pelayo Acevedo
- 12:15 - 12:30 ID 127. Spatial and temporal distribution of Mycobacterium tuberculosis complex infection in Eurasian badger (Meles meles) and cattle in Asturias, Spain**
Cristina Blanco Vázquez, Thiago Doria Barral, Beatriz Romero, Manuel Queipo, Isabel Merediz, Pablo Quirós, José Ángel Armenteros, Ramón Juste, Lucas Domínguez, Mercedes Domínguez, Rosa Casais, Ana Balseiro
- 12:30 - 12:45 ID 234. Stable prevalence of Coxiella burnetii in wildlife after a decade of surveillance in the Basque Country (northern Spain)**
Ion I. Zendoia, Aitor Cevitanes, Patricia Vázquez, Jesús F. Barandika, Ana Hurtado, Marta Barral, Ana L. García-Pérez
- 12:45 - 13:00 ID 222. Small mammals are reservoirs for multiple zoonotic pathogens**
Elisabeth Schmidt

ROOM 2

- 11:30 - 13:00 Session 12. Integrated monitoring of wildlife populations and disease.**
Chairs: Gudrun Wibbelt & Erik Ågren
- 11:30 - 11:45 ID 318. MAMMALNET project: citizen and open science at the service of mammal population monitoring in Europe**
Graham Smith, Pelayo Acevedo, Marco Apollonio, Daniel Beltran-Alcrudo, Jose Antonio Blanco, Jim Casaer, Ezio Ferroglio, Mark Hovari, Patrick Jansen, Oliver Keuling, Rafal Kowalczyk, Tomasz Podgorski, Massimo Scandura, Joanna Stojak, Rachele Vada, Stefania Zanet, Joaquin Vicente
- 11:45 - 12:00 ID 320. Retroviral infection affects reproduction and survival of female wild turkeys**
Stephanie A. Shea, Matthew B. Gonnerman, Erik J. Blomberg, Kelsey M. Sullivan, Pauline L. Kamath
- 12:00 - 12:15 ID 314. Health of wild fish exposed to contaminants of emerging concern in freshwater ecosystems utilized by a Minnesota Tribal community**
Jessica R. Deere, Mark D. Jankowski, Alexander Primus, Nicholas B. D. Phelps, Mark Ferrey, Joanna Borucinska, Matteo Convertino, Joseph L. Servadio, Yvette Chenaux-Ibrahim, E. J. Isaac, Randall S. Singer, Dominic A. Travis, Seth Moore, Tiffany M. Wolf
- 12:15 - 12:30 ID 375. Operationalizing two-eyed seeing around wildlife health in the Arctic**
Andrea J. Hanke, Xavier Fernandez Aguilar, Amanda Niptanatiak-Dumond, Monica Angohiatok, Lisa Marie Leclerc, Amélie Roberto-Charron, Fabien Mavrot, Susan Kutz



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- 12:30 - 12:45 *ID 361. Pulmonary health in Barataria Bay dolphins in the 8 years after the deepwater horizon oil spill*
Cynthia R. Smith, Teresa K. Rowles, Forrest M. Gomez, Ryan Takeshita, Jeanine S. Morey, Kathleen M. Colegrove, Eric S. Zolman, Brian C. Balmer, Todd R. Speakman, Jennifer M. Meegan, Marina Ivancic, Randall S. Wells, Forrest I. Townsend, Lori H. Schwacke
- 12:45 - 13:00 *ID 365. Cardiac assessments of bottlenose dolphins (*Tursiops truncatus*) in the Northern Gulf of Mexico following exposure to Deepwater Horizon Oil*
Barbara K. Linnehan, Forrest M. Gomez, Sharon M. Huston, Adonia Hsu, Ryan Takeshita, Kathleen M. Colegrove, Craig A. Harms, Ashley Barratclough, Alissa C. Deming, Teri K. Rowles, Whitney B. Musser, Eric S. Zolman, Randall S. Wells, Eric D. Jensen, Lori H. Schwacke, Cynthia R. Smith

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- 15:00 - 16:30 **Awards' Ceremony**
- 17:00 - 21:15 **Evening Session**
- 17:00 - 17:45 **Plenary talk AAWV AI Franzmann**
The Mother of Invention: New Tools for an Old Foe
Chair: Joaquín Vicente
Speaker: Dr. Daniel J. O'Brien
- 17:50 - 19:05 **Session 13. Wildlife disease control.**
Chairs: Susan Kutz & Joaquín Vicente
- 17:50 - 18:05 *ID 256. Robust interaction between predator pressure and disease prevalence during the peak phase of a rodent species with cyclic demography: a large-scale replicated experiment*
Javier Fernandez-De-Simon, David González-Barrio, Lara Royo-Hernández, Alfonso Paz, David López-Idiáquez, Jesús Martínez-Padilla, Jesús T. García, Pedro P. Olea, Francisco Ruiz-Fons, Javier Viñuela
- 18:05 - 18:20 *ID 60. Modeling host-pathogen transmission dynamics to support scientific decision making*
Robin Russell, Tonie Rocke, Daniel Walsh, John Grider
- 18:20 - 18:35 *ID 201. Modeling epidemic prevention and detection strategies for introduced pathogens in the Channel Island fox (*Urocyon littoralis*)*
Jessica N. Sanchez, Brian R. Hudgens
- 18:35 - 18:50 *ID 111. Optimizing risk management strategies for the control of *Philornis downsi* - a threat to birds in the Galápagos Islands*
Irene Bueno, Randall S. Singer, Charles Yoe, Dominic A. Travis, Rees Parrish, Julia B. Ponder
- 18:50 - 19:05 *ID 150. Harvest management & chronic wasting disease prevalence trends in western mule deer herds*
Mary M. Conner, Mary E. Wood, Anne Hubbs, Justin Binfet, A. Andrew Holland, Luke R. Meduna, Annette Roug, Jonathan P. Runge, Todd D. Nordeen, Margo J. Pybus, Michael W. Miller

ROOM 2

- 17:50 - 19:05 **Session 14. Host-pathogen interactions in wildlife.**
Chairs: Tabitha Viner & Gregorio Mentaberre
- 17:50 - 18:05 *ID 144. Bi-seasonal dynamics of a multi-host pathogen: the role of environment in the dynamics of anthrax*
Yen-Hua Huang, Kyrre Kausrud, Ayesha Hassim, Louis Van Schalkwyk, Edgar Dekker, Alexander Buyantuev, Claudine Cloete, Werner Kilian, Henriette Van Heerden, Wendy Turner
- 18:05 - 18:20 *ID 376. Environmental factors determine the seasonal seropositivity of *Erysipelothrix rhusiopathiae*, an emerging pathogen in caribou*
O. Alejandro Aleuy, Michelle Anholt, Karin Orsel, Fabien Mavrot, Catherine Gagnon, Kimberlee Beckmen, Steeve Côté, Christine Cuyler, Andrew Dobson, Brett Elkin, Lisa-Marie Leclerc, Joëlle Taillon, Susan Kutz



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- 18:20 - 18:35 *ID 299. Unravelling the pathogenesis of Herpesvirus-Associated Proliferative Skin Disease in frogs and toads*
Francesco C. Origi, Patricia Otten, Petra Lohmann, Ursula Sattler, Thomas Wahli, Antonio Lavazza, Veronique Gaschen
- 18:35 - 18:50 *ID 325. Using multivariate analyses to explore evolutionary patterns in disease pathology*
Rachel M. Ruden, Amberleigh E. Henschen, Dana M. Hawley, James S. Adelman
- 18:50 - 19:05 *ID 211. An outbreak of Plasmodium related Disease and mortality in a conservation breeding population of greater sage grouse (Centrocercus urophasianus)*
Sandra R. Black, Douglas P. Whiteside, Adriana R. Pastor, Yiran Li, Dayna Goldsmith
- 19:05 - 19:30 **Break / networking / e-posters**

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- 19:30 - 21:00 **Session 15. Molecular epidemiology of wildlife pathogens.**
Chairs: Sandra Díaz & Pelayo Acevedo
- 19:30 - 19:45 *ID 185. Syphilis seropositivity and Treponema paraluisleporidarum strain diversity in European brown hares*
Linda Hisgen, Lena Abel, Erik Ågren, Alexander Barlow, Marcus Fährndrich, Linda Grillová, Miklós Gyuranecz, Luisa Hallmaier-Wacker, Antonio Lavazza, Simone Lüert, Markéta Nováková, Carlo Pacioni, Christian Roos, Egbert Strauß, Tiziana Trogu, Roser Velarde, Ulrich Voigt, David šmajš, Sascha Knauf
- 19:45 - 20:00 *ID 265. Impact of the genomic architecture of Lagovirus europaeus/GI.2 recombinants in the clinical course of rabbit hemorrhagic disease*
Ana Margarida Lopes, Raquel Machado Marques, Madalena Costa, Luzia Teixeira, Ana Pinto, João Vasco Côrte-Real, Maria João Magalhães, Pedro José Esteves, António Costa Silva, Aleksija Neimanis, Dolores Gavier-Widén, Paula Gomes Ferreira, Joana Abrantes
- 20:00 - 20:15 *ID 269. Decreased immunity of wild rabbits against rabbit hemorrhagic disease virus in Azores (2015-2019)*
Ana M. Lopes, João V. Côrte-Real, João Faria, Fabiana Neves, Tereza Almeida, Tiago M. Rodrigues, Maria J. Magalhães, Esther Blanco, Juan Bárcena, Manuel Leitão, Paulo C. Alves, Pedro J. Esteves, Pedro Monterroso, David Gonçalves
- 20:15 - 20:30 *290. Frequency and molecular diversity of protist enteroparasites in Western chimpanzees (Pan troglodytes verus) from Ivory Coast, Senegal, and Sierra Leone*
Pamela C. Köster, Juan M. Lapuente, Laia dotras, Justinn Renelies-Hamilton, Andrea Pizarro, Manuel Llana, Alejandro Dashti, Begoña Bailo, Aly Salimo Muadica, David González-Barrio, Rafael Calero-Bernal, Francisco Ponce-Gordo, Isabel Fuentes, David Carmena
- 20:30 - 20:45 *ID 191. American mink (Neovison vison) as potential reservoir of Leishmania infantum*
Iris Azami- Conesa, José Sansano- Maestre, Rafael Alberto Martínez- Díaz, María Teresa Gómez- Muñoz
- 20:45 - 21:00 *ID 310. Clinical babesiosis in a North American river otter (Lontra canadensis) and the prevalence and genetic characterization of this Babesia microti-like species in the eastern United States Molecular epidemiology of wildlife pathogens*
Kayla Buk Garrett, Ashlyn Halseth, James Beasley, Mark G. Ruder, Mourad Gabriel, Michael J. Yabsley

ROOM 2

- 19:30 - 20:45 **Session 16. Mixed thematic areas.**
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- 19:30 - 19:45 *ID 224. Highly pathogenic avian influenza in the Netherlands, 2020/2021: H5N8 virus expands its host range to barnacle geese*
Valentina Caliendo, Jolianne M. Rijks, Erik Kleyheeg, Roy Slaterus, Marcel A.h. Spierenburg, Hans Verdaat, Nancy Beerens, Ron A.m. Fouchier, Thijs Kuiken
- 19:45 - 20:00 *ID 329. Unravelling the interface: farm connectivity provided by spotless starling (Sturnus unicolor) movements*
Alberto Sánchez-Cano, Cosme López-Calderón, Teresa Cardona Cabrera, Andy J. Green, Ursula Höfle
- 20:00 - 20:15 *ID 287. Yellow-legged gulls (Larus michahellis) and Audouin's gulls (Larus audouinii) from Barcelona as a source of Campylobacter of public health relevance.*
Alicia Manzanares Pedrosa, Teresa Ayats, Sara Sabaté, Tomàs Montalvo, Marta Cerdà - Cuéllar
- 20:15 - 20:30 *ID 54. Physiological effects of azaperone and midazolam on netgun-captured mule deer*
Annette Roug, Randy Larsen, Xaela Walden, Kent Hersey, Brock Mcmillan, Nigel Caulkett
- 20:30 - 20:45 *D123. Fibropapillomatosis and chelonid alphaherpesvirus 5 infection in Kemp's ridley sea turtles (Lepidochelys kempii)*
Annie Page-Karjian, Liam Whitmore, Brian A. Stacy, Justin R. Perrault, Jessica A. Farrell, Hilary Frandsen, Jennifer S. Walker, Donna J. Shaver, Elina Rantonen, Craig A. Harms, Terry M. Norton, Charles Innis, Kelsey Yetsko, Cody R. Mott, Michael J. Bresette, David J. Duffy

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21:00 - 21:15 **Closure**



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STUDENT AWARD E-POSTERS



ALECTORIS RUFA
Red-legged partridge

María García Romero



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ID 63. A metatranscriptomic approach to parasitic, viral, and bacterial surveillance in hunter harvested primates in an indigenous reserve in Guyana, South America.

Marissa S. Milstein, Laramie L. Lindsey, Christopher A. Shaffer Phillip Suse, Elisha Marawanaru, Suzanne Stone, Tiffany M. Wolf, Peter A. Larsen

ID 232. Alpine ibex hybrids: fairy tale or reality in our mountains?

Barbara Moroni, Alice Brambilla, Luca Rossi, Pier Giuseppe Meneguz, Bruno Bassano, Paolo Tizzani

ID 190. Anticoagulant rodenticide exposure in raptors from Ontario, Canada.

Grace L. Thornton, Brian Stevens Shannon K. French, Leonard J. Shirose, Felipe Reggeti, Nick Schrier, E. Jane Parmley, Alexandra Reid, Claire M. Jardine

ID 4. Assessing Strain-Specificity In Acquired Resistance Response To *Batrachochytrium Dendrobatidis*.

K.M. Barnett, Taegan McMahon, David Civitello

ID 315. California serogroup viruses: Revealing the reservoir potential of cervids in Arctic and Subarctic ecosystems.

Kayla Buhler, Antonia Dibernardo, Robbin Lindsay, Michael Drebot, Jane Harms, Heather Fenton, Javier Fernandez Aguilar, Lisa-Marie Leclerc, Ellen Avard, John Blake, Adrián Hernández Ortiz, Patrick Leighton, Emily Jenkins

ID 305. Cross-sectional survey of vector-borne diseases at the wildlife-livestock interface: Bluetongue, Schmallenberg disease and Q fever in Doñana National Park (Spain).

Saúl Jiménez-Ruiz, Joaquín Vicente, María Ángeles Risalde, Pelayo Acevedo, Patricia Barroso, David Cano-Terriza, David González-Barrio, Ignacio García-Bocanegra

ID 157. Description of novel adenoviruses and herpesviruses in Galapagos giant tortoises (*Chelonoidis* sp.).

Ainoa Nieto Claudin, Sharon Deem, Kathleen Apakupakul, Fernando Esperón

ID 327. Detection of *Lactococcus garvieae* in feral fish and environmental DNA of four California Lakes.

Taylor Abraham, Zeinab Yazdi, Eric Littman, Khalid Shahin, Taylor Heckman, Eva Quijano Carde, Diem Thu Nguyen, Ruixue Hu, Mark Adkison, Tresa Veek, Kavery Mukkatira, Christine Richey, Kevin Kwak, Ian Gardner, Timothy J Welch, Esteban Soto

Establishing the safety, pharmacokinetics, and efficacy of fluralaner as a novel treatment for sarcoptic mange in the bare-nosed wombat (*Vombatus ursinus*).

Vicky Wilkinson, Kotaro Takano, David Nichols, Alynn Martin, Roz Holme, David Phalen, Kate Mounsey, Michael Charleston, Alexandre Kreiss, Ruth Pye, Elizabeth Browne, Christina Næsberg-Nielsen, Shane A. Richards, Scott Carver

ID 115. Evaluation of contact network between commensal wild birds and domestic poultry around a French duck farm

Chloé Le Gall-Ladevèze, Pierre Fievet, Julien Cappelle, Claire Guinat, Jean-Luc Guérin, Guillaume Le Loc'H

ID 194. First description of *Sarcoptes scabiei* cross-transmission between Iberian ibex (*Capra pyrenaica*) and wild boar (*Sus scrofa*).

Marta Valldeperes, Barbara Moroni, Luca Rossi, Roser Velarde, Jorge Ramón López-Olvera, Emmanuel Serrano, Gregorio Mentaberre, Santiago Lavín, Anna Rita Molinar Min, Samer Angelone, José Enrique Granados

ID 247. First known outbreak of *Salmonella* serovar *Choleraesuis* in Swedish wild boar.

Karin M. Olofsson, Linda Ernholm, Caroline Bröjer, Gustav Averhed, Erik Ågren



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ID 228. *Flavivirus infection of wild birds in a wildlife-livestock interaction gradient in continental Iberia.*

Laia Casades Martí, Rocío Holgado Martín, Sara Baz Flores, Raúl Cuadrado Matías, Yolanda Fierro, Francisco Ruiz Fons

ID 51. *Global conservation implications for health assessment studies in non-captive wildlife.*

Sara Kophamel, Björn Illing, Ellen Ariel, Leigh C. Ward, Diana Mendez, Lee F. Skerratt, Mark Hamann, Morgan Difalco, Suzanne L. Munns

ID 189. *Identification of a novel neorickettsia species in kemp's ridley sea turtles with granulomatous renal lesions and development of a quantitative PCR assay.*

Brittany Liguori, Brian Stacy, Linda Archer, April Childress, Donna Shaver, James Wellehan

ID 218. *Listeriosis and viral coinfections in multiple wildlife species in the southeastern United States.*

Alisia A. W. Weyna, Kevin Niedringhaus, Melanie R. Kunkel, Heather Fenton, M. Kevin Keel, Amy H. Webb, Charlie Bahnson, Brandon Munk, Rebecca Radisic, Nicole M. Nemeth

ID 134. *Long-term study of ranaviruses drivers, associated with mortality events on Rana temporaria in the French National Park of Mercantour.*

Loïc Palumbo, Sylvain Larrat, Guillaume Le Loc'H, Claude Miaud

ID 130. *Microbiome diversity and its relation to the pathogen of different tick species collected in Sarawak, Malaysian Borneo.*

Alice Lau, Mohamed Abdallah Mohamed Moustafa, Yongjin Qiu, Wessam Mohamed Ahmed Mohamed, Manabu Onuma, Nobuyoshi Nakajima, Ryo Nakao, Michito Shimozuru, Jayasilan Mohd-Azlan, Toshio Tsubota

ID 294. *Monitoring of Schmallenberg virus in zoo animals in Spain, 2002-2019.*

Débora Jiménez-Martín, Javier Caballero-Gómez, Ignacio García-Bocanegra, Nuria Navarro, Rafael Guerra, Cati Gerique, Eva Martínez-Navado, Pilar Soriano, Sabrina Castro-Scholten, Adrián Beato, David Cano-Terriza

ID 212. *Multi-systemic spirochidiasis and gastrointestinal parasitism in louisiana red-eared sliders (trachemys scripta elegans).*

Rebecca Radisic, Heather Fenton, Jim Lacour, A. Nikki Anderson, Kevin Niedringhaus, Michael J. Yabsley, Nicole Nemeth

ID 98. *Pathological Findings in White-Beaked Dolphins (Lagenorhynchus albirostris) and Atlantic White-Sided Dolphins (Lagenorhynchus acutus) from the South-eastern North Sea.*

Luca Aroha Schick, Lonneke L. Ijsseldijk, Miguel L. Grilo, Jan Lakemeyer, Kristina Lehnert, Peter Wohlsein, Christa Ewers, Ellen Prenger-Berninghoff, Wolfgang Baumgärtner, Andrea Gröne, Maria J.I. Kik, Ralf Oheim, Julian Stürznickel, Ursula Siebert

ID 216. *Seroprevalence of West Nile virus in game bird populations in the United States.*

Melanie R. Kunkel, Lisa Williams, Mary Jo Casalena, Mitchell Blake, Samantha E. Allen, Leslie Schreiber, David Moscicki, Christopher Moorman, Daniel G. Mead, Mark G. Ruder, Nicole M. Nemeth

ID 242. *Spillover event of recombinant Lagovirus europaeus/GI.2 into the Iberian hare (Lepus granatensis) in Spain.*

Roser Velarde, Joana Abrantes, Ana M. Lopes, Josep Estruch, João V. Côrte-Real, Pedro J. Esteves, Ignacio García-Bocanegra, Jordi Ruiz-Olmo, Carlos Rouco



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ID 197. Squirrels (*Sciuridae*)- neglected reservoirs for emerging zoonotic pathogens.

Viola C. Haring, Valerie Allendorf, Laura Vesper, Vanessa Schulze, Kore Schlottau, Elisabeth Schmidt, Peter W. W. Lurz, Dirk Höper, Donata Hoffmann, Kerstin Wernike, Martin Pfeffer, Dennis Rubbenstroth, Martin Beer, Rainer G. Ulrich

ID 122. Synurbization increases zoonotic hepatitis E hazard posed by wild boar.

Marc López-Roig, Raquel Castillo-Contreras, Abir Monastiri, María Escobar, Gregorio Mentaberre, Carles Conejero, Marta Valdeperes, Joan Roldan, Jose María López-Martín, Jordi Serra-Cobo, Jorge Ramón López Olvera

ID 227. Usutu and Plasmodium co-infection in Eurasian blackbirds (*Turdus merula*).

Giuseppe Giglia, Gianfilippo Agliani, Bas B. Oude Munnik, Reina Sikkema, Famke Schaafsma, Alinda Berends, Maria Teresa Mandara, Marja Kik Jooske Ijzer, Jolianne M. Rijks Marion P. G. Koopmans, Helene Verheije, Andrea Gröne, Chantal B. E. M. Reusken, Judith M. A. Van Den Brand

ID 270. Validation of a drop-net system to trap wild boar according to the Agreement on International Humane Trapping Standards.

Carles Conejero, Jorge R. López-Olvera, Enric Vila, Santi Oms, Jordi Vigué, Enric Ullar, Carlos González-Crespo, Arián Ráez-Bravo, Raquel Castillo-Contreras, Roser Velarde, Gregorio Mentaberre

ID 114. Wildlife diversity among villages in Chad, Africa with various levels of *Dracunculus medinensis* (Guinea worm) infections in domestic dogs: insights into possible reservoirs?

Avery L. Korn, Christopher A. Cleveland, Levi Ellington, Michael J. Yabsley

ID 307. Zoo animals as sentinels for Bluetongue virus monitoring in Spain.

Javier Caballero-Gómez, David Cano-Terriza, Joan Pujols, Eva Martínez-Nevado, María Dolores Carbonell, Rafael Guerra, Jesús Recuero, Pilar Soriano, Noelia De Castro, Sabrina Castro-Scholten, Jesús Barbero, Ignacio García-Bocanegra



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GENERAL POSTERS



CANIS LUPUS SIGNATUS

Iberian wolf



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Ecosystem health, global change and diseases

ID 6. *Effect of urban habitat use on parasitism in mammals: a meta-analysis.*

Courtney S. Werner, Charles L. Nunn

ID 56. *Coprological approach to parasites of the California kingsnake (*Lampropeltis californiae*); an invasive species in Gran Canaria, Spain.*

Kevin M. Santana-Hernández, Simon L. Priestnall, Eligia Rodríguez-Ponce

ID 57. *A potential conservation threat to Macaronesian raptors: First documented case of fatal viral hepatitis in a Canary Islands Kestrel (*Falco tinnunculus canariensis*).*

Kevin M. Santana-Hernández, Simon L. Priestnall, Alejandro Suárez-Bonnet, Pablo A. Lupiola-Gómez, Eligia Rodríguez-Ponce

ID 59. *A passenger from a long-distance traveler? Story of *Lutztrema attenuatum* (Digenea: *Dicrocoeliidae*) carried by a blackbird (*Turdus merula*).*

Kevin M. Santana-Hernández, Simon L. Priestnall, Pascual Calabuig Miranda, Eligia Rodríguez-Ponce

ID 62. *Prevalence of respiratory disease in Eastern grey squirrels (*Sciurus carolinensis*) in relation to levels of air pollution found in London (UK).*

Irene Torres-Blas, Simon L. Priestnall, Patricia Brekke

ID 68. *Regional and Inter-sectoral Gaps in the One Health Research; Future Directions.*

Touseef Ahmed, Muhammad Farooq Tahir, Tigga Kingston

ID 75. *Gross Evaluation and Suspected Cause of Mortality in Indian Elephants (*Elephant maximus indicus*) in Southern India.*

Laura A. B. Aguilar, N. Kalaivanan, Sridhar Kanniappan, Easwaran Vijayaraghavan, Gregory B. Walth, Andrew S. Atuan, Sarah Laws, Govindaraju Sivasubramanian, Puliyur S. Mohankumar, Joerg Mayer

ID 101. *Current status of *Toxoplasma gondii* in foxes (*Vulpes spp.*) from northern Canada.*

Émilie Bouchard, Adrián Hernández-Ortiz, Kayla Buhler, Michaël Bonin, Heather Fenton, Ellen Avar, Jim Roth, Chloé Warret Rodrigues, Matilde Tomaselli, Carla Pamak, Audrey Simon, Patrick Leighton, Emily Jenkins

ID 117. *Antimicrobial resistant *Moellerella wisconsensis*; a potentially zoonotic pathogen isolated from wild birds in Greece.*

Zoi Athanasakopoulou, Marina Sofia, Dimitris C. Chatzopoulos, Efthymia Petinak, Vassiliki Spyrou, Charalambos Billinis

ID 135. *Toxins from harmful algae in fish from Scottish coastal waters.*

Joanna Kershaw, Ailsa Hall

ID 151. *Insights on the Diet of Urban American White Ibis (*Eudocimus albus*) Nestlings.*

Julia Silva Seixas, Elizabeth Kurimo-Beechuk, Katherine F. Christie, Sonia M. Hernandez



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Andreia Manuela Garcês, Justina Praga, Anabela Alves, Adelina Gama, Celso Santos, Filipe Silva, Isabel Pires

ID 173. *Giardia spp. in wild rodents from a landscape dominated by exotic plantations in Chile.*

Natalia Huerta, Maira Riquelme, Javier A. Simonetti, Fernando Fredes, André V. Rubio

ID 177. *Tick risk in roe deer fawns: what links with environment and individual characteristics?.*

Léa Bariod, Sonia Saïd, Clément Calenge, Stéphane Chabot, Gilles Bourgoïn

ID 196. *Cross-sectional serological survey of Aujeszky's Disease virus and Classical Swine Fever virus in white-lipped peccary (*Tayassu pecari*) and collared peccary (*Pecari tajacu*) in the Peruvian Amazon.*

Maria Fernanda Menajovsky, Johan Espunyes, Gabriela Ulloa, Artuto Mamani, Stephanie Montero, Winnie Contreras, Andrés Lescano, Meddy Santolalla, Oscar Cabezón, Pedro Mayor

ID 217. *Effects of Low Salinity Exposure on Bottlenose Dolphins (*Tursiops truncatus*).*

Abby M McClain, Risa Daniels, Forrest M. Gomez, Sam H Ridgway, Ryan Takeshita, Eric D. Jensen

ID 231. *Screening of vector-borne pathogens in Icelandic arctic foxes, *Vulpes lagopus*.*

Sándor Hornok, Kristin Mühldorfer, Nóra Takács, Regina Hofmann-Lehmann, Marina L. Meli, Miklós Gyuranecz, Ester R. Unnsteinsdóttir, Alex D. Greenwood, Gábor Árpád Czirájék

ID 260. *Liver parasite *Pseudamphistomum truncatum* infects mainly subadult Baltic ringed seals.*

Marja Isomursu, Kaarina Kauhala

ID 262. *Multi-drug resistant *E. coli* isolated from free-living griffon vultures (*Gyps fulvus*) and cinereous vulture (*Aegypius monachus*) from Central Spain.*

Bárbara Martín-Maldonado, Fernando González González, Irene López Márquez, Laura Suárez Regalado, Virginia Moraleda Fernández, Natalia Pastor Tiburón, Francisco Javier García-Peña

Emerging and re-emerging wildlife diseases

ID 39. *Eastern equine encephalitis outbreak in white-tailed deer (*Odocoileus virginianus*) in Michigan, USA, 2019 to 2020.*

Julie R Melotti, Thomas Cooley, Straka Kelly, Kathryn Farinosi, Scott Fitzgerald, Steven Bolin

ID 45. *A novel herpesvirus detected in three different species in the order testudines.*

John M. Winter, James F.x. Wellehan, Kathleen Apakupakul, Jamie L. Palmer, Maris Brenn-White, Kali Standorf, Kristin H. Berry, April Childress, Michael M. Garner, Peter Koplos, Sharon L. Deem

ID 89. *Vector-borne Viruses in Ungulates in southern Ontario, Canada: Distribution and Orbivirus Establishment.*

Samantha E Allen, Claire M Jardine, Stacey L Vigil, Tara Furukawa-Stoffer, Nicole Colucci, Kathleen Hooper-Mcgrevy, Aruna Ambagala, Jamie L Rothenburger, David L Pearl, Mark G Ruder, Nicole M Nemeth

ID 91. *Novel approaches for diagnosing tuberculosis in wildlife in resource-poor countries.*

Wynand Johan Goosen, Tanya Jane Kerr, David Cooper, Peter E Buss, Leanie Kleynhans, Robin Warren, Paul Van Helden



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ID 113. *Invasion pathways and public health risks of the raccoon and its roundworm *Baylisascaris procyonis* in the Netherlands.*

Miriam Maas, Rea Tatem-Dokter, Jolianne M. Rijks, Cecile Dam-Deisz, Hester Van Bolhuis, Mike Heddergott, Anna Schleimer

ID 116. *Toxigenic *Corynebacterium ulcerans* emerges from widespread hedgehog (*Erinaceus europaeus*) disease.*

An Martel, Filip Boyen, Jörg Rau, Tobias Eisenberg, Andreas Sing, Anja Berger, Koen Chiers, Sarah Van Praet, Serge Verbanck, Muriel Vervaeke, Frank Pasmans

ID 137. *Feline leukaemia virus in free-ranging Eurasian Lynx (*lynx lynx*) – a pathogen to keep an eye on.*

Iris Andrea Marti, Simone Roberto Rolando Pisano Sven Signer, Christine Breitenmoser-Würsten, Urs Breitenmoser, Ole Anders, Tomma Lilli Middelhoff, Florian Brandes, Regina Hofmann-Lehmann, Marina Luisa Meli, Marie-Pierre Ryser-Degiorgis

ID 140. *Seroprevalence of Crimean-Congo haemorrhagic fever in wild ungulates from north-eastern Spain.*

Johan Espunyes, Oscar Cabezón, Lola Pailler, Andrea Dias-Alves, Lourdes Lobato-Bailón, Ignasi Marco, Maria Puig Ribas, Sebastian Napp

ID 161. *Multiple strains of a novel hantavirus in voles in Continental Europe.*

Kathrin Jeske, Stephan Drewes, Melanie Hiltbrunner, Petra Straková, Guy-Alain Schnidrig, Linas Balciauskas, Laima Balciauskiene, Rasa Petraityte-Burneikiene, Gerald Heckel, Rainer G. Ulrich

ID 208. **Emydomyces testavorans* surveillance in multiple free-ranging terrestrial and aquatic chelonian species in Illinois.*

Kelcie Fredrickson, Laura Adamovicz, Karen Terio, Alexis Davidson, Michelle Waligora, Kayla Ladez Samantha Bradley Matthew Allender

ID 225. *Outbreaks of digital necrobacillosis in wild reindeer in Norway.*

Malin Rokseth Reiten, Kjell Handeland, Knut Madslie, Turid Vikøren, Jørn Våge

ID 226. *Serological Investigation of Selected Vector-Borne Viruses in Migratory Free-Living Passerine Birds Captured During Autumn Migration in Slovenia.*

Joško Racnik, Tomi Trilar, Mateja Jelovšek, Miša Korva, Zoran žlabavec, Brigita Slavec, Olga Zorman Rojs Tatjana Avšič županc

ID 233. *First report of *GI.2* in a Cape hare (*Lepus capensis*) from Africa.*

Faten Ben Chehida, Ana Margarida Lopes, João Vasco Côrte-Real, Soufien Sghaier, Thameur Ben Hassine, Lilia Messadi, Joana Abrantes

ID 291. *RNA in situ hybridization and virus characterization of skunk adenovirus in North American wildlife demonstrates severe multisystemic infections and genetic variation in a broad host range.*

Laura A. Bourque, Ole Nielsen, Mason Jager, Davor Ojkic, Chantale Provost, Carl Gagnon, Betty Chow-Lockerbie, Hein Snyman, Brian Stevens, David Needle, Shotaro Nakagun, Sherri Cox, Jessica Kohdadad, Megan Jones

ID 293. **Emydomyces testavorans* associated shell disease in an endangered population of Northwestern pond turtles in Washington, USA.*

Karen A. Terio, Katherine Haman, Jennifer Tepavich, Tori Mcklveen, Lisa Hallock



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ID 346. Diffuse Large B Cell Lymphoma and a Novel Gammaherpesvirus in Two Northern.

Elephant Seals, Margaret Martinez, Emily Trumbull, Michelle Rivard, Emily Whitmer, Nicole I. Stacy, Cara Field, Linda L. Archer James, F.X. Wellehan Jr., Salvatore Frasca Jr. , Padraig J. Duignan

ID 347. Moose (*Alces alces*) with suggested spontaneous Chronic Wasting Disease in Sweden. Erik Olof

Ågren, Gustav Averhed, Dolores Gavier-Widén, Kaisa Sörén, Karolina Wall, Sylvie L. Benestad, Linh Tran, Neele Doose, Jørn Våge, Maria Nöremark

ID 349. Finding elusive *Echinococcus* tapeworms in Sweden.

Erik Olof Ågren, Eva Osterman Lind, Jenny Frössling

ID 378. Cytopathic effects of *Trichomonas gallinae* on cell culture after environmental persistence trials.

Kathryn Erin Purple, Richard Gerhold

Host-pathogen interactions in wildlife

ID 69. Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming *Enterococcus* sp. Bacteria (*Enterococcus lacertiformus*) Identified in Reptiles.

Jessica Esther Agius , David Norton Phalen, Karrie Rose, John-Sebastian Eden

ID 80. Patterns and pathogen infection of deer keds (*Diptera: Hippoboscidae*) and ticks (*Ixodida: Ixodidae*) found on white-tailed deer (*Odocoileus virginianus*) in the eastern United States

Karen C. Poh, Jesse R. Evans, Michael J. Skvarla, Pia U. Olafson, Graham Hickling, Jennifer M. Mullinax, Erika T. Machtinger

ID 82. Gastrointestinal parasites prevalence and season dynamics in an endangered brown bear (*Ursus arctos*) population in Greece: preliminary results.

Antonios Synapalos, Stefanos Sgardelis, Anastasia Diakou, Dionysios Youlatos, Giorgos Mertzanis

ID 83. A preliminary study of endoparasites in live loggerhead sea turtles.

Marina García Piqueras, Jose Sansano Maestre

ID 108. Unravelling Elephant Herpesvirus Pathogenicity with Transcriptomics.

Jack Johnson, Adam Blanchard, Arun Zachariah, Rachael Tarlinton

ID 136. Molecular identification of *Sarcocystis* wobeseri-like parasites in a new intermediate host species, the white-tailed sea eagle (*Haliaeetus albicilla*).

Tammy Shadbolt, Ann Pocknell, Anthony Sainsbury, Stephen Egerton-Read, Damer Blake

ID 147. The Salmonella Dynamics of American White Ibis (*Eudocimus albus*) Nestlings.

Katherine Fredrica Christie, Julia Silva Seixas, Erin K. Lipp, William Norfolk, Ralph Scott Rozier, Sonia M. Hernandez

ID 148. Avian Influenza Virus Dynamics in Urban Nestling and Juvenile American White Ibis (*Eudocimus albus*).

Katherine Fredrica Christie, Julia Silva Seixas, Rebecca L. Poulson, Sonia M. Hernandez

ID 163. Tick-borne encephalitis in the Swedish moose (*Alces alces*).

Elina Thorsson, Tomas Bergström, Kristina Nyström, Peter Norberg, Anette Roth, Gustav Averhed



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Saskia Keller, Walter U. Basso, Diana S. Gliga, Gaia Moore-Jones Francesco C. Origi, Caroline F. Frey, Marie-Pierre Ryser-Degiorgis

ID 184. *Experimental Mycobacterium microti infection in bank voles (Myodes glareolus).*

Enric Vidal, Judit Burgaya Lorraine Michelet, Claudia Arrieta-Vilelgas, Guillermo Cantero, Michelle Di Bari, Romolo Nonno, Maria Laura Boschioli, Bernat Pérez De Val

ID 195. *Effect on Pulmonary Health of White-tailed Deer Under Presence of Lungworm.*

Nathan Daniel Wilson, Amy C. Dechen Quinn, Madeline A. Hilger

ID 198. *Genomic resistance to anthrax (Bacillus anthracis) in plains zebra (Equus quagga).*

Caroline C. Dickson, Melanie B. Prentice, Wendy C. Turner, Henriette Van Heerden, Pauline L. Kamath

ID 237. *In sickness and in health: plasma proteomics of hibernating European and North American myotis bats.*

Gábor Árpád Czirják, Alexander M. Hecht-Höger, Eberhard Kraus, Christian C. Voigt, Beate Braun, Alex D. Greenwood

ID 240. *Prevalence of gastrointestinal parasites in wild carnivore species from Central Spain.*

Pablo Matas, David Carmena, Ana Montoya, Marta Mateo

ID 251. *The spatiotemporal dynamics of exposure of wild ungulates to Flavivirus shapes the patterns of West Nile virus outbreaks in Spain.*

Laia Casades Martí, Raúl Cuadrado Matías, Roxana Triguero Ocaña, Patricia Barroso, Saúl Jiménez Ruiz, Pablo Palencia, Eduardo Laguna, Alfonso Peralbo Moreno, Sara Baz Flores, Yolanda Fierro Francisco Ruiz Fons

ID 296. *Meta-transcriptomic profiles of rodents at the rodent-agricultural interface.*

Laramie L. Lindsey, Nusrat A. Jahan, Adam Reinschmidt, Evan J. Kipp, Bradley J. Heins, Suzanne Stone, Peter A. Larsen

ID 297. *Experimental West Nile and Bagaza virus infections in quails.*

Francisco Llorente, Cristina Cano-Gómez Elisa Pérez-Ramírez, Pilar Aguilera-Sepúlveda, María Del Carmen Barbero Mathieu Sarasa Jovita Fernández-Pinero Miguel Ángel Jiménez-Clavero

ID 323. *The 'vicious circles' of host condition, infection susceptibility and intensity may be less common than expected.*

Cristina Garrido-Amaro, Roser Velarde, Anna E. Jolles, Jorge R. López-Olvera, Emmanuel Serrano

ID 330. *The spatiotemporal dynamics of Crimean-Congo haemorrhagic fever virus in enzootic Iberian scenarios.*

Raúl Cuadrado-Matías, Laia Casades-Martí, Ana Balseiro, Sara Baz-Flores Roxana, Triguero-Ocaña, Patricia Barroso, Saúl Jiménez-Ruiz, Pablo Palencia, Eduardo Laguna, Alfonso Peralbo-Moreno, Francisco Ruiz-Fons

ID 340. *Oral yeasts and lesions in cinereous vulture (Aegypius monachus) nestlings: Risk factors and importance.*

Ángela Mercedes Sánchez Arévalo, Úrsula Höfle, Javier De La Puente, Alberto Sánchez-Cano, Teresa Cardona Cabrera



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ID 355. Suspected Brucella-associated Abortion in a Hawaiian Monk Seal (Neomonachus schauinslandi).

Cara Lisa Field, Gregg Levine, Megan Mcginnis, Kathleen Colegrove, Karen Terio, Andrea Packham, Tracey Goldstein, Claudia Cedillo, Michelle Barbieri

ID 366. Patterns of Bartonella infection in small mammal from intensive farmlands, NW Spain.

Silvia Herrero-Cófreces, Raquel Escudero, François Mougeot, Nerea Castro, Juan José Luque-Larena

ID 381. The bird, the parasite, and the virus: Co-infection of free-living red-legged partridges (Alectoris rufa) with Bagaza virus and avian malaria.

Teresa Cardona Cabrera, Alberto Sánchez-Cano, María De Los Angeles Risald, Vidal Montoro-Angulo, José Antonio Ortiz, Ursula Höfl

Impact of diseases on wildlife conservation

ID 7. Locomotor Biomechanics Of Chinese Pangolins (Manis Pentadactyla) With Normal And Amputated Limbs/Tails.

I-Ting Tu, Peter Bishop, Yu-Mei Chang, Ting-Yu Chen, Hsuan-Yi Lo, Hsuan-Ya Yu, John Hutchinson

ID 78. Assessment of Urethral Catheterization for Semen Collection and Characterization of Normative Seminal Traits in Wild Ocelots (Leopardus pardalis) and Bobcats (Lynx rufus) in South Texas.

Ashley M. Reeves, William F. Swanson, Clayton D. Hilton, Tyler A. Campbell, Landon Schofield, Jason V. Lombardi, Michael E. Tewes, Debra L. Miller

ID 107. The risk from SARS-CoV-2 to bat species in England.

Sophie M. Common, Tammy Shadbolt, Katherine Walsh, Anthony W. Sainsbury

ID 155. Ricketts-like syndrome in two free-ranging Iberian lynx (Lynx Pardinus) kittens.

Elena Crespo, Fernando Najera, Amalia García, Tomás Castiella, Rebeca Grande, Francisco Sanchez, Manuel Mata, Javier Cáceres, Javier Herrera, Víctor Díez, Marino Lopez, Rafael Cubero, Antonio Aranda

ID 192. Assessing Deer Carcass Transportation, Processing, and Disposal Habits Among Minnesota Hunters Statewide and Within Disease Management Areas.

Kyle Smith, Adam Landon, David Fulton

ID 282. Multi-species Clostridial Outbreaks in Neonatal, Juvenile and Adult Greater Sage Grouse (Centrocercus urophasianus) in a Conservation Breeding Program.

Adriana R. Pastor, Sandra R. Black, Douglas P. Whiteside, Yiran Li, Dayna A. Goldsmith

ID 371. Survey of Arkansas Wildlife Rehabilitators: Perspectives, Motivators, and Opportunities for Collaboration.

Jennifer R. Ballard, Kimberly Sparks

Infection transmission at the wildlife-livestock-human interface

ID 38. A prevalent cryptic bacterium in the endangered Darwin's fox: genetic diversity, risk factor assessment and effects of infection.



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ID 40. Molecular detection of kobuviruses in domestic and wild animals in Northwestern Italy.

Irene Melegari, Serena Robetto, Paola Fruci, Cristina Guidetti, Andrea Palombieri, Emanuele Carella, Federica Di Profio, Vittorio Sarchese, Fulvio Marsilio, Riccardo Orusa, Barbara Di Martino

ID 52. Toxoplasma gondii sero-prevalence in wild cervids in Denmark.

Anna-Sofia Steensgaard, Mita Eva Sengupta, Mariann Chriel, Stine Thorsø Nielsen, Heidi Huus Petersen

ID 55. North American co-invaders? Serovars of Salmonella enterica carried by the invasive California kingsnake (Lampropeltis californiae) in Gran Canaria, Spain.

Kevin M. Santana-Hernández, Eligia Rodríguez-Ponce, Inmaculada Rosario Medina Begoña Acosta-Hernández, Simon L. Priestnall, Clara Marin, Santiago Vega, Teresa García Beltrán, Pablo A. Lupiola-Gómez

ID 65. Feral cats colonies as carriers of Salmonella spp. with impact on Public Health.

Maria Isabel Calcines Macías

ID 79. Detection of a novel Mycoplasma gallisepticum-like species in Common Starling (Sturnus vulgaris) around poultry farms in France.

Chloé Le Gall-Ladevèze, Laurent-Xavier Nouvel, Marie Souvestre, Guillaume Croville, Marie-Claude Hygonenq, Jean-Luc Guérin, Guillaume Le Loc'H

ID 124. Large-scale survey for canine vector-borne parasites in different bioclimatic regions of Chile: first description of Babesia in dogs and Hepatozoon in foxes.

Sophia Di Cataldo, Aitor Cevidanes, Claudia Ulloa-Contreras, Javier Cabello, Delia Gambino, Valeria Gargano, Constanza Napolitano, Irene Sacristán, Nicole Sallaberry-Pincheira, Juliana Vianna, Gerardo Acosta-Jamett, Domenico Vicari, Domenico Otranto, Javier Millán

ID 141. Are griffon vultures (Gyps fulvus) spreaders of antimicrobial resistant enteropathogens?

Johan Espunyes, Marta Cerdà-Cuellar, Lourdes Migura-Garcia, Lucía Illera, Andrea Dias-Alves, Lourdes Lobato-Bailón, Maria Puig Ribas, Teresa Ayats, Alicia Manzanares, Ignasi Marco

ID 149. A framework for more consistent reporting of wildlife-livestock contact data.

Sonny A. Bacigalupo, Linda K. Dixon, Simon Gubbins, Adam J. Kucharski, Julian A. Drewe

ID 166. Antimicrobial resistance profiles in wild and domestic ruminants: an One Health approach.

Camilla Smoglica, Simone Angelucci Anna Rita Festino, Muhammad Farooq, Antonio Antonucci, Alberto Vergara, Fulvio Marsilio Cristina Esmeralda Di Francesco

ID 167. Influenza A virus infection in urban and rural populations of wild boars in Spain.

María Escobar, Paloma Encinas José Enrique Granados, Gregorio Mentaberre, Arián Ráez-Bravo, Raquel Castillo-Contreras, Carles Conejero, Jorge R. López-Olvera, Gustavo Del-Real

ID 168. A species independent double-antigen ELISA allowing for CCHFV antibody detection in wildlife.

Loic Comtet

ID 174. Mycoplasma ovipneumoniae in Yukon: surveillance and the domestic-wildlife interface.



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Kristenn Magnusson, N. Jane Harms, Michelle Thompson, Maud Henaff, Jesse Walchuk, Matthew Larsen, Meghan Larivee, Mary Vanderkop

ID 220. Health surveillance to improve understanding of wildlife-livestock disease transmission risks and guide decision-making in antelope conservation reintroductions.

Stephanie Brien, Marie Petretto, Ouled Ahmed Hatem, Erhan Yalcindag, Melissa Marr, Mark Bronsvort, Rob Ogden

ID 238. The worst avian influenza (HPAI-H5N8 and H5N5) season ever in wild birds and poultry in Sweden.

Caroline Bröjer, Henrik Uhlhorn, Siamak Zohari, Malin Grant, Maria Nöremark, Elina Thorsson, Elisabeth Bagge, Gustav Averhed, Helena Eriksson, Karin Olofsson-Sannö, Minerva Löwgren, Pernille Engelsen-Etterlin, Désirée S. Jansson

ID 243. Generalized tuberculosis due to Mycobacterium caprae in a blind red fox (Vulpes vulpes) and its epidemiological context.

Roser Velarde, Enric Vidal, Josep Estruch, Zoraida Cervera, Abel Muñoz, Carlos Solano-Manrique, Albert Sanz, Carles Riera, Bernat Pérez De Val

ID 252. Reduce the Risk of Disease Emergence And Protect wildlife health By Adopting The One Health Approach.

Sophie Muset, Tiggy Grillo

ID 258. Antimicrobial resistant Escherichia coli in Bonelli's eagle (Aquila fasciata) in Spain and France.

Beatriz Sánchez-Ferreiro, Alicia Aranaz, Bárbara Martín-Maldonado, Laura Suárez Regalado, Virginia Moraleda Fernández, Alicia Carrero Ruiz, Natalia Pastor Tiburón, Fernando González González, Irene López Márquez

ID 259. Antimicrobial resistant Salmonella isolated from chelonians admitted to a Wildlife Rescue Center in Central Spain.

Sandra Sevilla-Navarro, Bárbara Martín-Maldonado, Natalia Pastor Tiburón, Irene López Márquez, Laura Suárez Regalado, Virginia Moraleda Fernández, Alicia Carrero Ruiz, Fernando González González, Clara Marin Orega

ID 288. Detection of African swine fever virus in wild boar in Southeast Asia.

Alice Porco, Emily Denstedt, Jusun Hwang, Alice Latinne, Nga Thi Thanh Nguyen, Ngoc Thi Bich Pham, Hai Kim Lam, Sokha Chea, Sreyem Sours, Kongsy Khamvong, Phonesavanh Milavong, Sothyra Tum, San Sorn, Davun Holl, Bounlom Douangngeun, Watthana Theppangna, Long Van Nguyen, Phuong Thanh Nguyen, Quang Tin Vinh Le, Hung Van Vo, Hoa Thi Nguyen, Anh Le Dao, Amanda Fine, Mathieu Pruvot

ID 292. Integrated control of tuberculosis at the wildlife-livestock interface in outdoor Iberian pig farms in Spain.

Saúl Jiménez-Ruiz, María Ángeles Riscalde, Ignacio García-Bocanegra, Eduardo Laguna, Débora Jiménez-Martín, David Cano-Terriza, Joaquín Vicente, Pelayo Acevedo

ID 304. Passive and targeted health surveillance of wild boar (Sus scrofa) populations in north-eastern Italy.

Marco Bregoli, Gabrita De Zan, Letizia Ceglie, Monia Cocchi, Martina Ustulin, Andrea Cadamuro, Manlio Palei Denis Vio

ID 313. Infectious disease surveillance at the wildlife-domestic interface of a partridge farm.



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Marta Barral, Vega Alvarez, Xeider Gerrikagoitia, Miriam Serrano, Olalla Torrontegi, Nekane Kortabarria, Ursula Höfle

ID 335. Are wild ungulates in close contact to humans exposed to SARS-CoV-2?

Elisa Ferreras-Colino, Mercedes Domínguez, María Escobar, Marta Valdeperes, José Antonio Infantes-Lorenzo, Inmaculada Moreno, Christian Gortázar, Jorge R. López-Olvera

ID 338. Spatial representation of the interfaces between wild and domestic ungulates in Spain: potential use for the control of shared diseases.

Carmen Ruiz-Rodríguez, Javier Fernández-López, Sonia Illianas, Pelayo Acevedo, José Antonio Blanco-Aguiar, Joaquín Vicente

ID 341. Anaplasma and Piroplasm co-infection in small ruminants from Portugal.

Marta Sánchez-Sánchez, Alberto Moraga-Fernández, Carla Alves, Vidal Montoro, Miguel A. Habela Rafael Calero-Bernal, Jesús Félix Lina Costa, Luís Manuel Madeira De Carvalho, José De La Fuente, Isabel G. Fernández De Mera

ID 343. Use of dynamic network in the wildlife-livestock interface to study endemic and emerging diseases.

Roxana Triguero-Ocaña, Eduardo Laguna, Saúl Jiménez-Ruiz, César Herraiz, Ignacio García-Bocanegra, María Ángeles Risalde, Vidal Montoro, Joaquín Vicente, Pelayo Acevedo

ID 348. Twenty years overview: spatio-temporal analysis of European surveys on zoonotic diseases in the main large game species.

Ana Carolina Abrantes, Maria Madalena Vieira-Pinto

ID 350. Global geographic pattern of studies on zoonotic diseases in wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*).

Ana Carolina Abrantes, Maria Madalena Vieira-Pinto

ID 351. Serological and molecular detection of *Anaplasma* species in domestic and wild ruminants from Eastern Spain.

Maite Masià-Castillo, Iris García-Bacete, Jose Sansano-Maestre

ID 367. Estimating interactions between livestock and wildlife in the Selva Lacandona, Mexico.

Salvador Romero Castañón, Francisco Ruiz Fons, Isabel G. Fernandez De Mera

Integrated monitoring of wildlife populations and disease

ID 3. Adipose tissue estimation in green turtles (*Chelonia mydas*) using deep learning, diagnostic imaging and bioelectrical impedance analysis.

Sara Kophamel, Leigh C. Ward, Dmitry A. Kononov, Ellen Ariel, Diana Mendez, Ian Bell, Nathan Cassidy, María T. Balastegui Martínez, Suzanne L. Munns

ID 8. Gapeworm (*Syngamus Spp.*) Infection In A Subset Of Collared Greater Prairie Chickens (*Tympanuchus Cupido*) In Wisconsin.

Jacob A. Shurba, Rebecca A. Cole, Matthew Broadway, Constance Roderick, Jason D. Riddle, Shelli A. Dubay



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ID 42. *Usutu virus surveillance in wild birds of Emilia-Romagna Region, North Italy.*

Alessandra Lauriano, Annalisa Santi, Paolo Bonilauri, Elena Carra, Gabriele Casadei, Giorgio Galletti, Arianna Rossi, Marco Tamba

ID 43. *A focus on ten years of wildlife surveillance in Emilia-Romagna region (Italy).*

Arianna Rossi, Annalisa Santi, Gabriele Casadei, Giorgio Galletti, Alessandra Lauriano, Marco Tamba

ID 66. *Estimating the prevalence of a globally-emerged pathogen in a Chilean amphibian assemblage: effects of imperfect pathogen detection and individual pseudoreplication.*

Hugo Sentenac, Andrés Valenzuela-Sánchez, Natashja Haddow-Brown, Claudio Azat, Andrew Cunningham

ID 70. *Size Doesn't Matter, Fit Does: microRNAs as Biomarkers of Immunomodulation.*

Anne-Fleur Brand, Marcel Klaassen, Courtney Alice Waugh, Veerle Leontina Bernard Jaspers

ID 76. *Tracking an invader: Wildlife Surveillance for Haemaphysalis longicornis in the Eastern U.S.*

Alec Thompson, Seth White, Emily Doub, Prisha Sharma, Kenna Frierson, David Shaw, Stacey Vigil, Mark Ruder

ID 86. *Monitoring of alopecia in wild carnivores using camera-trapping: insights for the study of sarcoptic mange.*

Julieta Rousseau, Jorge Costa, Mônia Nakamura, Helena Rio-Maior, Francisco Álvares, Nuno Santos, Luís Madeira De Carvalho

ID 95. *Uncovering Tuberculosis in South African Wildlife – What ante-mortem diagnostic tools are out there?*

Tanya Jane Kerr, Netanya Bernitz, Leanie Kleynhans, Wynand Johan Goosen, Michele Ann Miller

ID 96. *Ruminant interferon-gamma release assay (IGRA) shows potential for detection of Mycobacterium bovis infection in antelope species.*

Tanya Jane Kerr, Leanie Kleynhans, Peter Buss, Michele Ann Miller

ID 104. *Long-term determinants of the seroprevalence of the bluetongue virus in deer species in southern Spain.*

Patricia Barroso, María A. Risalde, Ignacio García-Bocanegra, Pelayo Acevedo, Jose A. Barasona, Pablo Palencia, Francisco Carro, Saul Jiménez-Ruiz, Joan Pujols, Vidal Montoro, Joaquín Vicente

ID 105. *Long-term determinants of the seroprevalence of the Hepatitis E virus in wild boar (Sus scrofa).*

Patricia Barroso, María A. Risalde, Ignacio García-Bocanegra, Pelayo Acevedo, Jose A. Barasona, Javier Caballero-Gómez, Saúl Jiménez-Ruiz, Antonio Rivero-Juárez, Vidal Montoro, Joaquín Vicente

ID 112. *Assessing the Eurasian otter (Lutra lutra) population health in Schleswig-Holstein, Germany – preliminary results from 2015-20.*

Simon Rohner, Peter Wohlsein, Ellen Prenger-Berninghoff, Christa Ewers, Patrick Waindok, Christina Strube, Christine Baechlein, Paul Becher, Ursula Siebert

ID 128. *Pathogens of common palm civets (Paradoxurus philippinensis, Jourdan 1837), domestic cats (Felis catus L.), and domestic dogs (Canis familiaris L.) in Mt. Makiling Forest Reserve, Luzon Island, Philippines.*

Desamarie Antonette P. Fernandez, Maria Catalina T. De Luna, Anna Pauline O. De Guia

ID 129. *A WebGIS to support the epidemiological surveillance of trichinellosis in North-East Italy.*



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*ID 154. Outcomes, mortality causes and pathological findings in European hedgehogs (*Erinaceus europaeus*, Linnaeus 1758): a seventeen-year retrospective analysis on the North of Portugal.*

Andreia Manuela Garcês , Vanessa Soeiro, Sara Lóio, Roberto Sargo, Luis Sousa, Filipe Silva , Isabel Pires

*ID 158. Blood mercury in three populations of endangered whooping crane (*Grus americana*).*

Barry Hartup , Paige Smith, Sarah Warner, Elsbeth Mcphee

ID 159. Exploring Epigenetics in Endangered Cetaceans.

Ashley Barratclough, Lori Schwacke, Forrest Gomez Ryan Takeshita, Ana Tatsch, Eduardo Secchi, Pedro Fruet, Abby McClain Celeste Parry, Steve Horvath, Cynthia Smith

*ID 175. The first three years period of European golden jackal (*Canis aureus moreoticus*) health surveillance in Italy (2018-2021).*

Marco Bregoli, Stefano Pesaro, Paola Beraldo, Gabrita De Zan, Giovanni Binato, Maria Serena Beato, Federica Gobbo, Patrizia Danesi, Paola De Benedictis, Paolo Benedetti, Stefano Filacorda, Federica Obber, Luca Lapini

ID 132. External evaluation and improvements of the epidemiological surveillance of amphibians in French National Parks.

Loïc Palumbo, Claude Miaud, Guillaume Le Loc'H, Sylvain Larrat

*ID 199. Hematology, plasma biochemistry, and pathogen discovery in Illinois headstarted and wild-reared populations of Blanding's turtles (*Emydoidea blandingii*) in two northern Illinois counties.*

Alexis Davidson, Michelle Waligora, Kayla Ladez, Samantha Bradley William Graser, Gary Glowacki
Laura Adamovicz Emilie Ospina Matthew C. Allender

*ID 200. RNA PATHOGEN DETECTION IN FREE-RANGING BLANDING'S TURTLES (*Emydoidea blandingii*).*

Samantha Bradley, Laura Adamovicz, Kayla Ladez, Gary Glowacki, Matthew C Allender

*ID 210. Spatial analysis of hematologic variables and pathogen detection in Blanding's (*Emydoidea blandingii*) and painted (*Chrysemys picta*) turtles in Kane County, Illinois.*

Michelle Waligora, Alexis Davidson, William Graser, Laura Adamovicz, Emilie Ospina, Matthew Allender

*ID 219. Characterization of Erythrocyte Sedimentation Rate in South American Sea Lions (*Otaria byronia*) as an Indicator of Inflammation.*

Samantha Johnson, Michael Adkesson, Susana Cárdenas Alayza, Karisa Tang, Matthew Allender

ID 230. Non-invasive investigations of the microbiome and antimicrobial resistance patterns in cetaceans: a one health approach to ecological health in Hong Kong.

Nathalie France Mauroo, Hein Min Tun, Frederick Chi-Ching Leung, Katie Wing In So , Mickey Hiu Chin Tsang, Yorkie Yu Ki Wong, Key Ho Man Cheung, Dengwei Zhang, Hogan Kok-Fung Wai



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ID 241. *The cost of synurbization for wild boars in Barcelona, Spain.*

Carles Conejero, Jorge R. López-Olvera, Carlos González-Crespo, Raquel Castillo-Contreras Marta Valdeperes, Roser Velarde, David Risco, Emmanuel Serrano, Gregorio Mentaberre

ID 266. *Impact of GI.1 and GI.2 rabbit haemorrhagic disease variants on wild rabbit populations based on Spanish national hunting bag.*

Juan Antonio Aguayo-Adán, Simone Santoro, Carlos Rouco

ID 301. *Are zoo mammals potential sentinels for zoonotic flaviviruses monitoring?*

Javier Caballero-Gómez, David Cano-Terriza, Sylvie Lecollinet, María Dolores Carbonell, Rosa Martínez-Velarde, Eva Martínez-Navado, Daniel García-Párraga, Steve Lowenski, Adrián Beato, Jesús Barbero, Ignacio García-Bocanegra

ID 306. *HPAI H5N1 outbreak investigation in wild birds, Cambodia 2021.*

Alice Porco, Sokha Chea, Sreyem Sours, Chamnan Hong, Savet Eang, Sothya Tum, San Sorn, Davun Holl, Erik Karlsson, Vanneng Sok, Vanna Chhuon, Bunna Um, Simon Mahood, Sereyrotha Ken, Mathieu Pruvot, Sarah H. Olson, Amanda Fine

ID 324. *Actualization of the feral American mink (*Neovison vison*) distribution in Europe: a potential risk species for SARS-Cov2.*

Rachele Vada, Pelayo Acevedo, Tim Adriaens, Marco Apollonio, Jose Antonio Blanco, Guillaume Body, Maria Isabel Garcia Fernandez, Ezio Ferroglio, Patrick Jansen, Sonia Illanas, Oliver Keuling, Santiago Palazon, Kamila Plis, Tomasz Podgorski Podgorski, Massimo Scandura, Graham Smith, Koen Van Den Berge, Stefania Zanet, Joaquin Vicente, ENETWILD Consortium

ID 333. *Mercury exposure and risk assessment for Eurasian otters (*Lutra lutra*) in Denmark.*

Miriam Dibbern, Morten Elmeros, Christian Sonne, Rune Dietz, Jens Søndergaard Anders Michelsen

ID 334. *Comparison of trap-bias and health outcomes between two small rodent live-traps in Wisconsin, United States.*

Gebbienna M. Bron, Hannah Fenelon, Susan M. Paskewitz

ID 356. *Modelling density wild boar populations in Europe for wildlife disease control.*

Sonia Illanas, Javier Fernández-López, José Antonio Blanco-Aguiar, Carmen Ruiz, Pelayo Acevedo, Joaquín Vicente

ID 357. *Cause of Death in Florida Farmed White-tailed Deer (*Odocoileus virginianus*) during 2017–2020 and their use as sentinels to monitor hemorrhagic diseases outbreaks.*

An-Chi Cheng, Sydney L. Cottingham, Olivia Goodfriend, Zoe S. White, Kristen N. Wilson, Julia C. Loeb, John A. Lednicky, Kuttichantran Subramaniam, Heather D. S. Walden, Thomas B. Waltzek, Samantha M. Wisely, Juan M. Campos Krauer

ID 359. *Non-Lethal Sampling Techniques in Invertebrates: Practical Replacements and Refinements to Improve Invertebrate Welfare.*

Sarah J. Wahltinez, Elizabeth A. Nunamaker, Nicole I. Stacy

ID 360. *Freshness might determine the outcome of wildlife health surveillance based on coprology.*

Catarina Fontoura-Gonçalves, Érica Portocarrero, Josep Estruch, Jesús Cardells, Gemma Alfaro Deval



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, Victor Lizana, Omar López-Garrido, Jorge R. López-Olvera, Santiago Lavín , Barbara Moroni . Luca Rossi , Emmanuel Serrano

Molecular epidemiology of wildlife pathogens

ID 37. Occurrence of Chlamydiaceae in raptors and crows in Switzerland.

Sandro Stalder , Nicole Borel, Hanna Marti (, Sarah Albini, Barbara Renate Vogler

ID 58. Subcutaneous mites from an endemic laurel pigeon (Columba junoniae), an endangered reintroduced species in Gran Canaria, Spain.

Kevin M. Santana-Hernández, Pilar Foronda, Simon L. Priestnall, Natalia Martín-Carrillo, Jose Pestano-Brito , Eva Betancor, Eligia Rodríguez-Ponce

ID 63. Molecular identification of Betacoronavirus in bats from Sardinia (Italy): first detection and phylogeny.

Roberta Lecis , Mauro Mucedda , Alberto Alberti

ID 84. Protist diversity of Culex quinquefasciatus mosquitoes in Grenada.

Maria Eugenia Ramos-Nino, Daniel M Fitzpatrick, Lindsey M Hattaway, Andy N Hsueh, Jaelene D. D Haynes, Scott Tighe, Korin M eckstrom, Julie A. A Dragon, Sonia Cheetham

ID 99. Characterizing epidemiological and genotypic features of Mycobacterium bovis infection in wild dogs (Lycaon pictus).

Christina Meiring, Roxanne Higgitt, Anzaan Dippenaar , Eduard Roos, Peter Buss, Jennie Hewlett, Dave Cooper, Peter Rogers, Lin-Mari De Klerk-Lorist, Louis Van Schalkwyk, Guy Hausler, Paul Van Helden, Marlo Moller, Rob Warren, Michele Miller

Detection of a novel species of circovirus in a tawny owl (Strix aluco) in Southern Italy.

Laura Grassi, Matteo Legnardi , Giovanni Franzo, Maria Luisa Menandro, Giulia Faustini, Adriano Minichino, Ludovico Dipineto, Alessandro Fioretti, Mattia Cecchinato

ID 126. First report of Canine circovirus and Canine parvovirus in red foxes of North-Eastern Italy.

Laura Grassi, Maria Luisa Menandro, Federica Obber, Carlo Citterio, Giulia Faustini, Michele Drigo, Giovanni Franzo

ID 138. Limited evidence for detrimental effects of Leucocytozoon infections among emperor geese (Anser canagicus) breeding on the Yukon-Kuskokwim Delta, Alaska.

Andrew M Ramey, Raymond M Bucheit, Brian D Uher-Koch, John A Reed, Maria Andreína Pacheco, Ananias A Escalante Joel A Schmutz

ID 176. Analysis and selection of genes encoding the expression of protective antigens of the African swine fever virus for further development of a vaccine based on adeno-associated virus vector.

Marina Efimova, Elena Zakirova, Vladimir Kuzmin, Alexander Aimaletdinov, Lenar Garipov, Kamil Khaertynov, Yuri Davidyuk, Eduard Shuralev , Albert Rizvanov, Rustam Ravilov

ID 205. Detection of Herpesviruses in Wild Bird Casualties in Slovenia.



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Joško Racnik, Zoran žlabravec, Brigita Slavec, Irena Bahc, Sabina Bolha, Tjaša Sernel, Darja Krelj, Nina Kocar, Maruša škrbec, Zlatko Golob, Olga Zorman Rojs

ID 254. Rickettsia aeschlimannii in Hyalomma marginatum and H. rufipes ticks from trans-Saharan migratory passerines in Spain.

Alberto Moraga-Fernández, Marta Sánchez-Sánchez, Francisco Ruiz-Fons, Xabier Cabodevilla, Mario Fernández-Tizón, Isabel García Fernández De Mera

ID 264. Blood microbial 16S rRNA metataxonomic analysis reveals infectious risks carried by wild black and brown bears.

Mohamed Moustafa, Wessam Mohamed, Ayaka Sasaki, Koji Yamazaki, Shinsuke Koike, Junpei Tanaka, Hiroo Tamatani, Masami Yamanaka, Tsuyoshi Ishinazaka, Mariko Sashika, Michito Shimozuru, Ryo Nakao, Toshio Tsubota

ID 273. Molecular description of gastrointestinal helminths of the Great Bustard (Otis tarda) in two areas of the Iberian Peninsula.

Paula Bolívar, Luis Miguel Bautista, Francisco Ponce, Rafael A. Martínez-Díaz, María Teresa Gómez-Muñoz

ID 279. A preliminary study of viral and bacterial pathogens present in Spanish bats: Identification of new tick-borne pathogen genetic variants.

Marta Sánchez-Sánchez, Alberto Moraga-Fernández, Joaquín Vicente, Xosé Pardavila, Isabel G. Fernández De Mera

ID 283. Prevalence and genotyping of enteric protist parasites in wild ungulates in Spain.

David González-Barrio, Miguel Ángel Habela, Fátima Vioque, Alejandro Dashti, Pamela C. Köster, José Antonio Ortiz, Begoña bailo, Carolina Hernández-Castro, Rafael Calero-Bernal, Guillermo A. Cardona, David Carmena

ID 285. Prevalence, molecular diversity, and evidence of zoonotic transmission of enteric protists between captive non-human primates and their caretakers in four Spanish zoos.

Pamela C. Köster, Alejandro Dashti, Begoña Bailo, Sheila Ortega, Eva Martínez-Nevado, Hugo Fernández-Bellon, Teresa Abelló, Manuel De La Riva-Fraga, Andrea González, David González-Barrio, Rafael calero-Bernal, Francisco Ponce Gordo, David Carmena

ID 286. Occurrence of Chlamydiaceae in Wild Birds.

Sandro Stalder, Nicole Borel, Sarah Albini, Hanna Marti, Barbara Renate Vogler

ID 321. Evaluation of Chlamydiaceae in wild Black-headed Vulture (Coragyps atratus).

Mayan Press Goldfreind, Tânia De Freitas Raso

ID 374. Molecular evidence of piroplasmid infections in Spanish wild ruminants from Valencian Community, (Eastern Spain).

Maité Masià-Castillo, Iris García-Bacete, Jose Sansano-Maestre

Neglected wildlife diseases

ID 106. Persecution of birds of prey in Flanders between 2011-2019: a retrospective study.

An Garmyn, Lieze Oscar Rouffaer, Tom Roggeman, Marc Verlinden, Katleen Hermans, Marleen Cools,



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Mark Van Den Meersschaut, Siska Croubels, An Martel

ID 109. *Adiaspiromycoses in alpine wild rodents from Pyrenees, Catalonia (North-Eastern Spain)*

Marc Ramon , Judit Burgaya, Johan Espunyes, Maria Puig Ribas, Lourdes Lobato-Bailón, Andrea Días-Alves, Axelle Lacombe, Paula Alonso, Catarina Baptista, Ignasi Marco, Bernat Perez De Val, Enric Vidal, Óscar Cabezón

ID 179. *Molecular identification of bot flies (Cuterebra baeri) infesting grey-legged night monkeys (Aotus griseimembra) and howler monkeys (Alouatta seniculus) in Colombia.*

Silvia Rondón, Serena Cavallero , Andrés Link, Manuela De Meo, Camila González, Marco Pombi, Stefano D'Amelio

ID 180. *Detection of Atypical Porcine Pestivirus (APPV) in wild boars in Northern Italy.*

Tiziana Trogu, Sabrina Canziani, Giovanni Parisio, Cristina Malucelli, Sara Salvato, Ilaria Barbieri, Davide Lelli, Ana Moreno, Antonio Lavazza, Enrica Sozzi

ID 244. *Molecular analysis suggests that Namibian cheetahs (Acinonyx jubatus) are definitive hosts of a yet unknown Besnoitia species.*

Gereon Schares, Maike Joeres , Franziska Rachel, Mareen Tuschy, Gábor Árpád Czirják, Pavlo Maksimov, Franz J. Conraths, Bettina Wachter

ID 250. *Yersinia pseudotuberculosis outbreak in Eurasian blackcap (Sylvia atricapilla) in Ebro Delta, Spain.*

Roser Velarde , Marta Cerdà , Míriam Lleixà , Josep Estruch , Stephania Tampach , Johan Espunyes, Lourdes Lobato , Núria Aloy, Carles Durà , Francesc Vidal , Ignasi Marco

ID 281. *Wildlife poisoning in Switzerland.*

Nicole Diana Wolf , Philippe Berny , Hermann Ammer , Marie-Pierre Ryser-Degiorgis, Iris Andrea Marti

ID 295. *Edwardsiella tarda septicemia in an adult striped dolphin (Stenella coeruleoalba).*

Sophie Labrut, Silvia Turci

ID 311. *Lymphoproliferative disease virus and reticuloendotheliosis virus: comparison of tissue tropism and microscopic lesions in wild turkeys (Meleagris gallopavo) in the United States.*

Kayla G Adcock, Chloe C Goodwin , Mark G Ruder, Daniel G Mead, Nicole M Nemeth

ID 352. *Selection of samples to determine the prevalence of Salmonella spp. in free-living Trachemys scripta turtles.*

Inmaculada Gallardo-Coll, Jose Sansano-Maestre

V380. *First description of Metacuterebra baeri infesting a critically endangered Ecuadorian White-fronted Capuchin monkey (Cebus albifrons aequatorialis) in Tumbes, Peru.*

Fernando Vilchez-Delgado, Xiomara Merino-Merino, Luis Fernando Ramírez-Montano , Renzo Randy Ojeda-Juárez , Maximiliano Espinoza-Román, Alejandra Duarte-Quiroga

ID 303. *Susceptibility of anurans, lizards, and fish to infection with Dracunculus species larvae and implications for their roles as paratenic hosts.*

Erin Box, Michael Yabsley, Kayla Garrett, Alec Thompson, Seth Wyckoff, Christopher Cleveland

ID 326. *Copepod consumption by amphibians and fish with implications for transmission of Dracunculus species.*



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ID 308. Surveillance for Echinococcus species infections among wild canids in Pennsylvania, USA.

Kayla Buck Garrett, Justin D Brown, Mark G Ruder, Kyle Vanwhy, Michael J Yabsley, Christopher A Cleveland

ID 312. Detection of Mycobacterium tuberculosis antibodies in Asian elephants in Sri Lanka.P.A.U.

Sewwandi, M.R.B.N. Bandara, H.P.R.N.S. Karunarathne, K.K. Sumanasekara , E.M.E. Liyanage, K.M.P. Perera, P. Ediriwarne, Åsa Fahlman, N.P. Sunilchandra

ID 317. Posterior paralysis: An overlooked challenge in big cat conservation.

Elias Rowther B, Arjun C P, Jacob Alexander, Krishna Kiran, Suriya Sartaj .

New technological insights into wildlife disease surveillance

ID 72. Assessing the national programme for general wildlife health surveillance in Switzerland.

Elisabeth Heiderich, Francesco Origgi, Samoa Zürcher-Giovannini, Stéphanie Borel, Iris Marti, Patrick Scherrer, Simone Roberto Rolando Pisano, Saskia Keller, Irene Adrian-Kalchhauser, Marie-Pierre Ryser-Degiorgis

ID 146. Metagenomic surveillance of foodborne pathogens and phenotypic characterization of antibiotic resistance of Escherichia coli isolated from farm dwelling rodent pests.

Nusrat Annie Jahan, Laramie L. Lindsey, Petet A. Larsen, Evan Kipp, Bradley J. Heins, Amy M. Runck

ID 165. Experimental evaluation of a PIT-tagging method without anesthetic in urodeles.

Paula Alonso Almorox, Maria Puig Ribas, Oscar Cabezón, Johan Espunyes, Lola Pailler García, Diego Martínez-Martínez, Albert Martínez-Silvestre

ID 221. Developing next-generation sequencing tools for health surveillance at the wildlife-livestock interface.

Stephanie Brien, Melissa Marr, Marie Petretto, Ouled Ahmed Hatem, Erhan Yalcindag, Mark Bronsvort, Rob Ogden

ID 257. Intraocular pressure reference values in adult Bonelli's eagles (Aquila fasciata).

Virginia Moraleda Fernández, Laura Suárez Regalado, Natalia Pastor Tiburón, Alicia Carrero Ruiz, Bárbara Martín-Maldonado, Irene López Márquez Fernando González González

ID 328. Sevoflurane anaesthesia in common kestrel (Falco tinnunculus).

Eva Rodríguez-Duarte, Casilda Rodríguez, Irene López, Virginia Moraleda, Laura Suárez, Fernando González

ID 342. Method comparison of glucose concentrations obtained via glucometer, Nova analyzer, and plasma chemistry analyzer and performance of three glucometers in cold-stunned Kemp's ridley turtles (Lepidochelys kempii)

Kathryn A. Tuxbury, Deana Edmunds, Justin R. Perrault, Nicole I. Stacy

Wildlife disease control



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ID 41. Treatment of Batrachochytrium Dendrobatidis in eastern hellbenders (Cryptobranchus alleganiensis alleganiensis) with terbinafine.

Daniella Guzman, Stephen Spear, Priscilla Joyner

ID 44. Health status of the Alpine ibex in the northwestern Italian Alps.

Riccardo Orusa, Maria Cristina Bona, Giuseppe Ru, Maria Lucia Mandola, Francesca Rizzo, Oriana Sparasci, Maria Silvia Gennero, Loretta Masoero, Margherita Messina, Bruno Bassano, Liliana Costanzi, Paolo Oreiller, Christian Chioso, Laura Martinelli, Arianna Menzano, Luca Maurino, Cristina Guidetti, Serena Robetto, Emanuele Carella

ID 53. Overview of post-mortem lesions in free-ranging red foxes (Vulpes vulpes) in northern Belgium in 2018-2020.

Han Versnaeyen, Nermin Caliskan, Veronique Saey, Sanne Terryn, Steven Van Gucht, Muriel Vervaeke, Stefan Roels

ID West Nile virus seroconversion in Eastern loggerhead shrike (Lanius ludovicianus migrans) after vaccination with a killed vaccine.

Kerry Schutten, Amy Chabot, Hazel Wheeler

ID 81. Applicability of ultrasonography in the clinical management of cystic Echinococcosis in captive langurs of the genera Trachypithecus and Pygathrix.

Szilvia Kalliopi Kalogeropoulou, Alyse Ann Klein, Elke Schwierz, Phuong Tran Quang, Michael Meyerhoff, Bonnie Leslie Raphael

ID 100. The Importance of Mange Diagnostics and Some Unusual Clinical Cases in Wildlife.

Ryan K. Grunert, Justin D. Brown, Kayla B. Garrett, Melanie R. Kunkel, Maureen Murray, Nicole M. Nemeth, Kevin D. Niedringhaus, Lisa A. Shender, Alisia A. W. Weyna, Michael J. Yabsley

ID 102. Butorphanol combinations for anesthesia of domestic goats: Models for small wild ruminants.

Mark L. Drew

ID 121. Modelling feline Leukemia virus in the Iberian lynx (Lynx pardinus) from an outbreak: applications for disease management in reintroduction programs.

Fernando Nájera, Guillermo López, Luis A. Fernández

ID 125. Water sports could contribute to the translocation of ranaviruses.

Rosa Casais, Asier Rodríguez Larrinaga, Kevin P. Dalton, Paula Domínguez Lapido, Isabel Márquez (1), Eloy Bécares, E. Davis Carter, Matthew J. Gray, Debra L. Miller, Ana Balseiro

ID 178. Wildlife rabies control and management in Tatarstan (Russian Federation).

Danil Mingaleev, Almaz Khisamutdinov, Iana Shabakaeva, Kamil Khaertynov, Eduard Shuralev, Marina Efimova, Rustam Ravilov

ID 223. Cavers care deeply about bats – but there are some important gaps in knowledge and biosecurity habits regarding White Nose Syndrome. A survey of delegates to an international caving conference (SPELEO 2017).

Jasmin Hufschmid, Soraya Salleh, Keren Cox-Witton

ID 249. First report of suggested septicaemia in a European otter (Lutra lutra) caused by the fish pathogen Yersinia



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ruckeri.

Karin M Olofsson, Minerva Löwgren, Paulina Hysing, Norbert Van De Velde, Erik Ågren, Charlotte Axén

ID 300. A case study of wild boar and TB: giving up the reservoir role?

Miriam Lleixà, Enric Vidal, Bernat Pérez De Val, Xavier Olivé-Boix, Josep V. Jovaní, Albert Sanz Artigas, Gregorio Mentaberre

ID 302. Surveillance of Chronic Wasting Disease in Sweden.

Gustav Averhed, Maria Noremark, Kaisa Sörén, Maria Cedersmyg, Karolina Wall, Dolores Gavier-Widén, Erik Ågren

Wildlife disease dynamics

ID 97. Feeding habits of cormorant in the province of Trento (Italy) and its role as vector of fish viruses.

Eleonora Franzago, Sara Andreatta, Marica toson, Claudia Casarotto, Manuela Dalla Pozza, Rosita Quartesan, Andrea Marsella, Laura Bille, Fabrizio Baldessari, Ruggero Giovannini, Deborah Dellamaria, Anna Toffan

ID 188. Pathogens of zoonotic and conservation concern in Los Angeles County, California.

Sarah Helman, Amanda Tokuyama, Katherine Prager, Riley Mummah, Hazel Byrne, Anthony Friscia, Jessica Lynch, James Lloyd-Smith

ID 207. Beak and feather disease virus detection and load in multiple tissues and blood in a wild parrot population.

Berta Blanch-Lázaro, Anthony Chamings, Raoul F. H. Ribot, Mathew L. Berg, Soren Alexandersen, Andy T. D. Bennett

ID 248. Investigating the sarcoptic mange outbreak in the Iberian ibex population from Ports de Tortosa i Beseit, Spain.

Marta Valldeperes, Gregorio Mentaberre, Emmanuel Serrano, David Chaparro, José Enrique Granados, Jorge Ramón López-Olvera

ID 263. Surveillance for *Batrachochytrium dendrobatidis* and possible association with skin keratin abundance in red-spotted newts (*Notophthalmus viridescens viridescens*) and mole salamanders (*Ambystoma talpoideum*).

Corinna M Hazelrig, Kayla B Garrett, Corrie J Navis, John C Maerz, Nicole M Nemeth, Michael J Yabsley

ID 364. Seroepidemiological study of *Toxoplasma gondii* in wild and domestic lagomorphs in Spain.

Sabrina Castro-Scholten, David Cano-Terriza, Juan A. Aguayo-Adán, Carlos Rouco-Zufiaurre, Daniel Vázquez-Caler, Sonia Almería, Leonor Camacho-Sillero, Débora Jiménez-Martín, Saúl Jiménez-Ruiz, Félix Gómez-Guillamón, Jitender P. Dubey, Ignacio García-Bocanegra



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PLENARY TALKS



CAPRA PYRENAICA

Iberian ibex



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RESERVOIRS SANS FRONTIÈRES: CAN ECOLOGY HELP US PREDICT VIRAL SPILLOVER RISK FROM BATS?

Dr. Olivier Restif

University of Cambridge, UK.

Abstract:

In the last 20 years, bats (Order Chiroptera) have been identified as a major source of zoonotic viruses, on a par with rodents. A small number of bat-borne viruses causing high fatality diseases in people and domestic animals (rabies, Ebola, Hendra, Nipah, SARS, MERS, and of course COVID-19) have caused bats to be portrayed as the ultimate wildlife villains around the world. Yet, like most wild mammals, many bat species are increasingly endangered or threatened by human activities and climate change. Given the vital ecosystem services provided by bats, from pollination to pest control, misguided attempts to cull or displace bat colonies can have far-reaching costs.

Under the One Health umbrella, the aim of my research is to reduce the risk of zoonotic spillover while protecting bats and their habitat. There are growing indications that these two objectives are complementary and that it is possible to improve public health and biodiversity in synergy. However, gathering field evidence and integrating data from multiple scientific disciplines remains a major challenge which requires long-term financial and institutional support. For this purpose, the Bat One Health consortium was established by Dr Raina Plowright to federate multiple international teams of ecologists, virologists, epidemiologists and social scientists with a shared interest in One Health.

In this talk I will focus on henipaviruses in Old-World fruit bats (family Pteropodidae). Despite their very old associations with several species of bats across Australia, Asia and Africa, these viruses were discovered only 20 years ago following zoonotic outbreaks in Australia, Malaysia, Bangladesh, and most recently in India. I will present two case studies from Ghana and Australia respectively, which combine sampling strategies with mathematical models to investigate the dynamics of virus circulation and shedding within bat colonies.

In Ghana, we have been monitoring a captive, breeding colony of *Eidolon helvum* for over ten years, and used serology to monitor the circulation of endemic henipaviruses within a closed population of 100 bats. This unique longitudinal dataset provides strong statistical support for a model of persistent infection with a low transmission rate. PCR testing of urine samples has confirmed the circulation of multiple paramyxoviruses in this colony.

In Australia, we started by reanalysing data from an earlier field survey led by CSIRO scientists. In particular, one bat colony was monitored for over a year, combining serology, individual urine samples and pooled urine samples. Prevalence of Hendra virus shows strong seasonal cycles, which our model was able to link to temporal variations in viral shedding. This points to potential physiological drivers of virus spillover in bats.

I will conclude with an outlook on current and future work which we hope will generate a step change in our understanding of bat-virus dynamics and spillover risk.



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ILLEGAL WILDLIFE TRADE AND EMERGING INFECTIOUS DISEASES: PERVERSIVE IMPACTS TO SPECIES, ECOSYSTEMS AND HUMAN HEALTH.

Prof. A. Alonso Aguirre

Department of Environmental Science and Policy, George Mason University, 4400 University Drive MSN: 5F2, Fairfax, VA 22030-4400 USA

Abstract:

Emerging infectious diseases (EIDs) can be traced to anthropogenic factors. The risk of spillover is clearly linked to human culture, habits and behavior related to close contact to several animal groups, i.e., wet markets, bushmeat hunting, illegal trade, and exotic species introduction. It is well known that avian influenza viruses emerged in China and SE Asia (Vietnam) and spread to the rest of the world from there. Habitat destruction and new animal interactions are key in the spread of new diseases. For example, releasing domestic ducks into rice fields where wild ducks also feed provide excellent conditions for viral exchange. Wet markets, bushmeat consumption and over harvesting of wild animal species are not only hastening species extinction but are changing human-wildlife interactions in a way not witness based on behavioral and cultural traits ingrained in humans for millennia. Interactions across species are facilitated by the rise of the internet and social media that facilitate illicit trade in endangered and other species across the globe. IWT is associated with corruption, money laundering, degradation of the rule of law, national insecurity, spread of zoonotic disease, undercutting sustainable development investments, erosion of cultural resources and convergence with other serious crimes. Recently, we documented links between IWT and EIDs. A total of 83 publications and 249 identified pathogen cases between 1990-2020. Over 60% were pathogens with known zoonotic potential and five cases directly referenced zoonotic spillover events. The diversity of pathogens by taxa included 49 in birds, 47 in mammals, 16 in reptiles, three in amphibians, two in fish, and one in invertebrates. This is the highest diversity of pathogens reported literature related to IWT. However, it is likely not a fully representative sample due to needed surveillance and monitoring of IWT and more frequent pathogen testing on recovered shipments. Poverty, deforestation, habitat loss and human behavior are key factors leading to EIDs; most likely these triggered the COVID-19 outbreak. Local capacity building, integrative research and transdisciplinary collaborations will be the only way to begin untangle these complex issues that may in many cases result in devastation to humanity. Simply banning these markets will not make them disappear but may cause them to be driven underground. Therefore, efforts must be made to address all elements of the supply chain and the corruption that facilitates it. Existing collaborations among human and veterinary health scientists seldom consider wildlife trafficking in zoonotic pathogen surveillance, biosafety, and security (SB&S) efforts. Critical SB&S can be supported through novel scientific collaborations creating new -- and enhancing existing -- capacity to address issues at the intersection of human-animal-ecosystem health using operations research and location science. Improved ability to detect pathogens in trafficked wildlife can significantly enhance technical capacity for effective detection networks, outbreak analysis, and surveillance strategies, thereby decreasing transmission of these pathogens to people and animals. Also, integration of systems analysis and decision science methods within a triple-bottom line (economic, environmental, and social) ecosystem perspective are needed. Finally, decision support models toward behavioral change policies will dramatically enhance local ability to prevent, detect, and respond to pathogen risks. Transdisciplinary science teams are uniquely positioned to help enhance understanding about the intersectionality of wildlife trafficking-related risks and zoonotic pathogens to human health, animal health, and ecosystem health. Together, such teams offer critical refocusing on issues such as priority zoonotic pathogens of security concern and pandemic potential.

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WILDLIFE THROUGH THE LENS OF ONE HEALTH: AN AFRICAN PERSPECTIVE.

Anita L Michel^{1, 2} & Michael D Kock³

1 Department Veterinary Tropical Diseases, Bovine Tuberculosis and Brucellosis Research programme, Faculty of Veterinary Science, University of Pretoria, South Africa 2 Centre for Veterinary Wildlife Research, Faculty of Veterinary Science, University of Pretoria, South Africa 3 International Wildlife Veterinary Services, Western Cape, South Africa

Abstract

One Health (OH) considers the interdependence of human, animal and environment health but in reality, OH is in most cases dominated by a homocentric view and a bias towards infectious diseases. As a result wildlife in the context of OH is primarily seen as a culprit for its ability to transmit zoonotic agents to humans. With 43% of the zoonotic emerging infectious diseases (EIDs) reported to originate from wildlife, this seems indeed a reason for global concern and increased surveillance in those regions of the world, including Africa, where EIDs are more likely to emerge (Jones et al. 2008). Little attention is, however, paid to the fact that epidemic disease outbreaks are typically driven by human-to-human transmission rather than by ongoing wildlife-to-human transmission (Haider et al. 2020). African wildlife interacts with domestic animals and humans at many different levels, including ecotourism, transhumance, agricultural activities, habitat encroachment and exploitation, be it sustainable or unsustainable. This multi-faceted interface between wild and domestic animals and humans, facilitates direct as well as indirect pathogen transmission from domestic animals and humans to wildlife, with potentially devastating effects for individuals as much as for populations. The past decades have witnessed major disease spillover events e.g. of canine distemper virus and rabies virus to wild carnivores as well as the establishment of wildlife disease reservoirs such as the African buffalo (*Syncerus caffer*) for bovine brucellosis and tuberculosis. The onward spread of the latter is considered a potential conservation threat to vulnerable and endangered wildlife species such as African wild dogs (*Lycan pictus*) and black rhinoceros (*Diceros bicornis*). On the other side of the coin, control measures to contain the disease are at the same time in the way of genetic exchange and wildlife conservation. The co-inhabitation of protected areas by wildlife and humans and their livestock is also a frequent source of human-wildlife conflict at the interface, resulting in negative economic, social and health impacts including crop damage, livestock predation and the loss of lives of wildlife and humans. The extent of the human wildlife conflicts increases with the human population and the demand for resources (Mekonen 2020). Innovative interventions to protect communities without harming wildlife have been developed and new ideas are being sought. Thirdly, OH is intricably connected to conservation of biodiversity, i.e. by protecting and ensuring the survival of plant and wildlife species in their natural habitats with the aim of a sustainable co-existence of people with wildlife and natural resources in healthy ecosystems (WHO 2005). *Anthropogenic threats including habitat encroachment, livestock grazing and illegal hunting contribute at the same time to alarming wildlife declines (Rija et al. 2020). Therefore the protection of indigenous wildlife in protected wilderness areas must form part of a strategic OH approach, able to link the conservation of biodiversity, wildlife and health. As Africa's rural communities are interconnected with the natural systems they live in, community-based programmes are key to providing sustainable solutions for livestock production, food security and household income at the interface (https://itswild.org/).*

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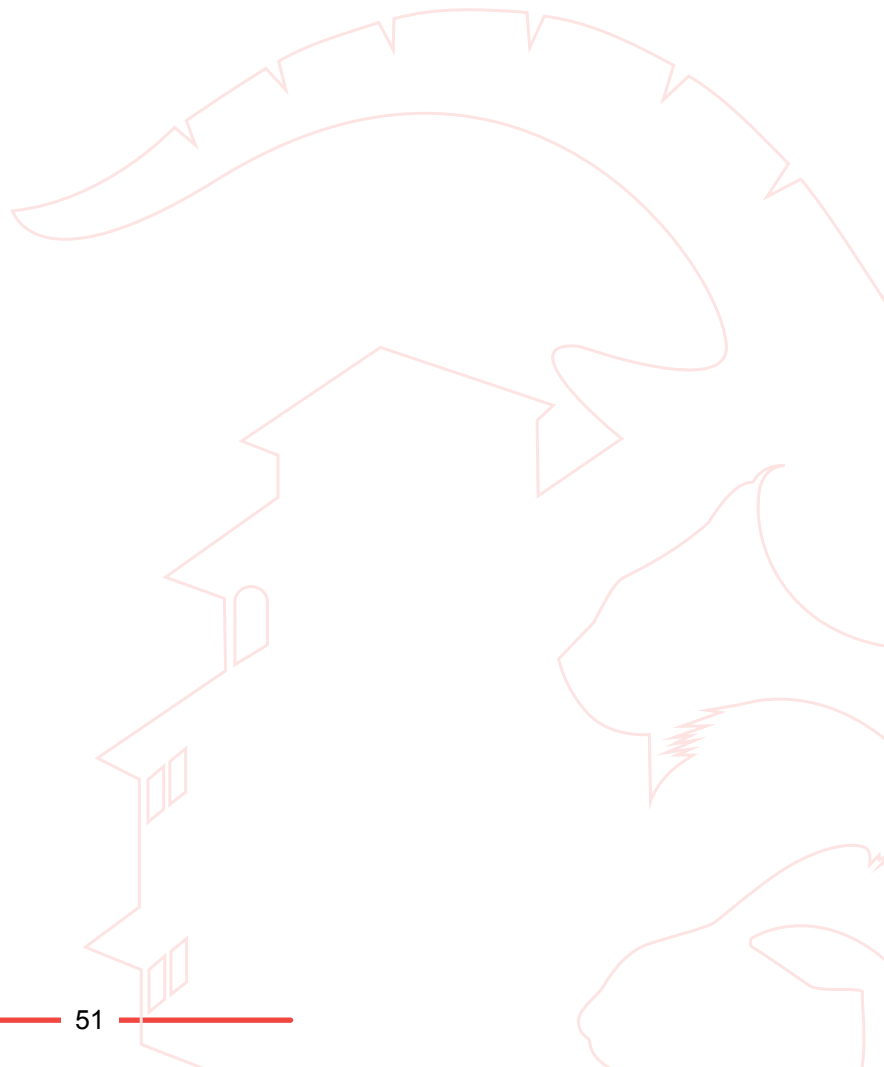
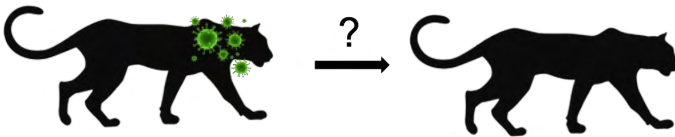
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UNDERSTANDING PATHOGEN TRANSMISSION IN A SOLITARY, SECRETIVE CARNIVORE (PUMA CONCOLOR).

Prof. Meggan Craft

Abstract Text

In this era of the Anthropocene, human impacts on the environment affect wildlife and wildlife disease. How will we manage disease in the face of anthropogenic changes? To understand how to manage disease threats, is it important to understand the basic process of transmission. For example, what conditions promote transmission from an infected to a susceptible individual? And how might pathogen transmission be shaped in human-dominated landscapes? To investigate these questions, I will focus on puma (*Puma concolor*) and highlight how we have leveraged serology, contact networks and simulation modeling, and pathogen genomics to investigate these questions in a solitary, secretive carnivore.





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THE ECOLOGY, ECONOMICS AND EVOLUTION OF EMERGING PATHOGENS.

Prof. Andrew P. Dobson

Abstract Text

This talk will have three main themes: ecology, economics and evolution. Although each section of the talk will focus on one of them, interactions with each of the others will also be considered. As we have seen with Covid-19, it is impossible to understand how to control emerging pathogens without considering their ecology, evolution and the economic impact of the pathogen and resultant control measures. Increasingly we realize that we have to consider interactions between each of these factors, they are far from independent, and all constantly changing. Over the last one hundred years viral pathogens of humans appear to emerge at a relatively steady rate of two new species recorded each calendar year [1]. Most of these events fail to lead to an epidemic. Nonetheless, spillover events that generate large epidemics that spread to multiple continents are increasing in frequency, roughly appearing at the rate at which nations elect new leaders. The most dramatic example has been Sars-CoV-19, but the past emergence of HIV, Zika, and Dengue should warn us that we need to be constantly vigilant to prevent new outbreaks occurring. We can make an initial cost of the average annual cost of these outbreaks by collating data for the last hundred years on size of outbreaks, number of deaths, and impact on local, national, or global economy. The methodology for doing these calculations needs to be better organized, there is no consensus on what to include, so the “true cost” of a global pandemic is consistently underestimated by an unknown and variable proportion. I will first briefly describe a conservative way of undertaking these calculations, and mention factors that are missed from most economic calculations. Our estimates suggest that prevention strategies that curtail the risk of any epidemic by half, would save 1.6 million lives a year, reducing mortality costs by \$10 trillion. Additional economic costs may double this figure. Any combination of strategies that cost less than this should be economically defensible. The primary drivers of pathogen emergence are deforestation of tropical forests, the wildlife trade and intensive agriculture [2]. When we estimate the costs of reducing all these activities to levels that might reduce risk of emergence by 90%. We find that the costs of primary prevention are ~1/100th of the low-end annualized value of lives lost to emerging viral zoonoses and <1/40th of the annualized economic losses. Essentially the annual costs of preventing emergence are a tiny proportion of the average annual cost of emerging pathogens. Several vital initiatives could be created that are central to pandemic prevention: the Global Virome Project, a decade long project that seeks to identify 70% of the unknown potentially zoonotic viruses in wildlife globally, has an estimated budget of US\$1.2 to 3.4 billion over 10 years. This will provide a huge, globally accessible data-base of viruses, their geographical distribution, and their level of host specificity. It would also provide a resource for the development of tests and vaccines needed when future pathogens spillover. Significantly reducing tropical deforestation would obviously help save biodiversity and concomitantly increase our potential to absorb CO₂ from the atmosphere and slow, or reverse, climate change. Viruses evolve at much faster rates than their hosts. This leads initially to the production of novel strains and subsequently to selection for strains that can avoid the host immune system, which will occur when levels of infection in the host population are sufficiently high for the viral infective stage to consistently be partially blocked by immunologically resistant hosts. The rate at which new strains appear is likely a simple linear function of number of hosts who are currently infected. If you half the number of infected hosts by vaccination or changes in behavior, then you double the time until novel strains appear. If you reduce number of infected hosts by 90%, then it will take ten times longer for novel strains to emerge. Novel strains that appear before a high proportion of hosts are immune, will always be more transmissible than earlier emerging strains, these will sequentially replace the less transmissible earlier strains. High levels of herd immunity change the selection pressure on the virus in ways that select for strains that can circumvent host immunity [3]. Pathogens that exhibit an asymptomatic transmission phase before virulence is expressed will tend to evolve higher levels of virulence, than those where virulence and transmission are more sharply connected [4]. A crucial component of global preparedness for pandemic prevention is the need to train many more veterinarians, particularly wildlife veterinarians. These are the front-line troops in our defenses against emerging pathogens. It looks to me as if members of the audience attending this talk will be very, very busy over the coming decades.

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PLENARY TALK AL FRANZMANN AAWV.
THE MOTHER OF INVENTION: NEW TOOLS FOR AN OLD FOE.

D.J. O'Brien,¹ L.C.M. Salvador²

1. Wildlife Disease Laboratory, Michigan Department of Natural Resources, Lansing, Michigan, USA, 2. Department of Infectious Diseases, College of Veterinary Medicine, Institute of Bioinformatics, University of Georgia, Athens, Georgia, USA

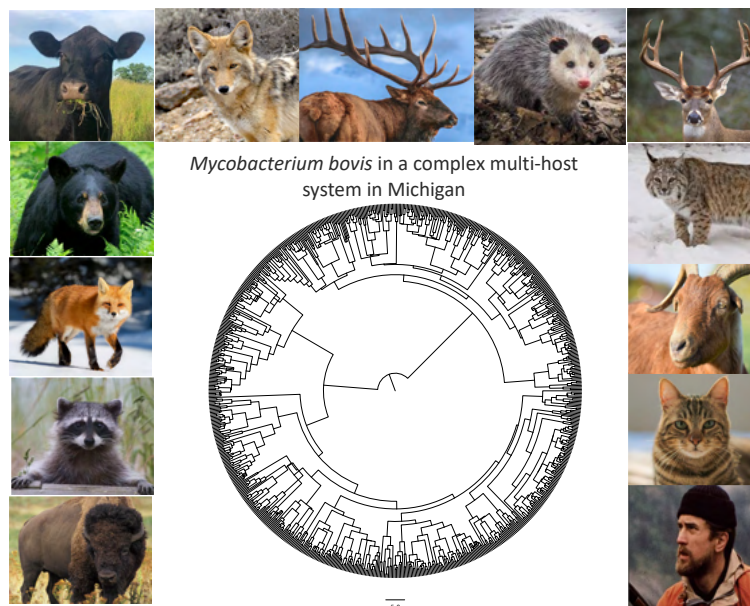
Abstract Text

In the age of the ongoing Covid-19 pandemic, the attention of the One Health community is necessarily focused on emergent, highly contagious viral pathogens. Yet below the surface of the current crisis bides the biggest infectious killer in human history, tuberculosis (TB). Globally, tuberculosis has killed more than a billion people in the past two centuries, far outpacing such formidable diseases as smallpox, malaria, plague, influenza and cholera. Caused by bacteria of the *Mycobacterium tuberculosis* complex, it includes both human and animal pathogens, many of which are shared. Predominantly due to *Mycobacterium bovis* and long neglected, effectively confronting zoonotic tuberculosis is integral to the United Nations' stated goal of ending the global TB epidemic by 2030. In its 2017 document Roadmap for Zoonotic Tuberculosis, the World Health Organization and partners point out that "the implications of zoonotic TB go beyond human health", and reiterate the status of people at risk of zoonotic TB as "a neglected population deserving further attention". They have also set the stage for the enormity of the task, and the necessity and aptness of a One Health approach. In terms both ominous and elegant, the WHO has noted that "The human burden of disease cannot be reduced without improving standards of food safety and controlling bovine TB in the animal reservoir".

If only it were so simple. While organisms that fail to adapt perish, *Mycobacterium bovis* is one of the most well-adapted generalist pathogens on the planet. Even a cursory survey of the ecological systems where *M. bovis* has become established in free-ranging wildlife displays the global diversity of bovine TB outbreaks, the unique challenges posed in each, and the resilience of responses. But what all hold in common is the necessity of developing novel approaches to deal with the constantly shifting challenges posed by the tenacity of this ancient disease.

By way of example, we describe some of the current efforts to progress against the endemic, multispecies bovine TB outbreak in Michigan, USA. From the seminal epidemiologic insights provided by phylogenetic analysis of *M. bovis* whole genome sequences, to novel quantitative metrics required to adapt to changing surveillance data, to outreach efforts evolving to sustain support for disease management in publicly-owned wildlife, necessity is, as ever, the Mother of Invention.

The Mother of Invention: new tools for an old foe





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STUDENT PLENARY TALKS



LYNX PARDINUS
Iberian Lynx

María García Romero



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FELINE LEUKEMIA VIRUS (FeLV): AN EMERGING THREAT TO WILD FELIDS WITHOUT PROTECTION FROM ENDOGENOUS FELINE LEUKEMIA VIRUS (enFeLV)

Elliott Chiu¹, Roderick Gagne², Simona Kraberger³, Mark Cunningham⁴, Lara Cusack⁵, Melody Roelke-Parker⁶, Sue Vandewoude¹

1. Colorado State University, Fort Collins, United States, 2. University of Pennsylvania, Philadelphia, United States, 3. Arizona State University, Tempe, United States, 4. Florida Fish and Wildlife Conservation Commission, Tallahassee, United States, 5. Atlantic Veterinary College, Charlottetown, Canada, 6. National Cancer Institute, Bethesda, United States

Abstract Text

Threats to wild felids include habitat destruction, depredation conflicts, and disease emergence. Incidence of pathogenic feline leukemia virus (FeLV) has increased in a number of wild felid species. The purpose of these studies is to examine the source of a contemporary FeLV outbreak in Florida panthers (*Puma concolor coryi*) and to determine genetic resistance factors present in the host species. Our phylogenetic analysis of the contemporary 2010-2016 FeLV outbreak further implicated domestic cats (*Felis catus*) as the origin of FeLV infections in wild felids. Furthermore, we detected a recombinant oncogenic variant in Florida panthers that is believed to be non-horizontally transmissible. These field studies prompted us to examine the cellular basis of infection and intrinsic resistance to the virus. We hypothesize that wild felids may be at greater risk of FeLV infection compared to domestic cats due to the lack of endogenous FeLV (enFeLV) in wild felid genomes. Using *in vitro* infections of puma (*P. concolor*) and domestic cat cells, we have demonstrated that puma cells support greater infection and replication. Additionally, we documented related enFeLV elements in domestic cats that are negatively correlated with FeLV infection. Data-mining the domestic cat transcriptome revealed that cells resistant to FeLV infection transcribe more enFeLV elements than susceptible cells. We identify a biologically active enFeLV-derived small interfering RNA capable of restricting FeLV replication. Wild felids lack enFeLV altogether, which may leave them more vulnerable to FeLV infection. As urbanization forces niche overlap and contact between wild and domestic felids, wild felids will face increasing pressure from FeLV infection. It is imperative to consider domestic cats in wild felid conservation action plans.



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AN APATHOGENIC VIRUS PREDICTS TRANSMISSION DYNAMICS OF A PATHOGEN AND REVEALS PARADOXES AND SYNERGIES IN PATHOGEN MANAGEMENT IN THE FLORIDA PANTHER (*PUMA CONCOLOR CORYI*)

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Abstract Text

Identifying drivers of transmission prior to an epidemic is a formidable challenge for proactive pathogen management efforts. To overcome this gap, we tested a novel approach, hypothesizing that an apathogenic virus (feline immunodeficiency virus, FIV) could elucidate drivers of transmission processes, and thereby predict transmission dynamics of an analogously transmitted pathogen (feline leukemia virus, FeLV) in a model system, the Florida panther (*Puma concolor coryi*). FeLV caused a significant outbreak among panthers in 2002-04 and continues to threaten panther population health, necessitating ongoing management efforts in the face of uncertain intervention optimization. To test our novel predictive approach, we derived a transmission network using FIV whole genome sequences, used exponential random graph models to determine drivers structuring this network, and used these drivers to predict FeLV transmission dynamics. We then used our transmission analysis pipeline to simulate proactive and reactive FeLV management interventions in the contemporary panther population. Comparing our simulated FeLV predictions to the 2002-04 FeLV outbreak, prospective FIV-based predictions of FeLV transmission dynamics performed at least as well as simpler, often retrospective approaches, and FIV-based predictions best captured the spatial structuring of the observed FeLV outbreak. In addition, management simulations showed that inadequate proactive vaccination can paradoxically increase the number of disease-induced mortalities in FeLV outbreaks, while combinations of proactive vaccination with reactive test-and-removal or vaccination had a synergistic effect in reducing FeLV impacts. Our finding that an apathogenic agent can predict transmission of an analogously transmitted pathogen holds promise for improving predictions of pathogen transmission in novel host populations, and can thereby revolutionize proactive pathogen management in human and animal systems. We demonstrated this value in our management simulations, which highlighted the importance of integrating management and modeling approaches to identify unexpected consequences and synergies in pathogen management interventions and aid in conservation of at-risk species.



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ESTABLISHING ESOPHAGEAL MEASUREMENTS OF CORE BODY TEMPERATURE IN FLORIDA MANATEES (*TRICHECHUS MANATUS LATIROSTRIS*) TO ADVANCE THE MEDICAL MANAGEMENT OF COLD-STRESS SYNDROME

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Abstract Text

In free-ranging Florida manatees (*Trichechus manatus latirostris*) cold-stress syndrome (CSS) is one of the leading causes of mortality. Manatees are frequently presented with CSS to rehabilitation facilities in cold months, however the inability to acquire core body temperatures in CSS manatees has limited veterinary clinical assessments due to a lack of clinically applicable and accurate temperature measurement methodologies. The currently utilized temperature measurement techniques, oral and rectal measurements, are known to be unreliable indicators of core body temperature in manatees. The objective of this study was to establish a clinically reliable measurement of core body temperature in manatees to advance the medical management of CSS. A novel clinically applicable non-invasive temperature methodology was established in manatees: esophageal measurements were collected via the Digi-Sense thermometer (Cole-Parmer, Vernon Hills, IL) placed with an orogastric tube, and were compared to current oral and nasal methods in twenty clinically healthy manatees. Statistical analysis indicated the esophageal as the most accurate and precise methodology ($P > 0.01$, mean 35.4, SD 0.24, range 35.1-35.9°C), compared with nasal ($P = 0.33$, mean 32.5, SD 1.80, range 29.1-34.7°C) and oral (mean 33.0, SD 1.61, range 29.8-34.8°C). The esophageal measurements were consistent with manatee core body temperature, facilitating generation of the first reference interval for core body temperature in healthy manatees (34.97-35.84°C). Three CSS manatee medical cases were evaluated with the newly validated esophageal temperature methodology, which established the first confirmed hypothermic CSS manatees. The application of this newly developed temperature measurement that is logistically practical for field assessments and rehabilitation settings in manatees will improve clinical assessments and further the understanding of CSS, thereby advancing the rehabilitation of manatees.



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ORAL PRESENTATIONS



AQUILA ADALBERTI
Iberian imperial eagle

María García Romero



PATHOLOGICAL CHANGES AND VIRAL ANTIGEN DISTRIBUTION IN TISSUES OF IBERIAN HARE (LEPUS GRANATENSIS) INFECTED WITH MYXOMA VIRUS

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Keywords: Immunohistochemistry, Iberian Hare, Lesions, Myxoma Virus

Abstract Text

Myxomatosis is an enzootic disease caused by myxoma virus (MYXV; genus *Leporipoxvirus*) in several continents. Despite MYXV causes clinical and even fatal disease in European rabbits (*Oryctolagus cuniculus*), only sporadic cases of myxomatosis have been reported in brown hare (*Lepus europaeus*) and mountain hare (*Lepus timidus*) in Europe. However, a cross-species jump was confirmed in 2018 when a novel recombinant MYXV causing high mortalities was isolated in Iberian hare. The aim of this work was to evaluate the main lesions, and organs and target cells of MYXV infection in Iberian hares. For it, anatomopathological and immunohistochemical studies were carried out in twenty-eight hares in which MYXV infection was confirmed by PCR. The main external macroscopic lesions were blepharitis, epistaxis and occasional rectal bleeding, as well as oedema of nasal, oral, anal and genital orifices. The histopathological examination revealed a hyperplastic epidermis with predominant hyperkeratosis, where bacterial colonies were occasionally observed. Likewise, keratinocytes showed widespread hydropic degeneration and eosinophilic cytoplasmic inclusion bodies. Myxomas were not found at the base of ears, eyelid or other skin areas. However, microscopically the dermis of most animals presented a loosely arranged slightly basophilic myxoid matrix admixed with oedematous areas, and with the presence of inflammatory infiltrates. Several internal organs and body cavities showed an intense congestion and haemorrhages. Furthermore, alveolar oedema and interstitial pneumonia in lung, dramatic depletion of lymphocytes in spleen and necrosis in liver and testis were observed. The main target cells of MYXV were epithelial and myxoma cells, hepatocytes, Leydig and Sertoli cells in specific organs, as well as macrophages, lymphocytes, fibroblasts, dendritic shape-like cells and endothelial cells in several organs. These findings, characterized by an acute or hyperacute presentation, are compatible with the amyxomatous forms of the disease. Further studies are needed in order to understand MYXV immunopathogenesis in Iberian hare.



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ENVIRONMENTAL FACTORS DETERMINE THE SEASONAL SEROPOSITIVITY OF *ERYSIPELOTHRIX RHUSIOPATHIAE*, AN EMERGING PATHOGEN IN CARIBOU

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Keywords: Caribou, Environmental Factors, Erysipelothrix Rhusiopathiae, Seasonality

Abstract Text

Caribou (*Rangifer tarandus*) are core to the structure of northern ecosystems and communities and are facing unprecedented population declines coincident with the rise of several emerging pathogens. The generalist bacterium, *Erysipelothrix rhusiopathiae*, was described for the first time in the Arctic associated with widespread unusual mortality and population declines in muskoxen (*Ovibos moschatus*) and has also been reported in other Arctic species like caribou and arctic foxes (*Alopex lagopus pribilofensis*). We investigated the epidemiology and environmental factors influencing the seroprevalence of *Erysipelothrix* in caribou. A total of 3170 serum samples collected from captured and hunted caribou between 1980 and 2015 spanning migratory herds from Alaska to Greenland were analyzed using a modified ELISA. We investigated the influence of sex, age, season and herd in *Erysipelothrix* seroprevalence, the association of seroprevalence in four Alaskan herds with environmental variables from the specific seasonal herd ranges, and the trends in seroprevalence during the study period. Males had a significantly higher seroprevalence than females (Odds ratio OR= 1.4, 95% CI= 1.09-1.75). Similarly, seropositivity tended to be lower in immature compared to adult caribou (OR= 0.7, 95% CI= 0.49-1.00). *Erysipelothrix* had a clear seasonal pattern with higher seroprevalence during warmer months reaching a peak in September and significantly decreasing in October. The intensity of this seasonal pattern was positively associated with oestrid index from the previous summer, icing and snowing events on the fall-winter-spring ranges, and precipitation in the summer range from the same year, and negatively associated with growing degree-days on the calving range during the same year. The variability in the seroprevalence of *Erysipelothrix* increased during the later years of the study period. Understanding the trends of *E. rhusiopathiae*, as well as the environmental factors influencing these trends, is instrumental for developing predictive frameworks to anticipate and mitigate climate change disease risk



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AMERICAN MINK (*NEOVISON VISON*) AS POTENTIAL RESERVOIR OF *LEISHMANIA INFANTUM*

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Keywords: Leishmania Infantum, American Mink, Invasive Species, Zoonosis, PCR

Abstract Text

Leishmania infantum is a zoonotic parasite that affect multiples species of domestic and wild animals, including humans. It is an endemic disease in the Mediterranean basin, where interaction of wildlife and *L. infantum* has been studied. Nevertheless, invasive species, as American mink (*Neovison vison*), have been scarcely studied as potential reservoir of this parasite, even though its role as reservoirs of multiples pathogens, including nematodes, protozoan and viruses has been demonstrated. In this study, we have analyzed the presence of DNA of *L. infantum* from twenty-two American minks coming from Valencian Community (Spain), by five PCR methods, using four different targets: kDNA (two methods), ITS1, SSUrRNA and Repeat region. In addition, a strain of *L. infantum* and a positive bone marrow sample from an infected dog were used to determine the limit of detection for each method. The highest sensitivity employing the control samples were obtained with PCR of the kDNA (using primers RV1 and RV2), SSUrRNA and Repeat region, while ITS1 and kDNA with primers 13A and 13B showed lower sensitivity. Twenty spleen samples from American minks were positive by PCR, but only two PCR methods were able to detect the parasite, PCR of the Repeat region and PCR of SSUrRNA. These results reflected those obtained with both controls (strain and positive sample) although PCR of kDNA did not work in the same way with our samples. This fact can be explained by the presence of inhibitors in the spleen. The obtained results and the previous reports in farms in Mediterranean countries, show the potential role of the American minks as reservoir of *L. infantum*, both in natural environments and in captivity, and should be including in control programs of leishmaniasis in endemic areas.



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WHAT IS BLACKHEAD DISEASE IN FREE-RANGING WILD TURKEYS (*MELEAGRIS GALLOPAVO*)?: COMPARISON OF *TETRATRICHOMONAS GALLINARUM*, *SIMPLICIMONAS SP.*, AND *TRITRICHOMONAS SP.* INFECTIONS WITH *HISTOMONAS MELEAGRIDIS*

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Keywords: Protozoa, *Simplicimonas Sp.*, *Tetratrachomonas Gallinarum*, *Tritrachimonas Sp.*, Wild Turkey

Abstract Text

The wild turkey (*Meleagris gallopavo*) is a national icon and popular game bird species in North America. Since 2015, several wild turkeys at the Southeastern Cooperative Wildlife Disease Study (SCWDS) were diagnosed with protozoal disease with similar clinical manifestations and lesions suggestive of histomonosis ("blackhead disease"; caused by *Histomonas meleagridis*), but with differing etiologies and varied anatomic lesion distribution. We reviewed wild turkey cases (1975-2020) to determine protozoal disease incidence, including histomonosis, and to document pathology and coinfections among wild turkeys infected with less common or novel protozoans. Histomonosis was the sole protozoan disease diagnosed among 44/1,028 (4.3%) wild turkeys from 1975-2020, most of which had classic lesions of necrotizing typhlitis and hepatitis. However, from 2015-2020, other protozoans comprised 7/9 (43.8%) of fatal protozoan disease and included *Tetratrachomonas gallinarum* in 5 turkeys from North Carolina, Kentucky, West Virginia, Mississippi, and *Tritrachimonas sp.* and *Simplicimonas sp.*, in one turkey each from Pennsylvania and Kentucky, respectively. Grossly, 5/7 of these turkeys had cecal cores and 3/7 had pale hepatic foci; microscopically, 4/7 had necrogranulomatous hepatitis and 6/7 had necroulcerative enteritis/typhlitis. Molecular assays and sequence analysis were used to determine the causative agents in these cases. Coinfections included lymphoproliferative disease virus (3/7), avian poxvirus (2/7) and reticuloendotheliosis virus (1/7), *Listeria monocytogenes* (2/7), *Escherichia coli* (1/7); *Raillietina sp.* and skin mites were noted in 1 turkey each. These cases represent rare detections of fatal disease due to *Tetratrachomonas gallinarum*, *Tritrachimonas sp.* and *Simplicimonas sp.* infections in wild turkeys and associated disease was similar to histomonosis, but more often was limited to the intestinal tract. These protozoa should be considered as a rule out for severe intestinal disease in wild turkeys, which may have been historically misdiagnosed as histomonosis due to lack of or limited use of appropriate diagnostic (i.e., molecular) tools.



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INVESTIGATING THE TRANSMISSION OF GASTRO-INTESTINAL NEMATODES BETWEEN LIVESTOCK AND ROE DEER USING DEEP-SEQUENCING ANALYSES

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Keywords: Strongyle, Livestock, Metabarcoding, Nemabiome, Wildlife

Abstract Text

The spread of livestock activities and the expansion of wild ungulates populations favor the share of grazing pastures among species, increasing opportunities for direct or indirect cross-transmission of pathogens. While most studies focused on major economic and public-health infectious diseases, comparatively few studies focused on the epidemiology of gastro-intestinal nematode (GIN) parasites at the wildlife/livestock interface. These parasites are ubiquitous and of major concerns for both domestic and wild ungulates, as they may cause disease or loss of productivity. Although breeders can use anthelmintic drugs to control the infestation of livestock by gastrointestinal nematodes to limit diseases and loss of productivity, those parasites are also hosted by wildlife which can contribute to their circulation. In this study, we aimed to assess the influence of sharing pastures with livestock on the parasitism of roe deer in southern France. Using DNA metabarcoding of ITS-2 rDNA from larvae isolated from fecal samples, we analyzed the gastrointestinal nematodes communities (termed "nemabiome") of roe deer and sheep inhabiting a heterogeneous rural landscape. While the dominant GIN species found in roe deer and sheep are generalist species (*Haemonchus contortus*, *Trichostrongylus axei*), we also detected in wild roe deer GIN species usually found in wild cervids (e.g., *Ostertagia leptospicularis*, *Spiculoptera* spp.), but at low frequency. Nemabiome in roe deer varied along the sampling period, revealing seasonal variation of gastrointestinal species in this species. In addition, we detected a low variation of nemabiome related to the proximity of roe deer samples to livestock pastures. Our results suggest exchanges of gastrointestinal nematodes between and within domestic and wild ungulates in this rural landscape. It emphasizes the role of domestic ungulates in contaminating wild species, but also the potential role of wild ungulates as reservoirs and spreaders of parasites –including drug resistant parasites– between locations.



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STRUCTURED DECISION-MAKING: A TOOL FOR DISEASE RISK ANALYSIS AND MANAGEMENT PLANNING IN THE FACE OF UNCERTAINTY

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Keywords: Structured Decision-Making, Disease Risk Analysis, Wildlife Reintroduction, Pasteurella Multocida, Madagascar Pochard Aythya Innotata

Abstract Text

There is scope to better integrate disease risk analysis (DRA) in wildlife conservation planning. DRA helps identify risks of disease to wildlife, domestic animals and humans. However, its utility can be compromised because of uncertainties around the impact of infectious agents and their proposed management on conservation objectives. Structured decision-making (SDM) provides a management decision-making framework whereby alternative actions are evaluated against fundamental project objectives, i.e. the key outcomes of concern. We used a combined DRA and SDM approach for Madagascar pochard (*Aythya innotata*) reintroduction. A preliminary DRA identified *Pasteurella multocida*, cause of avian cholera (a common disease in domestic poultry in Madagascar), as a potential but unquantified threat to released pochards. Through SDM, we aimed to determine optimal management approaches to this hazard, alongside evaluation of the wider translocation strategy. A multi-disciplinary expert group refined the fundamental project objectives, which included maximising pochard population establishment and welfare, and used an age-based population model and quantitative welfare scale to predict outcomes with respect to these objectives. Predictions were elicited concerning the likelihood of pochard exposure to *P. multocida* and the consequences of associated disease on population establishment and welfare under different management strategies. Management alternatives such as 'ring vaccination' of local poultry, and vaccination and corralling of pochards in the event of an outbreak, were predicted to reduce pochards' likelihood of exposure to the pathogen and improve establishment and welfare, but these outcomes were uncertain. Clearly presenting the uncertain predicted outcomes across alternative management actions allowed project managers to more easily interpret expert knowledge and therefore judge risks and benefits against fundamental project objectives. DRA combined with SDM enabled effective integration of disease considerations in translocation planning. Other benefits of this approach included strengthening team cohesion, truly multidisciplinary working, and the explicit consideration of welfare outcomes in project design



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AN OUTBREAK OF PLASMODIUM RELATED DISEASE AND MORTALITY IN A CONSERVATION BREEDING POPULATION OF GREATER SAGE GROUSE (*CENTROCERCUS UROPHASIANUS*)

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Keywords: Conservation Breeding, Disease Outbreak, Plasmodium, Sage Grouse

Abstract Text

Greater sage grouse (*Centrocercus urophasianus*) are an endangered species in Canada, having undergone a significant decline and extirpation from much of their range due to habitat loss and disturbance. In 2014, the Calgary Zoo, with support from provincial and federal partners, initiated a conservation breeding and reintroduction program for this species. In September 2020, after an unusually wet summer, clinical signs of dyspnea, inappetance, and lethargy were noted in multiple birds. A total of 35 cases occurred over a period of 5 weeks with death in 12 breeding adults and 18 juvenile and subadult birds. Gross pathology included tracheopulmonary edema and haemorrhage, coelomic and pericardial effusion, cardiomegaly, splenomegaly, and nephropathy. Initial histopathology revealed multisystemic subacute to chronic lymphohistiocytic inflammation and vasculitis with no identifiable pathogens. Molecular diagnostics for multiple viral and bacterial etiologies were negative. Midway into the outbreak, a single protozoan schizont was identified in a splenic endothelial cell in one case. Immunohistochemistry was negative for *Toxoplasma*, *Neospora*, and *Chlamydia*. A brain smear from a subsequent case with neurologic signs demonstrated the first finding of gametocytes in erythrocytes. Histologic examination identified large numbers of schizonts within endothelial cells of brain capillaries. Gametocytes increasingly became visible in blood smears as the outbreak progressed. Pan-hematozoan and *Plasmodium* specific PCR and sequencing confirmed *Plasmodium* sp. (BT7 lineage), which is widely reported from multiple avian genera worldwide. Treatment with chloroquine and primaquine was successful in preventing mortality in 5/17 cases. This outbreak highlights the significant negative impact of disease in conservation breeding programs.



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SPATIAL AND TEMPORAL DISTRIBUTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX INFECTION IN EURASIAN BADGER (*MELES MELES*) AND CATTLE IN ASTURIAS, SPAIN

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Keywords: Atlantic Spain, Badger/Cattle, Mycobacterium Tuberculosis Complex, Serology, Isolation

Abstract Text

In Europe, Eurasian badgers (*Meles meles*) are recognized as major tuberculosis (TB) reservoir hosts with the potential to transmit infection to associated cattle herds. The present work investigated the prevalence as well as spatial and temporal distribution of TB in free-ranging Eurasian badgers and in cattle in Asturias (Atlantic Spain) during 13-year follow-up. The study objective was to assess the role of badgers as a TB reservoir for cattle and other sympatric wild species in the region. Between 2008 and 2020, 673 badgers (98 trapped and 575 killed in road traffic accidents) in Asturias were necropsied and their tissue samples were cultured for Mycobacterium tuberculosis complex (MTC) isolation. Serum samples were tested in an in-house indirect P22 ELISA to detect antibodies against the MTC. In parallel, data on single intradermal tuberculin test results were obtained from the Spanish National Program for the Eradication of Bovine TB. A total of 27/639 badgers (4.23%) were positive for MTC based on bacterial isolation, while 160/673 badgers (23.77%) were positive by P22 ELISA. The rate of seropositivity was higher among adult badgers than subadults. Badger TB positive proportion was spatially and temporally associated with cattle TB prevalence. Our results cannot determine the direction of possible interspecies transmission, but they are consistent with the idea that the two hosts may exert infection pressure on each other. This study highlights the importance of wildlife monitoring of infection and disease during epidemiological interventions in order to optimize outcomes. In this regard, the P22 ELISA might be a useful screening tool, faster, more cost-effective and even sensitive in early or latent stages of disease than MTC isolation. Funding: Ministerio de Ciencia, Innovación y Universidades (MCIU), the Agencia Estatal de Investigación (AEI) reference project RTI2018-096010-B-C21 (FEDER co-funded), PCTI 2018–2020 (GRUPIN: IDI2018-000237), and FEDER and Ministerio de Agricultura, Pesca y Alimentación.



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DEMOGRAPHIC TRENDS AND SKIN LESION PREVALENCE OF STRANDED BOTTLENOSE DOLPHINS FOLLOWING A FRESHWATER EVENT

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Keywords: Ecosystem Health, Estuary, Mobile Bay, Prolonged Freshwater Exposure, Salinity

Abstract Text

An increased number of bottlenose dolphins (*Tursiops truncatus*) with skin lesions indicative of freshwater exposure stranded in Alabama, USA, during Spring 2020. Little is known about the salinity threshold and duration of exposure required for lesions to appear. Grossly, these lesions present acutely as combinations of pale, proliferative skin with areas of erosion and ulceration. These lesions progress to multifocal and coalescing erosions, with blubber involvement and algal matting in presumably more chronic cases. In this study, presence/absence of skin lesions and stranding location, age class, and sex were analyzed for freshly dead and moderately decomposed dolphins (n=35) stranded between 1 January to 31 August 2020. To better understand the salinity threshold and timeline for lesions to appear, discharge from major rivers and downstream salinity data were examined during the same period. A 40-year flood event occurred in Mobile Bay during early 2020, with the highest rate of discharge in February (12,714 m³s⁻¹, 2.4x greater than the 8-month average), followed by the lowest salinity in March (0.45 psu, 8 psu lower than the 8-month average). Forty-six percent (n=16) of examined *T. truncatus* had evidence of freshwater-associated lesions. Individuals with freshwater lesions were more likely to strand inside Mobile Bay (n=13) than outside the Bay (n=3). Prevalence of lesions was highest in adults but did not differ between sexes. Most individuals with freshwater lesions stranded in April (n=10), only one month after the lowest recorded salinity. Discounting intercurrent disease, this finding suggests that an extreme freshwater event may lead to death in as little as one month. This information contributes to understanding of the salinity threshold and timeframe of freshwater exposure effects in dolphins and highlights the need for management considerations in advance of extreme or prolonged freshwater inputs.



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FATE OF LYNX ORPHANS IN SWITZERLAND: A RETROSPECTIVE STUDY.

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Keywords: Animal Care, Conservation, Health, Management, Rehabilitation

Abstract Text

In Central and Western Europe, Eurasian lynx (*Lynx lynx*) occur in small isolated populations with poor genetic diversity, urging for pan-European conservation strategies. In Switzerland, health surveillance of the lynx population consists in a combination of clinical examinations of captured live lynx and necropsy of lynx found dead conducted in parallel to population monitoring (radio-telemetry, camera trapping). Besides other concerns, orphaned lynx management has been very challenging since species reintroduction, due to animal welfare, conservation and political issues. The aim of this study was to document previous experiences with lynx orphans and formulate conservation-oriented recommendations. We analyzed data on 120 presumptive orphans, 75 found alive and 45 found dead, and described the fate of live individuals taken to a wildlife care center, and the causes of death of orphans found dead. We assessed the management options of orphaned lynx applied in Switzerland from 1981 to 2019. Orphans were either culled (n=32, no conservation value and questionable regarding animal welfare) or taken to a wildlife care center (n=42). Of these, 18 (43%) died prematurely because of pre-existent health impairments or, rarely, of captivity-related injuries, 15 (36%) were placed in a zoo (no conservation value and questionable regarding welfare), and eight (19%) were rehabilitated. All released lynx survived at least one month, and at least three survived the first year. Finally, an orphan was successfully fed in the wild. Among individuals found dead, the main causes of death were trauma (42%, mainly traffic accident (29%)) and starvation (42%). In conclusion, premature separation from the mother is a major cause of juvenile loss. Orphans found alive could contribute to conservation actions but their rehabilitation requires pre-established procedures and clearly defined responsibilities. If the management option chosen implies (provisory) captivity, a suitable infrastructure with competent staff needs to be identified in advance.



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GUT MICROBIOTA DIVERSITY AND COMPOSITION IS ASSOCIATED WITH INFECTION AND COINFECTION STATUS AND INDIVIDUAL PATHOGENS IN WILD BANK VOLES (*MYODES GLAREOLUS*)

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Keywords: Gut Microbiota, Pathogen-Microbiota Interaction, Wild Animal Microbiota, Coinfection,

Abstract Text

Many pathogen infections have been associated with changes in gut microbiota, potentially affecting the host-pathogen interactions. The type and magnitude of microbiota changes can depend on the pathogen species, duration of the infection, and potentially co-occurrent infections. Though common in the wild, coinfections and their potential impact on host gut microbiota have been poorly studied. Here, we determined the status of four pathogen infections (*Anaplasma phagocytophilum*, *Babesia microti*, *Borrelia burgdorferi* s.l. and Puumala orthohantavirus) and used 16S rRNA gene sequencing to characterize the gut microbiota of wild bank voles to understand how a) the presence of infection, b) coinfection status and c) individual pathogens associate with gut microbiota diversity and composition. We found that having at least one pathogen infection was associated with higher phylogenetic diversity and a shift in gut microbiota community composition. Coinfection status was associated with differences in community composition and dispersion (inter-individual variation) and from the four pathogens detected, only Puumala orthohantavirus infection was associated with higher α -diversity and altered community composition. This study demonstrates that the gut microbiota of wild animals is associated not only with the presence or absence of pathogen infection but also coinfection status. Thus it is important to characterize the potential effects of coinfection and interactions between co-infecting pathogens to understand the host-pathogen-microbiota relationship.



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OPTIMIZING RISK MANAGEMENT STRATEGIES FOR THE CONTROL OF PHILORNIS DOWNSI - A THREAT TO BIRDS IN THE GALÁPAGOS ISLANDS

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Keywords: Birds, Cyromazine, Galápagos, Nest Parasite, Risk Analysis

Abstract Text

One of the most concerning threats to Galápagos bird populations, including some critically endangered species, is the invasive parasitic fly *Philornis downsi*. While long-term sustained solutions are under study, immediate actions are needed to reduce the impacts of this fly. Application of permethrin to birds's nests has been successfully done, but there might be potential long-term reproductive effects to birds. Cyromazine, an insect growth regulator, has been proposed as an alternative, but its risks and effectiveness are unknown. The goal of this study was to determine which combination of chemical (permethrin or cyromazine) and mode of application (injection, spray, and self-fumigation) was most effective to control *P. downsi* while minimizing toxicity to small land birds in Galápagos, maximizing the feasibility of application, and minimizing uncertainty (criteria). A semi-quantitative risk assessment consisting of a multi-criteria decision analysis (MCDA) model was conducted. For the six potential alternatives resulting from the combination of chemical and mode of application, the criteria were given a score from 1-6 supported by available evidence from the literature and from expert opinion. In addition, three different scenarios with different sets of weights for each criterion were assessed with stakeholder's input. Considering the scenario with higher weight to effectiveness of the method against *P. downsi* while also weighing heavily to minimize the toxicity to birds, cyromazine spray followed by permethrin injection were the preferred strategies. Self-fumigation was the mode of application with highest uncertainty but with much potential to be further explored for its feasibility. The approach taken here to evaluate mitigation strategies against an important threat for avian species in Galápagos is not only useful and applicable to the Galápagos system. It can also be used in other conservation programs when making decisions in the face of uncertainty.



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HIGHLY PATHOGENIC AVIAN INFLUENZA IN THE NETHERLANDS, 2020/2021: H5N8 VIRUS EXPANDS ITS HOST RANGE TO BARNACLE GEESE

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Keywords: Avian Influenza, Wild Birds, Anseriformes, Barnacle Goose, The Netherlands

Abstract Text

Since the emergence of the Goose/Guangdong H5 lineage, highly pathogenic avian influenza (HPAI) outbreaks have become frequent in wild birds. To quantify deaths among species groups with known susceptibility for H5 during the start of the latest outbreak in the Netherlands, from October 1, 2020 to February 28, 2021, daily mortality data of wild birds were recorded, thanks to the cooperation among Dutch ornithologists, virologists, animal health organizations and citizen scientists. Citizens were encouraged to submit records of birds found dead, and contributed substantially to the information collected. A total of $\approx 6,000$ wild birds of 140 species were reported dead. Waterbirds accounted for 80%, and land birds for the remaining 20% of the total mortality reports. Anseriformes represented 60% of the total mortality reports. Based on the numbers of reported dead birds, barnacle goose (*Branta leucopsis*), greylag goose (*Anser anser*) and mute swan (*Cygnus olor*) had the highest mortality rates. H5 infection was confirmed in 284 live and dead birds of 22 species. Six virus subtypes were identified (H5N1, H5N2, H5N3, H5N4, H5N5, H5N8), and H5N8 subtype was the most frequently detected. Twelve commercial poultry farms and 1 commercial duck farm in the Netherlands were infected with HPAI H5 virus. The locations of these farms partially matched with high concentrations of waterbirds in the Netherlands, suggesting that infection of farmed birds is enhanced by high presence of waterbirds. An unusual feature of this outbreak was the large proportion of geese, especially barnacle geese, which were hardly involved in previous years. Citizen science was a fundamental resource in this study and made possible to obtain a wider impression of the actual scale of mortality in wild birds, otherwise limited to the data of the official surveillance. We recommend including such methods of data collection in other countries.



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INVESTIGATING THE RISK FROM DISEASE IN A PROPOSED ASSISTED COLONIZATION OF AN EXTINCT IN THE WILD SPECIES, THE SIHEK (GUAM KINGFISHER, *TODIRAMPHUS CINNAMOMINUS*)

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Keywords: Assisted Colonization, Conservation Translocation, Disease Risk Analysis, Extinct In The Wild, *Todiramphus Cinnamominus*.

Abstract Text

The extinct in the wild sihek (Guam kingfisher, *Todiramphus cinnamominus*), once endemic to Guam, currently exists only in conservation facilities under human care. A conservation translocation is being planned to re-establish a wild sihek population, but the bird's cause of extinction, the introduced brown tree snake (*Boiga irregularis*), is still present in Guam. Therefore, assisted colonization to a site outside the indigenous range is being considered. Assisted colonization provides a powerful tool for species recovery where reintroduction is not possible, yet it raises additional risks to recipient ecosystems. We adopted a multi-component assessment to quantify the risks to sihek and the recipient ecosystem. We used the IUCN's EICAT (Environmental Impact Classification of Alien Taxa) method to elicit perspectives from a range of experts (N=19) on which risk factors are likely of concern for sihek assisted colonization. As EICAT identified disease as a heightened risk we evaluated infectious and non-infectious hazards following methods promoted by the IUCN/OIE, including a hazard prioritisation step utilizing opinions from multiple wildlife health experts (N=12). 63 potential hazards were evaluated by this expert panel, including parasites known to be present in sihek or closely related taxa, as well as multi-host parasites, and non-infectious agents. The panel also considered apparent commensal parasites. Most hazards were deemed low risk, but 8 hazards were prioritized as higher risk. Therefore, we developed a translocation pathway with these hazards in mind and quantified their risks. The translocation pathway included strict quarantine from before hatching to arrival at destination and this management method was predicted to reduce the likelihood of co-introduction of pathogenic hazards. Overall, we assessed disease risk as low and acceptable. Our work recognised that disease could be a substantial threat, but that thorough assessment alongside carefully designed mitigation can provide confidence in the utility of assisted colonization.



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SEARCH AND FIND: ZOOSES OF URBAN WILD BOAR IN BARCELONA, SPAIN

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Keywords: Sus Scrofa, Synurbic Wild Boar, Zoonoses, Urban Habitat

Abstract Text

More than half of the emerging infectious diseases in humans originate from wildlife. Wild boar (*Sus scrofa*) populations are increasing and expanding across Europe, leading to growing interactions with humans. In urban environments, the zoonoses carried by wild boars have received little attention. Our aim is to compile knowledge about the zoonotic pathogens detected in wild boars from the Metropolitan Area of Barcelona (MAB), in order to assess this potential public health hazard. We compiled data from 1005 wild boars sampled in the MAB between 2010 and 2019. *Campylobacter lanienae*, *Campylobacter coli* and *Campylobacter hyointestinalis* (59.9%; 95% CI: 51.3–67.8%) and *Salmonella enterica* subsp. *enterica* (3.1%; 1.2–7.6%) were isolated from faecal swabs, and zoonotic *Streptococcus suis* serotypes (40.7%; 31.9–50.2%) from nostril and tonsil swabs. Hepatitis E virus RNA was detected by PCR in faeces (12.1%; 8.3–17.2%) and sera (16.4%; 11.8–22.3%). In addition, resistance to at least one antimicrobial agent was detected in faecal isolates in 24/24 *Campylobacter*, 1/4 *Salmonella*, 4/40 indicator *Escherichia coli*, 18/20 indicator *Enterococcus faecium* and 6/12 indicator *Enterococcus faecalis*. Four tick species were found parasitizing the wild boars (infestation prevalence: 59.6%; 54.9 – 64.1%), and spotted fever group rickettsiae were detected in the ticks (minimum prevalence: 8.7%, 7.0–10.8%). Finally, antibodies against *Brucella* sp. (6.2%, 4.1 – 9.4%), influenza A virus (31.4%, 21.7 – 43.0%), and hepatitis E virus (26.4%, 22.5 – 30.6%) further indicated the exposure of wild boars to these zoonotic pathogens. The detection of these zoonotic pathogens and the associated hazards in urban and periurban wild boars is a cause of concern because of the close interactions with humans in the MAB. Since acquisition and dissemination pathways are not clear for all the aforementioned pathogens, their implications for public health should be further addressed, in order to better quantify these hazards.



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EVALUATING INTERSPECIFIC TRANSMISSION OF TICKS, FLEAS AND CANINE VECTOR-BORNE PATHOGENS BETWEEN DOGS AND FOXES IN A HUMAN-DOMINATED LANDSCAPE

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Keywords: Interspecific Transmission, Ticks, Fleas, Vector-Borne, Carnivores

Abstract Text

Landscape anthropization may facilitate pathogen transmission between domestic hosts and wildlife. Andean foxes (*Lycalopex culpaeus*) thrive in human-dominated landscapes around Santiago (Chile), where free-ranging dogs abound. We aimed to determine whether sympatric free-ranging dogs and wild foxes share ectoparasites and vector-borne pathogens (VBP). Infestation by ticks and fleas and the prevalence of selected VBP were determined in 111 free-ranging dogs and 87 foxes and compared between the two hosts. Ectoparasites and pathogens were genetically characterized. Drivers of transmission were tested by correlating the pathogen/parasite occurrence in foxes with three proxies of the probability of contact with dogs: i) spatial analysis (fox distance to the nearest household and household density into the fox's home range); ii) fox exploitation of food of anthropogenic origin throughout stable isotope analysis; and iii) burden of antimicrobial resistance genes in fox feces analyzed by qPCR. A clear parasite-host association was observed. While *Rhipicephalus sanguineus* (RS) tick and *Ctenocephalides* (CT) fleas predominated in dogs, *Amblyomma tigrinum* (AT) tick and *Pulex irritans* (PI) flea predominated in foxes. A similar tendency was observed for *Hepatozoon* sp. (probably transmitted by AT, only found in foxes), and *Anaplasma platys* (transmitted by RS, much more prevalent in dogs). Although the prevalence of *Mycoplasma haemocanis* was similar in both species, genotypes network analysis indicated that interspecific transmission predominates, with occasional interspecific transmission. No clear association was observed between contact probability proxies and the occurrence of pathogens/parasites in foxes. Close proximity to human settlements does not seem to be necessary for dog-to-fox pathogen transmission. In general terms, a limited transmission of ectoparasites and VBP between free-ranging rural dogs and sympatric wild foxes is taking place in heavily anthropized environments of central Chile.



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MODELLING THE EFFECT OF CLIMATE CHANGE ON SPATIOTEMPORAL TRANSMISSION OF PARASITIC DISEASE IN REINDEER

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Keywords: Modelling, Reindeer, Climate, Parasites

Abstract Text

Reindeer (*Rangifer tarandus* ssp.) face multiple threats from the changing climate including increased threat of parasitic disease. *Elaphostrongylus rangiferi*, commonly known as brainworm, is a protostrongylid nematode which causes neurological disease in reindeer. The sporadic outbreaks occurring in reindeer across Norway have been associated with permissive climatic conditions, and the thermal suitability for development of the larvae has increased over the past decades. This study aimed to determine the effect of climate change on *E. rangiferi* transmission. Species distribution models (SDMs) were developed using Maxent for a range of potential intermediate host species in order to determine areas of the reindeer ranges with high potential for transmission. Both the SDMs and a degree-day model representing development from first to third stage larvae within a range of intermediate hosts were applied to climate change scenarios in order to determine potential future transmission risk. The areas of the reindeer habitat suitable for gastropod hosts remained relatively unchanged throughout the climate change predictions, with areas in the north of Norway and at higher elevations remaining unsuitable for habitation. Thermal suitability is predicted to increase with the changing climate allowing a shift from the 2-year lifecycle, which is currently predominant, to a 1-year lifecycle across the entire reindeer range. This increased rate of development is expected to result in increased transmission risk to the semi-domesticated and wild reindeer, and co-grazing small ruminants, potentially affecting the livelihoods of the indigenous Sami reindeer herders. Further developments to this model will allow the inclusion of intermediate host mortality and spatiotemporal movement of reindeer in order to improve advice on risk mitigation strategies.



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SEMI-QUANTITATIVE SEROLOGY UNVEILS THE EPIDEMIOLOGY OF MYXOMA AND RABBIT HAEMORRHAGIC DISEASE VIRUSES IN THE EUROPEAN RABBIT

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Keywords: Capture-Mark-Recapture, Enzyme-Linked Immune Serum Assay, GI.2 Variant, Longitudinal Study, *Oryctolagus Cuniculus Algerus*

Abstract Text

The European rabbit (*Oryctolagus cuniculus*) was classified as Endangered by the International Union for Conservation of Nature due to >50% reduction in population size in the last decade. Myxoma (MYXV) and Rabbit Haemorrhagic Disease (RHDV) viruses are important drivers of the population decline of this keystone species, however their epidemiology is poorly known, particularly for the emerging GI.2 variant of RHDV. Our study aimed to uncover the epidemiology of MYXV and RHDV in wild rabbits. A serological assessment of MYXV and RHDV was performed over 2 years in two populations of *Oryctolagus cuniculus algerus* in southern Portugal, in a capture-mark-recapture study. Data on gender, weight, and ear length was recorded and the scaled mass index estimated as a proxy of body condition. The semi-quantitative ELISA results for antibodies against MYXV and RHDV GI.2 on 189 sera were analysed using linear mixed models. The RHDV model (conditional $R^2=0.974$) revealed a negative quadratic relationship with body condition ($p<0.05$), peaking at intermediate values. Both the RHDV and MYXV (conditional $R^2=0.962$) models revealed a positive quadratic relationship with weight ($p<0.05$), presenting a nadir at weights suggestive of 3-7 months of age. The ELISA results highlighted a slow progressive decline of antibodies against both viruses from their peaks. Semi-quantitative serology showed seasonal dynamics for both viruses, with a simultaneous nadir in August. Peaks were observed in January and May for RHDV, and in January, September and October for MYXV. We found evidence of antibodies against MYXV and RHDV, possibly of maternal origin, in juvenile rabbits up to 2 months of age. Semi-quantitative serology supports maternal passive immunity to RHDV GI.2 and MYXV in *O. c. algerus*. Immunity to both viruses following natural infection is likely lifelong. Semi-quantitative serological data contains epidemiological information, otherwise lost when the assay results are converted into binomial positive/negative data.



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HARVEST MANAGEMENT & CHRONIC WASTING DISEASE PREVALENCE TRENDS IN WESTERN MULE DEER HERDS

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Keywords: Chronic Wasting Disease, Control, Harvest, Mule Deer, Prion

Abstract Text

We analyzed retrospective data on harvest management practices and corresponding chronic wasting disease (CWD) prevalence trends in 36 western US and Canadian mule deer (*Odocoileus hemionus*) management units (“units”). Our analyses employed logistic regression and model selection, exploiting variation in practices within and among jurisdictions to examine relationships between harvest management and apparent prevalence (the proportion of positive animals among those sampled). Despite notable differences in hunting practices among jurisdictions, our meta-analysis of combined data revealed strong evidence that the amount of harvest was related to CWD prevalence trends among adult male mule deer in the 32 units where prevalence at the start of the analysis period was <5%. All competitive models included the number of male deer harvested or number of hunters 1–2 yr prior as an explanatory variable, with increasing harvest leading to lower prevalence among males harvested in the following year. Competitive models also included harvest timing. Although less definitive than the number harvested, median harvest dates falling closer to breeding seasons were associated with lower prevalence in the following year. Our findings suggest harvest - when sufficient and sustained – can be an effective tool for attenuating CWD prevalence in adult male mule deer across western ranges, especially early in the course of an epidemic. Evidence of a broad relationship between the amount of harvest and subsequent changes in CWD prevalence among adult male mule deer provides an empirical basis for undertaking adaptive disease management experimentation aimed at suppressing or curtailing CWD epidemics.



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HEALTH OF WILD FISH EXPOSED TO CONTAMINANTS OF EMERGING CONCERN IN FRESHWATER ECOSYSTEMS UTILIZED BY A MINNESOTA TRIBAL COMMUNITY

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Keywords: Fish Health, Chemicals Of Emerging Concern, Ecosystem Health, Indigenous Peoples

Abstract Text

Fish play a critical role in the aquatic food web and are sensitive indicators of habitat degradation, environmental contamination, and ecosystem productivity. Fish are particularly susceptible to contaminants of emerging concern (CECs) - chemicals such as pharmaceuticals, hormones, and personal care products - as uptake can occur via both dermal and gill surfaces, orally through the diet, or maternally via the transfer of contaminants through eggs. While some effects from CECs are documented, the effects of CECs on fish health are not fully understood. Laboratory and in vitro studies have documented links to adverse effects in fish exposed to these chemicals. However, these are limited in the diversity of species examined, the effects of specific contaminants and other water chemistry interactions, population-level effects, and the long-term effects of low-level contaminant exposures. Therefore, in situ studies complement experimentally controlled research in overcoming some of these limitations. This study will evaluate the health of wild fish exposed to CECs in waterbodies across northeastern Minnesota by utilizing three fish health metrics: high-throughput (ToxCast) in vitro assays; a refined fish health assessment index (rFHI), and a histopathological index. These measures were applied to subsistence fish, and CECs detected within them, collected from waterbodies in northeastern Minnesota, within the Grand Portage Indian Reservation (GPIR) and 1854 Ceded Territory. Across two years, 26 CECs were detected in fish tissues. Results from this study reveal potential biological effects and the adverse outcome pathways most likely to be relevant for the identified chemicals and chemical mixtures identified, as well as histological and gross tissue and organ abnormalities of subsistence fish harvested for consumption. A better understanding of how the health of wild fish is affected by CECs will help prioritize risk management research efforts and could ultimately be used to guide fisheries management decisions.



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EXPOSURE TO LOW SALINITY WATERS IDENTIFIED AS CAUSE OF THE 2019 NORTHERN GULF OF MEXICO BOTTLENOSE DOLPHIN UNUSUAL MORTALITY EVENT

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Keywords: Prolong Low Salinity Exposure, Bottlenose Dolphins, Northern Gulf Of Mexico, Skin Lesions

Abstract Text

An unusual mortality event (UME) of bottlenose dolphins (*Tursiops truncatus*) occurred in the Northern Gulf of Mexico (nGOM; including Louisiana, Mississippi, Alabama, and the panhandle of Florida) from February to November 2019 (n= 337 strandings), which was a four-fold increase compared to historical average (n=83 during non-UME years from 2002 to 2018). The 2019 UME coincided with record breaking levels of precipitation in mid-United States during winter and spring months. This resulted in an extreme flood event causing massive influx of freshwater discharge into the nGOM, especially from the Mississippi River which was compounded by opening of spillways for flood control measures. This caused a dramatic drop in salinity in the nGOM for over 4 months (February to June 2019). Of the 337 bottlenose dolphin that stranded, the majority occurred from February through June (88%; 297/337) and strandings were highest in Mississippi (n=138) and Louisiana (n=113) followed by Alabama (n=48) then Florida (n=38). Stranding networks collected external photographs, performed necropsies and collected samples from fresh and moderately decomposed carcasses for gross examination of skin, histologic evaluation, infectious disease and harmful algal bloom toxin (HABs) testing. Working with hydrologists and water managers, information was obtained on salinity profiles over time. The stranding patterns (temporally and geographically) were compared to salinity levels within the UME region. The most significant finding was skin lesions consistent with low salinity exposure. The high prevalence of skin lesions coincided with low salinity levels (<5ppt) that extended for several months prior to the spikes in strandings. Brucella, morbillivirus, HABs and fisheries interactions were ruled out as the cause of the UME. These findings support the cause of this UME to be exposure to low salinity water in the nGOM due to extreme flood event of 2019, particularly associated with the Mississippi River watershed impacting the Mississippi Sound.



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PROTECT PEOPLE, PROTECT BATS, AVOID RABIES!

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Keywords: Bats, Conservation, Film, Human-Caused Mortality; Rabies

Abstract Text

Healthy bat populations are critical to maintaining a balanced environment; however, they are experiencing excessive mortality from a variety of directions. Millions are dying in the United States because of the emerging fungal pathogen, *Pseudogymnoascus destructans*, the cause of white-nose syndrome (WNS). WNS has devastated bat populations in North America yet many aspects of the disease remain outside our control. In addition, bats can be a reservoir of the rabies virus which is virtually 100% fatal to humans if medical attention is not sought early. Therefore, fear of bats in general, a lack of understanding of both normal bat behavior and what constitutes an actual rabies exposure, can lead to indiscriminate and unnecessary human-caused bat mortality. One way to advance the conservation and recovery of surviving bat populations is to mitigate human-caused sources of mortality that have additional detrimental effects. This film seeks to provide a clear and consistent message about bats and rabies across agencies at multiple levels of government. This film was created to accurately characterize bats and rabies and promote a One Health message that integrates human health, wildlife health, and environmental health, in an effort to enhance rabies risk awareness to reduce indiscriminate bat mortality. Two important goals of the film are to alleviate the public's fear of bats in general and to raise awareness for rabies prevention and control in humans and animals. By clarifying the relationship between bats and rabies, and what constitutes a rabies exposure, this film will help to disseminate information that reduces human exposure to the disease and reduces the number of bats euthanized for rabies testing. The film will also raise awareness about bat conservation and why bats are so important to human health, the environment, and the economy.



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POPULATION CONNECTIVITY PROTECTS DESERT BIGHORN SHEEP FROM INFECTIOUS PNEUMONIA

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Keywords: Bighorn, Connectivity, Disease Ecology, Ecoimmunology, Genetic Diversity

Abstract Text

Habitat fragmentation is an important driver of biodiversity loss and can be remediated by increasing connectivity in metapopulations. Connectivity may protect populations from infectious diseases by maintaining immunogenetic diversity and disease resistance. However, increased connectivity may also exacerbate the risk of infectious disease spread across vulnerable populations. We tracked the spread of a novel strain of *Mycoplasma ovipneumoniae* in a metapopulation of desert bighorn sheep (*Ovis canadensis nelsoni*) in the Mojave Desert to investigate how variation in connectivity among populations influenced disease outcomes by quantifying disease exposure, genetic diversity, and immunophenotype. Here we show that connectivity was correlated with lower disease risk in invaded populations, higher immunogenetic diversity, and stronger immune responses. *M. ovipneumoniae* rapidly reached all but one of the bighorn sheep populations we evaluated, indicating that the relative isolation of many of these populations did not protect them from infection. Variation in immune function predicted infection risk in individual bighorn sheep and was associated with heterozygosity at genetic loci linked to adaptive immune signaling (interferon gamma) and antigen presentation (major histocompatibility complex 1). Our findings suggest that the genetic benefits of population connectivity can outweigh the risk of infectious disease spread and support conservation management that enhances connectivity in metapopulations.



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OPPOSING MECHANISMS LEAD TO NON-MONOTONIC PATTERNS BETWEEN COMPETITORS AND DISEASE: A THEORETICAL INVESTIGATION WITH A DIRECTLY-TRANSMITTED ZOOZONOSIS

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Keywords: Density-Dependent Transmission, Emerging Infectious Diseases, Interspecific Competition, Hantaviruses, Mathematical Models

Abstract Text

The “dilution effect” and “amplification effect” hypotheses predict negative and positive monotonic, linear relationships, respectively, between species diversity and infectious disease risk. However, community composition, such as heterospecific competitors, could in fact be more important than diversity per se in dictating disease risk in ecological communities. The underlying mechanistic drivers of dilution and amplification have been studied less with directly-transmitted disease systems. Here, we carried out a theoretical investigation to understand how the density of a heterospecific competitor could affect disease outcomes in such systems, by incorporating multiple yet relevant mechanisms within the same modeling framework. We used Sin Nombre virus, hosted by the North American deermouse (*Peromyscus maniculatus*), an example of a directly-transmitted zoonotic system, with voles (*Microtus* spp.) serving as the competitor to mimic a natural community. Empirical evidence suggests that vole competitors could affect deermouse density, behavior, and physiological stress, all of which can determine disease prevalence. Therefore, we used a validated mathematical model with density-dependent transmission, to explore the theoretical outcomes possible when competitor density is allowed to influence disease prevalence through all these various mechanisms (either singly or combined). Our results indicated that, although disease dilution was more commonly predicted than amplification, an unexpected non-monotonic relationship (increase then decrease), was the most commonly predicted outcome in the parameter space we examined for this host-parasite system. Taken together, our findings broadly highlight that heterospecific competitors could, in theory, generate non-monotonic disease outcomes within the same system irrespective of scale, when mechanistic drivers can antagonize one another. These non-monotonic relationships could indeed be more common than previously thought and subject to misinterpretation in natural systems.



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SENSITIVITY OF INTERNATIONAL NOTIFICATION SYSTEM OF WILDLIFE DISEASES: A CASE STUDY USING WAHIS DATA ON TULAREMIA

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Keywords: OIE-WAHIS, Capture-Recapture, Wildlife Health Framework, Tularemia

Abstract Text

The OIE has recently developed a Wildlife Health Framework to respond to the need of Members to manage the risk from emerging diseases at the animal-human-ecosystem interface. One of its objectives is to improve surveillance systems, early detection and notification of wildlife diseases. OIE Members share information on disease occurrence by reporting through the OIE World Animal Health Information System (OIE-WAHIS). To evaluate the capacity of a surveillance system to detect disease events, it is important to understand the gap between actual events and information officially notified. This study used capture-recapture analysis to estimate sensitivity of the OIE-WAHIS system for OIE-listed wildlife diseases by comparing information from publicly available sources used to estimate undetected events. A case study on tularemia occurrence in countries in North America and Europe during the period 2014-2019 is presented. First, an analysis using three data sources (OIE-WAHIS, ProMED, Epidemic Intelligence from Open Sources) was conducted. Next, a second model was built integrating information from a fourth source (scientific literature collected in PubMed). Using the three-source approach, the predicted number of tularemia events was 93 (95% CI 75-114), with an OIE-WAHIS sensitivity of 90%. In the four-source approach, the number of predicted events increased to 120 (95% CI 99-143) and the sensitivity of OIE-WAHIS dropped to 70%. The results indicate a good sensitivity of the OIE-WAHIS system using the three sources approach, but low sensitivity when including information from scientific literature. Further analysis should be undertaken to identify diseases and regions for which the international reporting presents a low sensitivity. This will allow evaluation and prioritisation of underreported OIE-listed wildlife diseases on which actions identified in the Wildlife Health Framework should focus. This study also highlights the need for stronger collaborations between academia and National Veterinary Services to enhance surveillance systems for notifiable diseases.



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ROBUST INTERACTION BETWEEN PREDATOR PRESSURE AND DISEASE PREVALENCE DURING THE PEAK PHASE OF A RODENT SPECIES WITH CYCLIC DEMOGRAPHY: A LARGE-SCALE REPLICATED EXPERIMENT

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Keywords: Disease Propagation, Francisella Tularensis, Pest Management, Predator-Prey Relationships

Abstract Text

Predation and diseases are widely known factors that shape ecological communities and population dynamics, but their interactive role in wild conditions is largely unknown. Two major opposing hypotheses may be proposed: i) predators remove sick prey, reducing disease propagation and being favorable for prey populations' health, and ii) predators induce fear in prey, producing immunosuppression and disease propagation, being unfavourable for prey populations' health. It is unknown which hypothesis prevails, particularly for cyclic rodents. Here we studied infection of common voles *Microtus arvalis* to *Francisella tularensis* in experimentally manipulated predation areas in Castilla y León (north-western Spain), during a vole peak year. Over 300 voles were sampled in three study areas, each of which with a treatment plot with nest-boxes for predators (*Falco tinnunculus* and *Tyto alba*) and a paired control plot (no nest-boxes). Overall, treatment plots totalled 300 nest-boxes. We tested *F. tularensis* infection in preyed, live and naturally dead voles by qPCR analyses in vole spleens. Despite *F. tularensis* prevalence varied among study areas, voles in experimentally-increased predation plots consistently showed higher prevalence of *F. tularensis* than voles in control plots. Unsurprisingly, dead voles showed higher prevalence than predated or live voles, with no significant differences between the latter two groups. Therefore, it is likely that raptors do not select infected individuals but could inflict prey's fear and immunosuppression, so their continued presence could increase *F. tularensis* infection in voles. No reported human cases of tularemia in municipalities with the highest prevalence in voles suggest that other factors such as vector abundance, presence of dead voles in landscape or spilling through aerosols or water bodies may be involved in the epidemiology of tularemia human epidemics. Nest boxes being effective in controlling voles in their surroundings, their outcome in infection prevalence seems a side effect to consider.



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WHAT ARE THE EFFECTS OF PATHOGENS IN PREGNANCY AND BODY CONDITION OF TUNDRA CARIBOU?

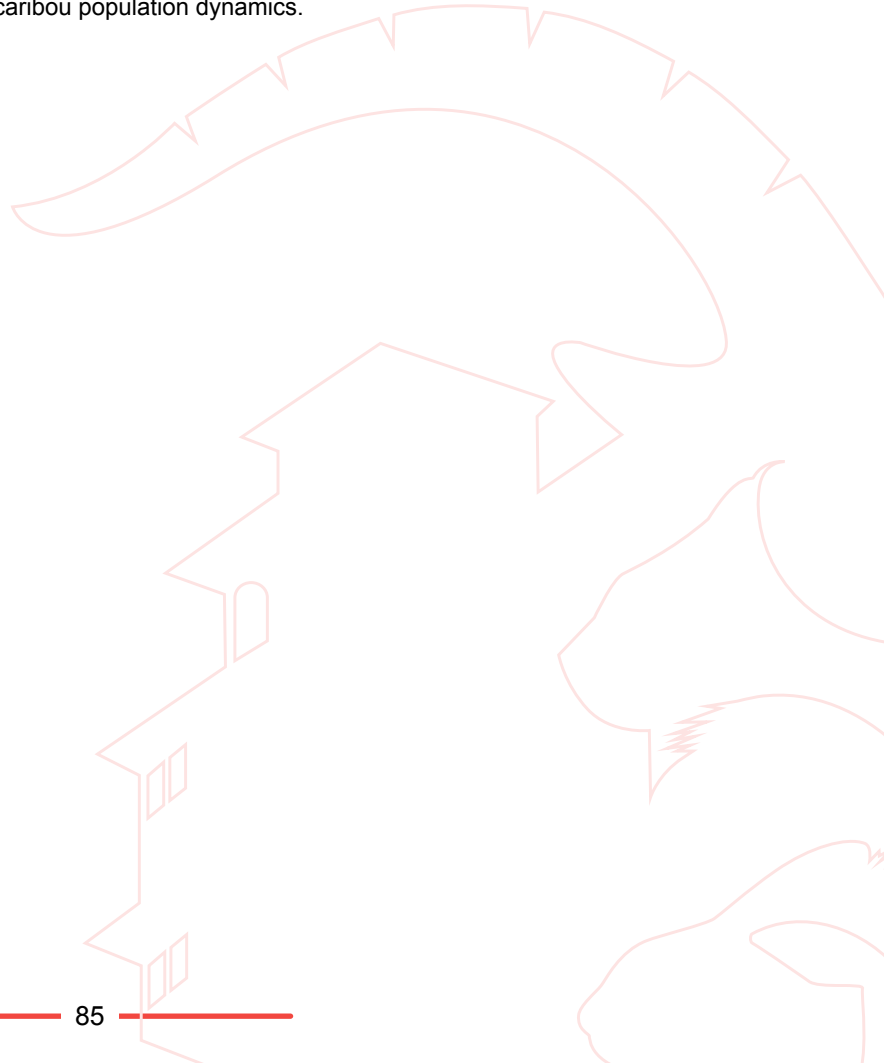
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Keywords: Caribou Health, Pathogens, Reproductive Loss, Disease, Partial Least Square Regression

Abstract Text

Infectious diseases and parasites can affect population dynamics by impairing reproduction or survival. Tundra migratory caribou maintain several infectious agents that can cause reproductive loss or detrimental health costs, however, their effects remain largely unknown. We used cross-sectional data from the hunter-base surveillance program established in Kugluktuk (NU, Canada) to assess the effects of selected infectious agents on pregnancy and body condition. Samples were collected from Dolphin and Union Caribou (*Rangifer t. groenlandicus* x *pearyi*) and barren-ground caribou (*Rangifer t. groenlandicus*) in early Spring (April and May). Antibodies against Pestivirus, alpha-herpesvirus, *Erysipelothrix rhusiopathiae*, *Toxoplasma gondii*, and *Brucella* spp. were assessed and larvae of protostrongylid parasites (DSL) recorded by coprology. We used a partial least square regression (PLSR) approach for exploring the role of age, pathogen exposure and DSL (X block variables) on the pregnancy status and body condition (Kidney Fat index, KFI, as determined using the Riney method) of caribou (Y block variables). Preliminary PLSR analyses from 2018 and 2019 provided a X component explaining 38.0% of the observed variability of pregnancy and RFI (correlations y-U 0.9 and 0.8, respectively). Most of this component's variance was due to *Brucella* ($W^2=70.5\%$) and DSL ($W^2=19.1\%$), and the effect of the rest of predictors was negligible. *Brucella suis* biovar 4 is known to cause reproductive disease in Rangifer, however these hidden effects on body condition may also affect caribou fitness. Knowledge on the effects of pathogens in caribou fitness is important to understand tundra caribou population dynamics.





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EVALUATING THE APPLICATION OF A NOVEL SEROLOGICAL ASSAY IN WILD RED DEER FOR A TUBERCULOSIS SURVEILLANCE PROGRAM IN SPAIN

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Keywords: Tuberculosis, ELISA, Gross Pathology, Red Deer

Abstract Text

Animal tuberculosis (TB) persists in Iberia in a multi-host system which includes domestic and wild ungulates and European badgers (*Meles meles*). Red deer (*Cervus elaphus*) are regarded as an important component of the *Mycobacterium tuberculosis* complex (MTC) host community. However, information about time series and trends of prevalence is scarce. Therefore, developing a consistent TB surveillance program in wild red deer would be of great interest. Generally, the diagnostic of TB has been widely based on gross pathology and bacteriological culture. Recently, new immunological tools have been developed in this species, which could improve the sensibility and specificity of the diagnosis. Thus, we hypothesized that a suitable diagnostic technique for large-scale screening based on detection of anti-MTC antibodies and TB-like lesions would produce comparable results for TB diagnosis in wild red deer, improving the epidemiological surveillance of the disease in this species. The objective of the present study was to assess the potential application of a novel serological technique, an indirect enzyme-linked immunosorbent assay (ELISA) based on P22, for TB surveillance in wild red deer in Spain. We performed P22-ELISA with 5,095 red deer sera from 13 populations over the last two decades and compared resulting prevalences with those obtained by gross TB-compatible lesions. We found mean seroprevalences ranging locally from 1.22% to 25.35%, while the prevalence of TB-like lesions ranged from 0.00% to 62.64%. We observed a North-South gradient of increasing TB prevalence and a stability over time. The risk of testing positive was higher for stags from high-density deer populations. These findings agreed with prior data of TB distribution in red deer in the Iberian Peninsula. However, we found poor agreement (0.214) between serology and gross pathology. Thus, TB-lesion based prevalence and seroprevalence cannot be regarded as equivalent for disease surveillance in wild red deer populations.



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ENETWILD PROJECT: TOWARDS HARMONISING MAMMAL INTEGRATED MONITORING IN EUROPE

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Keywords: ENETWILD, Monitoring, Harmonization, Wildlife, Disease

Abstract Text

Through the project carried out by the ENETWILD consortium (www.enetwild.com), the European Food and Safety Authority (EFSA) aims to improve European capacities to monitor wildlife populations, develop standards for the collection and validation of data (population and disease) and, finally, create and promote a data repository with which to analyse the risks of shared diseases (e. g. ASF) among fauna, livestock and humans. ENETWILD initially focused on the collection of wild boar abundance and distribution data and is now moving to other groups of species (migratory birds relevant to bird flu, as well as other ungulates and carnivores). The project has set up the standards of harmonized data collection in Europe, and those for wildlife diseases are coming next. The process is the following: (i) building the inventory of available data, checking up on missing information, (ii) developing of a data collection model (standards), (iii) data collation and collection through the network and collaborators, and (iv) integration in a common database. The standards must follow the criteria of a) having sufficient quality to produce high quality maps and models and b) being compatible with existing biodiversity/disease data collection systems to optimize inter-operability between them. Similarly, users can upload methods for density estimation of wildlife on a local scale, and a network (first European observatory of wildlife population) is under construction, involving several collaborators from different countries. We open discussion in relation to the need for a common basis for the surveillance of diseases in wildlife in Europe, exemplifying the very variable responses of governments to the emergency created by the spread of ASF in wild boar, that were not always based on scientific knowledge.



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EXPERIMENTAL SUSCEPTIBILITY OF NORTH AMERICAN RACCOONS (*PROCYON LOTOR*) AND STRIPED SKUNKS (*MEPHITIS MEPHITIS*) TO SARS-COV-2

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Keywords: Experimental Infection, One Health, Raccoons, SARS-CoV-2, Striped Skunks

Abstract Text

Recent spillback from humans to animals has raised concerns about SARS-CoV-2 becoming endemic in wildlife species. A sylvatic cycle of SARS-CoV-2 could present multiple opportunities for repeated spillback into human populations and susceptible wildlife species. Striped skunks (*Mephitis mephitis*) and raccoons (*Procyon lotor*) represent a high likelihood of susceptibility and ecological opportunity to infection with SARS-CoV-2. We hypothesized that both species would be susceptible to infection, develop disease, shed virus, transmit virus to other conspecifics via direct contact, and seroconvert after intranasal inoculation of SARS-CoV-2. Eight animals of each species were intranasally inoculated with SARS-CoV-2; four with 103 PFU and four with 105 PFU. To evaluate direct transmission, a naïve animal was added to an identically inoculated pair at day 1 post-inoculation. At predetermined intervals, we collected nasal and rectal swabs to quantify virus shed via virus isolation, detect viral RNA via rRT-PCR, and blood for serum neutralization. Lastly, animals were euthanized at staggered intervals to capture disease progression through histopathology and immunohistochemistry. No animals developed clinical disease. All intranasally inoculated animals seroconverted, suggesting both species are susceptible to SARS-CoV-2 infection. The highest titers in skunks and raccoons were 1:128 and 1:64, respectively. Low quantities of virus were isolated from 2/8 inoculated skunks for up to day 5 post-inoculation, however no virus was isolated from inoculated raccoons or direct contacts of either species. Neither species had gross lesions but recovering mild chronic pneumonia consistent with viral insult was recorded histologically in 5/8 inoculated skunks. Unlike other SARS-CoV-2 infection trials in these species, we detected neutralizing antibodies in inoculated raccoons and demonstrated lack of cage-mate transmission; thus, future wildlife serologic studies must be interpreted with caution. However, continued outbreaks in non-domestic species, wild and captive, highlight that additional research on the susceptibility of SARS-CoV-2 in wildlife, especially musteloidea, is needed.



CAPTURE AND TRANSPORT OF WHITE RHINOCEROSSES (*CERATOTHERIUM SIMUM*) CAUSE SHIFTS IN THEIR GUT BACTERIAL MICROBIOTA COMPOSITION MORE TOWARDS POTENTIAL PATHOGENS

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Keywords: Gut-Health, Microbiome, Rhinoceros, Stress, Translocation

Abstract Text

Translocation of Rhinocerotidae plays a central role in rhinoceros conservation programs, but exposes the animals to a variety of stressors. The gut is inhabited by a vast number of microbiota that provide health benefits for the individual. Stress may change the composition of gut microbiota, which can impact animal health and welfare. White rhinoceroses in particular, commonly develop anorexia, diarrhea and enterocolitis after they have been captured and transported. To investigate the impact of translocation on the rhinoceros' bacterial gut microbiota we collected paired fecal samples from seven adult semi-captive white rhinoceroses at capture and after 30-hours road transport. DNA was isolated from these samples and submitted to high-throughput amplicon sequencing of the variable region 4 of the 16S rRNA gene and processed with QIIME2. Alpha and beta diversity indices of the rhinoceros' fecal microbiota at these two sample time points were compared using the Mann-Whitney U test and PERMANOVAs, respectively, with the R environment. Our results showed no significant differences in alpha diversity levels between the two groups, but significant differences in beta diversity. In line with previous reports, the most represented bacterial phyla in rhinoceros fecal samples at capture were Firmicutes and Bacteroidetes (85.76 % of all sequences) represented by the Lachnospiraceae, Ruminococcaceae, Prevotellaceae and Rikenellaceae families. After transport, the phyla Proteobacteria ($p = 0.001$) and Actinobacteria ($p = 0.002$) were enriched. Potentially pathogen bacterial families such as Enterobacteriaceae ($p < 0.001$), Pseudomonadaceae ($p = 0.001$), Mycobacteriaceae ($p = 0.016$), Corynebacteriaceae ($p = 0.043$) and Clostridiaceae_1 ($p = 0.018$) increased in relative abundance. Important commensals such as the bacterial families Lachnospiraceae ($p = 0.001$) and Ruminococcaceae ($p = 0.007$) decreased in relative abundance. These results indicate that capture and transport cause an imbalanced intestinal microbiota in white rhinoceroses that may lead to dysbiosis and intestinal disorders.



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EPIDEMIOLOGY AND MOLECULAR CHARACTERIZATION OF CANINE BUFAVIRUS AND CACHAVIRUS IN GREY WOLVES (*CANIS LUPUS*) OF THE NORTHWEST TERRITORIES

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Keywords: Co-Infection, Divergence, Molecular Characterization, Parvovirus, Wolves

Abstract Text

Canine bufavirus (CBuV) and cachavirus (CachaV-1) are parvoviruses in the subfamilies Parvovirinae and Hamaparvovirinae, respectively. CBuV has previously been found in free-ranging canids and domesticated dogs, whereas CachaV-1 has only been found in domesticated dogs. Although both viruses have been associated with gastrointestinal symptoms their ability to cause clinical disease is undetermined. The focus of this study was to test for the presence of CBuV and CachaV-1 among grey wolves (*Canis lupus*) from the Northwest Territories (NWT) and molecularly characterize identified strains. DNA isolated from the spleens of 305 wolves (West N=28, East N=188, South=12) previously analyzed for other common dog viruses, was screened for CBuV and CachaV-1 using nested-PCR. Of the 305 samples, 131 were CBuV-positive (42.95%), and 50 (38.9%) of these presented with a co-infection. Eight samples were CachaV-1-positive (2.62%) and 7 (87.5%) of these presented with a co-infection. CBuV was significantly more prevalent and the co-infection rate for CachaV-1-positive animals was significantly higher. Sex and age were not significant in infection for either virus. There were significantly less CBuV infections in the west region than in the east, and all CachaV-1-positive samples with known sampling locations came from the east region. A partial nucleotide sequence was obtained from 28 CBuV- and 4 CachaV-1-positive samples and full genome sequences were obtained for 5 CBuV and 1 CachaV-1 strain. Maximum-likelihood phylogenetic trees revealed the presence of two distinct strains for both viruses. CBuV strains were 90.2-100% identical to each other and 85.5-100% identical to sequences in public databases, while CachaV-1 strains were 95.9-100% identical to each other and 95.5-100% identical to sequences in public databases. Our results indicate different lineages of these recently discovered parvoviruses of dogs are present within the NWT wolf population and warrant further investigation of any potential clinical significance to free-ranging or domestic canids.



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CARRIAGE OF ANTIBIOTIC RESISTANT BACTERIA IN ENDANGERED AND DECLINING AUSTRALIAN PINNIPED PUPS

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Keywords: Pinnipeds, Integron, Antimicrobial Resistance, Heavy Metals, Wildlife

Abstract Text

The rapid emergence of antimicrobial resistance (AMR) is a major concern for wildlife and ecosystem health globally. Genetic determinants of AMR have become indicators of anthropogenic pollution due to their greater association with humans and they are rarely present in environments less affected by humans. The objective of this study was to determine the distribution and frequency of the class 1 integron, a genetic determinant of AMR, in both the faecal microbiome and in *Escherichia coli* isolated from neonates of three pinniped species. Australian sea lion (*Neophoca cinerea*), Australian fur seal (*Arctocephalus pusillus doriferus*) and long-nosed fur seal (*Arctocephalus forsteri*) pups from eight breeding colonies along the Southern Australian coast were sampled between 2016-2019. DNA from faecal samples (n=309) and from *E. coli* (n=795) isolated from 884 faecal samples were analysed for class 1 integrons using PCRs targeting the conserved integrase gene (*intI1*). Class 1 integrons were detected in *A. p. doriferus* and *N. cinerea* pups sampled at seven of the eight breeding colonies investigated in 4.85% of faecal samples (n=15) and 4.52% of *E. coli* isolates (n=36). Integrons were not detected in any *A. forsteri* samples. DNA sequencing of the class 1 integron identified diverse genes conferring resistance to four antibiotic classes. The relationship between class 1 integron carriage and the concentration of five trace elements and heavy metals was also investigated, finding no significant association. The results of this study add to the growing evidence of the extent to which antimicrobial resistant bacteria are polluting the marine environment. As AMR determinants are frequently associated with bacterial pathogens, their occurrence suggests that these pinniped species are potentially vulnerable to potential health risks. The implications for individual and population health as a consequence of AMR carriage is a critical component of ongoing health investigations.



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ARE INTRODUCED RODENTS INVOLVED IN DISEASE OUTBREAKS THREATENING SUBANTARCTIC WILDLIFE?

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Keywords: Conservation, Invasive Species, Multi-Host Epidemiological Dynamics, Reservoir, Seabird

Abstract Text

Characterizing pathogen reservoirs is key to understand, and potentially limit, their re-emergence and spread. Due to their foraging behaviours, terrestrial predating and/or scavenging species have the potential to play critical roles in epidemiological dynamics by introducing, maintaining pathogens and/or enhancing their circulation among their preys. On Amsterdam Island (Southern Indian Ocean), avian cholera, caused by *Pasteurella multocida* bacteria, has been causing recurrent die-offs of albatross and penguin nestlings since the 1980's, threatening the viability of these populations. In addition, predation by introduced rats and mice also appear to impact nestling survival. We explored whether introduced rodents might also directly impact avian cholera dynamics by carrying and transmitting *P. multocida* to seabirds. Introduced rodents exposed to *P. multocida* were detected across the island. Prevalence was particularly high around seabird colonies affected by avian cholera outbreaks, indicating that transmission between seabirds and rodents likely happen. In addition, prevalence remained high in winter, when most seabirds have migrated at sea, suggesting that rodents might maintain *P. multocida* independently of seabirds, and facilitate its re-emergence in seabird populations. The presence of introduced rodents may thus explain the exceptional intensity and recurrence of avian cholera outbreaks on Amsterdam Island. In such contexts, the control of introduced species may represent an efficient strategy to control disease outbreaks in wild populations, highlighting a potential additional benefit of ecosystem restoration programs.



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CLINICAL BABESIOSIS IN A NORTH AMERICAN RIVER OTTER (*LONTRA CANADENSIS*) AND THE PREVALENCE AND GENETIC CHARACTERIZATION OF THIS *BABESIA* MICROTI-LIKE SPECIES IN THE EASTERN UNITED STATES

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Keywords: Babesia, Babesia Microti-Like Sp., North American River Otter, Parasite, Disease

Abstract Text

Babesia species are intraerythrocytic protozoan parasites that infect a diversity of hosts, including North American river otters (*Lontra canadensis*). In 2009, a 4-month-old, male river otter from Athens-Clarke County, Georgia at a rehabilitation facility died after a three-day history of lethargy, anorexia, and severe anemia. Antemortem blood smears revealed intraerythrocytic piroplasms. Supportive care and antiparasitic treatments were initiated but the animal died three days later. Gross necropsy revealed yellow discoloration of all adipose tissue throughout the carcass and a mildly enlarged, diffusely yellow/pale orange liver. Microscopically, moderate, centrilobular hepatocellular degeneration and necrosis was observed, consistent with hypoxia secondary to apparent hemolytic anemia. Piroplasms were observed in red blood cells in histologic sections. The near full-length 18S rRNA gene sequence was identical to a previously described piroplasm from river otters from North Carolina. To determine the prevalence and distribution of this parasite, spleen and/or blood samples were collected from otters in Georgia, North Carolina, South Carolina, Pennsylvania, and California. Samples were tested for piroplasms using PCR assays (one amplifies the *Babesia sensu stricto* (s.s.) and the other amplifies the *Babesia microti*-like sp.). To evaluate diversity and intraspecific variation, positive samples were genetically characterized by amplifying and sequencing partial 18S rRNA and cytochrome oxidase subunit 1 (cox1) genes. Of 45 otters tested, 18 (40%) were positive for the *Babesia microti*-like sp. All 18S sequences were identical to each other but 6 unique cox1 sequences were obtained and were not geographically distinct. Phylogenetic analyses for both gene targets support that this otter *Babesia microti*-like sp. is distinct from other *Babesia* spp. within this group. The high prevalence and broad distribution of this otter-specific *Babesia microti*-like sp. combined with the mortality of an infected young otter indicates that further research of this poorly understood group of parasites in meso-mammals is needed.



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A CENTURY OF CO-INFECTION RESEARCH: A REVIEW

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Keywords: Co-Infection, Coinfection, Concomitant Infections, Multiple Infections, Mixed Infection

Abstract Text

Co-infection, coinfection, and concomitant infections are used to describe the occurrence of more than one simultaneous infection in individual hosts, populations, or communities. With a growing number of pathogens being discovered, emerging and shifting among host species, co-infection appears to be the rule rather than the exception in nature. However, few works have evaluated the role of specific combinations of pathogens to assess their impact on disease severity, length, or transmission. Existing studies demonstrate a broad diversity in approaches and inconsistency in terminology, making comparison difficult. But what exactly does co-infection entail and what challenges and opportunities emerge with the growing body of evidence? The main aim of this study is to summarize the insights of co-infection research in wildlife during the last century. We conducted a systematic search in Web of Science database, obtaining 32,934 research articles published between 1920 and 2020. After screening the first 10,000 papers, we obtained 180 validated research articles and extracted valuable information about co-infection terms, population of interest, taxonomic groups, number of species studied, and statistical techniques used. We found a wide variety of patterns on co-infection. For example, we found co-infections within the same taxonomic groups (Arthropoda-Arthropoda, Bacteria-Bacteria, Fungi-Fungi, Helminths-Helminths, Protozoan-Protozoan, and Viruses-Viruses), and also between two or three taxonomic groups—like co-infection between Protozoan-Helminths-Bacteria or Protozoan-Viruses-Helminths. Some research involves up to 14 different pathogen species, but the majority only consider two. The study also identifies the range of terms used when referring to co-infection—such as co-infection with and without a dash, concomitant infections, multiple infections, and mixed infections. To date, the co-infection literature is afflicted by inconsistent terminology and definition of concepts, which require an update in light of the pressing demand to better understand the ecology of co-infection in time of global change induced disease spread in wildlife.



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USING METABARCODING TO STUDY EFFECTIVE CONTACT FOR BRAINWORM TRANSMISSION BETWEEN MOOSE AND GASTROPODS

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Keywords: Brainworm, Gastropods, Metabarcoding, Minnesota, Moose

Abstract Text

Moose (*Alces americanus*) are culturally, ecologically, and economically important to the United States, but experienced drastic (~50%) population declines in the midwestern portion of their range over the last three decades. Brainworm (*Parelaphostrongylus tenuis*), a nematode with a gastropod (Gastropoda) intermediate host and white-tailed deer (*Odocoileus virginianus*) definitive host, is associated with 25-33% of those deaths. Moose must consume infected gastropods to contract brainworm, making a sound understanding of this interaction crucial for preventing further moose declines. However, we lack empirical information regarding which gastropod species moose consume or when they consume them. The proliferation of high-throughput sequencing provides new opportunities to explore this interaction, specifically through metabarcoding of moose feces. In collaboration with the Grand Portage Band of Chippewa, for whom moose are a historically important subsistence species, we obtained 246 temporally stratified moose fecal samples near the Grand Portage Indian Reservation in Minnesota, USA and amplified a fragment of the mitochondrial cytochrome oxidase subunit I gene from each sample. We then sequenced the sample and compared the result to a known gastropod sequence database for species identification. In preliminary work, we detected moose consumption of one gastropod (*Punctum minutissimum*) in the first 20 samples sequenced, highlighting the potential utility of this metabarcoding approach. This study is an important first step in understanding effective contact between moose and gastropods in the brainworm transmission system and could provide a parameter value estimate for researchers trying to model transmission. It will also identify species for future studies of host competency and ecology. Ultimately, this information could be used by forest and wildlife managers to devise plans that reduce the presence of the implicated gastropod species in seasons when and areas where they are most likely to be consumed by moose.



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MALLARDS ON THE LEASH: WHY DON'T THEY BARK FOR HPAIV INTRUDERS?

Anja Globig, Anne Günther, Timm Harder, Angele Breithaupt, Christian Grund, Klaus Depner, Laura Zani, Frank Busch, Anne Pohlmann, Martin Beer, Thomas C. Mettenleiter

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Keywords: Mallards, HPAIV H5, Low Pathogenic Avian Influenza Viruses, Sentinel Surveillance

Abstract Text

In 1996, a highly pathogenic avian influenza (HPAI) H5N1-lineage emerged from domestic poultry in China (Goose/Guangdong/96 – Gs/Gd/96) as an ancestral virus that subsequently circulated, adapted and differentiated into a plethora of reassortant progeny that widely dispersed over vast geographic distances and time. HPAIV H5N8 clade 2.3.4.4 first appeared around 2010 in China and reached Europe in the autumn of 2014 (group A). A new and phylogenetically distinct group of the same clade (B) was then detected in October/November 2016 in Europe. The epidemics caused by HPAIV H5N8 clade 2.3.4.4 group B (H5N8B) were the most severe reported in Germany and Europe so far. Dabbling ducks play an important role in the maintenance and dissemination of low pathogenic avian influenza viruses (LPAIV), but likely also of H5-HPAIV, typically associated with lower mortalities as compared to other anseriform species. Since 2006, a small raft of mallard ducks (*Anas platyrhynchos*) were placed as sentinels in the shallows of the southern Baltic coast (Greifswald Bodden, Germany), in relation to circulating AIV. The ducks were usually held between 6-12 months in an aviary right beside the sea and in close contact to wild waterfowl and migratory birds. During 15 years of fortnightly testing for AIV infection in various batches of sentinel mallard ducks, HPAIV has not been detected until 2020/2021, although it could be demonstrated that H5N8B was abundantly circulating in wild ducks and gulls in the same geographical area in 2016/2017. Instead, several LPAIV infections of individual ducks were detected. In 2021, for the first time, we detected H5N8B in samples from clinically inconspicuous sentinel mallard ducks. We present the sentinel surveillance concept, including AIV data collected over the last 16 years and highlight the role that mallard ducks can play in the ecology of emerging HPAIV.



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DESCRIPTIVE EPIDEMIOLOGY AND GENETIC CHARACTERISATION OF TRICHOMONAS GALLINAE INFECTIONS IN ORNITHOPHAGOUS BIRDS OF PREY FROM NORTH-WESTERN FRANCE (2012-2015)

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Keywords: Descriptive Epidemiology, Raptors, T. Gallinae, Trichomoniasis, Wildlife Rehabilitation Centre

Abstract Text

Trichomoniasis in wild birds, a digestive disease caused by the protozoa *Trichomonas gallinae*, is worldwide distributed. Two lineages of *T. gallinae* are currently predominant: the C/V/N reference affecting mainly Columbids and the A/B lineage which emerged in 2005 in the UK causing since then an epizootic in Finches across Europe. Raptors can also develop trichomoniasis following ingestion of avian infected preys. Even if many studies have already been published on diseased or infected Raptors by one of the two lineages, no longitudinal study was performed in this group of birds in France to date. Our study both aimed at describing the epidemiology of *T. gallinae* infection and trichomoniasis among ornithophagous Raptors in France (infection and disease frequency per species, spatio-temporal distribution) and at providing a genetic characterisation of the strains involved. From August 2012 to June 2015, every bird from ornithophagous raptor species admitted at a wildlife rehabilitation centre from North-Western France was subjected to a thorough oropharyngeal clinical examination and swabs were collected for in vitro culture. Genetic identification of *T. gallinae* strains was then performed from positive cultures by ITS region PCR amplification and sequence analysis. Demographic and incident history data of the casualties were also collected. A total of 444 birds from 7 species (5 diurnal and 2 nocturnal) was included in the study. *T. gallinae* infection was found in 3 species only, with infection frequency ranging from 2.6% to 13.3%. 95% of the infected birds had macroscopical lesions. 75% of the cases were related to the ITS A/B epizootic lineage. The two lineages were found in one diurnal species only. Our work provides then innovative knowledge on *T. gallinae* infection and disease in French Raptors. It's also an additional illustration of the potential of rehabilitation centres to take part to wildlife disease epidemiological studies in France.



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NEW DIAGNOSTIC TECHNIQUES TO CHARACTERIZE FETAL, PLACENTAL, AND MATERNAL HEALTH IN BOTTLENOSE DOLPHINS FOLLOWING THE DEEPWATER HORIZON OIL SPILL

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Keywords: Deepwater Horizon, Dolphin, Health, Oil Spill, Reproduction

Abstract Text

In the aftermath of the Deepwater Horizon (DWH) disaster, a high rate of reproductive failure persists in bottlenose dolphins (*Tursiops truncatus*) within the oil spill footprint. To better characterize reproductive loss following DWH, new diagnostic techniques were developed with dolphins in managed care and applied to free-ranging dolphins living in oil-impacted Barataria Bay, LA (BB). An expanded reproductive ultrasound protocol was established to provide parameters and descriptive findings correlated with reproductive success. This protocol was then applied to failed pregnancy cases (calf survival ≤ 30 days) from managed care (N=22) (1996-2020) and to BB dolphin pregnancy exams (N=38) performed during capture-release health assessments (2011-2018). Serial monitoring of managed care dolphins with extensive health histories allowed for the identification of ultrasound parameters associated with reproductive failure. These included abnormal architecture and thickening of the uteroplacental unit (UPU), a large corpus luteum, and maternal peritoneal effusion. A newly developed case-analysis framework identified common underlying etiologies of failure. Maternal illness was unequivocally the most important etiology, followed by placental dysfunction, in-utero infection, and congenital defects. In BB, abnormalities associated with fetal hypoxia, UPU architecture and thickening, and umbilical cord coiling were detected. Synthesis of ultrasound findings with additional health parameters showed poor maternal health as the primary cause of persistent reproductive failure in DWH-impacted dolphins. Application of advanced diagnostic techniques for the identification of at-risk dolphin pregnancies during capture-release health assessments is now possible. These efforts can aid in the prediction of population recovery timelines, to support management decisions following environmental events.



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ASSESSING THE ANIMAL AND PUBLIC HEALTH HAZARD OF URBAN WILD BOARS USING AN AGENT-BASED MODEL APPROACH

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Keywords: African Swine Fever Virus, Agent-Based Model, Campylobacter, Hepatitis E Virus, Urban Wild Boar

Abstract Text

Wild boar (WB, *Sus scrofa*) populations are globally increasing, accompanied by growing synurbization in European cities (i.e. Barcelona, Spain), enhancing the major epidemiological role as pathogen host. Synurbization increases WB aggregation, contact rates and close interactions with humans, with the consequent risk of pathogen transmission, generating a new human-WB interface and creating epidemiological public health concern. This study aims to test epidemiological scenarios of three pathogens, two of them of zoonotic potential (i.e., hepatitis E virus, HEV, and antimicrobial-resistant *Campylobacter*, AR-CB) and one affecting suids (i.e., African swine fever virus, ASFV), at the WB-human interface in the (peri)urban area of Barcelona. Using the BCNWB-prototype, a validated agent-based model of the social-ecological factors driving the use of the urban ecosystem by synurbic WB and the related human-WB interactions in Barcelona, this study develops an epidemiological expansion, the BCNWB-EPI model, in order to inform animal and public health risk assessments and support risk-based decision-making. Citizen exposure was similar for HEV (0.79%) and AR-CB (0.80%) and agreed with the World Health Organization (WHO) estimates of global exposure for these pathogens. The similar human exposure despite the difference in pathogen prevalence previously found in WB (HEV, 20%; AR-CB, 60%), suggests a major role of feces in the transmission of pathogens to humans in urban areas, resulting in a non-negligible public health risk. The entire WB population was exposed to ASFV, through carcasses (87.6%) or direct contact (12.6%), 51-71 days after the first case. The outbreak lasted 71-124 days, reducing 95% of the initial population, similar to previous reports of ASFV outbreaks in European countries. The spatially-explicit epidemiological predictions generated by the model are valuable to evaluate the animal and public health risks posed by HEV, AR-CB and ASFV in Barcelona and could be easily adapted to other diseases at the WB-livestock-human interface.



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DOMESTIC TURKEYS AS AN EXPERIMENTAL MODEL FOR LYMPHOPROLIFERATIVE DISEASE VIRUS IN WILD TURKEYS

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Keywords: Lymphoproliferative Disease Virus, Wild Turkeys, Shedding, DNAemia, Experimental Inoculation

Abstract Text

Lymphoproliferative disease virus (LPDV) is an oncogenic retrovirus first documented in the western hemisphere in 2009, when it was confirmed in a wild turkey from Arkansas, USA. Subsequent surveillance demonstrated a high prevalence of LPDV infection in wild turkeys across portions of the U.S. and Canada; yet, vital information regarding pathogenesis, such as transmission route(s), shedding, and risk factors for disease development are unknown. To further investigate this disease in wild turkeys, we aimed to create a LPDV challenge model in domestic turkeys to determine appropriate inoculation routes, and assess for viral DNA shedding, tissue tropism, and lesion development. Twenty five, 4-week-old, domestic turkeys were inoculated using various routes: oral cavity (n=4), crop (n=4), nasal cavity (n=5), subcutaneous injection (n=6), or coelomic injection (n=6). Choanal and cloacal swabs, and whole blood were collected weekly. At 12-weeks post-inoculation (PI), birds were euthanized and necropsied. One week PI, three inoculated birds (14%) had DNAemia, which increased to 11 birds (48%) by the study endpoint, most commonly in subcutaneously inoculated turkeys (5/5). Development of DNAemia varied by inoculation group (i.e., 5/5 subcutaneous, 4/5 intraperitoneal, 1/5 intranasal, 1/3 crop, 0/3 oral cavity). The most consistent gross finding in turkeys with DNAemia was splenomegaly (8/11). One subcutaneously-inoculated turkey exhibited tan nodules on the intestinal serosa that were histologically consistent with lymphoid proliferation. In birds with detectable DNAemia, LPDV DNA was consistently detected in select tissues (liver, spleen, kidney, bone marrow, gonads). Testing of choana and cloacal swabs for LPDV DNA is underway. This study demonstrates that infection with LPDV in domestic turkeys can occur via numerous routes, subsequent DNAemia and shedding are commonly detected, and disease is experimentally reproducible. This research lays the foundation for investigations into pathogenesis, refinement of diagnostic strategies and techniques, and improved epidemiologic understanding of LPDV in wild turkeys.



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OPERATIONALIZING TWO-EYED SEEING AROUND WILDLIFE HEALTH IN THE ARCTIC

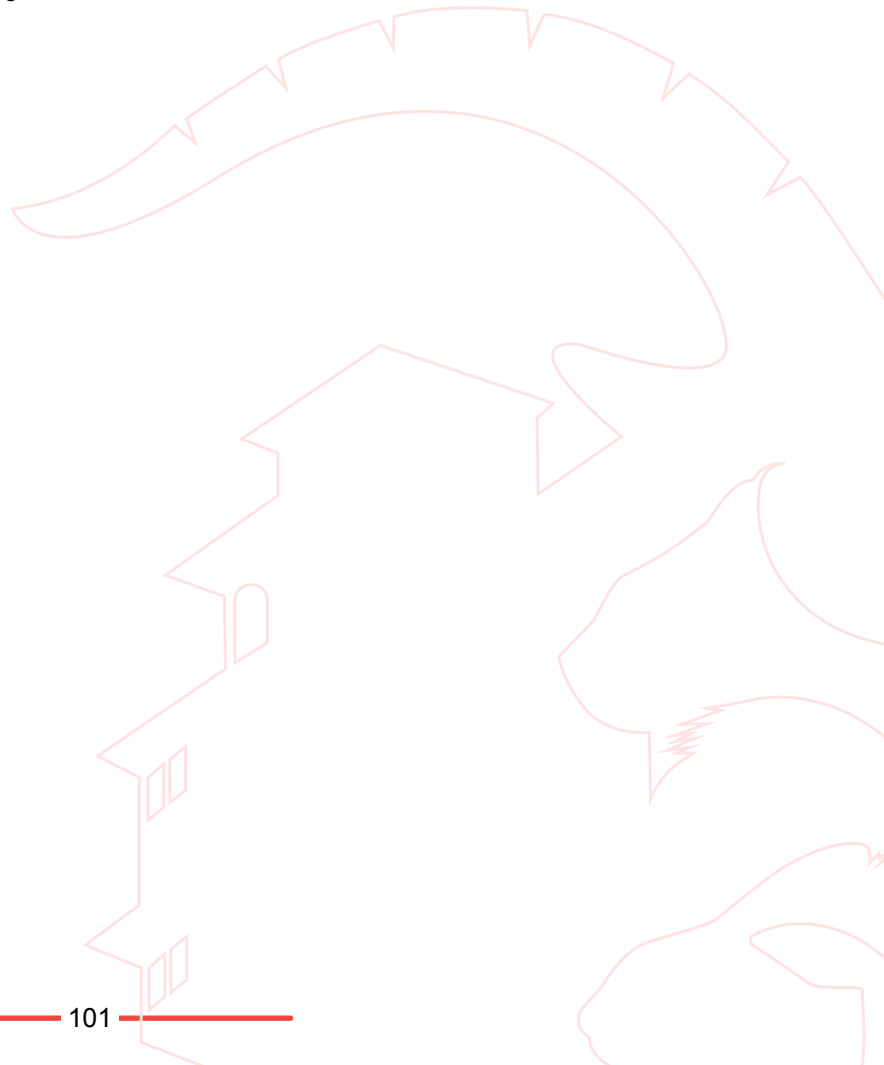
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Keywords: Arctic, Caribou, Community-Based Monitoring, Traditional Knowledge, Wildlife Co-Management

Abstract Text

The critical value of Indigenous Knowledge in natural resource management is increasingly recognized among government agencies, conservation organizations, and academics alike. How to respectfully mobilize this knowledge to affect wildlife conservation and management decisions is less well charted. In the Canadian Arctic, Inuit communities, government biologists, and academics are working together to understand the health and dynamics of the ecologically distinct and threatened Dolphin and Union caribou herd. We analyzed a series of historical 'orphaned' traditional knowledge interviews, facilitated new interviews, and established a harvester-based caribou health surveillance program to better understand this caribou herd. Through this mixed-methods approach, we found that Indigenous Knowledge from the historical interviews described behavioral and health changes that foreshadowed a decline that has resulted in this herd being assessed by the Committee on the Status of Endangered Wildlife in Canada as Endangered. Contemporary interviews have reinforced and deepened this knowledge and, together with harvester-based caribou surveillance, have provided substantial new insights on the history, health and ecology of the Dolphin and Union caribou herd. Finally, by respecting different knowledge sources and generating knowledge together, trust among co-management partners was strengthened and difficult decisions on herd management were made possible. Our results demonstrate how Indigenous Knowledge and scientific knowledge can be brought together to improve our collective understanding of this herd and its dynamic relationships, and facilitate wildlife co-management.





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EPIDEMIOLOGY OF OPHIDIOMYCOSIS IN LAKE ERIE WATERSNAKES (*NERODIA SIPEDON INSULARUM*)

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Keywords: Epidemiology, Lake Erie Watersnake, *Nerodia Sipedon Insularum*, Ophidiomycosis

Abstract Text

Ophidiomycosis, caused by the fungus *Ophidiomyces ophidiicola*, is an infectious disease of wild and managed snakes worldwide. Lake Erie watersnakes (*Nerodia sipedon insularum*, LEWS) were listed as threatened under the U.S. Endangered Species Act from 1999 to 2011 and were first diagnosed with ophidiomycosis in 2009. The purpose of this project was to characterize the current epidemiology of ophidiomycosis in LEWS. We hypothesized that the prevalence of skin lesions, *O. ophidiicola* DNA, and ophidiomycosis disease categories would show spatial and temporal variation, with higher prevalence at sites with greater human disturbance and prevalence increasing over time. Snakes were captured via visual encounter surveys at five surveillance sites across four islands and visually inspected for skin lesions suggestive of ophidiomycosis. Body swabs were collected to detect *O. ophidiicola* DNA using qPCR. Each snake was assigned an ophidiomycosis category based on the presence of skin lesions and *O. ophidiicola*. We evaluated 578 LEWS between 2017 and 2020 and detected ophidiomycosis at all five sites. Logistic regression analysis showed temporal and spatial variation in disease epidemiology, with skin lesions more likely in May, at lower temperatures, and in later years of the study, and *O. ophidiicola* detection more likely at sites with open space development and low intensity development. The presence of emerging herbaceous wetlands, urban land change, and certain soil types increased the odds of both lesion presence and qPCR detection of *O. ophidiicola*. Overall, ophidiomycosis epidemiology varied among sites: the disease appeared to be endemic at most sites and emerging at one site. Based on our results, ophidiomycosis does not pose a threat to LEWS conservation at this time, but we recommend ongoing efforts to monitor population health and disease prevalence, and mitigation may be necessary should population health become threatened by this disease.



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COCCIDIAN PARASITES IN HARVESTED BELUGA WHALE (*DELPHINAPTERUS LEUCAS*) AND CARIBOU (*RANGIFER TARANDUS*) IN THE CANADIAN NORTH

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Keywords: Beluga Whale, Caribou, Parasites, Toxoplasma, Sarcocystis

Abstract Text

Beluga whales (*Delphinapterus leucas*) and caribou (*Rangifer tarandus*) are important wildlife hunted and harvested as country food by Inuit communities, playing an important role in alleviating food insecurity, which is disproportionately high in the Canadian North. The consumption of wildlife has many benefits but may also increase the risk of transmission of food borne zoonotic pathogens such as *Toxoplasma gondii*. People living in some regions of the Canadian North have much higher seroprevalence of *T. gondii* than the mainstream North American population, and exposure has been linked to consumption of wildlife. The aim of the study was to determine the status of *T. gondii* and related, non-zoonotic coccidian parasites in harvested wildlife harvested by northern communities. Heart and brain were collected from caribou from Nunavik (northern Quebec) between 2018 and 2019, and belugas from the Eastern Beaufort Sea, Northwest Territories from 2014-2019. DNA of *T. gondii* was detected by magnetic capture qPCR in 1% (n=1/96; 95% CI:0-0.06) of beluga samples; however, all caribou samples were negative (n=56). DNA of *Sarcocystis* spp. was detected in heart tissue of both caribou and beluga by Melt curve analysis qPCR. Sequencing results from 26 isolates of *Sarcocystis* obtained from caribou indicated 99% identity with *S. grueneri*, previously reported in reindeer and wolves (as definitive hosts) from Europe. Further analysis is under way to identify species of *Sarcocystis* in belugas, which was not a close match to existing sequences. This study provides insight into the currently available tools to detect tissue coccidians and will help better understand if there is a potential risk of transmission of *T. gondii* to human populations who harvest and consume wildlife. As well, the study contributes to the knowledge of *Sarcocystis* diversity in wildlife from the Canadian North.



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SPATIAL EPIDEMIOLOGY OF ANIMAL TUBERCULOSIS AT THE WILDLIFE-LIVESTOCK INTERFACE AT NATIONAL SCALE

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Keywords: Animal Tuberculosis, Risk Factors Analysis, Spatio-Temporal Epidemiology, Wildlife-Livestock Interface

Abstract Text

Eradication of animal tuberculosis (TB) is a priority for European animal health authorities. Despite all efforts, most of Spain has not yet obtained the officially tuberculosis-free (OTF) status. Risk factors associated to TB have been widely studied both in domestic and wild reservoirs, but information regarding wildlife-livestock interface is scarcer. When explored, the role of wildlife is usually neglected or poorly assessed in large-scale studies. The National Wildlife Health Surveillance Plan now provides information about infection rates in wild reservoirs at national scale. Using Bayesian approach, we aimed to identify the risk factors associated to four TB parameters in cattle (one model per parameter): prevalence and incidence of infected farms, maintenance (positive-tested county consecutive years) and persistence (sum of consecutive positive-tested years) at county level in Spain during the period 2014-2019. Information about cattle herd abundance by aptitude (beef, dairy and bullfight), cattle movements, wild boar and red deer abundance, and TB prevalence in wild boar were used as predictors. Spatial autocorrelation, temporal correlation and space-time interaction were included as random effects. Predictors related to cattle movements were retained with a significant association in the four models. Bullfight abundance was associated with higher risk of incidence, maintenance, and persistence. The wildlife-related predictors were retained in the four models. TB prevalence in wild boar was significantly associated with incidence, maintenance, and persistence. Other wildlife-related variables were also significantly associated with those parameters, and non-significantly associated with prevalence. Our results reinforce previous studies reporting the relevance of movements and bullfight in TB infection rates and suggest, for first time at national scale, a relevant role of wild ungulates in the spatio-temporal variability of TB in cattle. Further analyses should be performed to disentangle the spatial variation for each predictor effect, which can provide directional hypotheses for TB control at regional scale.



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SYPHILIS SEROPOSITIVITY AND *TREPONEMA PARALUISLEPORIDARUM* STRAIN DIVERSITY IN EUROPEAN BROWN HARES

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Keywords: Lagomorphs, *Oryctolagus*, *Lepus*, Population Genetics, Infection

Abstract Text

The bacterium *Treponema paraluisleporidarum* causes syphilis in hares (ecovar *Lepus*, TPeL) and rabbits (ecovar *Cuniculus*, TPeC). To date, only a single complete genome of a rabbit-infecting strain has been whole-genome sequenced (NC_015714.1). Comparative genomic studies showed that rabbit infecting treponemes differ only in about two percent of their whole genome sequences (corresponding to ~1kbp) from human syphilis-causing treponemes (*T. pallidum* strain Nichols). Although several studies have demonstrated anti-*Treponema* antibodies in European brown hares (*Lepus europaeus*; EBH), serology is unable to distinguish infection with TPeL, TPeC or the genetically closely related *T. pallidum*. In a European-wide study, we screened >3,500 EBHs for the presence of TPeL infection. The majority of animals had no skin ulcers, which have been reported from infected rabbits and hares in others studies. However, we were able to confirm high seropositivity for anti-*Treponema* antibodies in all sampled populations (CZ:n=154/290, DE:n=631/1,226, ES:n=50/129, HU:n=116/192, IT:n= 418/1,025, and NL:n=15/29). The positive association of age suggests sexual transmission. The successful amplification of TPeL DNA from genital swabs further supports this notion. We present data on the genetic diversity of the newly discovered TPeL strains and compare the results with mitochondrial (mt) DNA-based genetics of the sampled hare populations. Our results show that the two selected TPeL loci are under positive selection, and that lagomorph infecting treponemes include a repeat region at the tp0548 locus that is not present in human syphilis-causing treponemes, which might contribute to the immune evasion strategy of TPeL. Yet, the geographic extent and high rate of infection in EBHs argues for the long-term existence of the pathogen in a panmictic hare population in western-central Europe. Further investigations are warranted on the fitness costs associated with infection and whole-genome sequences. The latter will provide information on the evolutionary history of human and lagomorph syphilis. Funding: DFG KN1097/7-1, GACR GC18-23521J



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EFFECTS OF HEAT STRESS ON THE RESPONSE OF WILD CAPTIVE BIRDS OF PREY AND OWLS TO HANDLING AND IMMUNIZATION AGAINST WEST NILE VIRUS

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Keywords: Climate Change, Heat Stress, Wildlife Rehabilitation, Birds Of Prey, Vaccination.

Abstract Text

Heat stress has been shown to selectively suppress immune response in commercial broiler chickens, negatively impacting performance, and response to vaccination. Although similar negative impacts of heat stress on free-living birds are likely information is scarce. Injured wild birds, especially birds of prey in wildlife rehabilitation centres must be captured for treatment administration, fitness or pre-release health checks which is a stressful event. On the other hand, due to the significant threat West Nile virus poses for endangered birds of prey in captive breeding projects or zoological collections vaccination is frequently part of sanitary protocols. Using flow cytometry, we analysed lymphocyte populations in peripheral blood collected on day 0, 7 and 15 in eight raptor species and European eagle owls (Buho buho) after manual capture and restraint during morning hours outside (controls) and during a heat wave. We also vaccinated individuals of the same species twice in a fortnight using a commercially available vaccine against West Nile virus during and prior to heat waves and quantified the antibody response by virus neutralization test (VNT) on day 0, 7, 15 and 28 after first vaccination. Heat stress significantly changed the leucocyte response to handling stress but differed in impact among species, with less severe changes in transsaharan migrants. It reduced B-lymphocytes in peripheral blood, and significantly increased T-lymphocytes in peripheral blood of 7/9 species, especially T-helper (CD4+) cells, while cytotoxic/suppressor T cells (CD8+) increased in only 5/9 species. In contrast to most species the endemic Spanish Imperial eagle showed a significant decrease in both CD4+ (Helper) and CD8+ (Supressor-T cells). Heat stress also reduced the levels of neutralizing antibody titres after vaccination (D15 and D28) although this reduction was only significant in two species. Thus, heat stress needs to be considered as an important factor in wildlife rehabilitation and vaccine delivery.



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BI-SEASONAL DYNAMICS OF A MULTI-HOST PATHOGEN: THE ROLE OF ENVIRONMENT IN THE DYNAMICS OF ANTHRAX

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Keywords: Anthrax, Disease Dynamics, Environmental Fluctuations, Transmission Mechanisms

Abstract Text

Seasonality in infectious diseases is common in wildlife diseases, however bi-seasonality or bimodal annual peaks in infections are less commonly reported. Bi-seasonality may involve complex drivers, and there are normally multiple triggers. We explored patterns in anthrax infection in two multi-host systems in southern Africa, central Etosha National Park in Namibia, and northern Kruger National Park in South Africa. We also assessed the possible transmission mechanisms behind anthrax dynamics, using associations with rainfall and remotely-sensed vegetation index. For both parks, anthrax infections showed two seasonal peaks, with each species having only one peak in a year, and host species shared in common between the two parks peaked in the same season across systems. Anthrax mortalities of plains zebra (*Equus quagga*), springbok (*Antidorcas marsupialis*), blue wildebeest (*Connochaetes taurinus*) and impala (*Aepyceros melampus*) peaked in wet seasons, while cases of greater kudu (*Tragelaphus strepsiceros*), African elephant (*Loxodonta africana*), and African buffalo (*Syncerus caffer*) peaked in dry seasons. We also found that multiple possible mechanisms exist. Zebra and elephant cases in Etosha are driven by behavioral responses to vegetation fluctuations, with positive and negative correlations with vegetation growth, respectively. Rainfall had negative correlation with kudu cases in Kruger, which supports the hypothesis that pathogen translocation by blowflies to leaves is involved in the transmission mechanism. Comparing across species and systems, mechanisms vary with species, and different mechanisms governed different seasonal peaks. These species-specific mechanisms are likely the causes leading to the uniqueness of multi-host anthrax seasonality and dynamics.



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CAVERS CARE DEEPLY ABOUT BATS – BUT THERE ARE SOME IMPORTANT GAPS IN KNOWLEDGE AND BIOSECURITY HABITS REGARDING WHITE NOSE SYNDROME. A SURVEY OF DELEGATES TO AN INTERNATIONAL CAVING CONFERENCE (SPELEO 2017).

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Keywords: Bats, Biosecurity, Caver, Survey, White Nose Syndrome

Abstract Text

White-nose syndrome (WNS) is a significant disease of insectivorous bats caused by the fungus *Pseudogymnoascus destructans* (Pd). The fungus is endemic in Europe and parts of Asia, and humans are thought to be responsible for introducing the disease to North America. Recent disease risk assessments for Australian bats identified cavers as relatively high risk for accidentally facilitating entry of the fungus into Australia. However, there is a worldwide lack of data on cavers' knowledge of and biosecurity attitudes towards WNS. This study aimed to provide some of this information, by surveying cavers about their knowledge of WNS and their caving and biosecurity habits. An anonymous qualitative survey was completed by delegates (n=134) from 23 countries at an international speleological conference in Sydney, Australia (SPELEO 2017). The results showed that the majority of respondents visit caves at least bi-monthly, and visits to caves in countries other than their own are common. Just over a fifth of respondents first heard about WNS in association with the conference. There was considerable uncertainty about the WNS status of specific countries, especially in Europe. Similarly, some of the surveyed delegates were unsure whether Pd occurred in their own country. While most were aware of current recommended biosecurity protocols, a minority of respondents fully adhered to them. However, most respondents also indicated a preparedness to change behaviours in response to education about WNS. Although the caving community as a whole has been very responsive to WNS and supportive of efforts to limit its impact on bat populations, there still appear to be significant knowledge gaps, and more education, including but not limited to promotion of appropriate decontamination practices may be needed. To the best of our knowledge, this survey provides the first objective data on caver awareness of and attitudes towards WNS.



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CLIMATE AND LONG TERM TRENDS IN PATHOGEN SEROPREVALENCE IN POLAR BEARS (*URSUS MARITIMUS*) IN THE WESTERN CANADIAN ARCTIC

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Keywords: Parasite, Pathogen, Climate Change, Zoonoses, Polar Bear

Abstract Text

Polar bears (*Ursus maritimus*) are an iconic indicator for the rapid and accelerating effects of climate change, especially in the Canadian Arctic, which is warming at triple the global rate. While there are obvious mechanisms for climate change to alter the transmission, survival, and impact of climate-sensitive pathogens, demonstrating these changes is often difficult due to lack of baseline data and long term studies. We examined 425 serum samples from 381 adult polar bears, collected in western Hudson Bay, Canada, for antibodies to selected pathogens across three time periods: 1986-1989 (n = 157), 1995-1998 (n = 159), and 2015-2017 (n = 109). We ran serological assays for antibodies to seven pathogens: *Toxoplasma gondii*, *Neospora caninum*, *Trichinella* spp. (*T. nativa*/T6), *Francisella tularensis*, *Bordetella bronchiseptica*, canine morbillivirus, and canine parvovirus. Seroprevalence of zoonotic parasites and bacteria (*T. gondii*, *Trichinella* spp., *F. tularensis*, and *B. bronchiseptica*) was high (>50%) and generally increased over the three periods. Antibodies to *Neospora caninum* and viruses did not change with time. *Toxoplasma gondii* seroprevalence was higher following wetter summers, supporting increased oocyst transmission either directly to bears or their prey species. Seroprevalence of *Trichinella* spp. was higher in polar bears previously captured in human settlements (especially adult males), and in years with warmer summer and winter temperatures, which may be due to increased access to and survival of muscle larvae in carcasses. Seroprevalence of antibodies to *F. tularensis* increased following years polar bears spent more time on land, suggesting that this pathogen is primarily transmitted from terrestrial rodents, freshwater, or insect vectors. As the Arctic continues to warm, the effects of pathogens on wildlife populations already under stress may be enhanced, and high trophic level carnivores and scavengers such as polar bears may serve as sentinels for enhanced transmission of climate-sensitive diseases.



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THE SHEDDING OF PARAMYXOVIRUS RNA IN THE URINE OF STRAW-COLOURED FRUIT BATS (*EIDOLON HELVUM*)

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Keywords: Chiroptera, *Eidolon Helvum*, Paramyxoviridae, RNA, Urine

Abstract Text

Two emerging bat paramyxoviruses, Hendra and Nipah, have caused spillover events with high case-fatality ratios in people. Fruit bats shed these henipaviruses in their urine. Most Hendra spillovers take place during Australian winters; some have been associated with nutritional stress in bats. Straw-coloured fruit bats (*Eidolon helvum*) carry similar viruses in Africa and little is known about the seasonality of their viral shedding. We aimed to determine paramyxovirus diversity and RNA-shedding patterns in a captive research colony of *Eidolon helvum* bats in Ghana by collecting weekly under-roost urine samples for a year. We extracted RNA and ran PCRs for two different regions of the paramyxovirus L-gene. Bands positive in electrophoresis were extracted and sent for Sanger sequencing. We estimated viral phylogeny with NCBI BLAST and by building phylogenetic trees. Shedding seasonality was estimated with sinusoidal logistic regression and associations with breeding season, temperature and humidity with logistic regression. We detected eight different viral sequences in the PCR with general paramyxovirus primers and six sequences with more Henipavirus-specific primers. Three sequences were novel. Some sequences were detected throughout the year but most only 1-3 times. The combined shedding of any paramyxovirus RNA in *Eidolon helvum* urine followed a biannual seasonal pattern with the clearest peak in July. Breeding season, temperature and humidity were not significantly associated with RNA detections. Our results provide a starting point for further studies looking into the effects of nutritional stress and other environmental stressors on paramyxovirus shedding in this species. The results also help to estimate possible viral spillover risks and plan for mitigation measures. Whole genome sequencing and virus isolation are still required to understand the exact relationships and spillover potential of these viruses, as well as to determine if the bats are shedding infectious virus and not only RNA.



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LINKING ZONOTIC DISEASE PREVALENCE TO HUMAN AND LIVESTOCK EXPOSURE RISK ACROSS A GRADIENT OF ANTHROPOGENIC LAND USE IN MADAGASCAR

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Keywords: Biodiversity, Habitat Degradation, One Health, Network Analysis, Zoonotic Disease

Abstract Text

Habitat degradation and anthropogenic land use contribute to biodiversity loss and alter community composition, often due to an increase in non-native species. Many of the same non-native species that colonize disturbed habitats are competent hosts for zoonoses, therefore, we expect pathogen communities to expand alongside their hosts. Investigating the links between habitat degradation, host diversity and human exposure requires data on disease prevalence combined with spatial data on human, native, and introduced wildlife and domestic animal hosts. These data provide a way to test if pathogen prevalence in small mammal host communities differs by land-use type and if areas accessed by the same livestock or people are contaminated with similar pathogens. We collected data on 160 introduced (*Rattus*, *Mus*, *Suncus*) and 99 endemic (*Tenrecidae*, *Nesomyidae*) small mammals, 32 livestock (*Bos indicus*, *Sus scrofa*), and 122 people from the area surrounding a rural village in northeastern Madagascar. We trapped small mammals along a gradient of degradation and anthropogenic use (6 grids, 143 traps each), and used PCR to test for *Leptospira*, Hanta-, Paramyxo-, Corona-, and Astro-viruses. We conducted pathogen and serologic screening on all sampled livestock and people, these subjects also wore a GPS tracker (iGot-U 120) for a minimum of one week. We then formed spatial overlap networks of people, domestic animals, and trap grids to 1) identify individuals with the highest centrality based on overlap, and 2) test whether these overlaps predicted pathogen sharing between individuals within specific habitats. We found that 60 people and 9 livestock overlapped with 4 of the trap grids. Pathogen prevalence rates differed for non-native and native species respectively for *Leptospira* (0.25, 0.07), Paramyxovirus (0.04, 0.07), and Astrovirus (0.21, 0). The degree and strength centralities of people, domestic animals, and trap grids suggest usage patterns, and thus exposure risk, varied by individual and location.



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METAGENOMIC DETECTION OF TICK-BORNE PATHOGENS USING NANOPORE ADAPTIVE SEQUENCING

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Keywords: Ixodes, Metagenomics, Nanopore Sequencing, Ticks, Vector-Borne Disease

Abstract Text

Ixodid ticks are capable of vectoring a wide diversity of pathogens to humans, domestic animals, and wildlife. In the United States, the blacklegged tick—*Ixodes scapularis*—is a major vector of at least seven zoonotic pathogens of which many are actively increasing in incidence and range. Despite its importance as a vector, detailed surveillance data for many *I. scapularis*-transmitted pathogens is lacking. Using the nanopore MinION platform, we aimed to develop a novel metagenomic strategy for comprehensive tick-borne pathogen surveillance from field-collected *I. scapularis* ticks. Termed nanopore adaptive sequencing (NAS), our approach utilizes an advanced real-time bioinformatic analysis to selectively enrich for sequences mapping against the genomes of *I. scapularis*-transmitted pathogens. We hypothesized that NAS would show substantial enrichment for tick-borne sequence data in comparison to an unenriched control experiment. Nanopore libraries were generated using genomic DNA from four adult female *I. scapularis* ticks. Data generated from both NAS and control libraries were independently analysed to estimate levels of pathogen read enrichment and genomic coverage. These data were compared against bacterial 16S sequencing results to determine detection accuracy. Four pathogens were detected across the ticks screened: *Borrelia burgdorferi* (s.s.), *Borrelia miyamotoi*, *Anaplasma phagocytophilum*, and *Ehrlichia muris euclairensis*. Three of four ticks were co-infected with multiple agents. Importantly, the library sequenced with NAS achieved roughly two-fold pathogen-associated read enrichment and generated long-read data to collectively span entire pathogen genomes. Our NAS data were in agreement with 16S sequencing results and plainly distinguished between closely related bacterial agents (e.g., *Borrelia* spp.). Using the NAS pipeline, we generated considerable genomic surveillance data on tick-borne pathogens using unprocessed *I. scapularis* genomic DNA. These results suggest that MinION sequencing with NAS may be leveraged for a variety of real-time metagenomic applications to accurately detect and characterize pathogens in complex systems.



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FREQUENCY AND MOLECULAR DIVERSITY OF PROTIST ENTEROPARASITES IN WESTERN CHIMPANZEES (*PAN TROGLODYTES VERUS*) FROM IVORY COAST, SENEGAL, AND SIERRA LEONE

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Keywords: Western Chimpanzee, Enteric Protists, Genotyping, Epidemiology

Abstract Text

Chimpanzee populations (*Pan troglodytes verus*) in West Africa have decreased by an 80% between 1990–2014 as direct consequence of anthropic activities (habitat destruction, poaching) and infectious diseases, and are currently classified as Critically Endangered. Little is known on the occurrence, molecular diversity, and clinical significance of enteric protist species and their impact in western chimpanzee populations. Between October 2016–January 2020, faecal samples from chimpanzees were collected at the Comoé National Park (CNP) in Ivory Coast (n=125), Dindefelo Community Nature Reserve (DCNR) in Senegal (n=247) and Tacugama Sanctuary (TS) in Sierra Leone (n=67). Chimpanzees in CNP have no contact with humans, whereas those in DCNR live in an anthropogenic landscape. TS represent a sanctuary population kept in semi-liberty. Enteric protists were identified and genotyped by molecular (PCR and Sanger sequencing) methods. Among pathogenic protists, *Giardia duodenalis* was the most prevalent species found (2–33%), followed by *Blastocystis* sp. (6–22%), and *Cryptosporidium hominis* (0–1%). *Entamoeba histolytica* and *Enterocytozoon bieneusi* were not identified in any of the three populations surveyed. Among commensal protists, *Entamoeba dispar* (2–19%) was the most common species found, followed by *Troglodytella abgrassarti* (1–2%). *Blastocystis* ST1 was the only subtype circulating in chimpanzees from CNP and DCNR, whereas zoonotic ST1, ST2, and ST3 were detected in chimpanzees in TS. Overall, chimpanzee populations in close proximity to humans had higher infection/colonization rates by enteric protists. *Blastocystis* ST1 allele 7 seems to be particularly well adapted to infect/colonize western chimpanzees. Human populations living in close proximity to natural areas might act, to a still unknown extent, as source of enteric protist infections to wildlife including chimpanzees, most likely through environmental contamination with faecal material of anthropic origin. Incorrect management of human faeces may/might pose a risk to endangered species such as chimpanzees.



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THINKING ABOUT TRANSFORMATIVE CHANGES IN WILDLIFE HEALTH ACTIVITIES

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Keywords: Biodiversity, Ecosystem Services, Sustainability, Transformative Changes, Wildlife Health

Abstract Text

In its 2019 global biodiversity assessment, the U.N. Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services concluded that “the biosphere, upon which humanity as a whole depends, is being altered to an unparalleled degree across all spatial scales” and that “biodiversity is declining faster than at any time in human history”. Their main recommendation stated that “goals for conserving and sustainably using nature and achieving sustainability cannot be met by current trajectories, and goals for 2030 and beyond may only be achieved through transformative changes, (...) a fundamental, system-wide reorganization across technological, economic and social factors, including paradigms, goals and values”. Given the above, it is time to discuss transformative changes that need to happen across society, including in the wildlife health field. As a starting point, we could assess our current paradigms, goals and values (‘narrative’ for short), decide what our new narrative should be, and reason how this will affect our wildlife health activities. In the current narrative, most of us have been brought up and live in an anthropocentric world, where humans are separate from nature. In wildlife health activities, our approach often is concerned about how wildlife disease affects human or domestic animal health. In a new narrative, we might take a more “EcoCentric” approach, which recognizes that all species, including humans, are inter-related in their life processes. We might recognize that we must tread lightly to maintain the Earth’s integrity in perpetuity, for the benefit of both human society and other species. We will discuss how the proposed new narrative could affect students’ education, institutes’ organization, the conduct of research, and the translation of research results into solutions to societal problems. By opening the discussion about transformative changes, people working in wildlife health can start to make the transition to a sustainable society.



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SUSCEPTIBILITY OF WILD TURKEYS (*MELEAGRIS GALLOPAVO*) TO EXPERIMENTAL WEST NILE VIRUS INFECTION

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Keywords: Experimental Infection, Histopathology, West Nile Virus, Wild Turkey, Viremia

Abstract Text

Since its introduction to North America in 1999, West Nile virus (WNV; Family Flaviviridae, Genus Flavivirus) is estimated to have had devastating impacts on numerous North American bird species. The potential impacts on free-ranging upland game bird species remain largely understudied. Although regional declines in wild turkey (*Meleagris gallopavo*) populations have been documented without a known cause, data on the susceptibility of this species to WNV-associated disease are lacking. To address this knowledge gap and to assess for age class variation in susceptibility to WNV, we subcutaneously inoculated two age cohorts (~6-week-old and ~16-week-old) of wild turkey poults with WNV (n=25) or sham (BA-1 medium; n=19). Clinical, virologic, pathologic, and serologic responses were monitored for 14 days post-inoculation (DPI). No WNV-inoculated or sham-inoculated, contact-control poults developed clinical signs or gross lesions attributable to WNV infection. Viremia was transient with low peak titers as compared to more susceptible avian species, such as some corvids and raptors. The mean peak viremia titer was similar between age cohorts (<104.0 plaque-forming units [PFU]/ml serum). Most poults shed transient, low levels of WNV orally and/or cloacally. One sham-inoculated, contact-control poult in the ~16-week-old cohort became viremic on 5 DPI, presumably via either direct or indirect bird-to-bird transmission. All inoculated poults in both cohorts, as well as the sham-inoculated, contact-control poult that became viremic, seroconverted by 14 DPI. West Nile virus rarely was isolated from the heart, spleen, kidney, and breast feathers and was not isolated from the brain or skeletal muscle of any inoculated poults. The most consistent microscopic lesions in infected poults of both age cohorts were mild myocarditis, encephalitis, and enteritis. These data suggest wild turkeys of both age cohorts have low susceptibility to WNV-associated morbidity and mortality, and individuals in neither age cohort likely serve as competent reservoir hosts for WNV.



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IMPLEMENTING ENVIRONMENTAL DNA DETECTION METHOD IN THE SURVEILLANCE OF AMPHIBIAN PATHOGEN *BATRACHOCHYTRIUM SALAMANDRIVORANS*

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Keywords: Bsal, Bd, Chytridiomycosis, Water Filtration, EDNA

Abstract Text

Environmental DNA (eDNA) is becoming an indispensable tool in biodiversity monitoring, including the monitoring of invasive species and pathogens. Aquatic chytrid fungi *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal) are major threats to amphibians. However, the use of eDNA for detecting these pathogens has not yet become widespread, due to technological and economic obstacles. Using the enhanced eDNA approach (a simple and cheap sampling protocol) and the universally accepted qPCR assay, we confirmed the presence of Bsal and Bd in previously identified sites in Spain, including four sites that were new for Bsal. The new approach was successfully tested in laboratory conditions using manufactured gene fragments (gBlocks) of the targeted DNA sequence. A comparison of storage methods showed that samples kept in ethanol had the best DNA yield. Our results showed that the number of DNA copies in the Internal Transcribed Spacer region was 120 copies per Bsal cell. Eradication of emerging diseases requires quick and cost-effective solutions. We therefore performed cost-efficiency analyses of standard animal swabbing, a previous eDNA approach, and our own approach. The procedure presented here was evaluated as the most cost-efficient. Our findings will help to disseminate information about efforts to prevent the spread of chytrid fungi



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HOST EXPOSURE HISTORY ALTERS PATHOGEN TRANSMISSION AND VIRULENCE IN A WILD SONGBIRD

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Keywords: House Finch, *Mycoplasma Gallisepticum*, Pathogen Transmission, Trade-Off Hypothesis

Abstract Text

Incomplete host immune memory from prior infection may select for higher pathogen virulence if virulent strains more effectively overcome pre-existing immunity and replicate sufficiently to transmit. If incomplete immunity reduces disease severity to secondary infection this may also affect the theorised trade-off that pathogens experience between virulence and transmission. We tested these possibilities in a wild songbird species, the house finch, in which prior exposure to a naturally occurring bacterial pathogen, *Mycoplasma gallisepticum* (MG), elicits significant but incomplete protection that favours colonization by more virulent pathogen strains. Specifically, we asked whether prior exposure level mediates the transmission potential of a host and whether prior exposure favours the transmission of more virulent strains. We created variation in prior exposure by experimentally inoculating wild-caught, MG-naïve house finches with varying amounts (both in dose and number of exposures) of an MG strain of intermediate virulence and allowed birds to recover. We then challenged these hosts with one of two MG strains that vary in virulence and assessed their pair-wise transmission potential to a naive cage-mate. Higher levels of prior exposure resulted in stronger reductions in transmission potential, regardless of strain virulence. However, the higher virulence strain was associated with significantly higher transmission potential, regardless of prior exposure. The combined but statistically independent effects of prior exposure and strain virulence on transmission potential manifested as successful transmission occurring only for the more virulent strain from hosts with high levels of prior exposure. Additionally, our results suggest that transmission in this system is optimal at high levels of within-host pathogen load and intermediate levels of disease, our proxy for virulence. These patterns are consistent with pathogens facing a trade-off between virulence and transmission, and a selection towards higher virulence in hosts with high levels of previous exposure.



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ECOLOGY OF WEST CAUCASIAN BAT LYSSAVIRUS (WCBV) IN A GROUP OF SCHREIBERS' BENT-WINGED BATS (MINIOPTERUS SCHREIBERSII) FROM ITALY AND ITS SPILLOVER TO A DOMESTIC CAT

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Keywords: Bats, Spillover, West Caucasian Bat Lyssavirus, Ecopathology

Abstract Text

While Europe is mostly free from terrestrial rabies, five lyssaviruses circulate in bats that can cause the same clinical disease in mammals. On June 2020, we diagnosed a lyssavirus infection in a domestic cat from the city of Arezzo (Italy) using immunofluorescence and molecular techniques. We characterized WCBV as aetiological agent, showing high identity across the whole-genome with the sole other isolate, founded in 2002 from a Schreibers' bent-winged bat in Russia. To track the source and triggers of infection, we investigated the possible interface between cats and bats using bioacoustics analyses, camera trapping, and implemented active and passive surveillance in bats. Despite the bent-winged bat was not expected to either roost or feed in urban settings, we identified a group of 20-350 individuals inhabiting a tunnel nearby the cat's house between August and November, and in April. Bioacoustics supported low foraging activity for this bat upon the entrance, while camera-traps showed frequent access of cats. Bent-winged bats showed antibodies specifically neutralizing WCBV in both seasons, but no virus in salivary swabs. Carcasses collected across the country regardless of the species were negative for the infection, while the cardiac exudate of bent-winged bats collected from the Veneto region reacted against WCBV. Overall, these results showed that WCBV circulates in Italian bent-winged bats and spilled over a domestic cat in Arezzo, further supporting its role as reservoir host. Fortunately, our data suggest that chances for virus transmission are reduced by the low prevalence of viral shedding and by the behaviour of these bats, which do not forage at the entrance and use this urban site only as transient roost during their migration between the hibernacula and the reproductive sites. In addition, this case confirmed that free-ranging cats are a potential hazard for public health other than for the conservation of bats.



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RT-QUIC DETECTION OF CWD PRION SEEDING ACTIVITY IN WHITE-TAILED DEER MUSCLE TISSUES

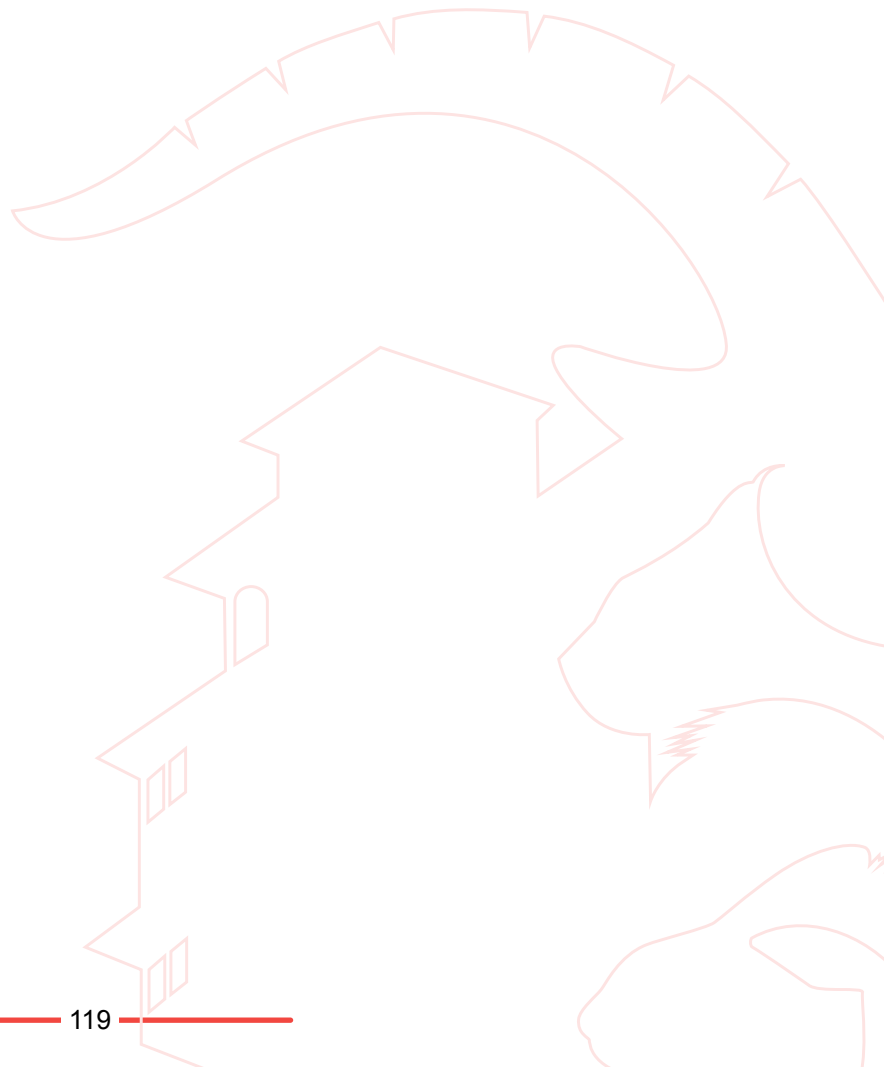
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Keywords: Chronic Wasting Disease, Odocoileus Virginianus, Real-Time Quaking-Induced Conversion, Skeletal Muscle, Venison

Abstract Text

Chronic wasting disease (CWD) is a prion disease circulating in wild and farmed cervid populations throughout North America (United States and Canada), Europe (Finland, Norway, Sweden), and South Korea. CWD is a long-term threat to all cervid populations and to cervid hunting heritage, with the potential to cause substantial economic losses across multiple sectors. In North America, hunting and farming industries focused on the processing and consumption of white-tailed deer (WTD) venison are particularly vulnerable to CWD prion contamination, as millions of WTD are consumed annually. Real-time quaking-induced conversion (RT-QuIC) is a highly sensitive assay amplifying misfolded CWD prions in vitro and has facilitated CWD prion detection in a variety of tissues and excreta. To date, no study has comprehensively examined CWD prion content across bulk skeletal muscle tissues harvested from individual CWD infected WTD. Here, we use RT-QuIC to quantify prion-seeding activity in a variety of skeletal muscles from both wild and farmed CWD-positive WTD. We successfully detected CWD prions in muscles commonly used for consumption (e.g., backstrap, tenderloin, etc.) as well as within tongue and neck samples of WTD. Our results indicate that CWD prions are more widely distributed across skeletal muscles of infected WTD than previously reported. We posit that RT-QuIC will be a useful tool for monitoring CWD prions in venison and that the method (with additional protocol optimization and high-throughput functionality) could be used to reduce and/or prevent CWD prions from entering animal and human food chains.





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CARDIAC ASSESSMENTS OF BOTTLENOSE DOLPHINS (*TURSIOPS TRUNCATUS*) IN THE NORTHERN GULF OF MEXICO FOLLOWING EXPOSURE TO DEEPWATER HORIZON OIL

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Abstract Text

The Deepwater Horizon (DWH) oil spill profoundly impacted the health of bottlenose dolphins (*Tursiops truncatus*) in Barataria Bay, LA (BB). To comprehensively assess cardiac health of dolphins living within the DWH oil spill footprint, techniques for in-water cardiac evaluation were refined with dolphins cared for by the U.S. Navy Marine Mammal Program in 2018 and applied to free-ranging bottlenose dolphins in BB (n=34) and Sarasota Bay, Florida (SB) (n=19), a non-oiled reference population. Cardiac auscultation detected systolic murmurs in the majority of dolphins from both sites (88% BB, 89% SB) and echocardiography showed most of the murmurs were innocent flow murmurs attributed to elevated blood flow velocity. Telemetric six-lead electrocardiography detected arrhythmias in BB dolphins (43%) and SB dolphins (31%), all of which were considered low to moderate risk for adverse cardiac events. Echocardiography showed BB dolphins had thinner left ventricular walls, with significant differences in intraventricular septum thickness at the end of diastole ($p=0.002$), and left ventricular posterior wall thickness at the end of diastole ($p=0.033$). BB dolphins also had smaller left atrial size ($p=0.004$), higher prevalence of tricuspid valve prolapse ($p=0.003$), higher prevalence of tricuspid valve thickening ($p=0.033$), and higher prevalence of aortic valve thickening ($p=0.008$). Two dolphins in BB were diagnosed with pulmonary arterial hypertension based on Doppler echocardiography-derived estimates and supporting echocardiographic findings. Histopathology of dolphins who stranded within the DWH oil spill footprint showed a significantly higher prevalence of myocardial fibrosis ($p=0.003$), regardless of age, compared to dolphins outside the oil spill footprint.



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DECREASED IMMUNITY OF WILD RABBITS AGAINST RABBIT HEMORRHAGIC DISEASE VIRUS IN AZORES (2015-2019)

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Keywords: Rabbit Hemorrhagic Disease, Wild Rabbit, Evolution, Azores

Abstract Text

Rabbit hemorrhagic disease virus (RHDV) is a highly contagious and lethal lagovirus that affects wild rabbit (*Oryctolagus cuniculus*) populations worldwide. Since the first appearance of a new genotype of RHDV (*Lagovirus europaeus*/GI.2) in France in 2010, the virus has spread to neighboring countries, but also to insular regions. This variant fatally affects young and adult rabbits, being responsible for sharp decreases in rabbit populations. In Azores, GI.2 was first reported in late 2014 and raised conservation concerns. Here we studied the evolution of the immunological status of rabbit populations from three Azorean islands. For that, we collected blood samples from rabbits hunted between 2015 and 2019 in Terceira (n=178), Graciosa (n=176) and São Miguel (n=196) and monitored, using ELISA, the prevalence of antibodies against RHDV. In parallel, we evaluated virus evolution by sequencing viral isolates from rabbits found dead in the same islands and estimated rabbit densities using a hierarchical distance sampling approach. Population density analysis revealed a sharp decrease in 2015 due to massive outbreaks of GI.2 in all islands. Consistent with this, surviving rabbits with antibodies were detected in the following years. The highest percentage of seropositive animals was found in 2015 in Terceira (88.5%) and Graciosa (92.9%), while in São Miguel the highest percentage was found in 2016 (40.0%). In 2019, values of seropositivity had decreased to 59.2% in Terceira, 14.0% in Graciosa, and 2.0% in São Miguel. Virological analysis confirmed circulation of GI.2 in all islands between 2015 and 2019, with an independent evolution in each island. Nonetheless, we observed a general decreasing trend in seropositivity in rabbit populations in the three islands across the years. These results raise concerns about the degree of protection against RHDV and maintenance of the wild rabbit populations in Azores.



IMPACT OF THE GENOMIC ARCHITECTURE OF LAGOVIRUS EUROPAEUS/GI.2 RECOMBINANTS IN THE CLINICAL COURSE OF RABBIT HEMORRHAGIC DISEASE

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Keywords: Disease, European Rabbit, Experimental Infection, Rabbit Hemorrhagic Disease Virus, Recombination

Abstract Text

Rabbit hemorrhagic disease virus is a Lagovirus of the Caliciviridae family that first emerged in 1984 as a pathogenic virus for wild and domestic adult European rabbits (*Oryctolagus cuniculus*). In 2010, a new genotype was described, Lagovirus europaeus/GI.2, with distinct antigenic and genetic characteristics. Indeed, GI.2 diverges ~15% from the original strains Lagovirus europaeus/GI.1, causes a fatal disease in young rabbits (<2 months old) that were resistant to GI.1 strains, has a broader host range with several instances of species jump reported in hares (*Lepus* spp.) and cottontails (*Sylvilagus* spp.), and partially escapes protection conferred by vaccines developed against GI.1.

All GI.2 strains characterized so far resulted from recombination with a breakpoint at the junction between the non-structural and the structural encoding regions. Strains associated with the first outbreaks were the product of intergenotypic recombination with a non-pathogenic enterotropic strain (GI.3) as donor for the non-structural part and GI.2 as parental strain for the structural part (GI.3P-GI.2, where P stands for the polymerase). Other recombination events occurred involving non-pathogenic GI.4, pathogenic GI.1b, and GII.1 (European brown hare syndrome virus) as donors for the non-structural part, forming GI.4P-GI.2, GI.1bP-GI.2 and GII.1P-GI.2 recombinants, respectively. A second recombination breakpoint was identified at the p16/p23 boundary which originated triple recombinants: GI.4(p16)-GI.1bP-GI.2 and GI.4(p16)-GI.3P-GI.2. In order to understand the implications of the different GI.2 genomic architecture in the clinical course of the disease, we experimentally inoculated young (25-30 days old) and adult rabbits (2-3 months old) with strains GI.3P-GI.2, GI.4P-GI.2, GI.1bP-GI.2, GI.4(p16)-GI.1bP-GI.2 and GI.4(p16)-GI.3P-GI.2. The combined analysis of the survival rates, biochemical alterations and immune response revealed differences between the tested recombinants, suggesting that the non-structural proteins, rather than the capsid, greatly influence the pathogenicity of GI.2. Disease management in the wild might benefit from knowledge on the genomic composition of the GI.2 circulating strains.



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YELLOW-LEGGED GULLS (*LARUS MICHAEHELLIS*) AND AUDOUIN'S GULLS (*LARUS AUDOUINII*) FROM BARCELONA AS A SOURCE OF *CAMPYLOBACTER* OF PUBLIC HEALTH RELEVANCE.

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Keywords: Antimicrobial Susceptibility, Campylobacter, MLST, PFGE, Virulence Potential.

Abstract Text

Wild birds, including certain gull species, are well-known reservoirs of *Campylobacter* and other zoonotic agents and play an important role in their dissemination and maintenance in the environment. In the last decade, yellow-legged gull (*Larus michahellis*) populations have increased dramatically, becoming a problem for human health because of its generalist insalubrious scavenging feeding habits, and its increasing direct and indirect interactions with human populations, compared with Audouin's gull (*Larus audouinii*). In Barcelona there is an important urban colony of yellow-legged gull, whilst Audouin's gulls have been reported to breed in the city only once in recent years, in 2013. To gain insight into *Campylobacter* epidemiology in these gull colonies, we assessed the occurrence, the virulence potential, the antimicrobial susceptibility, and the genetic diversity of *Campylobacter jejuni* isolates recovered from gull feces in different time periods during 2009-2018. *Campylobacter* prevalence was higher for Audouin's gulls (45%, 44/98; 2013) compared to yellow-legged gulls (13%, 44/331; 2009, 2010 and 2018). The prevalence of virulence-associated genes, which included those involved in motility, cell adhesion, invasion, cytotoxin production and a gene related to the T6SS, was high indicating that most isolates from both colonies had a high virulence potential. Most of the isolates were pansusceptible, however, a higher proportion of isolates from yellow-legged gulls, compared with those from Audouin's gulls, showed resistance to antimicrobials of relevance in human medicine (fluoroquinolones, tetracyclines). Despite we also found a high genetic diversity, we identified several *C. jejuni* genotypes (MLST, STs) from yellow-legged gulls which have been associated with human gastroenteritis (ST45, ST257, ST441, ST2197). These results suggest an environmental source of *Campylobacter* infection for humans within the wild birds niche. Results also highlight the public health risk that these two seagull species studied may pose, particularly yellow-legged gulls, in a human populated urban area such as Barcelona.



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A NOVEL APPROACH TO A NOVEL PATHOGEN: STUDENT-POWERED SURVEILLANCE OF BATRACHOCHYTRIUM SALAMANDRIVORANS

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Keywords: Batrachochytrium Salamandrivorans, Conservation, Emerging Pathogens, Pedagogy, Surveillance

Abstract Text

The emerging fungal pathogen *Batrachochytrium salamandrivorans* (Bsal) is threatening salamanders in Europe and North America. Bsal has yet to be detected in North America but its introduction is likely, making the early detection of Bsal essential for mitigating its negative impact. Unfortunately, early detection is inherently challenging, requiring broad spatiotemporal surveillance that can be expensive, time-consuming and logistically difficult. As the Bsal Surveillance & Monitoring Working Group of the North American Bsal Task Force, we are developing a new surveillance program that addresses some of the challenges of traditional surveillance approaches while providing a unique educational experience for undergraduate students. The Student Network for Amphibian Pathogen Surveillance (SNAPS) is a new program that leverages student power to conduct ongoing and cost-effective Bsal surveillance by incorporating surveillance into curricula. We are piloting SNAPS in April – June 2021 at three universities and will report results of both Bsal surveillance and our assessment of student learning outcomes. We predict that students will increase their recognition of emerging pathogens in general, and Bsal in particular, as a threat to biodiversity; understand how pathogen surveillance helps conservation; improve their skills in applying sterile techniques; and become more empowered to contribute to conservation. To surveil for Bsal, students will swab local amphibians. The USGS Amphibian Research and Monitoring Initiative and the National Wildlife Health Center will analyze these swabs for detection of Bsal and Bd using duplex real-time PCR. To assess learning outcomes, students will be invited to participate in anonymous surveys prior to, and shortly after, their engagement with SNAPS. Findings will inform our ongoing development of this new, student-powered model for Bsal surveillance and provide critical surveillance information. Our model represents a broad, scalable and potentially sustainable approach to help detect Bsal at the onset of a North American invasion.



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DOMESTIC DOGS AS BRIDGES FOR DISEASE BETWEEN WILDLIFE AND INDIGENOUS WAIWAI IN GUYANA, SOUTH AMERICA

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Keywords: Domestic Dogs, Bridge Hosts, Zoonoses, South America, Human-Animal Interactions

Abstract Text

The common presence of domestic dogs in urban, rural, and natural environments, as well as their interactions with wildlife and humans, make dogs uniquely suited to serve as bridge hosts for pathogen transmission. This is particularly true in Amazonian indigenous communities where the wildlife-human interface is extensive and dogs bridge that interface. In this study, we use quantitative and qualitative methods to characterize domestic dog health and their role among the Waiwai, an indigenous population in the Konashen Community Owned Conservation Area (KCOCA), Guyana, South America. We hypothesized that Waiwai village dogs, due to their role in hunting, their consumption of uncooked bushmeat, and their cultural importance in Waiwai society, will harbor pathogens that can be transmitted from wildlife to humans. We performed comprehensive physical examinations and serological screening (n=20), and fecal parasite analysis (n=16) on Waiwai domestic dogs. We administered questionnaires to Waiwai dog owners (n=20) to characterize the role of dogs in the community and identify potential transmission pathways. On physical exam, 80% of dogs had jigger flea (*Tunga penetrans*) lesions and/or active infections and 30% showed evidence of past and/or current bot fly (*Dermatobia hominis*) lesions. No hemoparasites were noted on peripheral blood film and all dogs (n=20) were negative on serology for: Canine Distemper Virus, *Brucella canis*, *Leptospiriosis interrogans* serovars, and *Trypanosoma cruzi*. One dog was positive for *Leishmania infantum*. Seventy-percent of owners reported that their dogs have been bitten by vampire bats (*Desmodontinae*) and 95% stated that their dogs consume raw meat. Although traditional diagnostics showed minimal evidence of underlying disease, our questionnaire data revealed important potential pathways for disease transmission in the community, specifically, the bat-dog-human interface. Understanding the role of domestic dog health and the social-cultural relationships dogs have with humans is critical in managing zoonoses and One Health in conservation.



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POPULATION IMPACTS OF DOMOIC ACID EXPOSURE IN SOUTHERN SEA OTTERS: AN INCREASING THREAT IN A CHANGING CLIMATE.

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Keywords: Cardiac Disease, Climate Change, Domoic Acid, Integrated Population Model, Sea Otter

Abstract Text

Toxins produced by harmful algal blooms can have profound detrimental effects on individual marine mammals, yet population-level impacts of biotoxins have not been well characterized. Southern sea otters (*Enhydra lutris nereis*) are a threatened species that faces many environmental hazards, including domoic acid (DA), an algal toxin that causes neurological and cardiovascular disease and mortality. We evaluated the impact of future DA exposure on sea otter population viability using an integrated population model (IPM), a stage-structured, spatially explicit matrix model that uses animal health, population trends, and survival data to project abundance. The IPM was modified to allow for DA exposure effects on cause-specific hazards of DA toxicosis and cardiomyopathy. We conducted a series of alternative scenarios to investigate how increased frequency and severity of future DA events (as might be expected with climate change) translated into changes in the projected abundance of sea otters in 50 years, relative to a baseline scenario (where DA event frequency and severity were based on observed values over the past 20 years). If the frequency and severity of high DA events increased six-fold, abundance would be 2,839 (95% CI: 1,116–4,920), a 34% reduction from baseline. When co-stressors and DA events increased, the impacts on population growth were substantial. If shark bite mortality and high DA event frequency and severity increased three- and six-fold, respectively, abundance would be 1,006 (95% CI: 320–1,755), a 76% reduction. Evidence of DA impacts on populations has not previously been presented. Our findings reveal that increased frequency and severity of high DA events in a future climate resulted in significant population reduction from baseline. The impacts of DA exposure on sea otter population viability highlight the need to improve our understanding of the widespread effects of algal toxins on marine mammal health in a rapidly changing environment.



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232 ALPINE IBEX HYBRIDS: FAIRY TALE OR REALITY IN OUR MOUNTAINS?

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Keywords: Alpine ibex, Goats, Hybridisation, Conservation, Livestock

Abstract Text

The Alpine ibex (*Capra ibex*) is a protected Alpine wild ungulate. A recognized threat for the species long-term conservation is represented by the hybridisation with domestic goats (*Capra hircus*), that may occur when domestic goats are left in the mountain at the end of the summer pasture.

Hybridisation between Alpine ibex and domestic goats has been documented in Switzerland, however, accurate data to understand the extent of this phenomenon in natural condition on the Alps are still lacking.

The main goal of this study was to collect unpublished evidence of hybridisation between Alpine ibex and domestic goats, and to map their distribution in time and space.

To this purpose, a questionnaire was sent to local Alpine wildlife authorities in five countries (Italy, Switzerland, France, Austria, Slovenia) to collect relevant information on the presence of suspected or confirmed hybrids, based either on phenotypic or genetic reports.

All the information were analyzed by experts and classified using reliability classes, taking into account the robustness of provided information.

The reports covered a temporal range between 1977 and 2021. Preliminary results showed that hybridisation events occurred in three countries (Italy, France, Switzerland). Most of the observations included single, likely F1 hybrids individuals. However, we also identified some back crosses as well as some hybridisation clusters, in the Piedmont region (Italy) where up to 9 individuals were observed in the same area in the last six years.

Our results suggest that hybridisation of Alpine ibex is a neglected phenomenon, raising important questions on the sanitary and conservation implications linked to the presence of feral goats on the Alps. Indeed, not only feral goats can transmit several pathogens at the livestock / wildlife interface, but they can also represent a threat for the genetic conservation of a species that already suffered significant genetic losses.



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THE ROLES OF MAMMALIAN PREDATORS IN THE EPIDEMIOLOGY OF FRANCISELLA TULARENSIS IN NORTH WEST SPAIN

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Keywords: Tularemia Epidemiology, Vole Predation, Shedder, Spreader, Bacterium

Abstract Text

Francisella tularensis, the agent of tularemia, is a notifiable Class A biothreat in Spain where >1,500 human cases were declared. Fluctuating populations of mammalian herbivores (lagomorphs and voles) shape tularemia dynamics and epidemiology. In NW Spain, common vole populations amplify the disease: tularemia prevalence increases with vole density, leading to environmental contamination and spillover. We report here on tularemia prevalence in epidemiologically relevant vole-eating mammalian predators. We studied prevalence in a specialist predator (weasel) and generalist predators that prey on voles when abundant (American mink, otter, red fox, Iberian wolf, and domestic cats). We hypothesized that mammalian predators consuming voles would become infected by *F. tularensis* and excrete the bacterium during and after the vole outbreak, contributing to *F. tularensis* spreading and persistence. We collected 199 faecal samples from mammalian predators in a tularemia hotspot during a vole abundance cycle including an outbreak and concomitant increase in human tularemia cases. After DNA extraction, faecal samples were analysed by PCR. We found that 11.1% of samples tested positive for *F. tularensis* subsp. *holartica*. Species-specific prevalence in scats were 20 % in common weasels, 9.5% in minks, 30.3% in foxes and 16,7% in wolves: %. *F. tularensis* was not detected in otter or cat faeces. As predicted, tularemia prevalence in predator faeces was maximum (28,5%) during the vole outbreak and was lower (0-12.5%) when voles were scarce. Interestingly, prevalence was 10.5% after the vole peak, indicating that predators continued to excrete the bacteria when voles were scarce. We conclude that mammalian vole predators act as shedders and are highly mobile spreaders of *F. tularensis*. They could further act as reservoirs during inter-epizootics or become infected by consuming other tularemia reservoir species (lagomorphs) when vole population have crashed. We suggest that screening predator remains could improve tularemia surveillance in endemic regions.



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CAUSES OF BALD EAGLE MORBIDITY AND MORTALITY IN THE EASTERN UNITED STATES FROM 1989 TO 2021

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Keywords: Eagle, Lead, Pathology, Toxicosis, Trauma

Abstract Text

Bald eagles (*Haliaeetus leucocephalus*) have historically been at risk of anthropogenic causes of mortality, most commonly through trauma (e.g., collisions, electrocution, and gunshot). As both apex predators and facultative scavengers, bald eagles also can suffer from various toxicoses, most notably from lead and anticoagulant rodenticides. More data are needed on causes of bald eagle mortality in the eastern U.S. to help determine and mitigate risks to population health. Our primary study objective was to determine the causes of morbidity and mortality in bald eagles in the eastern U.S., with a specific focus on assessing prevalence of trauma and toxicosis. Additionally, we sought to evaluate liver lead and anticoagulant rodenticide concentrations in conjunction with pathology findings and diagnoses. We retrospectively assessed diagnostic data from bald eagle cases submitted from 21 states from January 1989 to March 2021 and categorized primary and contributing causes of mortality. Diagnostic evaluations included gross and histopathology, with ancillary tests as applicable. Among 600 bald eagles examined, non-infectious causes of mortality (471; 78.5%) were more common than infectious etiologies (42; 7.0%), with 87 deaths of unknown cause (14.5%). The majority of noninfectious deaths were attributed to trauma (267; 56.7%), with vehicular collision (53) as the most common identifiable source. Toxicosis accounted for 187 cases (39.7%), primarily due to lead (92), aetokthonotoxin (i.e., vacuolar myelinopathy; 54), and anticoagulant rodenticide(s) (25). Lead toxicosis was diagnosed in birds with liver lead concentrations as low as 1.5 ppm, indicating that toxicosis may be associated with lower liver concentrations than previously thought. This study demonstrates challenges faced by bald eagles in the eastern U.S., emphasizing the potential impacts of human-associated activities on eagle populations. It also reveals the need for targeted studies to help decipher the diagnostic significance of liver concentrations of toxins commonly encountered by bald eagles in the environment.



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UNRAVELLING THE PATHOGENESIS OF HERPESVIRUS-ASSOCIATED PROLIFERATIVE SKIN DISEASE IN FROGS AND TOADS

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Keywords: Herpesvirus, Amphibians, Disease, Wildlife, Virus

Abstract Text

Amphibians are declining all around the world at an alarming rate. Several antropogenic factors have been associated with this major biodiversity loss. More recently, infectious diseases have surfaced as significant stressor contributing to this global decline. Among infectious agents, Chytrids and Ranavirus have been shown to be significant threats, however, limited investigations have been carried out towards additional potential pathogens. Within the last few years, two novel herpesviruses, named Ranid herpesvirus 3 (RaHV3) and Bufonid herpesvirus 1 (BfHV1) have been discovered and partially characterized in frogs (*Rana temporaria* and *R. dalmatina*) and in toads (*Bufo bufo*), respectively. Both these viruses are associated with similar proliferative skin disease, potentially suggesting a common pathogenesis. Accordingly, a thorough comparative study, including classic morphologic (histopathology), ultrastructural (electron microscopy) and molecular investigation (in situ hybridization and transcriptomics) has been carried out on tissues collected from infected frogs and toads. The results of this investigation revealed that the proliferative skin lesions are likely transitory with viral replication occurring in the upper layers only of the thickened epidermis, leaving the germinal layer unaffected. This compartmentalization of the lesions, supported by the in situ hybridization results, appears also to affect the immune response, which appears overall inconspicuous in the affected skin and overall limited to the lower layers of the epidermis. Transcriptomics revealed that the bulk of the most downregulated and upregulated host genes include those involved in signalling and cell remodelling, with seven of them homologous to human genes involved in neoplastic disease, consistently with the proliferative nature of the herpesvirus associated skin disease in anurans. At the light of the current finding, RaHV3 and BfHV1 associated skin disease appears to reflect a concerted process, functional to viral replication and with the presumptive involvement of signalling and gene remodelling host and immunomodulatory viral genes.



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FIBROPAPILLOMATOSIS AND CHELONID ALPHAHERPESVIRUS 5 INFECTION IN KEMP'S RIDLEY SEA TURTLES (*LEPIDOCHELYS KEMPII*)

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Keywords: Herpesvirus, Marine Turtle, Molecular Diagnostics, Tumor, Viral Metagenomics

Abstract Text

The Kemp's ridley sea turtle (*Lepidochelys kempii*) is a Critically Endangered species occurring in the Gulf of Mexico and waters off the eastern coastal United States. This species is susceptible to fibropapillomatosis, a debilitating neoplastic disease associated with chelonid alphaherpesvirus 5 (ChHV5) infection. Although historically FP has been only rarely reported in Kemp's ridleys, a number of cases have been documented in recent years, suggesting that prevalence may be increasing. The goals of this study were to: (1) characterize fibropapillomatosis in Kemp's ridley turtles, including case demographics and pathology; (2) detect ChHV5 DNA in tumor samples collected from Kemp's ridley turtles; and (3) analyze ChHV5 phylogenetics data in fibropapilloma tumor samples collected from Kemp's ridley turtles encountered in different regions of the coastal United States. We identified 19 cases of fibropapillomatosis in Kemp's ridley turtles encountered in Texas (N=7), Florida (N=6), North Carolina (N=3), Georgia (N=2), and Massachusetts (N=1) USA during 2006–2020. Twelve turtles (63%) were found stranded (including five dead), five (26%) were encountered during nesting, and two (11%) were incidental captures reported by fishermen. Seven (37%) of the turtles were juveniles, and 12 (63%) were adults. Individual turtles had an average of three tumors per turtle (range: 1–8); one turtle had associated internal tumors. Quantitative (q)PCR detected ChHV5 DNA in 10/11 (91%) tumor samples; mean viral copy number was 6.4×10^6 copies/ μ g DNA. Further viral sequencing detected ChHV5 in eight samples. Phylogenetic sequence analysis revealed that these samples cluster with known ChHV5 Florida variants A–C previously identified in two other sea turtle species. This indicates that ChHV5 variants have primarily evolved regionally among sympatric species rather than by host-virus coevolution, suggesting cross-species transmission and prompting concern for disease spread among Kemp's ridleys in regions of increasing spread in other species (e.g., green turtles, *Chelonia mydas*).



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SPATIAL MODELLING OF HYALOMMA LUSITANICUM TICKS SHAPE CRIMEAN-CONGO HAEMORRHAGIC FEVER VIRUS EXPOSURE IN DOÑANA NATIONAL PARK, SPAIN

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Keywords: Dynamics, Hyalomma, Prevention, Tick, Zoonosis

Abstract Text

Crimean-Congo haemorrhagic fever (CCHF) is an emerging tick-borne viral human disease in Spain. Migratory birds exchange *Hyalomma* spp. ticks infected with CCHF virus (CCHFV) between Europe and Africa. A crucial stopover on their route, Doñana National Park (DNP), also hosts abundant populations of wild ungulates (*Cervus elaphus*, Dama dama and *Sus scrofa*), cattle and horses that maintain large burdens of *H. lusitanicum* ticks, the presumed main vector of CCHFV in Iberia. This makes DNP a potential hotspot of CCHFV in Spain. Unravelling the factors shaping tick abundance and CCHFV distribution at different spatial scales may aid in better preventing CCHFV transmission to humans. So, the aim of this research was to model the spatial pattern of *H. lusitanicum* abundance and assess the link between vector abundance and CCHFV exposure risk. This was achieved through 11 years (2010-2020) of surveys of wild ungulates and their ticks in DNP. The presence of specific CCHFV antibodies in a selection of 435 red deer was analysed by a commercial double-antigen ELISA (IDvet, France). *Hyalomma lusitanicum* occurrence/abundance was spatially modelled with a series of host and environmental predictors using data of 20,501 *H. lusitanicum* collected on 1,965 wild ungulates in DNP. The abundance of *H. lusitanicum* was highly dependent on soil humidity traits. The models were projected at a 250x250m spatial resolution scale in DNP to map *H. lusitanicum* predicted abundance. Of the 435 deer tested, 323 were seropositive (74.3%; IC: 70.19-78.4%), but their distribution was not spatially homogeneous; 80.1% of the deer in the northern part of DNP were seropositive in contrast to the 45.7% in the south. We observed a high correlation between projected *H. lusitanicum* abundance and CCHFV exposure of deer, therefore pointing out that modelling *H. lusitanicum* abundance is a useful tool to predict CCHFV transmission risk.



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PREVIOUS USUTU VIRUS INFECTION INDUCES CLINICAL PROTECTION AGAINST WEST NILE VIRUS INFECTION IN GREY PARTRIDGES (*PERDIX PERDIX*)

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Keywords: Cross-Protection, Experimental Infection, Grey Partridge, Usutu Virus, West Nile Virus

Abstract Text

West Nile virus (WNV) and Usutu virus (USUV) are genetically related neurotropic mosquito-borne flaviviruses and are endemic in several European countries. Both viruses share the same mosquito vectors and avian populations as amplifying hosts. The potential cross-protection of USUV antibodies against WNV infection has been assayed in mice but it has never been evaluated in the natural reservoir. We performed an experimental study with 3 groups of grey partridges: a “test” group (n=10) of 11-week old birds with high levels of neutralizing USUV antibodies elicited after inoculation with USUV strain “Haut Rhin/2015” (France) was challenged subcutaneously with 104 pfu of Italy/08 WNV strain. Another group (“naïve”, n=10) received the same WNV dose, and a third group (“sham”, n=10) was sham-inoculated with diluent. Clinical signs were registered daily. Body weight, viremia, viral presence in feathers and oral swabs (by real-time RT-PCR) and neutralizing antibodies (by micro-VNT) were monitored for up to 15 days post-challenge (dpc). The “naïve” group suffered clinical disease with significant body weight loss, although no bird died. All the partridges in this group developed viremia and viral genome was detected in feathers and oral swabs. By contrast, the “test” group remained completely healthy with good body condition. These birds did not develop viremia and no viral genome could be detected in oral swabs or feathers (with the exception of the feathers of one bird at 3dpc). All WNV-infected birds developed WNV neutralizing antibodies, with higher titers in the “test” than the “naïve” group probably due to a prime-boost effect. Previous infection with USUV in grey partridges induced a complete clinical protection and a very strong virological protection against subsequent WNV infection. Such cross-protection could affect flavivirus transmission rates in susceptible birds in those areas where both virus co-circulate. Acknowledgements: this study was funded by the FNC (FNC-PSN-PR19-2015).



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COMBINED EFFECTS OF LAND USE PRACTICES AND WEATHER ON THE ABUNDANCE AND PRESENCE OF MOSQUITO-BORNE DISEASE VECTORS AND MOSQUITO DIVERSITY IN EASTERN ONTARIO

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Keywords: Land Use, Weather, Mosquito-Borne Disease Vectors, Abundance, Presence

Abstract Text

Mosquito-borne diseases (MBD) threaten human and wildlife health. Improving our understanding of vector ecology and their variation according to land use and weather changes are essential for a better management of MBD epidemiology. This study aims to estimate the separated and combined effects on weather and land use practices on mosquito species abundance and biodiversity in an Eastern Canadian context. Estimates of adult mosquito abundance and biodiversity were derived from biweekly field-based mosquito collection during late spring to early fall of 2017 and 2018 in eastern Ontario, Canada. Land use and meteorological variables were extracted from a one kilometer radius around mosquito trapping sites, then centered-reduced. Meteorological variables were averaged 5 days, 30 days and 90 days prior to mosquito capture. We modeled the abundance of 13 mosquito species of public health' relevance and the Shannon diversity index, by performing stepwise regressions, to the following explanatory variables: 1) land use, 2) weather conditions and 3) both land use and weather conditions. The effects of land use and meteorological variables were both species-specific. Mostly, the meteorological variables mean of at least 5 days prior to capture were associated to mosquito abundance and biodiversity. As an example, *Culex pipiens-restuans*, the main vector of West Nile virus, was negatively associated with mean minimum temperature over 5 days before mosquito capture, positively with mean precipitation over 90 days before the capture and the percent coverage of cropland. When land use and weather were simultaneously included in the model, more variables became significant and the model fit was improved. These findings support the added value to account for both meteorological and land-use changes while characterizing the evolution of the risk associated with MBD in North America under climate changes by improving models' performance. Therefore, urbanization and crop activities can increase the risk of exposure to MBD.



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INVESTIGATION ON THE ROLE OF RED FOX IN TB MAINTENANCE COMMUNITY – SECOND OPUS: EXPERIMENTAL INFECTION WITH A VIRULENT FIELD MYCOBACTERIUM BOVIS STRAIN

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Keywords: Animal Tuberculosis, Mycobacterium Bovis, Transmission, Fox, Pathology

Abstract Text

Animal tuberculosis (TB) due to *Mycobacterium bovis* infection is a problem that in Europe can concern multi-host communities including cattle but also wildlife species (wild boar, badgers, wild deer). Since 2014, numerous cases were detected in red foxes (*Vulpes vulpes*) in TB endemic regions in France and in the Iberian Peninsula, with *M. bovis* excretion in urine and feces observed in some individuals. To produce first data on the pathogenesis of *M. bovis* infection in foxes and the associated risk of excretion, we implemented an experimental infection by the oral route in 12 captive foxes using a French *M. bovis* field isolate. Immunology, molecular diagnosis, bacteriology and pathology protocols were performed 12 weeks post-infection (82 days post-infection, dpi). At post-mortem, only very few macroscopic lesions were observed. Histology showed small granulomas within lymph nodes, tonsils, liver and lung from a small number of foxes, with the presence of scarce acid-fast bacilli. All 12 foxes had at least four PCR positive samples (out of the 23 tested), and 11 foxes at least one culture positive sample. The culture negative fox was PCR positive in both retropharyngeal and the mesenteric lymph nodes, in line with the results on the rest of the animals. *M. bovis* was detected by PCR in the bladder of 3 foxes at 82 dpi and, at different time points of the experiment, in the oropharyngeal mucus of 3 individuals and in feces of 9 foxes, with one of them confirmed by bacteriology. This original study reproduces the pattern of infection observed in naturally TB-infected foxes in the wild and demonstrates a risk of mycobacteria excretion by foxes when infected by the oral route. If taken together with ecological traits of foxes, these results are useful to elucidate the putative role of foxes in the multi-host epidemiological system.



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PHYSIOLOGICAL EFFECTS OF AZAPERONE AND MIDAZOLAM ON NETGUN-CAPTURED MULE DEER

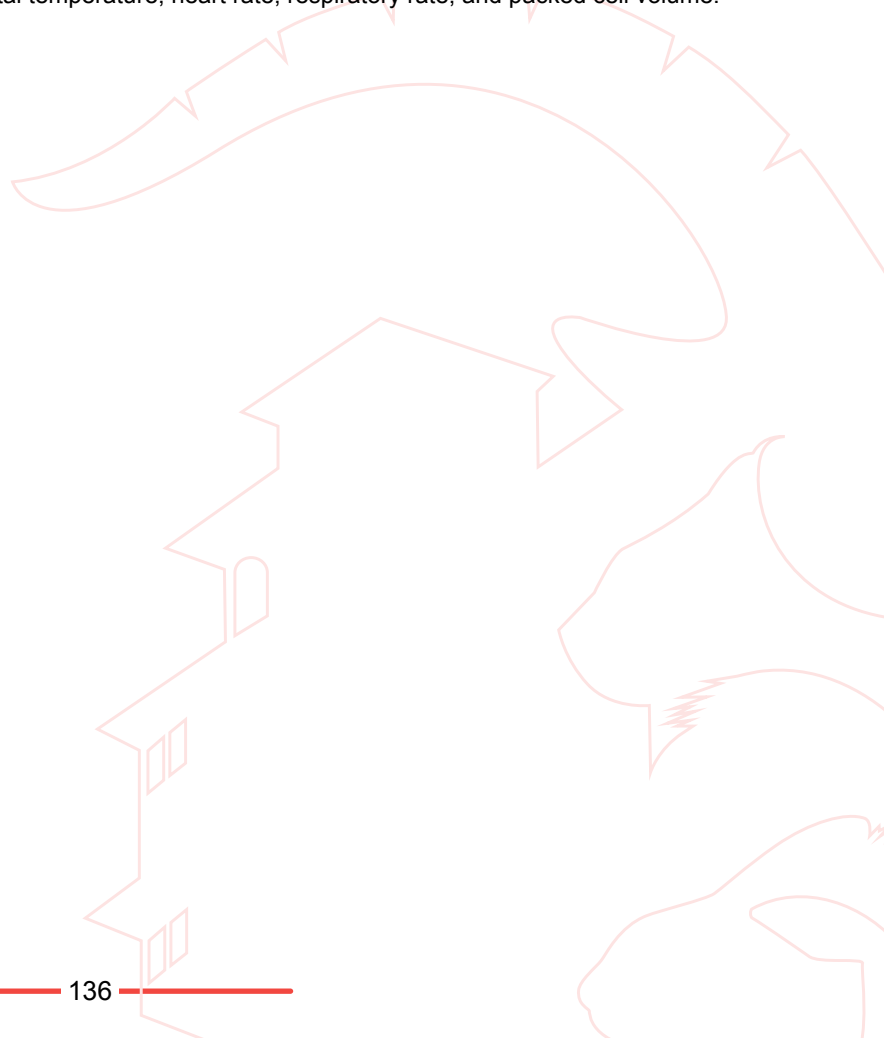
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Keywords: Deer, Netgun Capture, Tranquilizer

Abstract Text

Netgun capture is a commonly used capture method for mule deer (*Odocoileus hemionus*) in North America. Mortalities during netgun captures are generally low, and most often caused by trauma and occasionally fatal capture myopathy. Capture is a stressful event for wild animals, and subclinical capture myopathy is difficult to measure. The use of tranquilizers during netgun capture is not widespread. In this study, we compared physiological variables from netgun captured deer that did or did not receive an equal dose of midazolam and azaperone (mean of 0.14 mg/kg, SD = 0.02 mg/kg, range 0.08 – 0.21 mg/kg) at time of capture and before slinging to a processing location, with the goal of evaluating whether drug administration would improve or worsen physiological state of the animal. A total of 250 deer, 57 males and 193 females were included in the study. Deer were captured in association with management activities between December 2018 and March 2020. Of these, 132 deer received midazolam and azaperone at time of capture. Variables recorded included chase times, time from capture to arrival at the processing location, time from capture to release, rectal temperatures, heart rate, respiratory rate, body condition, age, sex, creatine kinase, aspartate aminotransferase, packed cell volume, red blood cell concentration, and hemoglobin, as well as serial venous pH, pCO₂, HCO₃⁻, and BE. All animals were GPS collared and monitored after release. There was no difference in survival after capture between drugged and non-drugged animals. All animals experienced severe metabolic lactic acidosis, which generally worsened with increasing chase time, highlighting the critical importance of limiting chase times during captures. Drug administration did not influence the degree of metabolic acidosis, however, it appeared to have a positive effect on several stress related indices including rectal temperature, heart rate, respiratory rate, and packed cell volume.





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USING MULTIVARIATE ANALYSES TO EXPLORE EVOLUTIONARY PATTERNS IN DISEASE PATHOLOGY

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Keywords: Community Analysis, Host-Pathogen Co-Evolution, Multidimensional Disease Space, Pathology, Shape Analysis

Abstract Text

Many wildlife diseases cause external pathology, providing a minimally invasive way to assess individual health in the field. Accordingly, researchers have developed several linear, multi-point scoring systems to capture disease severity across a range of hosts and pathogens. However, collapsing a complex, multidimensional trait (pathology) into a single, linear score can mask critical information about complex temporospatial interactions. Here, we describe a novel application of multivariate techniques (shape and community analyses) to explore potential patterns of co-evolution in a well-studied wildlife disease system: house finches infected with *Mycoplasma gallisepticum* (MG), which causes visible conjunctival pathology that facilitates transmission. We captured hatch-year house finches from two populations that differ in their history of pathogen emergence, one that has experienced seasonal epizootics for over 25 years (Virginia) and one that is naïve to the pathogen (Hawaii). After removing any individuals with prior MG exposure, we experimentally infected birds with either the original, low-virulence isolate or a more recent, high-virulence isolate and recorded: 1) observer-assigned severity scores (0, healthy - 3, severe), 2) changes in eye shape, and 3) presence of pathological descriptors (blepharospasm, crusting, erythema, eversion, exudate, and swelling). When infected with the low-virulence isolate, Virginia birds showed lower severity scores, milder distortions of the eye rim and depauperate suites of pathological descriptors when compared to Hawaii birds. When infected with the virulent isolate, these differences were more pronounced, with Virginia birds also expressing more variable descriptor communities than Hawaii birds. Notably, indicator analysis showed that all pathological descriptors ($p < 0.04$) except eversion ($p = 0.17$) were predictive of Hawaii as the population of origin. These patterns suggest that the pathogen's ability to induce eversion may have been selected for in Virginia and/or that host differences in tolerance or resistance may shape the expression of specific pathological phenotypes between populations.



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RABIES, LYSSAVIRUSES AND 'SMALL MAMMALS': RESERVOIRS, VECTORS, VICTIMS, PHANTASMS, OR ...?

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Keywords: Epidemiology, Lyssavirus, Rabies, Surveillance, Zoonosis

Abstract Text

Rabies is an acute, progressive encephalitis caused by a lyssavirus. More than 17 lyssavirus species are known, except in Antarctica. All warm-blooded vertebrates are believed susceptible, but predominantly, only mammalian species within the Orders Carnivora and Chiroptera appear important. Why certain wildlife hosts are responsible for essential rabies perpetuation, in contrast to others, is poorly understood. For example, among Eutherians, 'small mammals' (e.g., rodents, lagomorphs, shrews, etc.) represent the greatest number of described taxa. Historically, isolated cases of apparent dead-end, spill-over infections of rabies lyssavirus have been reported in several species of 'small mammals', in all enzootic regions, except Australia. Yet, given overt biodiversity, widespread distribution and relative abundance, no lyssavirus reservoirs have been documented among 'small mammals', despite focal laboratory-based surveillance, especially within Europe and North America. However, much less scrutiny has occurred within lesser developed countries (LDC) in Africa and Asia. Significantly, the reservoirs for Mokola lyssavirus in Africa are unknown, but suspected to be a representative 'small mammal'. The related issue of transmissibility is more controversial, and many doses of expensive and scarce biologics have been administered unnecessarily during human postexposure prophylaxis in LDC for suspected contact with non-rabid 'small mammals'. Although no human cases have been documented definitively, anywhere rabies is enzootic, human exposures to 'small mammals' should undergo a thorough risk assessment and appropriate diagnosis of biting animals using recommended criteria, such as after an unprovoked bite from an ill mammal. While rabies occurrence in 'small mammals' is possible (albeit uncommon), objectively, additional attempts at applied pathogen detection, viral characterization and ecological introspection within selected groups and regions are necessary, to better understand the evolution, emergence, epizootiology and significance of wildlife rabies from a more holistic, global perspective, especially given local anthropogenic perturbations, climate change and the 2030 plan of canine rabies elimination.



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MODELING HOST-PATHOGEN TRANSMISSION DYNAMICS TO SUPPORT SCIENTIFIC DECISION MAKING

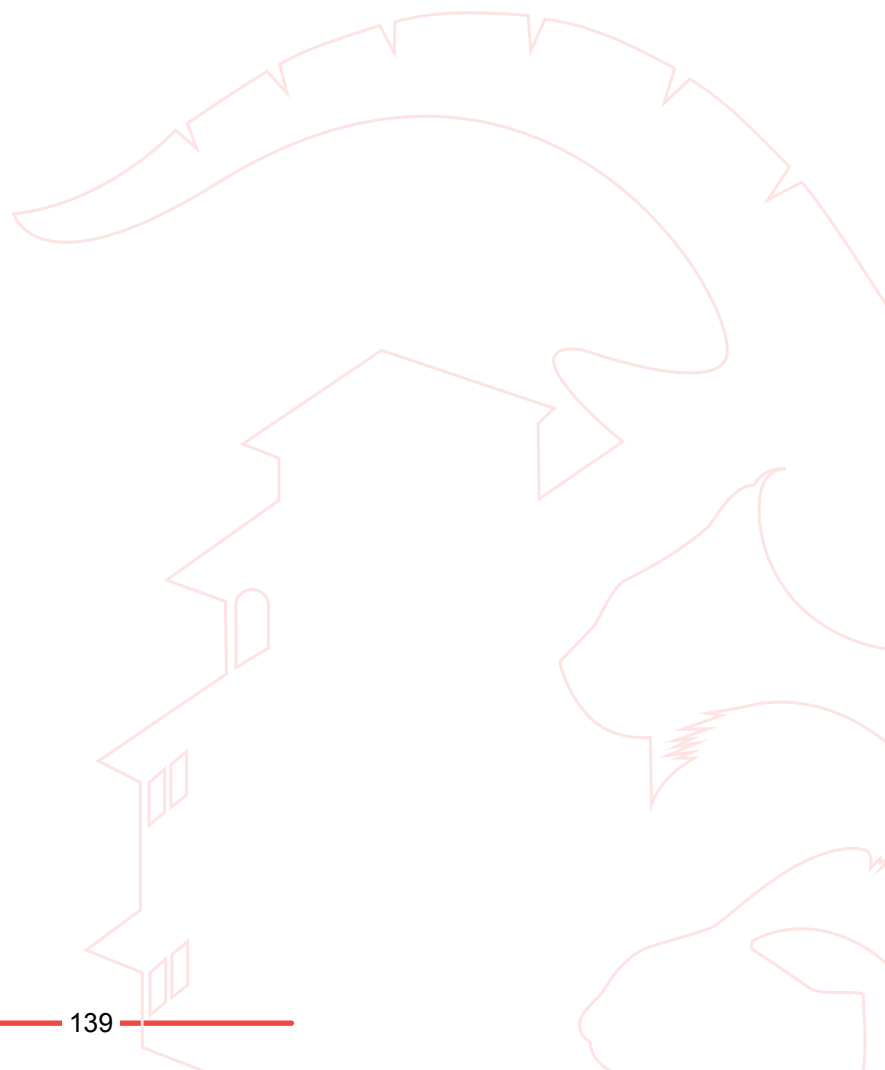
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Keywords: Host-Pathogen Models, Plague, Rabbit Hemorrhagic Disease, Vaccination, White-Nose Syndrome

Abstract Text

Diseases of wildlife are difficult to manage due to limited options, and numerous uncertainties, including uncertainty in wildlife responses to management actions, uncertainty in the identification of host species, and uncertainty in host species demographics and distributions prior to disease emergence. Host-pathogen models can provide guidance for decision makers particularly in the early stages of disease emergence and/or when new tools for management are developed. The development of host-pathogen models requires some knowledge of host distributions and demographics, pathogen transmission routes, and effects of pathogens on host populations. We have developed spatially-explicit, agent-based, host-pathogen models for plague and prairie dogs, rabbit hemorrhagic disease and rabbits, and white-nose syndrome and bats. These models can assist managers with assessing the potential impacts of disease mitigation tactics such as vaccination, the effort /cost needed to achieve desirable outcomes, and the influence of parameters on model results. Additionally, these models can assist with the identification of key uncertainties that require further research as well as mitigation strategies that are optimal across a range of conditions and therefore unaffected by model uncertainty. We discuss the importance of spatial structure (i.e. host distributions) on model outcomes, the commonalities among the host-pathogen systems, and the development of a generalizable framework to address emerging wildlife disease issues.





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CAN WE REDUCE THE RISK TO ECOSYSTEMS FROM CONSERVATION TRANSLOCATIONS THROUGH USE OF DISEASE RISK ANALYSIS?

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Keywords: Ecosystem Health, Conservation, Translocations, Surveillance, Disease Risk Management

Abstract Text

Given the widespread destruction of ecosystems during the Anthropocene, there has been, over the last century, a response through a burgeoning of conservation programmes, of which conservation translocations have been a part. Conservation translocations represent a risk from disease on account of (i) the movement of parasites (infectious agents) with the translocated hosts possibly leading to novel host-parasite interactions, and (ii) stressors placed on translocated wild animals and those in the recipient ecosystem. Over the last 32 years, the Disease Risk Analysis and Health Surveillance (DRAHS) project at ZSL, working with partners, has monitored the health of 38 translocated species and their recipient ecosystems. Disease risk analysis (DRA) was carried out for conservation translocations proposed after 2002 and 36 DRAs have been carried out on 32 translocation programmes in Europe, Asia, Australasia and North America. Where a conservation translocation programme pre-dated the implementation of DRA, we assessed disease risk management practices as soon as possible. The DRAs are published and freely available to assist other translocation managers. If a conservation translocation is approved, health is monitored through clinical and pathological techniques, prior, during and after translocation. Post-release health surveillance, primarily through pathological examination of wild animals found dead in the recipient ecosystem, is continued for as long as possible. For example, red kites *Milvus milvus* continue to be monitored more than 30 years after the first release, anticoagulant rodenticide poisoning has been shown to be a threat to the released population, and mitigation guidance has been issued for rodent control programmes. Integrated population dynamics monitoring assists in the interpretation of surveillance results for all species, whether invertebrates, amphibians, reptiles, birds or mammals. If data from DRA of conservation translocations demonstrates a disease threat, mitigation measures can be implemented and ecosystem health enhanced.



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UNRAVELLING THE INTERFACE: FARM CONNECTIVITY PROVIDED BY SPOTLESS STARLING (*STURNUS UNICOLOR*) MOVEMENTS

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Keywords: Avian Influenza Virus AIV, Salmonella, Spottless Starling, Telemetry, Interface.

Abstract Text

Highly Pathogenic Avian Influenza Viruses (HPAIV) are relevant pathogens for wild and domestic birds. Strict biosecurity is vital for outbreak prevention in domestic poultry and gamebird production. While aquatic birds are considered the reservoir of avian influenza viruses, circumstantial evidence and results from experimental infections suggest that passerine peridomestic birds that frequently enter barns and production facilities could act as bridge species for the introduction of HPAIV. Potential for such transmission has been experimentally demonstrated for the tree sparrow (*Passer montanus*) and Eurasian starling (*Sturnus vulgaris*). The spotless starling, a close relative of the European starling, is a frequent farm bird in Europe which forms large flocks especially in winter. We captured 27 starlings on a red-legged partridges farm (*Alectoris rufa*), took samples for pathogen detection, and equipped 21 with Pinpoint GPS Argos transmitters. We were able to track the movements of 17 spotless starlings, during 3-5 days in July and November. Though our sample size of tagged birds is small, these individuals belong to a large flock of starlings (i.e. roughly 500 individuals) and thus represent the movements of a much larger number of birds which potentially move together. None of the starlings tested positive for HPAIV by RtPCR on cloacal and oral swabs or had *Salmonella*, also none had antibodies against AIV. One individual was positive against West Nile (WNV), or cross-reacting Flaviviruses and one carried a multiresistant strain of *Escherichia coli*. Satellite transmitter data revealed mostly local movements of the starlings, connecting different types of farms with crops, several small waterbodies or streams and a village. Specifically, movements included visits to most different livestock farms in the region, such as pig, poultry, sheep farms as well as a horse stable. This suggests that the starlings could act as vectors for enteropathogens or AIV.



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MODELING EPIDEMIC PREVENTION AND DETECTION STRATEGIES FOR INTRODUCED PATHOGENS IN THE CHANNEL ISLAND FOX (*UROCYON LITTORALIS*)

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Keywords: Channel Island Fox, Disease, Epidemic, Spatially-Explicit Model, Vaccination

Abstract Text

Disease transmission and epidemic prevention are top conservation concerns for wildlife managers, especially for small, isolated populations. Previous studies have shown that the course of an epidemic within heterogeneous host populations is strongly influenced by whether pathogens are introduced to areas of relatively high or low host densities. We tested how disease monitoring and vaccination programs are influenced by spatial heterogeneity in host distributions by developing a spatially-explicit model, parameterized by field studies, simulating the spread of rabies and canine distemper in a spatially heterogeneous population of Channel Island foxes (*Urocyon littoralis*). Introductions into areas of high fox densities resulted in faster transmission and greater population reductions for both pathogens, compared to introductions to low fox density sites. When introduced to low fox density sites, rabies was >5x more likely to go locally extinct compared to high-density introductions, leaving an average of >99% of foxes uninfected. Canine distemper went extinct in >98% of simulations regardless of fox density at the site of introduction, but only after >90% of foxes were infected. Increasing the monitoring frequency of radio-collared foxes reduced the time to epidemic detection and percentage of foxes infected for both pathogens compared to increasing the number of collared foxes. The efficacy of vaccination was heavily influenced by local fox density at the site of pathogen introduction. A vaccine firewall far away from the site of pathogen introduction was generally the least effective strategy compared to a firewall close to the site of pathogen introduction or a random distribution of vaccines across the island. Our results highlight the challenges in mitigating an epidemic of novel disease in a naïve host population, in part due to complex interactions between pathogen biology and host behavior, exacerbated by the spatial variation of most host populations.



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A ONE HEALTH APPROACH TO THE IMPACT OF TRACE METAL CONTAMINATION FROM DERELICT LEAD MINES IN WALES

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Keywords: Contamination, One Health, Trace Metals

Abstract Text

Trace metals are naturally occurring elements that can be toxic to plant and animal life at relatively low concentrations. Through anthropogenic mining activities, trace metals can be extracted from the Earth's crust and accumulated to high concentrations. This results in environmental contamination, and can present a health risk to biota living around metalliferous mine sites. In this study, we aimed to (i) determine the distribution of trace metals at two sites in Wales impacted by historical lead mining activities, and (ii) understand the resulting impact on environmental and animal health. A survey of the areas showed that trace metals were dispersed beyond the mine sites, and were present in the water, sediment, and soil of surrounding areas at concentrations that exceeded established thresholds by up to three orders of magnitude. Trace metals were also found in high concentrations in plants, invertebrates, and vertebrates in these contaminated environments. In particular, wood mice (*Apodemus sylvaticus*) collected at contaminated sites had significantly higher tissue lead concentrations than wood mice from control sites (kidney: $\chi^2=107$, $df=2$, $p<0.001$; liver: $\chi^2=67.8$, $df=2$, $p<0.001$; bone: $\chi^2=115$, $df=2$, $p<0.001$). Domestic animals living at contaminated sites also exhibited elevated lead concentrations, specifically in chicken blood (1790 ± 121 $\mu\text{g/L}$), a horse liver (67.4 ± 3.64 mg/kg dw), and duck bones (1610 ± 945 mg/kg dw), indicating potential toxicity and possibly explaining adverse health impacts. We further identified a potential vector for human exposure through the consumption of lead-contaminated eggs produced by chickens living near the mine sites. The project is ongoing, and the potential health impacts on vertebrates, such as immune system suppression and gut microbiome community modifications, are currently being investigated. This project employs a true One Health approach to exploring the impact of trace metal contamination across an ecosystem, looking at possible effects on environmental, animal, and human health.



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TOXOPLASMA GONDII INFECTION IN THE PROTECTED EURASIAN LYNX (LYNX LYNX) IN SWITZERLAND

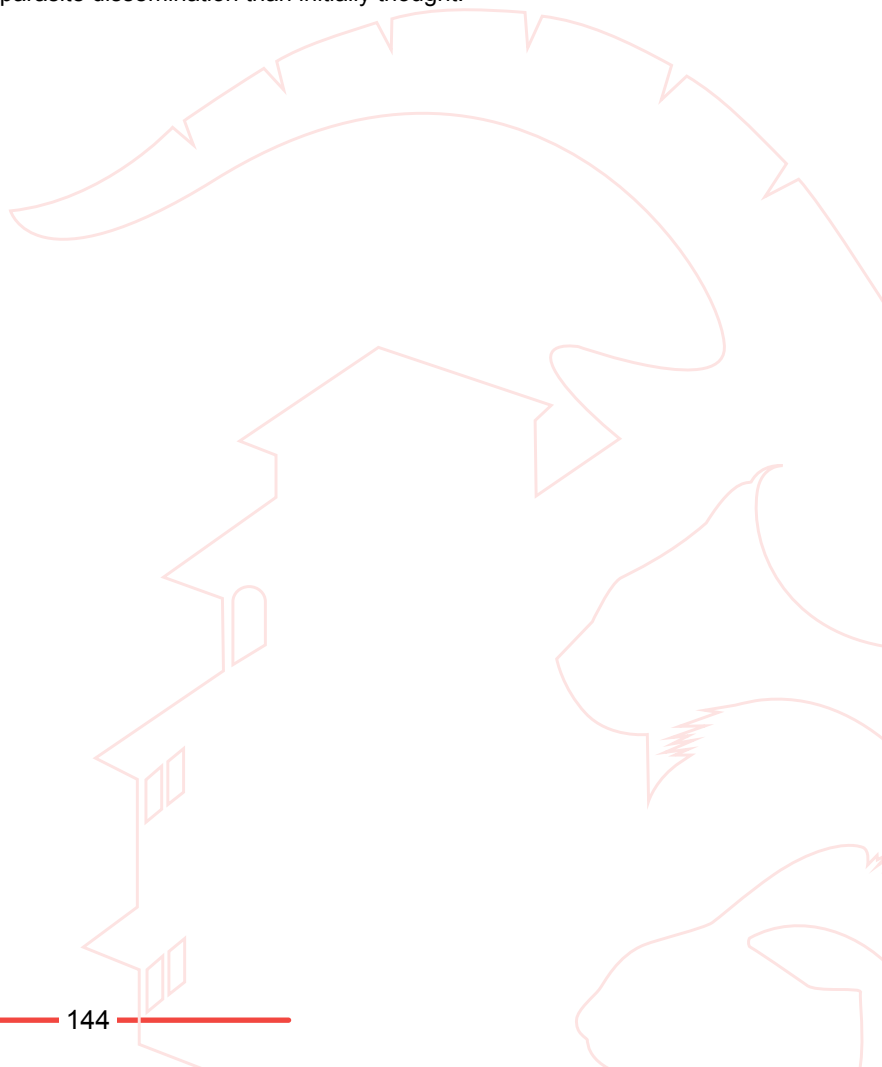
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Keywords: ELISA, IFAT, QPCR, Seroprevalence, Zoonosis

Abstract Text

Toxoplasma gondii is a coccidian parasite able to infect all warm-blooded species, including humans. It causes one of the most common zoonoses worldwide – toxoplasmosis. The Eurasian lynx (*Lynx lynx*) is one of the potential definitive hosts of *T. gondii* in Switzerland, besides domestic cats (*Felis catus*) and wildcats (*Felis silvestris*). Prevalence of infection in Swiss lynx is currently unknown. Due to increased human encroachment in wildlife habitats and growing domestic cat populations, mutual exposure becomes more likely. This may not only cause a problem for livestock but also increases the risk of infection for the local wild fauna. The aim of this study was to assess the role of the lynx as a potential intermediate and final host of *T. gondii* by determining seroprevalence of *T. gondii* in the Swiss lynx population, frequency of oocyst shedding, as well as potential risk factors that may favour infection. For the seroprevalence study 167 serum samples collected from dead lynx between 2002 and 2021 were tested by Enzyme-linked Immunosorbent Assay and Indirect Fluorescent Antibody Test. Samples with inconclusive results were further tested by Western Blot. A total of 141/167 (84.43%) samples tested positive for *T. gondii* antibodies. Additionally, 160 faecal samples were examined coprologically for endoparasites. *T. gondii*-like oocysts were observed in two (1.25%) of the samples. In both cases, they were confirmed as *T. gondii* by real-time PCR. Next steps include histologic and molecular examination of selected tissues (skeletal muscle, heart and brain), *T. gondii* genotyping studies and analysing metadata of each animal to assess risk factors for becoming seropositive. Our preliminary results indicate that the Swiss lynx population is often in contact with *T. gondii* and may play a more important role in parasite dissemination than initially thought.





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SMALL MAMMALS ARE RESERVOIRS FOR MULTIPLE ZOO NOTIC PATHOGENS

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Keywords: Leptospira Spp., Puumala Orthohantavirus, Bornaviruses, Coxiella Burnetii, TBEV

Abstract Text

Rodents and other small mammals are widespread throughout the world. In many regions they live in close contact to humans and farm animals. Small mammals are reservoir hosts of different zoonotic pathogens e.g. *Leptospira* spp., hantaviruses, bornaviruses, *Coxiella burnetii* or Tick-borne Encephalitis virus (TBEV). Coinfections with multiple pathogens are only rarely investigated, because research is mostly focussed on a particular pathogen. The aim of our study was a large-scale screening of small mammals for *Leptospira* spp., hantavirus, bornavirus, *Coxiella burnetii* and TBEV to create a comprehensive data set covering several zoonotic pathogens as well as their potential coinfection.

Samples of 2737 small mammals were analysed for *Leptospira* spp., Puumala orthohantavirus (PUUV), Tula orthohantavirus (TULV), Borna disease virus 1 (BoDV-1), variegated squirrel bornavirus 1 (VSBV-1), *Coxiella burnetii* and TBEV. Samples originated from regions with high human hantavirus case numbers or from TBE endemic areas in Germany in the years 2010 to 2020. RT-PCR/PCR was used to detect nucleic acids of *Leptospira* spp., PUUV, TULV, BoDV-1, VSBV-1, *Coxiella burnetii* and TBEV. Serological methods were applied to detect antibodies against PUUV, TULV and TBEV. First results of the still ongoing study show an overall *Leptospira* spp. prevalence of 8.7% (n=2230). PUUV prevalence depended on year, season and site and ranged from 0% up to 67% (n=2005). Antibodies against TBEV could only be detected in TBE endemic areas, with an overall prevalence of 17.9% (n=381). Out of 397 samples analysed for *Coxiella burnetii*, two samples yielded a positive result, further investigations are pending. Bornavirus infections were not detected (n=2246). Our study shows that zoonotic pathogens are widely spread in small mammal populations in Germany. We aim to improve the awareness that small mammals are reservoirs for multiple zoonotic pathogens and an important part of the One Health approach to achieve better public health outcomes.



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SETTING THE TERMS FOR ZOO NOTIC DISEASES: EFFECTIVE COMMUNICATION FOR RESEARCH, CONSERVATION, AND PUBLIC POLICY

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Keywords: Bats, Chiroptera, Conservation, Public Health, Science Communication

Abstract Text

Many of the world's most pressing issues, such as the emergence of zoonotic diseases, can only be addressed through interdisciplinary research. However, the findings of interdisciplinary research are susceptible to miscommunication among both professional and non-professional audiences due to differences in training, language, experience, and understanding. Such miscommunication contributes to the misunderstanding of key concepts or processes and hinders the development of effective research agendas, disease prevention or mitigation strategies, and public policy. These misunderstandings can also have devastating effects on conservation, such as the persecution of bats and even government calls to cull them. Here, we identify five types of miscommunication driven by the use of terminology regarding bats and the emergence of zoonotic diseases, which we have categorized based on their root causes: 1) Incorrect or overly broad use of terms; 2) Terms with unstable use or varying use between disciplines; 3) Use of common words as jargon; 4) Terms used correctly that spark incorrect inference; 5) Incorrect conclusions from evidence. We illustrate each type of miscommunication with commonly misused or misinterpreted terms, providing a definition, caveats and common misconceptions, and alternatives as appropriate. While we focus on terms specific to bats and disease ecology, we provide a general framework for addressing miscommunication that can be applied to other topics and disciplines for more effective research, problem-solving, and public policy.



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RETROVIRAL INFECTION AFFECTS REPRODUCTION AND SURVIVAL OF FEMALE WILD TURKEYS

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Keywords: Fitness, Lymphoproliferative Disease Virus, Meleagris Gallopavo, Reticuloendotheliosis Virus, Wild Turkey

Abstract Text

Understanding individual and spatial predictors of pathogen infection and the effect of infection on reproduction and survival is important for managing wildlife populations and diseases. Our research addresses this need by evaluating two retroviruses, lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV) in Maine's wild turkeys (*Meleagris gallopavo*). Infection with REV can result in immunosuppression, increased morbidity with viral co-infection, and reduced reproductive success in chickens, but has been relatively understudied in wild turkeys. Similarly, little is known about the effects of LPDV since it was recently discovered in the United States, though research suggests it may contribute to mortality and coinfection of wild turkeys. The goals of our study were to identify risk factors and fitness effects of LPDV and REV infection in Maine. We collected blood from 627 live-captured wild turkeys for molecular pathogen diagnostics and recorded age, sex, and location of capture. We attached radio-transmitter or GPS backpacks to a subset of females ($n = 163$) to gather data on land type usage and fitness metrics including survival rate, nest success, clutch size, and nest initiation. We identified sex, year, percent forest cover, and the interaction of age with percent agriculture cover and region as significant predictors of LPDV infection. Predictors of REV infection included region, year, and percent agriculture cover. Furthermore, REV infection and co-infection negatively affected survival of females, while LPDV infection reduced clutch size. We plan to use these results to inform population growth models to determine population level effects of infection, which is important for informing management decisions related to translocations, pathogen transmission between wildlife and poultry operations or captive breeding facilities, and harvest limits. These findings stress the value of consistent pathogen monitoring in game birds, and the inclusion of pathogen data in population estimation and growth models.



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WILDLIFE SURVEILLANCE AT MINK FARMS IN THE US FOLLOWING SARS-COV-2 OUTBREAKS

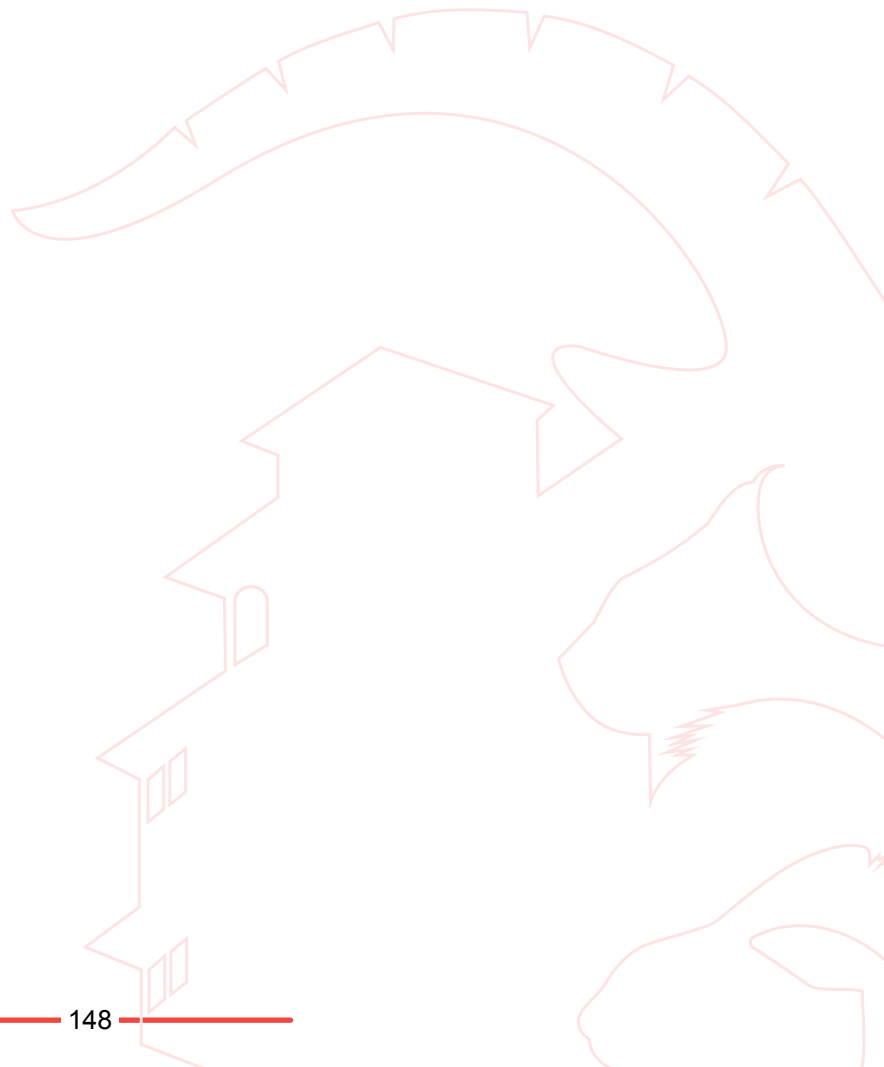
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Keywords: SARS-CoV-2, Mink, Spillover, Interface, Outbreak

Abstract Text

Outbreaks of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) on mink farms in Europe have shown that mink are highly permissive to infection and that transmission can occur bidirectionally between humans and mink. As of April 2021, 16 mink farms across four states in the United States have been confirmed with SARS-CoV-2 infections. We conducted wildlife surveillance at six of the affected mink farms across all four states to investigate potential SARS-CoV-2 spillover to nearby wildlife. In general, our trapping focused on meso-carnivores (raccoons, skunks, mink) and rodent-targeted trapping was conducted on two farms. Traps were typically placed outside mink barns or barrier fences with additional traps set within a 3.5-km buffer zone on some of the premises. We collected swabs and blood from all trapped animals, and tissues from a subset of animals, to test for evidence of SARS-CoV-2 infection or exposure. To date, over 250 mammals have been captured, including 26 house mice, 51 deer mic, 42 skunks, 32 raccoons, 29 opossums, and 21 mink (predominantly domestic escapees). We classified captured mink as either escaped or wild based on capture location, habitat, morphology, physiology, behavior, and genetics. We confirmed SARS-CoV-2 exposure in more than a dozen domestic escapees, most of which exhibited high antibody titers suggesting recent infection. We also confirmed SARS-CoV-2 in a nasal swab from one wild mink captured near one of the outbreak premises. Preliminary results indicate that the viral sequences from both the wild mink and an escaped mink associated with one of the outbreak farms were indistinguishable, indicating likely spillover from farmed mink to the wild mink, absent an intermediate host. While we did not document establishment of SARS-CoV-2 in wildlife, our results indicate that outbreaks of the virus at mink farms pose a potential spillover pathway to native wildlife.





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PULMONARY HEALTH IN BARATARIA BAY DOLPHINS IN THE 8 YEARS AFTER THE DEEPWATER HORIZON OIL SPILL

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Keywords: Deepwater Horizon, Oil Spill, Dolphin, Pulmonary, Health

Abstract Text

The Deepwater Horizon (DWH) disaster resulted in large-scale contamination of bays, sounds, and estuaries in the northern Gulf of Mexico (GoM), home to multiple stocks of bottlenose dolphins. Inhalation, direct aspiration, ingestion with subsequent aspiration, and dermal absorption of oil and its toxic components were all considered possible routes of exposure for dolphins living within the oil spill footprint. To determine if dolphins were adversely impacted, capture-release health assessments were performed in heavily-oiled Barataria Bay (BB), Louisiana, and in Sarasota Bay (SB), Florida, a comparison site with no DWH oil contamination. Initial studies were conducted as part of a Natural Resource Damage Assessment (2011-2014). To specifically evaluate pulmonary health, transthoracic ultrasound techniques previously developed for dolphins managed under human care were applied to wild dolphins. Results showed that BB dolphins were approximately 5 times more likely to have moderate to severe lung disease than SB dolphins in 2011, the year following the spill (0.34 in BB versus 0.07 in SB). Concurrent pathology investigations of dead dolphins in the northern GoM also reported more pulmonary health abnormalities than expected. In 2013 and 2014, moderate to severe lung disease persisted among BB dolphins, and remained elevated relative to the prevalence in SB dolphins. More recent capture-release health assessments (2016-2018) showed long-term persistence and potential worsening of moderate to severe lung disease in BB dolphins, specifically in animals alive during the oil spill (prevalence of 0.20, 0.35, and 0.55 in 2016, 2017, and 2018, respectively). Long-term monitoring of dolphin populations is critical to fully understand the potential for and timeline of individual and population recovery from the impacts of a large-scale oil spill event. In particular, BB dolphins provide valuable insight into the long-lasting effects of oil and oil-related contaminants on animal, human, and ecosystem health.



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MAMMALNET PROJECT: CITIZEN AND OPEN SCIENCE AT THE SERVICE OF MAMMAL POPULATION MONITORING IN EUROPE

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Keywords: MammalNet, Open Science, Citizen Science, Disease Surveillance, African Swine Fever

Abstract Text

The main objective of project MammalNet (www.mammalnet.com), funded by the European Food Safety Authority (EFSA) is to assess the potential of collaborative, open citizen science to reinforce, as a complementary approach (e.g. www.enetwild.com), monitoring schemes on mammal distribution and abundance in Europe. This project has set up some technological tools (iMammalia, MammalWeb, Agouti) to facilitate collaboration between researchers and citizens interested in nature. A first phase has been carried out in four countries (Croatia, Germany, Poland, Spain) where we communication campaigns have been developed to promote the project and the use of the apps among different audiences. Recently, after this successful pilot experience, MammalNet is expanding to other regions that are of interest because of local difficulties in generating, collecting, or accessing wild mammal distribution data. This will be very valuable to improve the European capacities to reliably predict the distribution and abundance of wild mammals over the continent, and to contribute to common framework of wildlife integrated monitoring and management. Our IT tools also have the potential to be used for wildlife disease surveillance, for instance, by alerting to the presence of dead animals. In this regard, iMammalia is being used in the Balkans for wild boar carcass reporting, in collaboration with FAO and national organizations, as an early detection system for African swine fever. To expand MammalNet to new Countries, apps are continuously updated with new languages and species to our apps. For this purpose, it is essential to increase participation in the project, for collaborators in several countries to support and promote the project and apps among the main audiences: public, naturalists, wildlife professionals, hunters, high-school students and academics/researchers. Being part of this network will be mutually beneficial for all researchers, institutions, organization, and administrations aiming at improving integrated wildlife monitoring, coordinated at European scale.



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SURVEILLANCE OF WEST NILE VIRUS (WNV) IN LIVING WILD BIRDS FROM PELOPONNESE REGION IN SOUTHERN GREECE

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Keywords: Living Wild Birds, Peloponnese Region, Spatial Analysis, Surveillance, West Nile Virus

Abstract Text

A surveillance system for West Nile Virus (WNV) in living wild birds was implemented in Peloponnese Region of Southern Greece during 2019-2020. In the context of this program, wild birds were captured in natural ecosystems, suburban and urban areas, while oropharyngeal swabs or/and blood samples were collected. Tissue samples were also obtained from wild birds that were found dead on the road network. A total of 493 wild birds from 25 different species were tested for the presence of WNV. RNA extracts from oropharyngeal swabs, whole blood or brain tissue samples were subjected to reverse transcription followed by PCR. Spatial analysis was used in order to predict and to model WNV geographical distribution and to investigate spatial patterns. In particular, Maximum entropy modelling, used positive wild birds' locations to test environmental variables including climatic conditions, topography and human activities. The goodness of fit of the model predictions was evaluated by the mean area under the curve (AUC) of the receiver operating characteristic (ROC) curve. WNV RNA was detected in 46 of the 493 wild birds. Of the environmental parameters, altitude, vegetation, human population density and distance from water collections gave substantial contribution to the model. The model was considered to be sensitive and descriptive since ROC analysis gave an AUC value of 0.983 which exceeded the value 0.5 of random prediction. Due to the early detection of WNV circulation in living wild bird species, preventive measures were implemented for the protection of public health and consequently, human cases of WNV were not reported in Peloponnese Region during 2019-2020. Acknowledgement: We thankfully acknowledge the financial support of the Prefecture of Peloponnese (PELOPONISSOS AE).



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OCCURRENCE AND SIGNIFICANCE OF PSITTACOSIS CAUSED BY CHLAMYDIA PSITTACI IN GARDEN BIRDS IN SWEDEN.

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Keywords: Chlamydia Psittaci, Bird, Zoonosis, Great Tit, Pigeon

Abstract Text

Psittacosis is caused by the bacterium *Chlamydia psittaci*. Birds are the main reservoir but mammals, including humans, can also be infected. The last decade has seen an increase in human infections associated with bird feeders in southern Sweden but little is known about the occurrence of *C. psittaci* in garden birds in Sweden. In this study, prevalence of *C. psittaci* was investigated in tissues from 275 garden birds archived in the National Veterinary Institute's (SVA) biobank between 2009-2019; finches (107), thrushes (52), corvids (50), pigeons (37), titmice (21), woodpeckers (3) and weavers (5). Real-time PCR was used to detect *C. psittaci* in pooled liver and lung tissue. For positive birds, samples were sequenced, PCR was performed on feces and microscopic examination was conducted. Six (2.2 %) birds, found between March and October, were positive for *C. psittaci* in pooled samples and feces; three great tits (*Parus major*), two rock pigeons (*Columba livia*) and one common wood pigeon (*Columba palumbus*). Two great tits and the wood pigeon had inflammation in air-sacs, pancreas and coelom with intralésional *C. psittaci*. The rock pigeons died from pigeon paramyxovirus infection and one great tit was too decomposed to establish cause of death. *C. psittaci* genotype A, the cause of most human cases, was detected in the Great tits and the wood pigeon by sequencing the *ompA* gene. Genotype B, considered endemic in pigeons, was detected in the rock pigeons. In conclusion, the prevalence of *C. psittaci* found in dead Swedish garden birds was 2.2 % (95% CI: 0.8-4.7%), similar to previous studies. *C. psittaci* infection was the cause of death in half of the positive birds, which also had the lowest Ct-values for *C. psittaci* in the gut. This highlights the risk for human infection via infected garden birds, especially great tits and pigeons.



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THE IMPLEMENTATION GAP IN MANAGING EMERGING DISEASE RISKS IN THE WILDLIFE TRADE.

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Keywords: Wildlife Trade, Emerging Disease, Risk, Intervention, Implementation

Abstract Text

The nature of future pandemics under global change, and how that might be influenced by interventions is uncertain. It is clear that something must be done about risks emerging from the wildlife trade but less clear on how to get it done. It is a quite different task to accumulate evidence on the presence of pathogens, their locations in the supply chain and their spillover to hosts than on effective ways to prevent and mitigate the effects of emerging disease. This study combined literature reviews with key informant interviews to assess evidence available to nominate risk management interventions. There is a growing literature on the presence of infectious hazards in the wildlife trade supply chain that can be used for inference or analogy but there are few direct measurements of the effectiveness, acceptability, or sustainability of risk management interventions. The absence of systematic evaluations or impact assessments of risk management options precluded identifying the most effective, efficient, or acceptable risks reduction policies or practices. The nature, magnitude, and likelihood of unintended consequences remain poorly quantified, precluding risk-benefit analyses of interventions. Biases in the literature to a subset of species and pathogens makes the bulk of the trade unexamined. Lack of implementation science prevents comment on the relative feasibility, impact, or sustainability of interventions including trade bans, market closures, or sanitary regulations. Evidence outside of the wildlife trade suggest tools used to control domestic animal disease and food safety risks are reasonable to implement but their effectiveness and unintended consequences cannot be forecasted. Uncertainty, interconnectedness, unpredictability, and context-dependence in the wildlife trade make this a complex and wicked problem. Rapid diffusion of evidence-based solutions is paramount to prevent and mitigate new emerging diseases. Adaptive management that is multifaceted and multisolving should underpin actions while the implantation gap is closed.



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RE-EVALUATING IDEAL RELEASE WEIGHT FOR REHABILITATED HARBOR SEAL (*PHOCA VITULINA*) PUPS

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Keywords: Body Condition Index, Harbor Seal, Rehabilitation, Weight

Abstract Text

Harbor seal (*Phoca vitulina*) pups are commonly rehabilitated and released in the United States, Canada, and Europe. Studies have shown that harbor seal body mass at release is positively correlated with post-release survival, however, there is currently no body weight or body condition recommendation for release. To better understand harbor seal growth during rehabilitation and ultimately, to improve release guidelines to increase post-release survival, we retrospectively analyzed release weights, lengths, and body conditions for rehabilitated harbor seals in the United States. We analyzed data from the National Oceanic and Atmospheric Association's Marine Mammal Health and Stranding Response database from seals admitted into rehabilitation as pups between January 1, 2005 and December 31, 2020. We calculated body condition index (BCI) and used linear regression models to understand how weight and BCI varied regionally and temporally. We also compared morphometrics of rehabilitated seals to recently weaned, free-range pups. We found significant spatiotemporal variations in weight, length, and BCI for rehabilitated and released seals between the east and west coasts of the United States and among different years. Currently, there is no recommended criteria for body condition index for release. Body condition may be more valuable than weight alone as animals of similar weights can have different body conditions. Length of time in rehabilitation varies and body condition for animals with the same weight may vary depending on the amount of time animals have been in rehabilitation. Our findings could help develop pre-release body condition criteria for harbor seals that could include weight, length, and/or girth.



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EVALUATING BLACK BEAR (*URSUS AMERICANUS*) SURVIVAL AND RECOVERY FROM SARCOPTIC MANGE

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Keywords: Black Bear, Ivermectin, Sarcoptic Mange, Sarcoptes Scabiei, Wildlife Tracking

Abstract Text

The parasitic mite *Sarcoptes scabiei* causes mange in over 100 species of mammals by burrowing under the skin, triggering hypersensitivity responses that can alter animals' behavior and result in extreme weight loss, secondary infections, and even death. Since the 1990's, sarcoptic mange has increased in incidence and geographic distribution in Pennsylvania black bear populations including expansion into surrounding states. However, recovery from mange in free-ranging wildlife has rarely been evaluated. We hypothesized that bears would be unlikely to survive and fully recover from mange without treatment. Following the Pennsylvania Game Commission's standard operating procedures, treatment consisted of one subcutaneous injection of ivermectin. To evaluate black bear survival and recovery from mange, from 2018 – 2020 we fitted 59 bears with GPS-collars, including 43 with mange, to track bear movements and recovery for up to three years. Bears were collared in triplicates according to sex and habitat, consisting of one bear without gross evidence of mange (healthy control), one bear with cytologically confirmed sarcoptic mange treated with ivermectin when collared, and one untreated bear with cytologically confirmed sarcoptic mange. Bear activity was monitored via GPS and activity sensor, and bears were re-evaluated for signs of mange during annual den visits, if recaptured during the study period, and after mortality events. Disease status and recovery from mange was determined based on outward gross appearance and presence of *S. scabiei* mites from skin scrapes. Of the 37 mange bears with known recovery status, 78% fully recovered regardless of treatment category, with 88% recovered after treatment (15/17) and 70% recovered without treatment (14/20). However, non-recovered status did not indicate mortality, and mange-related mortality was infrequent (2/37 bears). Overall, more bears were able to recover from mange than expected irrespective of treatment, potentially indicating a need for re-evaluation of the mange wildlife management paradigm.



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INVESTIGATION ABOUT MORTALITY IN A HEDGEHOG'S POPULATION IN NORTHERN ITALY

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Keywords: Coronavirus, Hedgehog, Italy, Reovirus, Salmonella Spp.

Abstract Text

Western European hedgehog (*Erinaceus europaeus*) is a common synanthropic mammal. It could be involved in maintenance and transmission of potentially zoonotic pathogens. In Ferrara province (Emilia Romagna region–North Italy), since the end of 2019, an increase of hedgehog's mortality was recorded. Necropsy was carried out on 88 hedgehogs. In most cases, no significant lesions were found, but in the latest cases in 2021 diffused liver necrosis, catarrhal enteritis, enteric/pulmonary hemorrhagic suffusions were observed. The diffused hemorrhages suggested a potential anticoagulant poisoning currently under investigation. Actually in one hedgehog traces of Brodifacoum and Bromadiolone were found. In few cases pulmonary worms of *Crenosoma striatum* species, and ticks of Ixodidae family were identified. Consequently, presence of tick-borne pathogens was investigated and cases of babesiosis (n=1) and rickettsiosis (n=2), one of these in coinfection with Tick Borne Encephalitis virus, were detected. All hedgehogs were tested for *Leishmania* spp. with negative results. Viscera were submitted to a panel of bacteriological and virological analyses: 34 resulted positive to *Salmonella*, in particular *S. enteritidis* (n=28) and *S. veneziana* (n=6). Analyses to detect canine distemper virus (CDV), Coronavirus and Reovirus are still in progress. Currently 1 sample resulted positive to CDV, 19 to Coronavirus (*Erinaceus betacoronavirus-EriCoVs*) and 11 to Reovirus. In 3 animals, a coinfection between Coronavirus and Reovirus was found. Moreover, EriCoVs was isolated in almost half of the hedgehogs affected by salmonellosis, and few coinfections between Reovirus and *Salmonella* was also recorded. The synergic effect of these pathogens related to anatomopathological findings could explain the increased mortality observed especially in 2021. However, toxicological and poisoning risk should also be further investigated. Present results suggest a potential role of hedgehogs as reservoir of zoonotic pathogens, including some viral agents, raising relevant issues that should be considered in the management of these species at the human-wildlife interface.



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PATTERNS OF GAMMAHERPESVIRUS REACTIVATION IN GENITAL TRACT LINKED TO STRESSORS IN EUROPEAN BADGERS (MELES MELES)

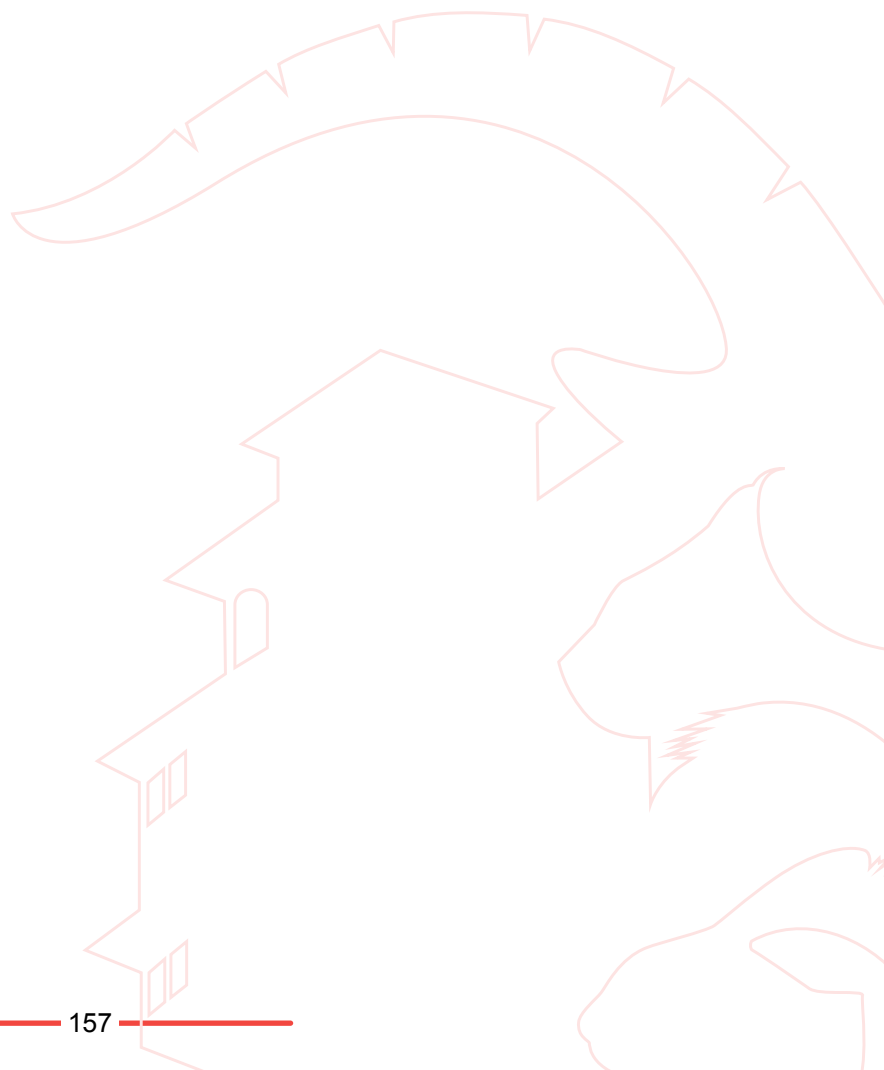
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Keywords: Sexually Transmittable Infections, Wildlife Disease, Epidemiology, Seasonal Effect, Weather Conditions

Abstract Text

Gammaherpesvirus reactivation can promote diseases or impair reproduction. Understanding reactivation patterns and associated risks of different stressors is therefore important. Nevertheless, outside the laboratory or captive environment, studies on the effects of stress on gammaherpesvirus reactivation in animals are lacking. Here we used Mustelid gammaherpesvirus 1 (MusGHV-1) infection in European badgers (*Meles meles*) as a host-pathogen wildlife model to study the effects of a variety of demographic, physiological and environmental stressors on virus shedding in the genital tract. We collected 251 genital swabs from 150 free-ranging individuals across 3 seasons and screened for MusGHV-1 DNA using PCR. We explored possible links between MusGHV-1 DNA presence and 7 variables reflecting stressors, using logistic regression analysis. The results reveal different sets of risk factors between juveniles and adults, likely reflecting primary infection and reactivation. In adults, virus shedding was more likely in badgers in poorer body condition and younger than 5 years or older than 7; while in juveniles, virus shedding is more likely in females and individuals in better body condition. However, living in social groups with more cubs was a risk factor for all badgers. We discuss possible explanations for these risk factors and their links to stress in badgers.





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INTERACTION PATTERNS BETWEEN WILDLIFE AND CATTLE ASSESSED BY CAMERA TRAPS REVEAL CHANCES FOR MYCOBACTERIA TRANSMISSION IN ATLANTIC HABITATS

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Keywords: Camera-Traps, Interactions, Non-Tuberculous Mycobacteria, Tuberculosis, Wildlife-Livestock Interface

Abstract Text

Interactions taking place between sympatric wildlife and livestock may contribute to interspecies transmission of mycobacteria included in the *Mycobacterium tuberculosis* complex or non-tuberculous mycobacteria, leading to the spread of agents responsible for relevant infections or for causing interference in the diagnosis of tuberculosis. The aim of this study was to characterize the spatiotemporal patterns of interactions between wildlife and cattle in the Basque Country, an Atlantic region from the Iberian Peninsula. Camera traps were set in 67 points during a one-year period (January to November 2017) in three farms with history of *M. bovis*-infected cattle and/or tuberculin skin test false positive reactor cattle due to non-tuberculous mycobacteria. For six species or group of species of wild mammals, the frequency and duration of visits, and the number of individuals per visit were analysed through generalized linear mixed models. The season, type of place, type of point and period of the day were the explanatory variables. A total of 1293 visits were recorded during 2741 camera days of observation. Only 23 visits showed direct contacts with cattle, suggesting that mycobacteria transmission at the wildlife-livestock interface, if any, would occur mainly through indirect interactions. A noteworthy diversity in interaction patterns was observed among the studied species. Cattle pastures represented the most appropriate habitat for interspecies transmission of mycobacteria, and badgers' latrines could represent a potential hotspot for mycobacteria circulation between badger, wild boar, fox and cattle. According to the interaction patterns observed and previous data on mycobacteria prevalence among wildlife from the Basque Country, badger, wild boar, fox and small mammals could be the most likely species or group involved in the epidemiology of mycobacterioses in the study area. Wildlife monitoring with camera trapping combined with epidemiological information can be a useful tool to design suitable disease control strategies.



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DIFFERENTIAL RESPONSE TO ANTHROPOGENIC DISTURBANCE BY CAVE-DWELLING BATS: AN ECO-IMMUNOLOGICAL APPROACH

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Keywords: Bat Disease Ecology, Eco-Immunology, Multi-Pathogen System

Abstract Text

Caves are high-quality roosts that subsidize bat diversity in forest fragments that otherwise may decline over time. However, habitat degradation may reduce individual health by forcing bats to forage in poor-quality habitats or by increasing commuting costs to reach suitable foraging areas. Thus, apparently healthy cave-roosting bat populations in modified landscapes may suffer from chronic stress with consequences in downstream effects on health, making them more susceptible to pathogens, thereby enhancing the spread of diseases. While some bat species may acclimatize to repeated stressors and even thrive in human-modified habitats, other species may experience higher stress levels that subsequently impair immunity. Due to their high species richness, bats display wide variation in morphology, foraging behavior, and habitat use, making them a good model to assess the physiological effects of human disturbance on wildlife. We conducted our study in 16 caves in Costa Rica along a gradient of human disturbance ranging from undisturbed caves in protected areas, to caves subject to high levels of disturbance surrounded mostly by agriculture, livestock, and other human-dominated landscape. Surveys were repeated in the dry and wet seasons. We collected samples from 1230 adult individuals, representing 12 species from four families with diverse ecological niches. We evaluated markers of physiological stress (neutrophil-to-lymphocyte ratio), downstream health measures (body condition and white blood cell counts), and innate (lysozyme) and adaptive (IgG) immune markers. We will contrast these results with infection prevalence of four common and divergent pathogens: Bartonella (242/1230), Leptospira (61/192), Trypanosoma (393/1230), and microfilaria (82/1230). Preliminary data shows divergent patterns among species to pathogen prevalence and immune markers. Factors that may explain this variation, such as species identity, ecological traits, season, sex, and human perturbation, will be examined. This work provides insight into the complex patterns of the immune function of wild bats in changing environments.



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USING WHOLE-GENOME SEQUENCING AND A ONE HEALTH APPROACH TO UNDERSTAND THE EPIDEMIOLOGY OF SALMONELLA AND ASSOCIATED ANTIMICROBIAL RESISTANCE AT THE HUMAN, WILDLIFE, ENVIRONMENTAL, AND LIVESTOCK INTERFACE IN SOUTHERN ONTARIO

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Keywords: Antimicrobial Resistance, Salmonella, Whole-Genome Sequencing, Raccoons, Zoonoses

Abstract Text

Non-typhoidal Salmonella infections represent a substantial burden of illness to human health, and the increasing prevalence of antimicrobial resistance among these infections is a growing concern. Using a combination of whole-genome sequencing data of isolates from human, raccoon, livestock and environmental sources, and epidemiological modeling, our objective was to assess for evidence of transmission of Salmonella and associated antimicrobial resistance determinants between these different sources. Outputs from bioinformatics analyses were used in logistic regression models to assess for potential associations between source type and the occurrence of select resistance genes and plasmid replicons. A total of 608 isolates were obtained from the following sources: human (n=58), raccoon (n=92), livestock (n=329), and environment (n=129). Population structure based on 3002-loci cgMLST suggests that transmission of Salmonella and associated plasmid types and resistance genes between humans, livestock, and water samples may be occurring. In contrast, none of the Salmonella isolates from raccoons clustered together with human isolates. Resistance genes of public health importance, including AmpC producers (i.e., blaCMY-2) were identified in human, livestock, and environmental sources, but not in raccoons. In addition, quinolone resistance proteins (e.g., qnrS1, qnrB20) were only identified in water and human samples, but not in livestock or raccoon isolates. Some plasmid incompatibility groups were strongly associated with certain sources; some were only isolated from raccoons and soil samples, whereas others were only isolated from human and livestock sources. Collectively, our findings suggest that rural populations of raccoons on swine farms in the Grand River watershed are likely not major contributors to antimicrobial resistant human Salmonella infections in this region. Further research, including a comprehensive examination of all human cases (including phenotypically susceptible ones), and examination of additional raccoon populations (urban and rural) may help to provide additional insight on the role of raccoons in human Salmonella infections.



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EVALUATING ASSOCIATIONS BETWEEN ENVIRONMENTAL PARAMETERS AND *OPHIDIOMYCES OPHIDIICOLA*, THE CAUSATIVE AGENT OF OPHIDIOMYCOSIS (SNAKE FUNGAL DISEASE)

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Keywords: Environmental Parameters, Geographic Information Systems (GIS), *Ophidiomyces Ophidiicola*, Snake Fungal Disease

Abstract Text

Ophidiomyces ophidiicola is the causative agent of ophidiomycosis (snake fungal disease, SFD) and is thought to persist in the soil as a saprobe. This study aimed to identify relationships between environmental factors and the presence of *O. ophidiicola* on snakes, as detected using qPCR. The complete dataset included qPCR results and geographic location from 2104 snakes of 92 species, sampled across the contiguous United States and Puerto Rico during 2008-2019. 391 snakes were positive for *O. ophidiicola* and 1713 were negative. The locations were geocoded using geographic coordinates of latitude and longitude. At each position, landscape characteristics were obtained from the National Land Cover Database, National Resources Conservation Service, and the Harmonized World Soil Database, and extracted using geographic information systems (GIS). Univariate and multivariate logistic regression analyses were performed to assess the odds of *O. ophidiicola* detection based on various landscape variables. Lower values of available water storage, mean elevation, calcium carbonate content, pH, base saturation, total exchangeable bases, and the cation exchange capacity of both soil and clay were found to increase the odds of *O. ophidiicola* detection; increasing values of albedo were associated with higher odds of *O. ophidiicola* detection. The findings of this study suggest that *O. ophidiicola* presence may be associated with certain habitat conditions. Further work is required to investigate how these relationships may affect the growth and survival time of this fungus, as well as its infectivity and pathogenicity.



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PREVALENCE OF HANTAVIRUS IN BANK VOLES AND HUMANS: THE EFFECT OF WILDLIFE AND ENVIRONMENTAL FACTORS

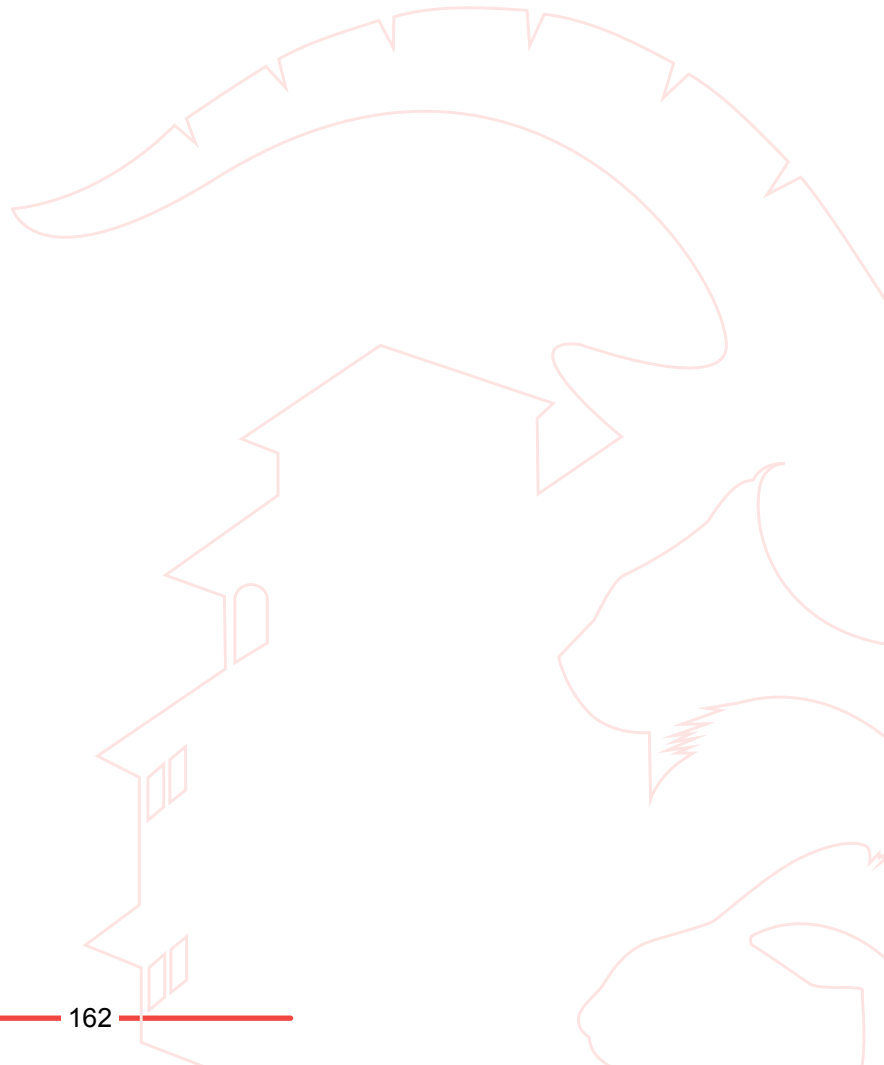
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Keywords: Zoonoses, Puumala Orthohantavirus, Juvenile Dilution Effect, Predators, Rodent Diversity

Abstract Text

Wildlife originated zoonoses are posing an increasing risk to humans. Understanding the factors that affect the pathogen transmission dynamics in the host population level is crucial to predict and prevent the risks that the pathogens cause to humans. Here we study the three mechanisms that may affect zoonotic Puumala orthohantavirus (PUUV) transmission, influencing the infection prevalence in the reservoir rodent host, the bank vole (*Myodes glareolus*) populations and infection incidence in humans. Specifically, we study the role of (i) rodent community composition related diluted effect, (ii) juvenile dilution effect and (iii) predator related dilution effect in PUUV infection prevalence in bank vole populations and infection incidence in humans in the region. We used 5-year rodent trapping and PUUV infection in bank vole data, collected from 30 sites and human PUUV infection incidence data in the same areas (i.e., 24 administrative regions). Our results support Juvenile dilution effect for PUUV prevalence in bank voles and PUUV incidence in humans. In addition, we found that PUUV prevalence in bank voles and PUUV incidence in humans was negatively associated with predators rather, whereas rodent diversity did not have an effect. Our results suggest that predator abundance can benefit human health through the control of pathogen prevalence and the number of infected individuals in wildlife.





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TEMPORAL AND SPATIAL PATTERNS IN CANINE DISTEMPER VIRUS CASES IN WILDLIFE DIAGNOSED AT THE SOUTHEASTERN COOPERATIVE WILDLIFE DISEASE STUDY (SCWDS), 1975-2019

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Keywords: Carnivore, Disease Ecology, Distemper, Model, Virus

Abstract Text

Canine distemper (CDV) is an important infectious disease that can affect many mammal species, particularly carnivores, and is responsible for substantial carnivore population declines. The primary objective of this study was to identify long-term spatial and temporal patterns in CDV cases in wildlife diagnosed at the Southeastern Cooperative Wildlife Disease Study (SCWDS). Additionally, we aimed to identify how outbreaks in different species may be related. Finally, we aimed to identify spatial patterns of infections with potential associations with human activity. Analysis was conducted on passive surveillance diagnostic data of wild mammals diagnosed with CDV that were submitted to SCWDS between January 1975 and December 2019. Overall, 964 cases were submitted to SCWDS from 17 states that were identified as CDV positive, comprising raccoons (n=646), gray foxes (n=254), striped skunks (n=33), coyotes (n=18), red foxes (n=4), gray wolves (n=3), black bears (n=3), two mink, and one long-tailed weasel. Raccoon and gray fox case data from the state of Georgia (n=441) were selected for further analysis. An auto regressive integrated moving average model used the numbers of gray fox CDV cases from the previous two months and of raccoon cases in the current month to predict the numbers of gray fox cases in the current month. There were temporal trends in CDV cases for both species, with cases more likely to occur during the breeding season. Cases were more likely to occur in areas of medium to high human population density. There are enough potential relationships suggested from this passively collected data which would support more comprehensive sampling of wild carnivores over time and space to try to elucidate spillover trends between species, particularly in suburban areas. This could inform decision making regarding vaccination and other strategies aimed at reducing transmission among both domestic and wild animals.



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EXPLORING THE USE OF THE ERYTHROCYTE SEDIMENTATION RATE AS AN INFLAMMATORY MARKER FOR FREE RANGING WILDLIFE - A CASE STUDY IN AFRICAN BUFFALO (*SYNCERUS CAFFER*)

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Keywords: Buffalo, ESR, Inflammatory Markers, Respiratory Disease, Anaplasma

Abstract Text

Measuring inflammatory markers is critical to evaluating both recent infection status and overall human and animal health; however, there are relatively few techniques of detecting inflammation among wildlife that do not require specialized equipment or personnel. Such techniques are useful in that they help determine individual and population-level inflammatory status without the highly specialized personnel and equipment used in more specific assays, such as polymerase chain reaction (PCR), fluorescence assays, or enzyme-linked immunosorbent assays (ELISA). One such technique, known as the erythrocyte sedimentation rate (ESR), is a measure of how quickly erythrocytes, or red blood cells, settle in serum. ESR is simple, inexpensive, and can be performed without specialized equipment; therefore, ESR has great potential as an inflammatory marker in wildlife field studies. We took advantage of a well-studied population of African buffalo (*Syncerus caffer*) to understand the utility of ESR in an important wildlife population. We first evaluated whether there was a correlation between ESR and other known markers of inflammation in African buffalo. We found that a faster ESR was marginally correlated with increased total globulin levels. We also found that a slower ESR was significantly correlated with increased RBC and albumin levels. We then evaluated whether or not ESR correlated to the incidence of five respiratory pathogens and infection with two tick-borne pathogens in African buffalo. Our results suggest that elevated ESR is associated with the incidence of bovine viral diarrhea virus infection, as well as parainfluenza virus and *Mannheimia haemolytica* infections, and current *Anaplasma marginale* and *Anaplasma centrale* co-infection. These findings suggest that ESR is a useful field test as an inflammatory marker in individuals and herds, helping us better monitor overall health status in wild populations.



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RETROSPECTIVE STUDY ON AVIAN PARAMYXOVIRUSES IN WILD BIRDS IN THE UNITED STATES IDENTIFIES SEVERAL PUTATIVE NEW SPECIES

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Keywords: Avian Paramyxoviruses, MinION, Phylogeny, Wild Birds

Abstract Text

Avian paramyxoviruses (APMV) have been isolated from wild and domestic birds from around the world. The International Committee on Taxonomy of Viruses (ICTV) currently defines 21 different APMV species, with Avian orthoavulavirus 1 viruses (APMV-1; a.k.a., Newcastle disease virus) being the most frequently studied due to their economic burden in the poultry industry. Less is known about other APMV species because of their lower impact on domestic poultry, but these have been implicated in respiratory disease and reproductive problems in wild and domestic birds. Additionally, there is limited knowledge on the genetic diversity and cross protection of APMVs circulating in wild birds. The goal of this project was to use MinION sequencing to genetically characterize APMVs isolated from blue-winged teal (*Anas discors*), mallard (*A. platyrhynchos*), and ruddy turnstone (*Arenaria interpres*) swabs collected in 2016–2018 in the United States. Total RNA was extracted from 37 egg-cultured, influenza-negative, hemagglutination-positive samples. Multiplexed MinION libraries were prepared using a random strand-switching approach. Raw reads were basecalled, trimmed, demultiplexed, and taxonomically classified and genome sequences were built using a reference-based consensus building method or a de-novo assembly. Thirty five samples had complete polymerase coding sequences that were speciated using the ICTV phylogenetic methodology. The phylogenetic analysis identified APMV-1, -4, -6, -8, and several putative novel species in the samples. Additionally, co-infections of APMVs were identified in a subset of the samples. Complete genomic coding sequences from all putative species and all other APMV species detected in this study were obtained, which allowed for further analysis of the fusion gene for genotyping and cleavage site identification for virulence prediction. This study expands the knowledge of APMV diversity and highlights the benefits of complete viral genome sequencing and characterization of viruses circulating in wild birds, which can be applied to future avian and non-avian studies



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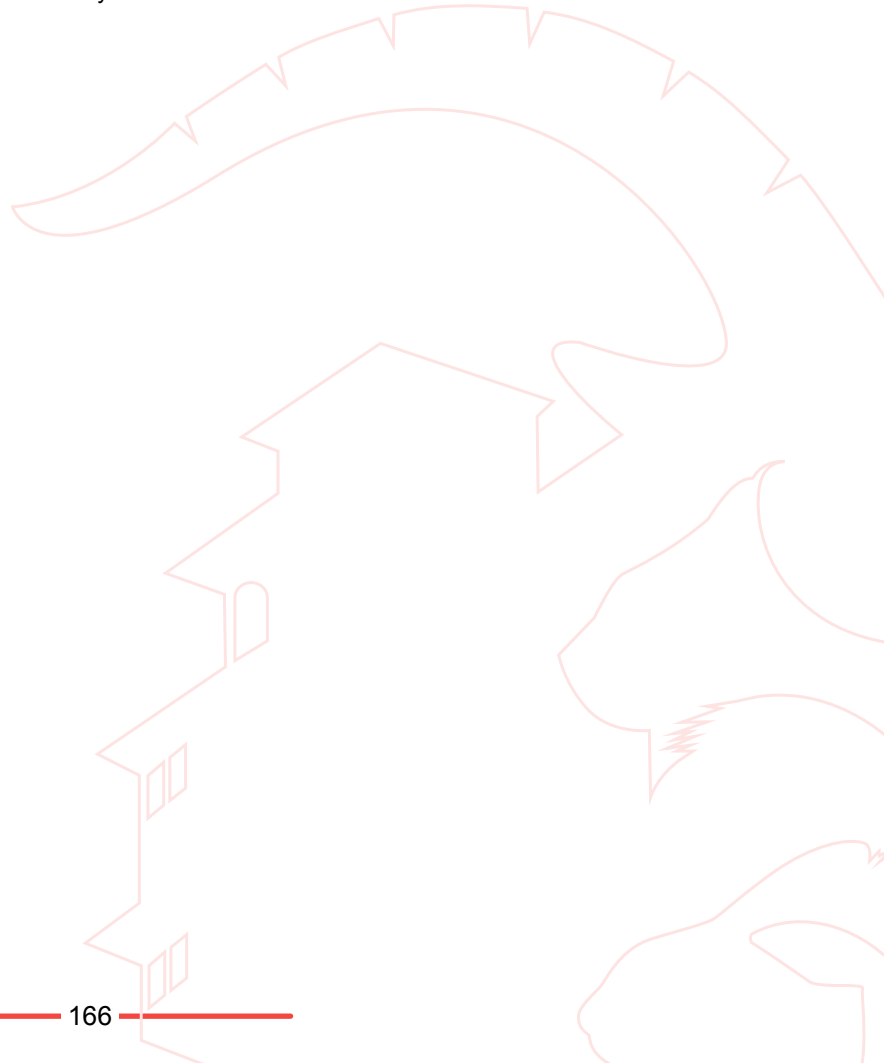
STABLE PREVALENCE OF COXIELLA BURNETII IN WILDLIFE AFTER A DECADE OF SURVEILLANCE IN THE BASQUE COUNTRY (NORTHERN SPAIN)

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Keywords: Birds, Coxiella Burnetii, Q Fever, Ungulates, Zoonoses

Abstract Text

Coxiella burnetii is an obligate intracellular zoonotic bacterium widespread in nature, which causes Q fever in animals and humans. The most common sources of human infection are domestic ruminants, but wildlife could also act as reservoir. In this study, tissues from 660 wild ungulates and 86 wild birds collected between 2011 and 2019 in the Basque Country (northern Spain) were analysed. DNA was extracted from spleen using a commercial kit and subjected to real-time PCR (IS1111 gene). *C. burnetii* DNA was detected in 6.9% (6/87) of roe deer (*Capreolus capreolus*), 1.8% (9/488) of wild boar (*Sus scrofa*) and 2.4% (2/85) of Iberian red deer (*Cervus elaphus*). All birds tested negative, including carrion species. The prevalence found in roe deer was significantly higher compared to that detected in wild boar ($2 = 7.4$, $p=0.006$). In order to assess whether wild species share genotypes with domestic ruminants, and whether these genotypes are related to human cases of Q fever, the identification of the genotypes of *C. burnetii* in these 17 animals is in progress. When the results of this study were compared with those obtained in the period 2001-2006 in the same area [5.1% of roe deer (4/78), 4.3% of wild boar (4/93), 11.0% of vultures (*Gyps fulvus*) (1/9) and 14.3% of black kites (*Milvus migrans*) (1/7) positive to the presence of *C. burnetii* DNA (Astobiza et al., 2011)], no significant differences were observed in the prevalence of *C. burnetii* in any of the wildlife species predominant in the area between both study periods. These results indicated stability in the prevalences observed. However, continuous surveillance is needed to monitor any future changes in the reservoir role of roe deer and wild boar associated to the population increase of both species observed in the study area in recent years. Funded by INIA-RTA2017-000055-C02-01





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327 DETECTION OF LACTOCOCCUS GARVIEAE IN FERAL FISH AND ENVIRONMENTAL DNA OF FOUR CALIFORNIA LAKES

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Keywords: California, Fish, Lactococcus, Outbreak

Abstract Text

Lactococcus garvieae is a gram-positive bacterium and the etiological agent of lactococcosis, an emergent disease of feral and captive fish worldwide. Outbreaks have resulted in significant economic losses in the aquaculture industry, specifically during the summer months. In 2020, *L. garvieae* was diagnosed for the first time in cultured trout in California, USA. Following the diagnosis, the pathogen was isolated in three other facilities in California. However, the source of this agent and presence in wild fish and the environment in California is unknown. This project aims to investigate the presence of *L. garvieae* in feral fish and environmental samples, specifically water and substrate, of four lakes near the affected facilities. During September 2020, 346 fish and 40 environmental samples were collected from four lakes in Victorville, California and analyzed for presence of *L. garvieae*. *Lactococcus garvieae* was detected in 2/4 and 4/4 of the lakes water and soil environmental DNA (eDNA) using species specific quantitative PCR (qPCR), respectively. Bluegill (n=140), largemouth bass (LMB) (n=119), catfish (n=48), prickly sculpin (n=12), green sunfish (n=4), carp (n=9), trout (n=11) and black crappie (n=3), were collected from the different lakes and subjected to necropsy and sample collection. Brain and posterior kidney samples were collected and inoculated in agar media for detection of *L. garvieae*. Additionally, brain and posterior kidney were subjected to molecular diagnosis. Although *L. garvieae* DNA was detected in several fish species, bluegill and largemouth bass tested with the highest prevalence by qPCR; however, *L. garvieae* was only isolated from two LMB fish. Interestingly, the recovered isolates were distinct from the virulent isolates recovered from rainbow trout using multilocus sequence analysis. Future characterization of the *L. garvieae* detected in environmental samples is necessary to gain a better understanding of the presence and distribution of pathogenic *L. garvieae* in California.



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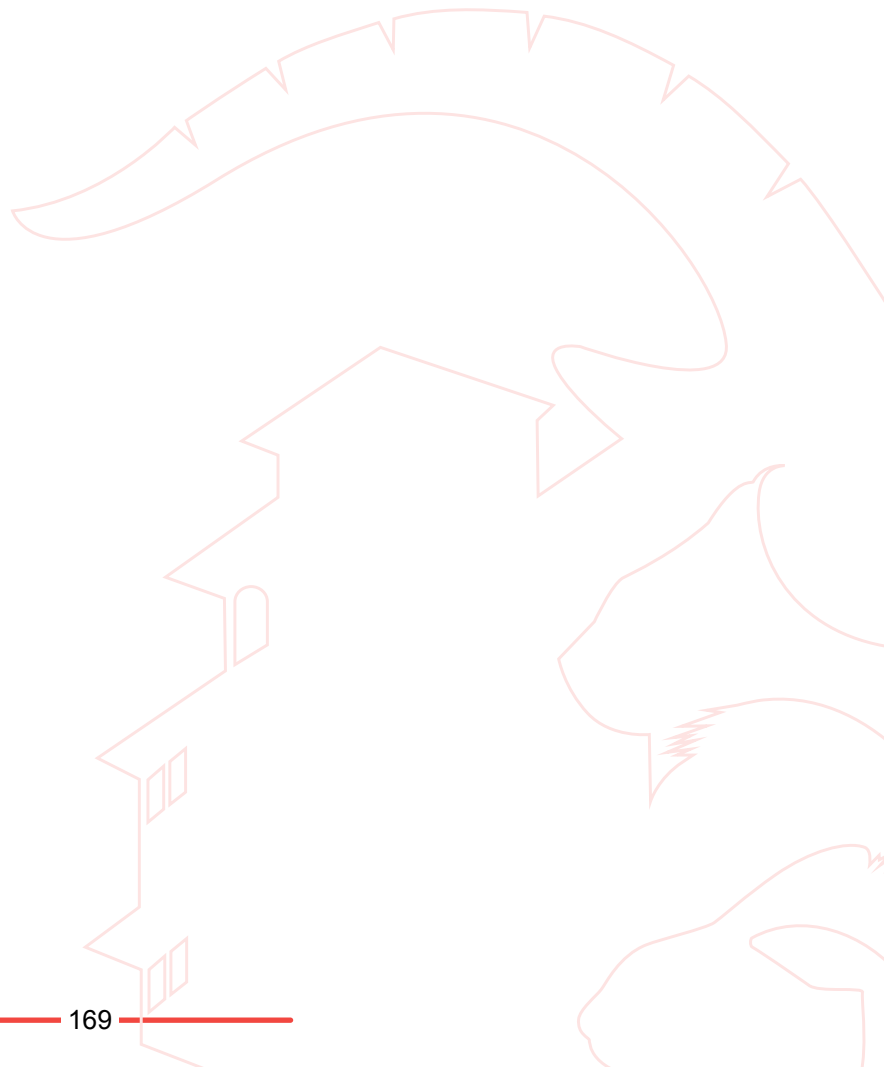
4 ASSESSING STRAIN-SPECIFICITY IN ACQUIRED RESISTANCE RESPONSE TO BATRACHOCHYTRIUM DENDROBATIDIS

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Abstract Text

Chytridiomycosis, an infectious disease of amphibians caused by the fungus *Batrachochytrium dendrobatidis* (Bd), poses an imminent conservation threat. The global emergence of Bd has led to mass mortality events in many species, even resulting in ~90 extinctions. Thus, novel management tools are urgently needed. Exposure to filtrate from Bd cultures can induce partial immunity against live Bd, suggesting the potential for vaccination. However, little is known about immunity to Bd, especially regarding strain specificity. We hypothesized that induced resistance could be specific to the vaccinating strain, and therefore provide weaker protection against other strains. To evaluate strain specificity of this induced immune phenotype, we conducted a 3x2 factorial experiment in which we crossed vaccination and live infection treatments with two Bd strains that differ in pathogenicity. Specifically, we exposed adult Cuban tree frogs, *Osteopilus septentrionalis*, to either filtrate isolated from a California strain, the global pandemic strain (Panama), or an artificial spring water sham-control. After twelve days of vaccination, we then exposed frogs to 9×10^5 zoospores of live Bd from either the California or Panama strain. After 16 days, we swabbed the frogs and used qPCR to quantify infection status and zoospore count. Using a zero-inflated negative binomial model, we found a significant interaction between vaccination strain and infection strain on Bd loads. Specifically, frogs vaccinated with the California-isolated strain and then exposed to the Panama-isolated strain had lower loads than frogs vaccinated with the Panama strain or the sham treatment. These results suggest that the magnitude of induced resistance is sensitive to the identities of the vaccinated and infecting strains. In addition, these results contradict the hypothesis that vaccination provides strain-specific protection. Follow up experiments are needed to determine the mechanisms underlying resistance phenotypes and the asymmetric cross-resistance observed here.





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315 CALIFORNIA SEROGROUP VIRUSES: REVEALING THE RESERVOIR POTENTIAL OF CERVIDS IN ARCTIC AND SUBARCTIC ECOSYSTEMS.

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Keywords: California Serogroup Viruses, Cervids, Vector-Borne Disease, Mosquitoes, Arctic

Abstract Text

As annual temperatures continue to rise in the Arctic, vector-borne pathogens have become a growing wildlife and public health concern. California (CAL) serogroup viruses are mosquito-borne viruses of zoonotic importance in North America. In a recent survey, almost one third of people in Alaska had antibodies to these viruses, suggesting that they may be widespread in the North. Wildlife reservoirs and sentinels have yet to be identified in Arctic and subarctic ecosystems.

Blood and/or sera collected from caribou in the Yukon, Northwest Territories, Nunavut, and Nunavik were tested with a competitive ELISA for antibodies to CAL serogroup viruses. Seroprevalence was 45% in the Yukon (68/152), 83% in the Northwest Territories (225/272), 80% in Nunavut (58/73), and 8% in Nunavik (4/50). A plaque reduction neutralization test on a subset of positive samples from the Northwest Territories and Nunavik indicated that animals had antibodies to Jamestown Canyon virus (JCV).

Reservoir potential was determined with an experimental infection study with a captive reindeer herd at the University of Alaska Fairbanks. Animals were tested for antibodies to CAL serogroup viruses, and all but 3 of 19 yearlings seroconverted following natural exposure in their first or second summer of life. Six animals were exposed to JCV injected subcutaneously over the shoulders to investigate antibody response, viremia, tissue predilection sites, and health effects. All animals were asymptomatic during the study. Naïve animals had a detectable antibody response 5 days post infection. Similarly, JCV was detected in the blood of animals on day 1 and 5 post infection. Tissues that contained viral RNA included the parotid lymph node, spleen, obex, and uterus. Viral RNA in the obex suggests that the infection can progress to the nervous system (similar to human infections) and the development of viremia verifies that these animals may serve as reservoirs.



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228 FLAVIVIRUS INFECTION OF WILD BIRDS IN A WILDLIFE-LIVESTOCK INTERACTION GRADIENT IN CONTINENTAL IBERIA

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Keywords: Emerging Zoonosis, Flavivirus, Horses, Vector-Borne Diseases, Wildlife-Livestock-Human Interface

Abstract Text

Flaviviruses of the Japanese Encephalitis complex such as West Nile (WNV) and Usutu (USUV) viruses are emerging as causes of viral meningoencephalitis cases in animals and humans in Spain. Wild birds are natural reservoirs for WNV and USUV and, in liaison with competent mosquitoes, responsible for their maintenance and transmission. However, the intimate link between wild birds, domestic animals (horses), mosquitoes and humans in continental Spain is not yet well understood. With the goal of better understanding the ecology of flaviviruses at the wildlife-livestock-human interface, we captured birds in 2018/2019 in a decreasing wildlife-livestock interaction gradient in 5 horse farms. Birds were captured with mist nets at three sites per farm: (1) the farm; (2) a site 500-1,000m away from the farm; and (3) a site at a 3-5 km distance from the farm without livestock. We collected blood from the brachial vein, oral and cloacal swabs, and growing feathers from captured birds (N=580). The presence of Flavivirus antibodies in bird sera was estimated by a multispecies blocking ELISA that is highly specific for WNV, whereas a duplex quantitative real-time reverse transcription PCR allowed detecting Flavivirus infection. Twenty-eight of 451 sera were positive (6.2%) and the highest proportion of positives occurred in the farms (8.1%) in comparison to sites 2 and 3 (4.6% and 5.8%, respectively). Four of the 503 PCR tests (feathers/swabs) were positive (0.8%) but only one sample (*Turdus merula*) could be confirmed by sequencing as USUV (99.6% homology). PCR positive birds were only found in sites 1 and 2. These findings confirm the active circulation of flaviviruses in continental Spain and, especially, close to horse farms. The interaction with wild birds is high in the environment of the farms, so these results show that horses (and humans) are at risk of developing viral meningoencephalitis caused by WNV.



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114 WILDLIFE DIVERSITY AMONG VILLAGES IN CHAD, AFRICA WITH VARIOUS LEVELS OF DRACUNCULUS MEDINENSIS (GUINEA WORM) INFECTIONS IN DOMESTIC DOGS: INSIGHTS INTO POSSIBLE RESERVOIRS?

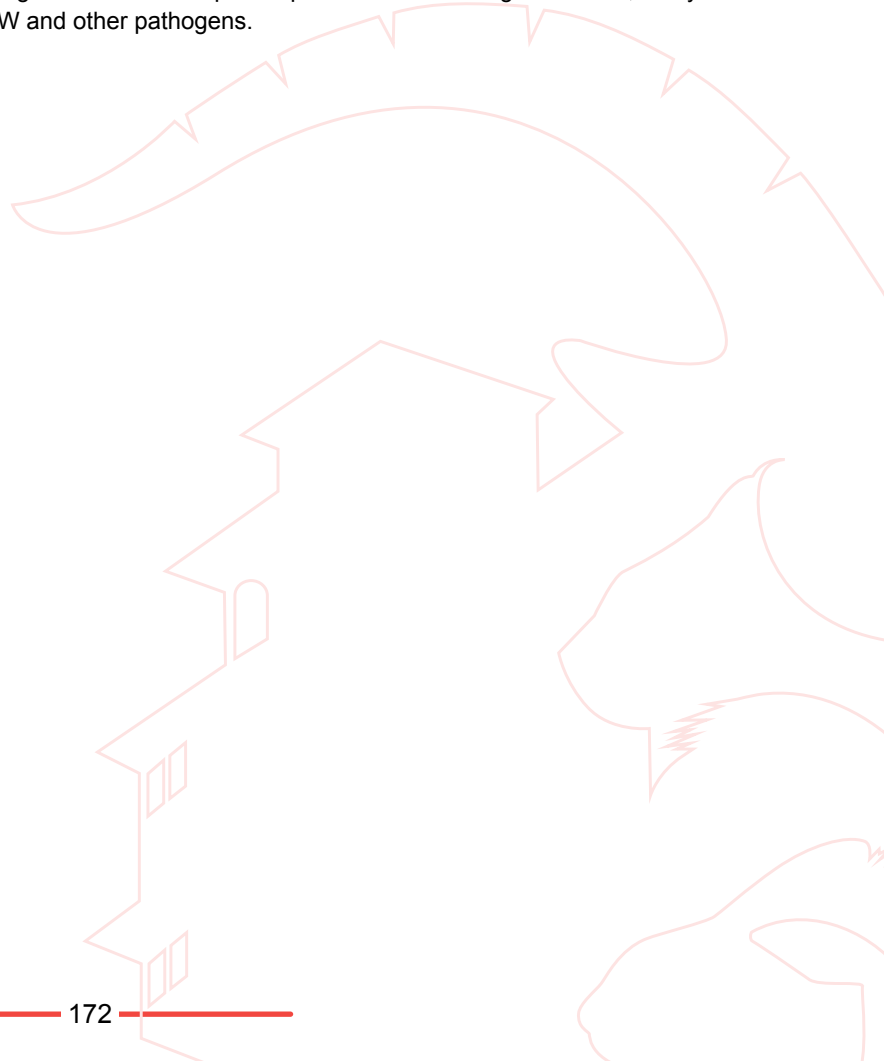
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Keywords: Game Camera, Occupancy Model, Transmission, Wildlife Host

Abstract Text

Guinea worm disease (dracunculiasis) is a painful infection caused by the filarial nematode *Dracunculus medinensis*. The Guinea Worm Eradication Program (GWEP) has reduced human cases from 3.5 million in 21 countries in 1986 to only 27 in 6 countries in 2020. Since 2012, Guinea worm (GW) infections have increased in domestic dogs (and cats), but have also been reported in baboons, wild cats, and one leopard. These infections have not followed typical epidemiology associated with water-borne transmission, suggesting alternative routes (e.g., paratenic/transport hosts) may be involved in transmission. We aimed to determine if possible wildlife hosts of GW vary in presence or diversity among villages with different levels of GW infections in domestic dogs. Seven villages in Chad were chosen for game camera placement based on surveillance intensity, accessibility, spatial independence, and GW endemicity (3 enzootic, 3 sporadic transmission, and 1 negative village). Eight game cameras were deployed at each village and recorded over three sessions in 2019: February-May, June-August, and September-November. All individuals detected were identified to the most specific taxonomy possible. Preliminary analysis was performed through frequency charts, which revealed tanzania monkeys (*Chlorocebus tantalus*) were detected highly frequently in enzootic villages, commonly in sporadic villages, and were absent from the negative village. These data suggest tanzania monkeys should be investigated as a possible GW wildlife host. Carnivore (e.g., jackals, genet, serval, wildcat, fox, etc.) detections were stable across villages; however, there may be other factors that would allow certain carnivores to host GW in one village but not another, so these results do not rule them out as possible hosts. Future analyses include creating occupancy models for selected wildlife species. Results will provide valuable knowledge on the wildlife species present around villages in Chad, a key step to understanding their role in transmission of GW and other pathogens.





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227 USUTU AND PLASMODIUM CO-INFECTION IN EURASIAN BLACKBIRDS (*TURDUS MERULA*)

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Keywords: Usutu Virus, Plasmodium, Avian Malaria, Co-Infection, Turdus Merula

Abstract Text

Usutu virus (USUV) is an emerging zoonotic arbovirus linked to various outbreaks in passerine birds in Europe. Recently, similarly to what has been described in humans with Dengue virus infection, a co-infection with haemoprotezoan parasites of the genus *Plasmodium* (Avian Malaria) has been described in USUV-infected Eurasian blackbirds (*Turdus merula*) in the Netherlands and Belgium. In humans, the simultaneous occurrence of Dengue and Malaria has been linked to an increase in severity of clinical and pathological findings. Similar studies regarding the role and effects of this co-infections are still lacking in birds.

To investigate the possible effects on lesions and disease severity of USUV and *Plasmodium* spp. co-infection, 160 blackbirds, submitted in the period 2016-2018 to the Dutch Wildlife Health Centre, were examined post-mortem. Molecular detection was performed for both agents, followed by sequencing and identification of the involved haemoprotezoan parasites. Concurrently, the assessment of lesions severity on histology was conducted. Finally, the statistical analysis was performed to assess a correlation between co-infection and lesion severity scores.

Results suggest an interplay between USUV and *Plasmodium* spp. for a high number of co-infected Eurasian blackbirds in the Netherlands, with increased severity of lesions in liver, spleen, heart and brain. To determine a causal relationship between *Plasmodium* spp. and USUV infection, further research is needed.

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197 SQUIRRELS (SCIURIDAE)- NEGLECTED RESERVOIRS FOR EMERGING ZONOTIC PATHOGENS

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Keywords: Emerging Pathogens, Bornaviruses, Hantaviruses, *Leptospira* Spp., Sciuridae

Abstract Text

The great diversity in species of the Sciuridae family is reflected in the varied habitats occupied and ecosystem services provided, like seed dispersal and pollination. Making them an important, but with regard to pathogen studies, a regularly overlooked group. Habitat fragmentation, hunting for bush meat and pet trade lead to increased human-animal interactions, which provoke zoonotic spill-over events as studies on variegated squirrel bornavirus-1 (VSBV-1; family Bornaviridae) have shown. This virus caused lethal encephalitis in humans following spill-over transmission from *Callosciurus prevostii* and *Sciurus variegatoides* kept in Germany. Further studies revealed the intensive and uncontrolled (exotic) squirrel trade in Europe as potential entry point for the import of an individual carrying this zoonotic virus. We aim to investigate squirrels as reservoir hosts and silent carriers of zoonotic pathogens to raise awareness of this neglected but critical aspect.

Between 2016-2021, we collected buccal swabs, faeces and tissue samples of deceased animals of endemic and non-endemic species from multiple European countries. The samples were screened with conventional or real-time RT-PCRs detecting either known squirrel-specific pathogens, such as VSBV-1 or squirrel adenovirus 1 (SqAdV-1, family Adenoviridae) or broad spectra of bornaviruses, hantaviruses or *Leptospira* spp. In addition, metagenome analysis was used to evaluate the presence of further viruses. First results for free-ranging squirrels in Europe (*Sciurus vulgaris*, *Sciurus carolinensis*) revealed no detection of hantaviruses (0/19) or VSBV-1 RNA (0/192), but detection of SqAdV-1 DNA (3/6). In exotic squirrel holdings VSBV-1-positive individuals (29/1187) were found. The concept of screening related animal species for a broad range of pathogens will help to close current knowledge gaps and might become even more important in future due to the ongoing destruction of natural habitats, climate alterations and increased movement of species. Future studies will focus on pathogen distribution of exotic squirrel species in their natural habitat.



70 VALIDATION OF A DROP-NET SYSTEM TO TRAP WILD BOAR ACCORDING TO THE AGREEMENT ON INTERNATIONAL HUMANE TRAPPING STANDARDS

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Keywords: Drop Net, Wild Boar, Humane Trapping, Welfare Standards, AIHTS

Abstract Text

In the last decades, wild boar (*Sus scrofa*) are causing conflicts with humans due to both their increasing abundance and ability to thrive in a wide variety of habitats, including urban areas. Wild boar population control remains the only cost-effective measure to manage human-wild boar conflicts in most cases. However, hunting is unfeasible in certain scenarios, then other management measures such as live trapping must be considered. Since the design and handling of live traps must assure animal welfare according to the Agreement on International Humane Trapping Standards (AIHTS), we aimed to evaluate a remote-controlled drop-net system (Estrateko®) to capture wild boars according to the AIHTS.

Six capture operations were performed in autumn 2017 in three different locations of the (peri)urban area of Barcelona (Spain), resulting in 32 wild boars trapped, anesthetized, and euthanized (average performance of 5.3 wild boar/capture event). Amongst these, 20 wild boars (minimum number required by the International Organization for Standardization) were randomly selected for pathological and histological examination according to ISO-10990-5.

Three wild boars (15%) displayed moderate to severe traumatic injuries associated with the drop-net system, 12 individuals showed low-grade abrasions or bruises, and the remaining five presented no injuries. The efficacy and the specificity were 100%.

Less than 20% of the examined wild boars presented moderate or severe injuries attributable to the capture method, hence fulfilling the AIHTS. Since moderate and severe injuries occurred in those events with a higher number of captured wild boars, the capture protocol should consider limiting the number of wild boars to be captured before triggering the system to prevent crowding under the net during the entangling phase and to minimize the time of handling. To the best of our knowledge, this is the first time that a drop-net capture system is assessed according to AIHTS.



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122 SYNURBIZATION INCREASES ZONOTIC HEPATITIS E HAZARD POSED BY WILD BOAR

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Keywords: Disease Dynamics, Hepatitis E Virus, Synurbic Wild Boar, Urban Wildlife, Zoonotic Hazard

Abstract Text

Wild boar (*Sus scrofa*) synurbization accompanies the generalized increase of wild boar populations worldwide. In addition, wild boar share diseases with domestic animals and humans, which can therefore be transmitted in the urban wildlife-human interface. Since wild boars are becoming an increasing reservoir of hepatitis E virus (HEV), its growing synurbic populations may pose a new zoonotic hazard. The aim of this study is to assess the dynamics of HEV infection in the synurbic wild boar population of Barcelona, Spain, combining ecological and health analyses, in order to assess its potential zoonotic hazard.

From September 2015 to June 2019, blood samples from 637 wild boars from the Metropolitan Area of Barcelona were obtained and tested for immunoglobulins G against the ORF2 and ORF3 of HEV-1 and HEV-3. Mean HEV seroprevalence was 36.1% (230/537, 95% confidence interval: 32.5-39.9%), increased with age and was higher in spring and summer, when wild boar presence was more frequent in the urban area.

Wild boars can be seasonally exposed to anthropogenic sources of HEV when exploring the city, and in turn could suppose a higher zoonotic dissemination hazard. Management measures aimed at reducing wild boar population and presence in urban areas could help to decrease wild boar-related HEV zoonotic hazard.



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305 CROSS-SECTIONAL SURVEY OF VECTOR-BORNE DISEASES AT THE WILDLIFE-LIVESTOCK INTERFACE: BLUETONGUE, SCHMALLEMBERG DISEASE AND Q FEVER IN DOÑANA NATIONAL PARK (SPAIN)

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Keywords: Reservoir, Shared Pathogens, Surveillance, Vector-Borne Diseases, Wildlife-Livestock Interface

Abstract Text

Vector-borne diseases (VBD) constitute a diverse group of diseases of increasing importance in human and veterinary medicine. In Mediterranean ecosystems, wild ungulates, livestock and arthropod vectors frequently share habitats, which can favor the maintenance and spread of VBD. A cross-sectional study was carried out to assess the circulation of selected vector-borne pathogens, including bluetongue virus (BTV) and Schmallenberg virus (SBV), both Culicoides-borne viruses, and *Coxiella burnetii*, which may be transmitted by ticks, within the ungulate host community of Doñana National Park (south-western Spain). Serum and spleen samples from 440 animals including 138 cattle, 102 red deer (*Cervus elaphus*), 101 fallow deer (*Dama dama*) and 99 wild boar (*Sus scrofa*) were analyzed to detect presence of antibodies (using a commercial ELISA) and infection (by molecular methods), respectively. High seroprevalence against BTV was found in red deer (97.0%) and fallow deer (64.7%). Cattle were not tested by BTV-ELISA because all of them were previously vaccinated against BTV. Antibodies against SBV were detected in 37.0% of cattle, 16.8% of red deer, 23.5% of fallow deer and 2.0% of wild boar. Thirty-eight animals (17 red deer and 21 fallow deer) were co-exposed to both viral agents. Seropositivity to *C. burnetii* was 0.7% in cattle, 3.0% in red deer, 1.0% in fallow deer and 1% in wild boar. BTV-4 infection was confirmed in red deer (10.3%; 4/39) and fallow deer (5.1%; 2/39). SBV-RNA was found in fallow deer (4.7%; 2/43). *Coxiella burnetii* DNA was detected in one out of three seropositive red deer. These results show a widespread distribution and active circulation of BTV and SBV in the study area, and a limited contact between *C. burnetii* and the surveyed species. Hence, this study highlights the importance of wildlife surveillance, particularly cervid species, for the success of VBD control programs in sympatric livestock.



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51 GLOBAL CONSERVATION IMPLICATIONS FOR HEALTH ASSESSMENT STUDIES IN NON-CAPTIVE WILDLIFE

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Keywords: Biodiversity Hotspots, Conceptual Framework, Diagnostic Methods, Reference Ranges, Systematic Review

Abstract Text

Wildlife health assessments help identify populations at risk of starvation, disease, and decline from anthropogenic impacts on natural habitats. We provide an overview of available health assessment studies in non-captive vertebrates, and propose a framework to strategically integrate health assessments in population monitoring. Using a systematic approach, we performed a thorough assessment of studies examining multiple health parameters of non-captive vertebrate species from 1982 to 2020 (n=261). We quantified trends in study design and diagnostic methods across taxa. We found a spatial mismatch between biodiversity hotspots and study location. Only 35% of studies involved international or cross-border collaboration. IUCN Red List non-threatened species represented 49% of species assessed, a trend likely associated with the regional focus of most studies. We identified a critical need for using statistically adequate sample sizes for studies establishing reference ranges, and strongly suggest following strict protocols when planning the study design. The main health assessment methods used across all taxa were blood analysis (89%), body composition assessment methods (81%), physical examination (72%) and faecal analysis (24% of studies). Based on our findings, we propose a conceptual framework for improved design and standardization for quality wildlife health assessments. Integrating a physiological and ecological understanding of species resilience towards threatening processes will enable informed decision making regarding the conservation of threatened species.



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307 ZOO ANIMALS AS SENTINELS FOR BLUETONGUE VIRUS MONITORING IN SPAIN

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Keywords: Bluetongue, Vector-Borne, Surveillance, Captive, Animal Health

Abstract Text

Bluetongue (BT) is an emerging and re-emerging communicable vector-borne disease of animal health concern. A serosurvey was performed to assess exposure to BT virus (BTV) in zoo animals in Spain and to determine the kinetics of seropositivity in longitudinally-sampled individuals during the study period. Serum samples were collected from 241 zoo animals belonging to 71 different species in five urban zoos (A-E) in Spain between 2007 and 2019. Twenty-four of these animals were longitudinally surveyed at three of the sampled zoos (zoos B, C and E) during the study period. Anti-BTV antibodies were found in 46 (19.1%; 95%CI: 14.1-24.1) of the 241 captive animals analyzed by commercial ELISA. Virus neutralization test confirmed specific antibodies against BTV-1 and BTV-4 in 25 (10.7%; 95%CI: 6.7-14.6) and five (3.0%; 95%CI: 0.3-4.0) animals, respectively. Two of the 24 longitudinally-sampled individuals (one African elephant (*Loxodonta africana*) and one aoudad (*Ammotragus lervia*)) showed anti-BTV antibodies at all samplings, whereas seroconversions were detected in one mouflon (*Ovis aries musimon*) in 2016, and one Asian elephant (*Elephas maximus*) in 2019. To the best of the authors' knowledge, this is the first large-scale survey on BTV conducted in both artiodactyl and non-artiodactyl zoo species worldwide. The results confirm BTV exposure in urban zoo parks in Spain, which could be of animal health and conservation concerns. Circulation of BTV was detected in yearling animals in years when there were no reports of BTV outbreaks in livestock. Surveillance in artiodactyl and non-artiodactyl zoo species could be a valuable tool for epidemiological monitoring of BTV.



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242 SPILLOVER EVENT OF RECOMBINANT LAGOVIRUS EUROPAEUS/GI.2 INTO THE IBERIAN HARE (*LEPUS GRANATENSIS*) IN SPAIN

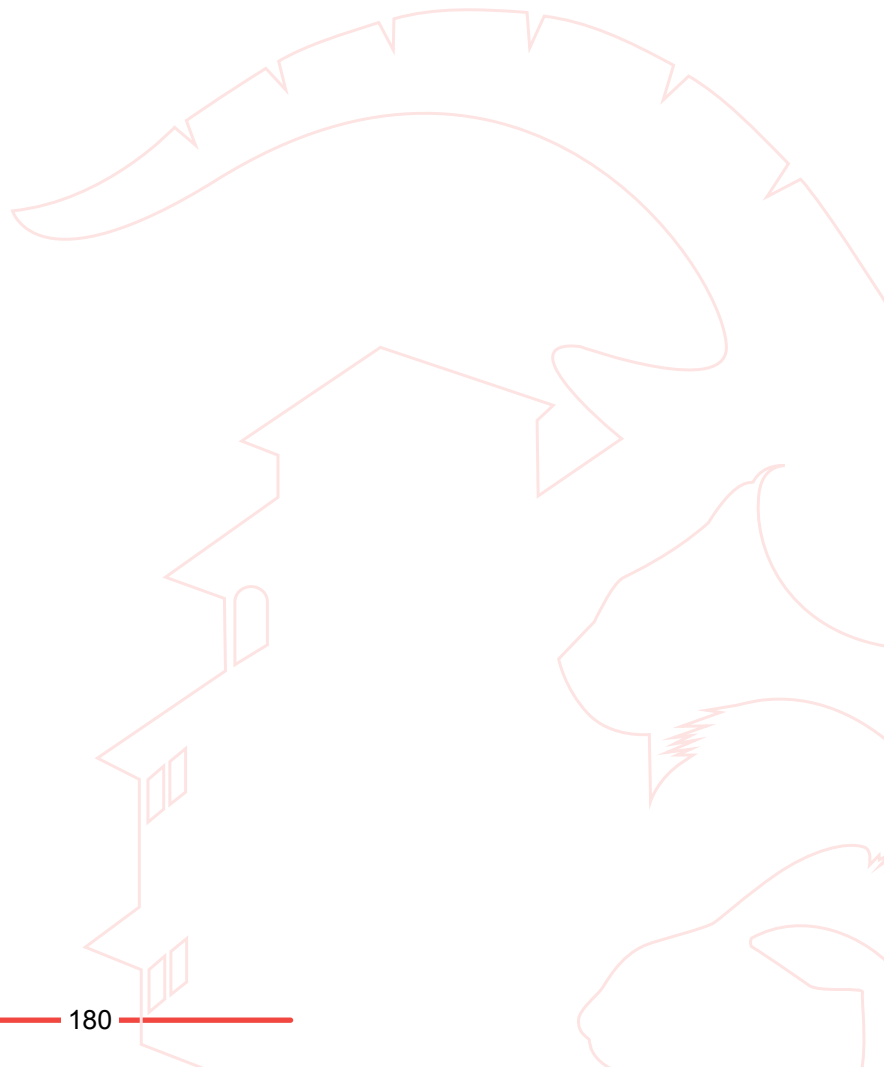
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Keywords: Iberian Hare, Lagovirus Europaeus/GI.2, Lepus Granatensis, Rabbit Haemorrhagic Disease

Abstract Text

Viruses that affect lagomorphs have decades of reported history of spillover events. One of these viruses is the causative agent of the so-called rabbit or "lagomorph" haemorrhagic disease (e.g., Lagovirus europaeus/GI.1 and L. europaeus/GI.2). In particular, L. europaeus/GI.2, has shown a great capacity to recombine with existing lagoviruses. In fact, it has replaced the former strains in the wild (i.e., L.europaeus/GI.2), and recently, an increase on spillover events has been detected among several lagomorph species including European and North American species of hares. In this study we report for the first time the infection of a wild Iberian hare with Lagovirus europaeus/GI.2/RHDV2/b, potential shedding and associated histopathological alterations. We identify the recombinant GI.4P-GI.2 as causative of the infection and we discuss plausible causes regarding the origin of the spillover event and its potential consequences for the Iberian hare wild populations, which is an endemic species of the Iberian Peninsula as well as an important game and prey species for many predators, including endangered species.





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294 MONITORING OF SCHMALLEMBERG VIRUS IN ZOO ANIMALS IN SPAIN, 2002-2019

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Keywords: Captive, Emerging, Schmallenberg, Surveillance, Vector-Borne

Abstract Text

Schmallenberg virus (SBV) is an emerging Culicoidesborne Orthobunyavirus that affects many domestic and wild animal species. In the present study, a serosurvey was carried out to assess SBV exposure in captive zoo animals in Spain and to determine the dynamics of seropositivity in longitudinally sampled individuals. Between 2002 and 2019, sera from 278 animals belonging to 73 different species were collected from five zoos (A–E). Thirty-one of these animals were longitudinally surveyed at three of these zoo parks during the study period. Seropositivity was detected in 28 (10.1 %) of 278 animals analyzed by blocking ELISA. Specific anti-SBV antibodies were confirmed in 20 (7.2 %; 95 %CI: 4.2–10.3) animals of six different species using virus neutralization test (VNT). The multiple logistic regression model showed that “order” (Artiodactyla) and “zoo provenance” (zoo B; southern Spain) were risk factors potentially associated with SBV exposure. Two (8.7 %) of the 31 longitudinally-sampled individuals showed specific antibodies against SBV at all samplings whereas seroconversion was detected in one mouflon (*Ovis aries musimon*) and one Asian elephant (*Elephas maximus*) in 2016 and 2019, respectively. To the best of the author’s knowledge, this is the first surveillance conducted on SBV in zoos in Spain. The results confirm SBV exposure in zoo animals in this country and indicate circulation of the virus before the first Schmallenberg disease outbreak was reported in Spain. Surveillance in zoological parks could be a complementary approach to monitoring SBV activity. Further studies are warranted to assess the impact of this virus on the health status of susceptible zoo animals.



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115 EVALUATION OF CONTACT NETWORK BETWEEN COMMENSAL WILD BIRDS AND DOMESTIC POULTRY AROUND A FRENCH DUCK FARM

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Keywords: Poultry, Wild Birds, Wildlife-Livestock Interface, Network, Host Community

Abstract Text

The role of commensal wild birds in introduction and dissemination of pathogens in poultry farms has been less studied than those of waterfowl. To characterize contacts between wild and domestic birds, a longitudinal observational study was implemented in a typical free-range duck farm of South-West France. Once a month for a year, standardised observations were conducted in outdoor parks to evaluate between-species contacts. For several periods of the day, number, behaviour and direct environment of each observed species were recorded, in addition with the surrounding density of domestic ducks. Network analysis methods were then applied to these data, each species being a node, and contacts between each other were quantified in frequency and intensity. General linear models were applied on most abundant species to identify the most favourable conditions for their presence.

Results showed a wide diversity of 50 species visiting outdoor parks. Among those, white wagtails (*Motacilla alba*) and sparrows (*Passer domesticus* and *Passer montanus*) were the most abundant species observed (in 91% and 78% of observation events, respectively), while all other species were observed in less than 25% of observation events. White wagtails and domestic sparrows were also the only species seen entering barns, only in current or recent presence of ducks. Moreover, white wagtails were observed most of the time on dry or wet ground, and their numbers were higher in presence of domestic ducks on outdoor parks. Network analysis confirmed the key role of white wagtails in linking domestic ducks and the avian community surrounding the farm, as well as sparrows to a lesser extent. The study highlighted the importance of least studied commensal wild birds in the host community of avian pathogens around poultry farms. It allowed to identify species on which sanitary surveillance and towards which contact-restriction measures in poultry farms must be prioritized.





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189 IDENTIFICATION OF A NOVEL NEORICKETTSIA SPECIES IN KEMP'S RIDLEY SEA TURTLES WITH GRANULOMATOUS RENAL LESIONS AND DEVELOPMENT OF A QUANTITATIVE PCR ASSAY

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Keywords: Kemp's Ridley, Kidney, Neorickettsia, Quantitative PCR, Sea Turtle

Abstract Text

The Kemp's Ridley sea turtle (*Lepidochelys kempii*) is classified as a critically endangered species. Distribution of this species is restricted to the Gulf of Mexico and Atlantic coast of the US. *Neorickettsia* is a genus of obligate intracellular Alphaproteobacteria in the order Rickettsiales, family Anaplasmataceae that are typically endosymbionts of parasitic trematodes. *Neorickettsia* may cause significant disease in vertebrate hosts including Potomac horse fever (*N. risticii*), Sennetsu fever (*N. sennetsu*), and Salmon poisoning disease (*N. helminthoeca*).

An adult male Kemp's Ridley was found dead on the coast of Kenedy County, Texas in August 2019. Death was attributed to severe, chronic nephritis in which heterophilic and chronic granulomas effaced much of both kidneys. No *Salmonella* sp. were isolated using selective culture and no organisms were observed in histological sections stained using Gomori methenamine silver and acid fast methods. Pan-bacterial 16S rRNA PCR and sequencing of affected tissue identified a *Neorickettsia* distinct from other known species to a degree consistent with a novel species. For further characterization, primers were designed for the groEL gene which was then sequenced, and the resultant sequence was used to design a probe-hybridization quantitative PCR (qPCR) assay. Quantitative PCR specific for this novel species identified the organism was also present as well in the liver and colon of the index case. A qPCR survey of additional stranded Kemp's Ridley sea turtle kidneys identified this species in three of seven animals. Recognition of this novel organism in a critically endangered species is concerning; additional work is underway to further characterize the potential of this organism as a pathogen and potential impacts on populations.



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212 MULTI-SYSTEMIC SPIRORCHIDIASIS AND GASTROINTESTINAL PARASITISM IN LOUISIANA RED-EARED SLIDERS (*TRACHEMYS SCRIPTA ELEGANS*)

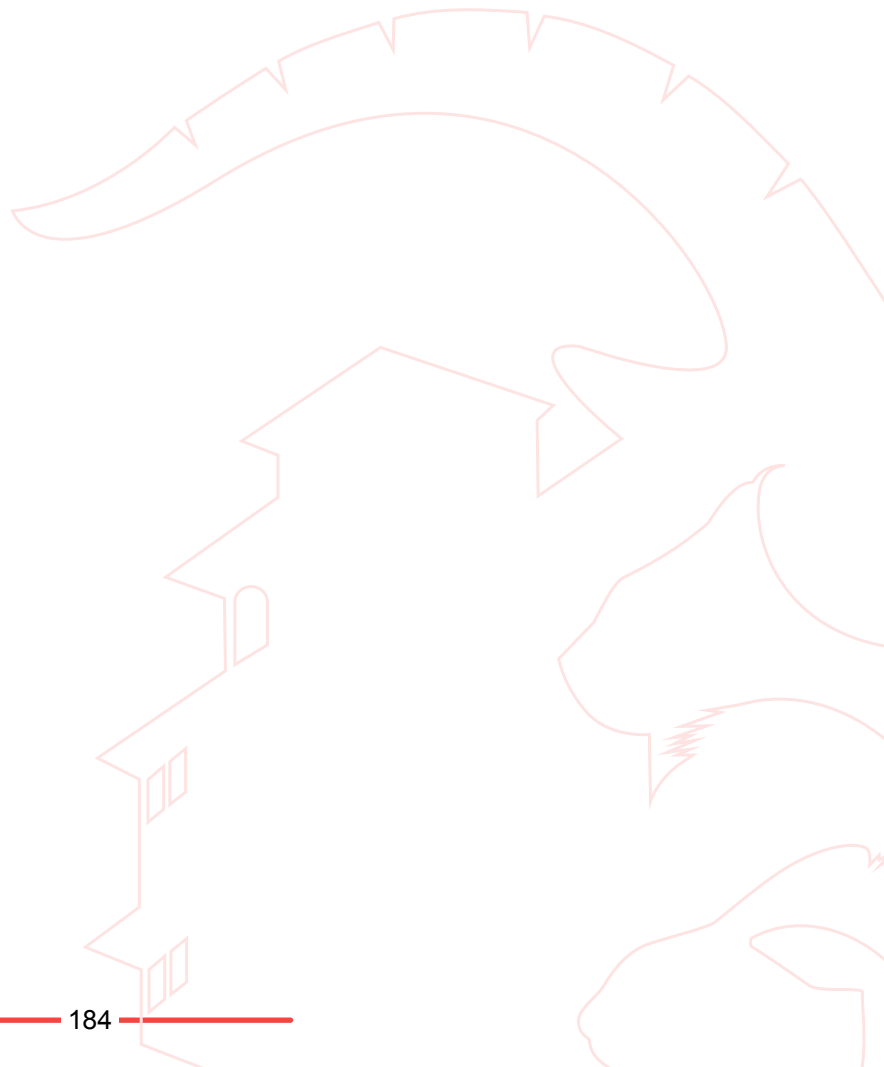
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Keywords: Louisiana, Mass Mortality, Red-Eared Slider, Spirorchidiasis, United States

Abstract Text

Recently, reports of mass mortality events have involved hundreds of red-eared sliders (*Trachemys scripta elegans*) in Louisiana. Red-eared sliders are considered an invasive species in much of the U.S. but are native in many areas of the southeast, including Louisiana. Our goal was to characterize gross and microscopic lesions and potential etiologies in red-eared sliders from three mortality events and assess for epidemiologic patterns. Postmortem diagnostic evaluation, including gross and histopathology and select ancillary tests, was performed on ten slider carcasses collected during annual die-offs in Louisiana during 2017, 2018 and 2020. Mortality events occurred in February and March near agricultural lands (e.g., crawfish and rice production ponds, cattle pastures) interspersed among natural aquatic habitats in northwestern and southern Louisiana. Death in all red-eared sliders was attributed to multi-organ parasitism, most notably with spirorchids eggs associated with granulomatous inflammation and necrosis in stomach and intestine (9/10), liver (8/10), pancreas (5/10), kidneys (5/10), lungs (5/10), spleen (3/10), skeletal muscle (2/10), uterus (2/10), ovaries (1/10), heart (1/10), and skin (1/10). *Serpinema trispinosum* (Nematoda: Spirurida: Camallanidae) and *Neoechinorhynchus* sp. (Acanthocephala) were identified morphologically in gastrointestinal tissue of seven red-eared sliders. No viruses, including ranavirus, were detected in pooled tissues (0/10). Large die-offs of red-eared sliders were attributed to multi-systemic disease associated with severe spirorchid infections, posing a health risk to this species. Further, red-eared sliders pose a conservation threat to native turtle species in some regions of the U.S. via potential pathogen transmission in shared environments. Seasonal (late winter/early spring) or habitat (e.g., agricultural use) associations may represent a disease risk and warrant continued monitoring.





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63 A METATRANSCRIPTOMIC APPROACH TO PARASITIC, VIRAL, AND BACTERIAL SURVEILLANCE IN HUNTER HARVESTED PRIMATES IN AN INDIGENOUS RESERVE IN GUYANA, SOUTH AMERICA

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Keywords: Disease, Surveillance, Transcriptomics, Wild Meat, Amazonia

Abstract Text

While wildlife hunting is a key component to the traditional subsistence strategies of millions of people throughout the tropical world, it is also a potential source of zoonotic disease. Although numerous studies have documented the emergence of zoonoses from wildlife hunting in Africa and Asia, little research has focused on infectious diseases from wild meat in the Neotropics. Here, we use next-generation metatranscriptomics to identify the parasitic, bacterial, and viral diversity in free-ranging primates harvested for meat by the Waiwai, an indigenous community living in the Konashen Community Owned Conservation Area in Southern Guyana, South America. We hypothesize that de novo molecular surveillance of primates harvested for food will identify potential zoonoses not previously described from other studies in the Guianan Shield and Central Amazonia. To test this hypothesis, we performed field necropsies on Waiwai harvested primates. A total of seven primates were sampled for molecular analysis (n=6 spider monkeys (*Ateles paniscus*) and n=1 bearded saki monkey (*Chiropotes sagulatas*)). Total RNA was extracted and sequenced on the Illumina NovaSeq, and processed through a bioinformatic pipeline for metatranscriptomic surveillance. Our metatranscriptomic analyses of primate samples indicate the presence of *Plasmodium vivax* and malariae, *Toxoplasma gondii*, and *Trypanosoma*. We also identified multiple bacteria and viruses closely related to those with known zoonotic potential including: *Listeria monocytogenes*, *Campylobacter jejuni*, *Klebsiella pneumoniae*, tick-borne bacteria closely related to *Borrelia*, *Rickettsia*, and *Bartonella*, and novel viruses including an Orthobunyavirus and a Chordopoxvirus. Given the difficulty of obtaining high quality tissue samples for RNA extraction from free ranging primates, the samples for this work are virtually unprecedented in similar research. Our research advances the knowledge of zoonoses from primate wild meat in the Neotropics and the use of high-throughput metatranscriptomics increases our ability to detect zoonoses from this zoonotic hotspot.



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157 DESCRIPTION OF NOVEL ADENOVIRUSES AND HERPESVIRUSES IN GALAPAGOS GIANT TORTOISES (*CHELONOIDIS SP.*)

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Keywords: Adenovirus, Conservation, Galapagos Tortoises, Herpesvirus, Wildlife Surveillance

Abstract Text

Emerging infectious diseases (EIDs) have been reported as causes of morbidity, mortality, and extinctions of free-living animal populations. Galapagos tortoises are endangered due to habitat change, invasive species, and other human impacts. Human activity also has spread diseases that have threatened turtle populations; however, the impact of EIDs on Galapagos tortoise conservation remain understudied. To determine the impact of infectious agents on Galapagos tortoises, we conducted health assessments of five species from the islands of Santa Cruz, Isabela, and Española. We performed health evaluations of 350 animals and PCR testing for pathogens relevant to other tortoise species. Through this screening, we identified two novel sequences of adenoviruses (ADVntST-1 and ADVntST-2) and four of herpesviruses (HVntST-1, HVntST-2, HVntST-3 and HVntST-4). Based on alignments of the DNA polymerase gene and maximum likelihood phylogenetic analyses, we found both novel adenoviruses to be most closely related to pancake tortoise adenovirus by nucleotide sequence (identities of 79% and 76.6%), and red footed tortoise adenovirus 2 based on amino acid sequence (79.1%, 76.1%). Analyses supported emydid herpesvirus 1 as closely related to herpesviruses HVntST-1, HVntST-2, and HVntST-3. These three sequences translated into the same deduced amino acid sequence; therefore, they could be considered the same viral species. HVntST-4 was highly divergent from any sequence previously detected and is closely related to a *Bubo bubo* herpesvirus based on nucleotide sequence (66.1%) and to loggerhead oro-cutaneous herpesvirus based on amino acids (66%). Our findings are considerations for Galapagos tortoise management based on our knowledge of how these agents are expressed in other chelonian species. Continued screening is crucial to determine if these viruses play a role in tortoise fitness, morbidity, and survival. This information will allow us to provide recommendations to the Galapagos National Park Directorate to improve the management and reintroduction plans for these unique species.



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247 FIRST KNOWN OUTBREAK OF SALMONELLA SEROVAR CHOLERAESUIS IN SWEDISH WILD BOAR

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Keywords: Domestic Pigs, Public Health, Salmonella Choleraesuis, Wild Boar (Sus Scrufa), Zoonosis

Abstract Text

An outbreak of *Salmonella enterica* subspecies *enterica* serovar *Choleraesuis* was diagnosed in a pig farm in the south of Sweden, in September 2020. This was the first diagnosed case of *Choleraesuis* in animals in the country since the 1970's, prompting extensive disease tracing, including initiating surveillance of wild boar (*Sus scrufa*). In the general wildlife disease surveillance, necropsied wild boar from all regions were sampled. A disease surveillance program for *Choleraesuis* in wild boar was set up with sampling of hunted wild boar in the two regions where the initial case and subsequent findings in wild boar occurred.

To date, the bacteria has been cultured from 10 out of 49 wild boars found dead or culled. Euthanized moribund wild boar showed gross lesions indicating septicaemia. The bacteria could be cultured from all sampled organs, including bone marrow. Additionally, 37 of the 244 wild boars sampled at hunting tested positive. Positive cases in wild boar have been detected in areas as far from the first case as 350 km.

The source of infection has not been identified neither in the pig farm nor in wild boar. Sweden and neighbouring countries have a favourable situation with low prevalence of salmonellosis in both domestic animals and wildlife. The current outbreak is therefore of utmost importance due to ecological and economic consequences for wild and domestic pigs. Also, of all *Salmonella* serotypes, *Choleraesuis* is the most prevalent cause of systemic disease in humans and the consumption of wild boar meat is increasing. Further investigations of bacterial isolates with molecular methods are currently ongoing and the surveillance areas of hunted wild boar are being expanded, aiming for national coverage. In conclusion, these findings underline the importance of a well-developed disease surveillance of the wildlife population, for both human and animal disease control.



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130 MICROBIOME DIVERSITY AND ITS RELATION TO THE PATHOGEN OF DIFFERENT TICK SPECIES COLLECTED IN SARAWAK, MALYSIAN BORNEO

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Keywords: Endosymbionts, Microbiome, Pathogen, Sarawak, Ticks

Abstract Text

In the tropics, ticks are the second most important vectors after mosquitoes causing human vector-borne diseases. Additionally, ticks harbor highly abundant symbiotic and commensal microorganisms, which play a role in tick development, reproduction, survival, and pathogen transmission. However, studies elucidating tick microbiome are limited in Malaysia.

To outline the endosymbionts and the associated pathogens of different tick species, a total of 210 tick samples from two primary forests and an oil palm plantation in Sarawak, Malaysian Borneo, were collected by flagging and rodents trapping. Six tick species of three genera: *Ixodes granulatus*, *Haemaphysalis shimoga*, *H. hystricis*, *Dermacentor compactus*, *D. steini* and *Dermacentor* sp. were included in Next-Generation sequencing (NGS) targeting the hypervariable region V3-V4. Data analyses were performed for the following groups: using all tick species, then with only adult ticks, and finally, *H. shimoga* was used for life stage and feeding status comparison.

Our results revealed that microbial diversity and composition were significantly different among the tick genera and species. Genus *Dermacentor* showed the highest microbial diversity. The microbial composition of *H. shimoga* formed a distinct cluster from *I. granulatus* and *Dermacentor* spp. We found the presence of dominant endosymbionts in some tick species, such as *Coxiella*, in most of the *H. shimoga*. *Rickettsiales* was mainly found in *I. granulatus* and, to some extent, *Haemaphysalis* spp. *Francisella* was primarily found in *Dermacentor steini* but not in other *Dermacentor* species. Additionally, the presence of pathogenic bacteria could affect the microbial composition of ticks, which was significantly demonstrated by the *Borrelia* infected and non-infected *I. granulatus*. Different life stages and feeding status had an impact on *H. shimoga* microbial diversity and composition; however, no significant difference was observed between the adult males and females. Altogether, this study's findings highlighted several important points that serve as pivotal information for future research work.



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98 PATHOLOGICAL FINDINGS IN WHITE-BEAKED DOLPHINS (*LAGENORHYNCHUS ALBIROSTRIS*) AND ATLANTIC WHITE-SIDED DOLPHINS (*LAGENORHYNCHUS ACUTUS*) FROM THE SOUTH-EASTERN NORTH SEA

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Keywords: Pathology, *Lagenorhynchus Albirostris*, *Lagenorhynchus Acutus*, North Sea

Abstract Text

In the North Sea, white-beaked dolphins (*Lagenorhynchus albirostris*) occur regularly and are the second most common cetacean in the area. Their close relative, the Atlantic white-sided dolphin (*Lagenorhynchus acutus*), prefers deeper waters of the northern North Sea and Atlantic Ocean. Strandings of both species have been observed regularly in the past three decades, however, numbers significantly decreased specifically in the southern North Sea more recently. Studies describing necropsy findings in stranded *Lagenorhynchus* spp. are, to date, still scarce.

Therefore, necropsy results from fresh *Lagenorhynchus* spp. which stranded along the southeastern North Sea between 1990 and 2020 were retrospectively assessed and compared. Main pathological findings as well as the causes of death were evaluated, in order to gain an insight into the health status of both species.

A full necropsy was performed on 25 white-beaked dolphins and three Atlantic white-sided dolphins. Samples of selected organs were taken for histopathological, bacteriological, mycological, parasitological and virological examination.

The most common findings included emaciation, gastritis and pneumonia. While gastritis and ulceration of the stomach were often associated with parasitic infections, pneumonia was most likely caused by bacterial infections. Encephalitis was found in three animals and morbillivirus antigen was detected immunohistochemically in one case.

There was no evidence of epizootic or mass stranding events in the monitored period.

The main causes of disease and causes of death described here will help assessing risk factors, like anthropogenic threats and climate change, and contribute to future conservation measures of both species.



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216 SEROPREVALENCE OF WEST NILE VIRUS IN GAME BIRD POPULATIONS IN THE UNITED STATES

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Keywords: Avian, Galliformes, Game Birds, Serosurvey, West Nile Virus

Abstract Text

Susceptibility to West Nile virus (WNV), a zoonotic mosquito-borne Flavivirus, varies greatly among avian species, which serve as the primary amplifying hosts for this virus. There remains a paucity of research on the potential impacts of WNV on many game bird species within North America. Some game birds, such as the greater sage-grouse (*Centrocercus urophasianus*) and ruffed grouse (*Bonasa umbellus*), are considered highly susceptible based on experimental infection trials and documented natural mortalities, while others, such as the wild turkey (*Meleagris gallopavo*), are considered less susceptible. The susceptibility of others, such as the American woodcock (*Scolopax minor*), remains poorly understood. Serosurveys provide a useful tool in determining the number of individuals that survive WNV infection. The objective of this study was to evaluate the WNV seroprevalence in free-ranging game bird species, specifically the ruffed grouse, wild turkey, and greater sage-grouse, and with opportunistic sampling of American woodcock, across the United States. From 2018 to 2021, blood-soaked Nobuto filter paper strips and/or serum from hunter-harvested and/or live birds were collected and tested for antibodies to WNV via plaque reduction neutralization test (PRNT) and subsequent co-titration to distinguish between antibodies to WNV and St. Louis encephalitis virus (SLEV) by a >4-fold difference in PRNT90 titers. The highest seroprevalence was in American woodcock (31%; 8/26) and wild turkey (28%; 133/477), followed by ruffed grouse (13%; 359/2805). Antibodies were not detected in any of the greater sage-grouse (0/57). Serosurveillance data should be interpreted in conjunction with species-specific susceptibility data (e.g., experimental infection trials and documented natural deaths attributable to WNV), but these results suggest that wild turkeys and woodcock survive WNV infection at greater rates than the other examined species in this study. These data will aid in conservation and management strategies of these valued game bird species.



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218 LISTERIOSIS AND VIRAL COINFECTIONS IN MULTIPLE WILDLIFE SPECIES IN THE SOUTHEASTERN UNITED STATES

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Keywords: Listeria Monocytogenes, Gray Fox, Wild Turkey, Canine Distemper Virus, Lymphoproliferative Disease Virus

Abstract Text

Listeria monocytogenes is a bacterium that can cause disease in a variety of vertebrate hosts, encompassing humans, livestock and wildlife. Increasing interactions at the human-livestock-wildlife interface, driven partially by changes in land and resource use, may facilitate increased pathogen transmission, including zoonoses. Our objectives were to determine host species diversity of listeriosis cases; assess geographic distribution; compare lesion patterns across species; and assess for co-infections. From 1991-2020, seven gray foxes, seven wild turkeys, a neonatal elk and a white-tailed deer fawn from mostly southeastern states (14; most commonly Georgia [4]), as well as Kansas (1) and Maryland (1) were diagnosed with listeriosis at the Southeastern Cooperative Wildlife Disease Study (SCWDS). All seven foxes had hepatitis and/or hepatic necrosis, and *L. monocytogenes* was cultured from liver (5/7) or lung (2/7). Liver (4/4), spleen (3/4), and lung (1/4) immunohistochemical labelled for *Listeria* spp. in foxes. All foxes were co-infected with canine distemper virus (CDV), two of which had been recently trapped and vaccinated for CDV. The wild turkeys had hepatocellular necrosis (3/7) or heterophilic hepatitis (1/7) with gram-positive bacilli, intrasinusoidal gram-positive bacilli without hepatic lesions (1/7), and/or granulomatous myocarditis (2/7). Five turkeys had immunohistochemical labeling for *L. monocytogenes* in liver, and the other two had immunolabeling in the heart. Tissues of 3 of 4 turkeys tested positive for lymphoproliferative disease virus with two of these concurrently positive for reticuloendotheliosis virus. Both cervids had systemic listeriosis and *L. monocytogenes* was cultured from the liver. We established *L. monocytogenes* as a cause of fatal disease in a variety of wildlife species, which suffered from concurrent infections and likely immunosuppression. A better understanding of the distribution across the landscape and varied epidemiology and pathogenesis of listeriosis in wildlife may help determine potential transmission pathways among wildlife, livestock, and humans and increase diagnostic awareness.



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190 ANTICOAGULANT RODENTICIDE EXPOSURE IN RAPTORS FROM ONTARIO, CANADA

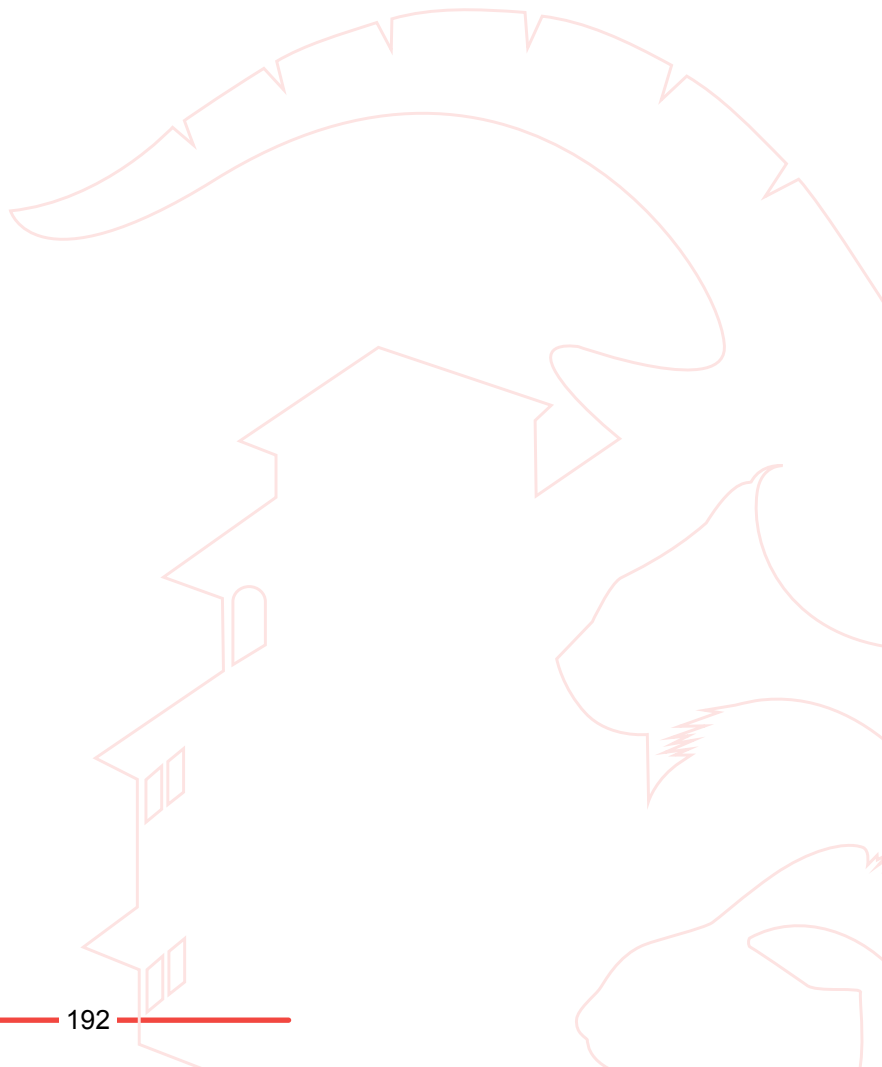
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Keywords: Anticoagulant Rodenticide, Brodifacoum, Bromadiolone, Difethialone, Raptors

Abstract Text

Anticoagulant rodenticides (ARs) are used globally to control rodent-pest infestations in both urban and agricultural settings. It is well documented that non-target wildlife, including predatory birds, are at risk for secondary anticoagulant exposure and toxicosis through the prey they consume. However, there have been no studies of AR exposure in raptors in Canada since new Health Canada legislation was implemented in 2013, attempting to limit exposure in non-target wildlife. Our objective was to measure levels of ARs in wild raptors in southern Ontario to assess their exposure. We collected liver samples from 133 raptors representing 17 species submitted to the Canadian Wildlife Health Cooperative in Ontario, Canada, between 2017-2019. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) was used to quantitatively assess the level of exposure to 14 first- and second-generation ARs. Detectable levels of one or more ARs were found in 82 of 133 (62%) tested raptors, representing 12 species. The most commonly detected ARs were bromadiolone (54/133), difethialone (40/133) and brodifacoum (33/133). Of AR-positive birds, 34/82 (42%) contained residues of multiple (>1) anticoagulant compounds. Our results indicate that there is widespread AR exposure in raptors living in southern Ontario, Canada. Our finding that brodifacoum, difethialone, and bromadiolone were observed alone, or in combination with one another in the majority of our sampled raptors indicates that legislative changes in Canada may not be protecting non-target wildlife as intended.





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194 FIRST DESCRIPTION OF SARCOPTES SCABIEI CROSS-TRANSMISSION BETWEEN IBERIAN IBEX (*CAPRA PYRENAICA*) AND WILD BOAR (*SUS SCROFA*)

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Keywords: Cross-Transmission, Immunohistochemistry, Multilocular Genotyping, Sarcoptic Mange, Wild Boar

Abstract Text

Sarcoptic mange is a globally distributed parasitic disease caused by the burrowing mite *Sarcoptes scabiei*. This mite is considered a single species with different varieties with a certain degree of host specificity. Interspecific cross-transmission is usually limited to phylogenetically related species, prey-predator relationships, and self-limited infestations in cases of close contact between individuals from phylogenetically distant species.

The last outbreak of sarcoptic mange in Iberian ibex (*Capra pyrenaica*) was detected in December 2014 affecting the ibex population of Ports de Tortosa i Beseit (PTB) in Catalonia (north-eastern Spain). On October 29th, 2018, a wild boar (*Sus scrofa*) with compatible lesions with sarcoptic mange was hunted in PTB and submitted to the Servei d'Ecopatologia de la Fauna Salvatge -Wildlife Health Service- (SEFaS) of the Universitat Autònoma de Barcelona for necropsy.

The presence of *S. scabiei* mites was confirmed through skin scraping and potassium hydroxide skin digestion. Histopathology (hematoxylin/eosin and toluidine blue stains) identified skin lesions consistent with sarcoptic mange as well as the occasional mite within those lesions. Through immunohistochemistry, a predominantly T-cell inflammatory infiltrate was described. The analysis of ten specific microsatellites for multilocular genotyping phylogenetically grouped the *S. scabiei* found in the wild boar with the mites found in the sympatric Iberian ibexes, separately from *S. scabiei* from other wild boars of the Iberian Peninsula. Altogether, the findings confirmed the first case of interspecific cross-transmission of sarcoptic mange from Iberian ibex to wild boar.



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134 LONG-TERM STUDY OF RANAVIRUSES DRIVERS, ASSOCIATED WITH MORTALITY EVENTS ON RANA TEMPORARIA IN THE FRENCH NATIONAL PARK OF MERCANTOUR

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Keywords: Amphibian, Epidemiology, Mortality, National Park, Ranavirus

Abstract Text

Ranaviruses, a major cause of die-offs and mass mortality events in amphibians worldwide have been identified in several European countries. Following the first French detection in the Parc National du Mercantour in common frogs (*Rana temporaria*) in 2011, surveillance of mortality caused by ranaviruses was implemented.

This surveillance provided a 10-year (2011-2020) database of mortality events associated with ranaviral infection status. These data are studied to try and identify the main drivers of ranavirus infections and to advise on control measures based on risk factors. Human activities (hiking, fishing and cattle breeding), temperature, and composition of local ecosystems (fishes, plants, invertebrates, herpetofauna) were hypothesised as possible contributing factors to the presence of ranavirus.

We analysed the impact of 25 variables describing the hypothetical drivers on the infection status, using logistic regression (univariate and multivariate models). Monthly temperature and cattle breeding had a significant effect, higher temperature and the presence of cattle being correlated to a higher risk of infection. The effects of other drivers were not statistically significant, with missing data and collinearity between most of the studied variables hampering analysis of some variables.

Although this study did not result in risk-based recommendations for management of ranavirus, it highlighted that further study of several possible drivers of ranaviral infection is warranted. Consequently, we propose relevant variables (temperature, altitude, presence of fish, reptiles and cattle, density and type of aquatic plants, presence, species and developmental stage of other amphibians) that should systematically be recorded along with mortality recording in the future.



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120 ESTABLISHING THE SAFETY, PHARMACOKINETICS, AND EFFICACY OF FLURALANER AS A NOVEL TREATMENT FOR SARCOPTIC MANGE IN THE BARE-NOSED WOMBAT (*VOMBATUS URSINUS*)

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Keywords: Efficacy, Fluralaner, Safety, Sarcoptic Mange, Wombat

Abstract Text

Sarcoptic mange, caused by *Sarcoptes scabiei* infestation, is the most significant infectious disease affecting free-living bare-nosed wombats (*Vombatus ursinus*). Enzootic across the species' range, the impacts of mange manifest as individual animal health and welfare compromise, population growth-limitation, and occasional local declines and extinctions. In situ interventions have involved the administration of macrocyclic lactones but success has been hindered by numerous drug-related factors. Fluralaner, a novel isoxazoline ectoparasiticide with several advantageous pharmacokinetic and -dynamic properties, represents a promising alternative warranting further investigation. This study aimed to establish the safety and pharmacokinetic profile of fluralaner in bare-nosed wombats and assess its efficacy against naturally acquired *S. scabiei* infections in this species. Fluralaner was administered topically at 25 mg/kg ($n = 5$) and 85 mg/kg ($n = 2$) to healthy captive bare-nosed wombats. Safety was assessed over 12 weeks by clinical observation and monitoring of haematological and serum biochemical parameters. Fluralaner plasma pharmacokinetics were quantified over the same period using ultra-performance liquid chromatography and tandem mass spectrometry. Efficacy was evaluated over 15 weeks through assessment of clinical responses to topical administration of 25 mg/kg fluralaner in sarcoptic mange-affected wild bare-nosed wombats ($n = 3$). No deleterious health impacts were detected following fluralaner administration. Fluralaner was absorbed and remained quantifiable in plasma throughout the monitoring period. For the 25 mg/kg and 85 mg/kg treatment groups, respective means for maximum recorded plasma concentrations (C_{max}) were 6.2 and 16.4 ng/ml; for maximum recorded times to C_{max} , 3.0 and 37.5 days; and for plasma elimination half-lives, 40.1 and 166.5 days. Complete clinical resolution occurred in all diseased animals within four weeks of treatment. Fluralaner is a safe, efficacious, and long-lasting treatment for sarcoptic mange in the bare-nosed wombat that represents a marked improvement in therapeutic capabilities and disease control prospects for the species.



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GENERAL POSTERS



LEPUS GRANATENSIS Iberian hare

María García Romero



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348 20 YEARS OVERVIEW: SPATIO-TEMPORAL ANALYSIS OF EUROPEAN SURVEYS ON ZOOBOTIC DISEASES IN THE MAIN LARGE GAME SPECIES

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Keywords: Hunting, Public Health, Red Deer, Zoonosis, Wild Boar

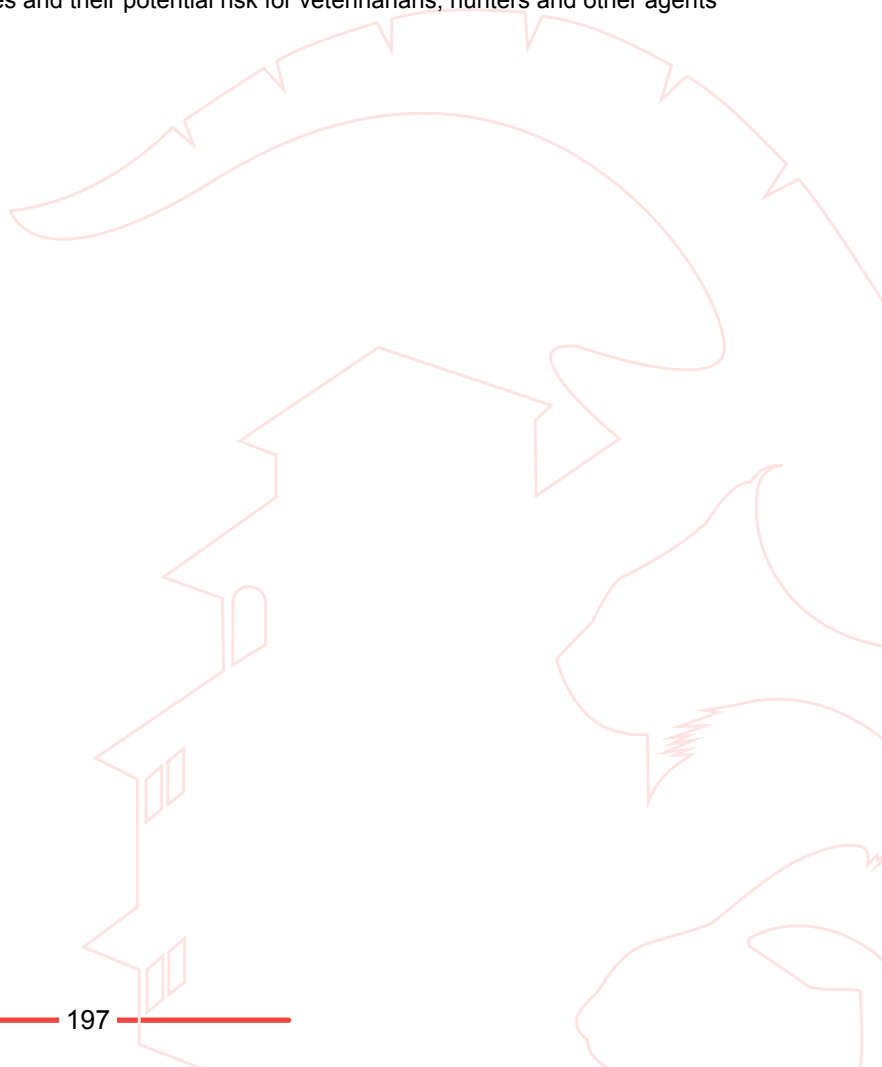
Abstract Text

Wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) are the main species hunted in Europe. They can also be a source of zoonotic infections for cohabiting humans and hunters. The objective of our systematic review was to analyse the spatio-temporal trends of surveys on zoonotic diseases of wild boar and red deer in the Europe in the last 20 years.

With the search strategy “((*sus scrofa* OR wild boar OR *cervus elaphus* OR red deer) AND (zoonosis OR zoonot* OR infectious disease))” in Pubmed and ScienceDirect databases, we got a total of 1419 articles. Following the inclusion criteria: species of interest – wild boar and red deer, confirmed zoonosis and presence of natural infection) and the exclusion filters: European study, stipulated timeline (2001-2020), written in English and open-access. To conduct this systematic review, 202 European surveys published in indexed journals were included.

Spatially, 103 survey (51%) are in the south Europe (mainly Spain and Italy). Followed by Western and Central (n=47) and East Europe (n=37). The North Europe presented a reduced number of revised surveys (n=15). Temporally, the pattern of number of publications about zoonotic diseases in wild boar and red deer oscillates, but with an increasing trend over the two decades under study. In the 1st decade of study (2001-2010) the maximum number is 6 (2009), but in the 2nd, ranging from 10 to 26, with a clear peak in 2015-2016 (n=51, 25% of total).

With the sharp increase in the population of wild boar and red deer in Europe and the previous gaps in their health profile, the number of studies has been promoted and increased in this continent in the last 20 years. Thus, improving knowledge about the occurrence of zoonotic diseases and their potential risk for veterinarians, hunters and other agents involved in the hunting sector.





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311 LYMPHOPROLIFERATIVE DISEASE VIRUS AND RETICULOENDOTHELIOSIS VIRUS: COMPARISON OF TISSUE TROPISM AND MICROSCOPIC LESIONS IN WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN THE UNITED STATES

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Keywords: Lymphoproliferative Disease Virus, PCR, Reticuloendotheliosis Virus, Retrovirus, Wild Turkey

Abstract Text

Lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV) are oncogenic retroviruses that can cause disease in wild and domestic fowl. LPDV infections are common (often $\geq 50\%$ prevalence) and widespread in wild turkeys (*Meleagris gallopavo*) in the USA and east-central Canada, while REV has been detected worldwide in various avian hosts, sometimes with economic impacts on avian production. LPDV infections in wild turkeys range from subclinical to fatal; the latter often attributable to concurrent tumor formation, immunosuppression, and cachexia. Recently, postmortem evaluation of wild turkeys at the Southeastern Cooperative Wildlife Disease Study revealed REV-infected individuals with neoplastic (lymphoproliferative) disease plus turkeys coinfecting with LPDV and REV. Thus, our aims were to compare infection prevalence of each virus (including coinfections), viral DNA tissue tropism, and lesion patterns among infected wild turkeys from across the southeastern USA. From December 2018 to April 2021, we tested a tissue subset (spleen, liver, and bone marrow with additional diagnostically relevant tissues) from 127 wild turkeys undergoing postmortem evaluation for LPDV and REV by PCR. 29.1% (37/127) of turkeys tested positive for LPDV-only and 11.0% (14/127) for REV-only in at least one tissue; 39.4% (50/127) were coinfecting. Among LPDV-infected turkeys (including coinfections), bone marrow most commonly tested positive (82/87; 94.3%) and the only tissue that tested positive in 7/35 (20.0%) cases. In REV-infected turkeys, bone marrow most commonly tested positive (43/97; 44.3%); all three tissues (spleen, liver, bone marrow) concurrently tested positive in 8/15 (53.3%) cases. Histopathology consistent with lymphoproliferative disease was evident in 15/125 (12.0%) turkeys tested, including one REV-only infected turkey. These results suggest LPDV tissue tropism for bone marrow, whereas REV may have broader tissue tropism and can be pathogenic in wild turkeys. These data will contribute to diagnostic strategies and assist in understanding potential impacts of these viruses on wild turkey populations.



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69 GENOMIC INSIGHTS INTO THE PATHOGENICITY OF A NOVEL BIOFILM-FORMING ENTEROCOCCUS SP. BACTERIA (*ENTEROCOCCUS LACERTIDEFORMUS*) IDENTIFIED IN REPTILES

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Keywords: Bacteria, Biofilm, Enterococcus, Reptiles, Whole Genome Sequencing

Abstract Text

Whole genome analysis of a novel species of enterococci, *Enterococcus lacertideformus*, causing multi-systemic and invariably fatal disease in critically endangered Christmas Island reptiles was undertaken to determine the genetic elements conferring its pathogenic nature, biofilm-forming capabilities, immune recognition avoidance, and inability to grow in-vitro. Comparative genomics with related and clinically significant enterococci were further undertaken to infer the evolutionary history of the bacterium and identify genes both novel and absent. The genome had a G+C content of 35.1% and was 2,419,934 bp in length. Multi-locus sequence typing (MLST), and single nucleotide polymorphism (SNP) analysis of multiple *E. lacertideformus* samples revealed they were highly clonal. *E. lacertideformus* was found to be located within the *Enterococcus faecium* clade and was closely related to *Enterococcus villorum* F1129D based on 16S rDNA and MLST house-keeping gene analysis. Antimicrobial resistance (*DfreE*, *EfrB*, *tetM*, *bcrRABD*, and *sat4*) and virulence genes (*Fss3* and *ClpP*), and genes conferring tolerance to metals and biocides (n=9) were identified. The detection of relatively few genes encoding antimicrobial resistance and virulence indicates that this bacterium may have had no exposure to recently developed and clinically significant antibiotics. Genes potentially imparting beneficial functional properties were identified, including prophages, insertion elements, integrative conjugative elements, and genomic islands. Functional CRISPR-Cas arrays, and a defective prophage region were identified in the genome. The study also revealed many genomic loci unique to *E. lacertideformus* which contained genes enriched in cell wall/membrane/envelop biogenesis, and carbohydrate metabolism. This finding and the detection of putative enterococcal biofilm determinants (*EfaAfs*, *srtC*, and *scm*) may underpin the novel biofilm phenotype observed. Comparative genomics revealed an absence of genes (n=54) that encode metabolic functionality, which potentially hinders nutrient acquisition/utilization by the bacterium and precludes growth in-vitro. These data provide genetic insights into the previously determined phenotype and pathogenic nature of *E. lacertideformus*.



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347 MOOSE (*ALCES ALCES*) WITH SUGGESTED SPONTANEOUS CHRONIC WASTING DISEASE IN SWEDEN

Erik Olof Ågren¹, Gustav Averhed¹, Dolores Gavier-Widén¹, Kaisa Sörén², Karolina Wall³, Sylvie L Benestad⁴, Linh Tran⁴, Neele Doose¹, Jørn Våge⁴, Maria Nöremark²

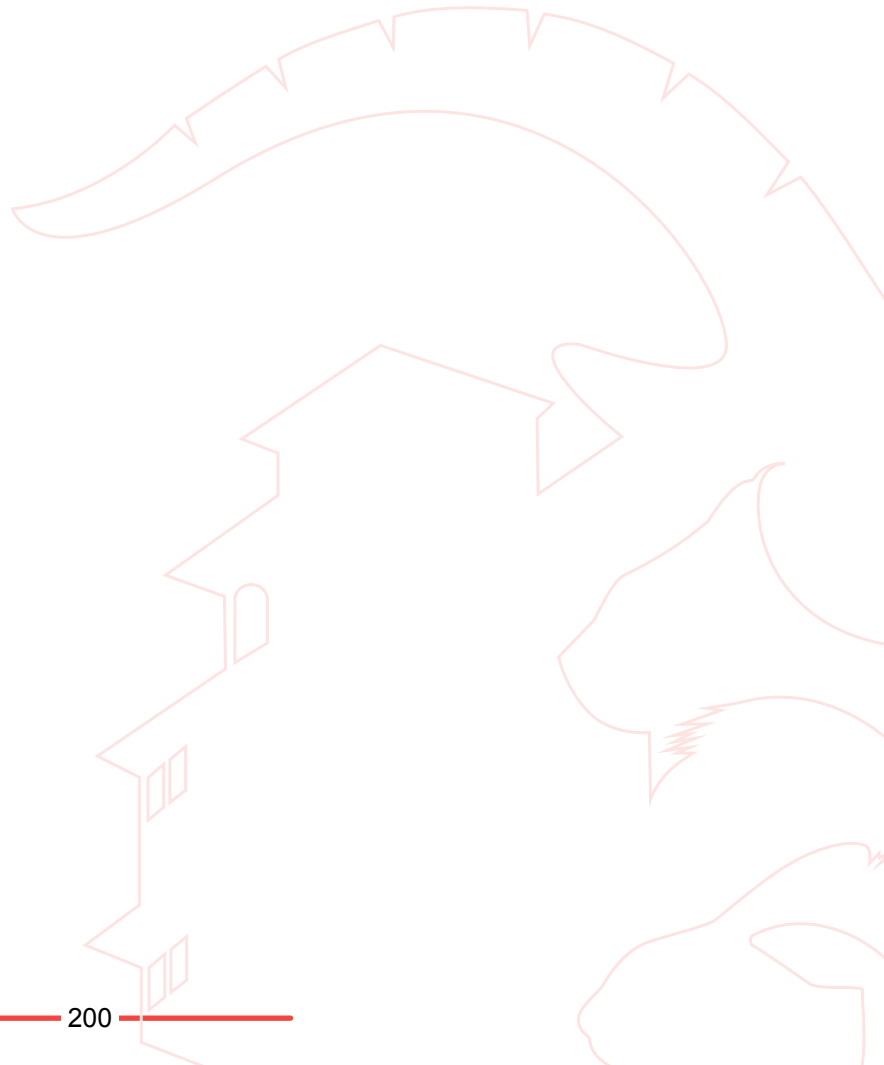
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Keywords: Chronic Wasting Disease, Surveillance, Moose (*Alces Alces*), Sweden, Prions

Abstract Text

Following the finding of CWD in 2016 in Norway in a wild reindeer, a European commission regulated surveillance of CWD was initiated in Sweden in 2018. The first two cases of CWD in Sweden were detected in the county of Norrbotten (Lat. 66°N) in March and May 2019, respectively. Both cases were 16-year-old female moose, both had been observed with behavioural changes and were euthanized. An intensified surveillance of 661 hunter harvested adult moose in this region detected a third positive case in September 2019. It was an apparently healthy, at least 10 years old female. A fourth moose case was found in the neighbouring county of Västerbotten in September 2020, when a 14-year-old female moose with some clinical signs of disease was euthanised. A locally intensified surveillance of 95 hunter harvested adult moose detected no further cases.

With screening tests all four moose were PrPCWD positive in brain tissue but negative in lymph nodes. Preliminary Western Blot glycoprofile and immunohistochemistry studies show similarities to described CWD cases in Norwegian moose, which differ from CWD in North American cervids. The CWD-cases in old moose in Nordic countries are suggested to be of spontaneous origin and not contagious. Further prion typing and epidemiological studies of these strains will be fundamental to understand the nature of this disease in moose as a basis for future management strategies.





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349 FINDING ELUSIVE ECHINOCOCCUS TAPEWORMS IN SWEDEN

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Keywords: Echinococcus, Wildlife, Zoonosis, Disease Surveillance, Sweden

Abstract Text

The tapeworms *Echinococcus granulosus*, sensu lato (E.g.) and *Echinococcus multilocularis* (E.m.) are both present in Sweden, but according to surveillance, at an apparently very low prevalence in focal areas or as rare findings in single animals, making them elusive to find and difficult to monitor or manage.

Echinococcus granulosus was not uncommon in the first half of the 20th century in semi-domesticated reindeer. Since the 1980's, only hydatid cysts have rarely been found in intermediate cervid hosts, mostly at meat inspection of slaughtered reindeer and hunter harvested free-ranging cervids. Biobank samples from wolves necropsied 2012 – 2020 were analysed in a retrospective study. Two out of 114 wolf fecal samples were PCR-positive for *E. granulosus*. The two positive wolves had both died in 2012. At this very low frequency of findings, the epidemiology of this parasite in Sweden is still enigmatic.

Echinococcus multilocularis was first found in Sweden in 2011, after 10 years of surveillance of red fox carcasses. After intensified surveillance 2011 – 2014, the parasite was found in five hot spots. In recent years, several cases of human alveolar echinococcosis have been found in Sweden where some patients could not be excluded to have been infected within the country. Therefore, monitoring of E.m. is now a priority for the Public Health Agency of Sweden. A second national screening is being initiated in 2021.

Also, in 2020, a focused screening of collected fox scats in the three of the five known hotspots showed PCR-positive scats in two areas; Uddevalla and Gnesta municipalities, indicating continued presence of the parasite at these sites. An expanded screening area is planned for 2021, to determine if the infection still is very localized and the hot spots could then be targeted for an attempt to eradicate the parasite by using medicated baits against tapeworm.



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266 IMPACT OF GI.1 AND GI.2 RABBIT HAEMORRHAGIC DISEASE VARIANTS ON WILD RABBIT POPULATIONS BASED ON SPANISH NATIONAL HUNTING BAG

Juan Antonio Aguayo-Adán¹, Simone Santoro², Carlos Rouco¹

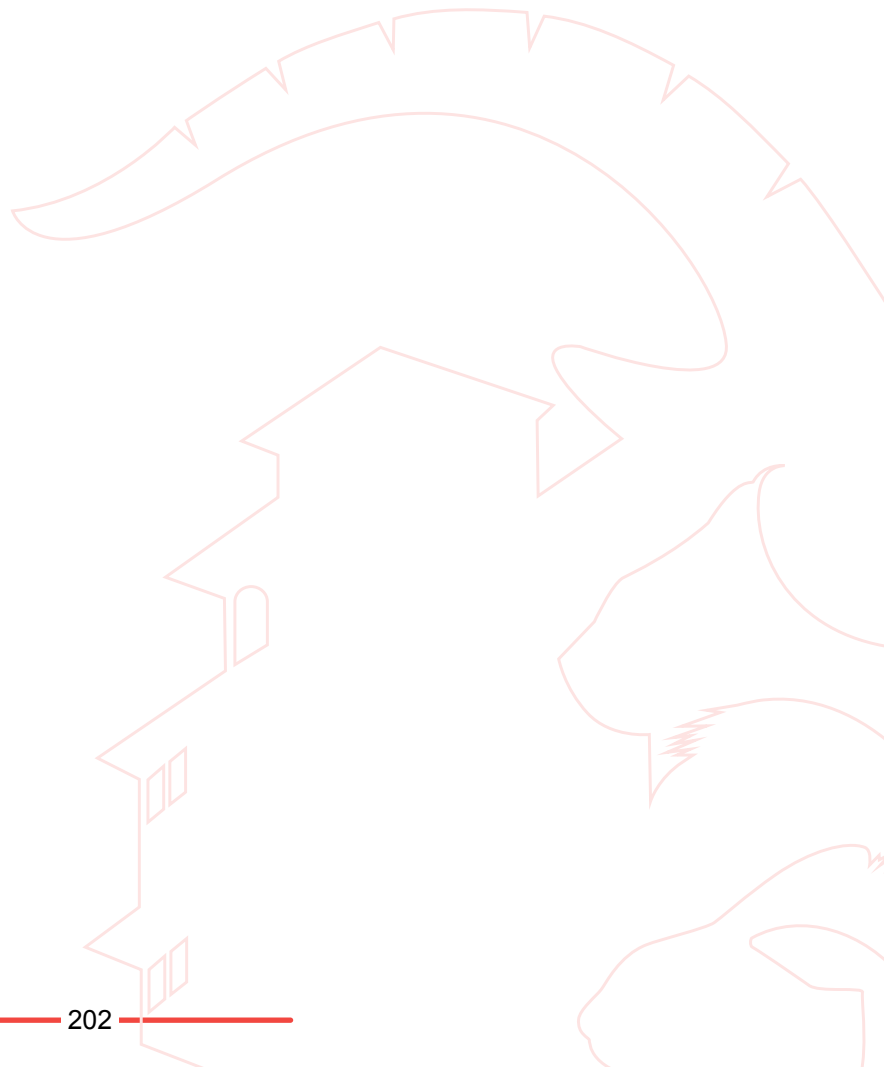
1. Universidad de Córdoba, Córdoba, Spain 2. Universidad de Huelva, Huelva, Spain

Keywords: Hunting Species, Lagovirus, *Oryctolagus Cuniculus*, RHD, Trend.

Abstract Text

Rabbit haemorrhagic disease (RHD) is an infectious disease that affects European wild rabbit. Its first outbreak in Spain was in June 1988. In 2010, a new RHD variant was discovered in France, followed by Spain in October 2011. While local evidence exists between the spread of this pathogen and the sharp decline over the last 50 years of wild rabbits' populations, there is a lack of information at a broader geographical scale. In Spain, the number of hunted pieces (hunting bags) must be declared by law and are publicly available from the yearbooks published by the National Institute of Statistics and the website of the Ministry of Agriculture and Fisheries, Food and Environment. We analyzed the impact of the two rabbit haemorrhagic disease variants in Spanish wild rabbit populations using an index of rabbit abundance (kills per licensed hunter based on the country-wide hunting bags of the most important game species).

Preliminary results revealed a significant decrease in rabbit abundance across the country following the GI.1 outbreak, but a slight increase following the GI.2 outbreak at the national level. Some Spanish regions experienced a decline in rabbit abundance after the GI.2 outbreak, although not as severe as after the GI.1 outbreak. On the other hand, in other regions, the population trend of wild rabbits according to the abundance index was less evident. A plausible explanation is that RHD does not affect the different regions homogeneously and that some areas are more vulnerable or affected than others. In this sense, hunting bags can provide a general abundance index that may help to assess diseases impact on the dynamic of wild rabbit population.





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266 REGIONAL AND INTER-SECTORAL GAPS IN THE ONE HEALTH RESEARCH; FUTURE DIRECTIONS

Juan Antonio Aguayo-Adán¹, Simone Santoro², Carlos Rouco¹

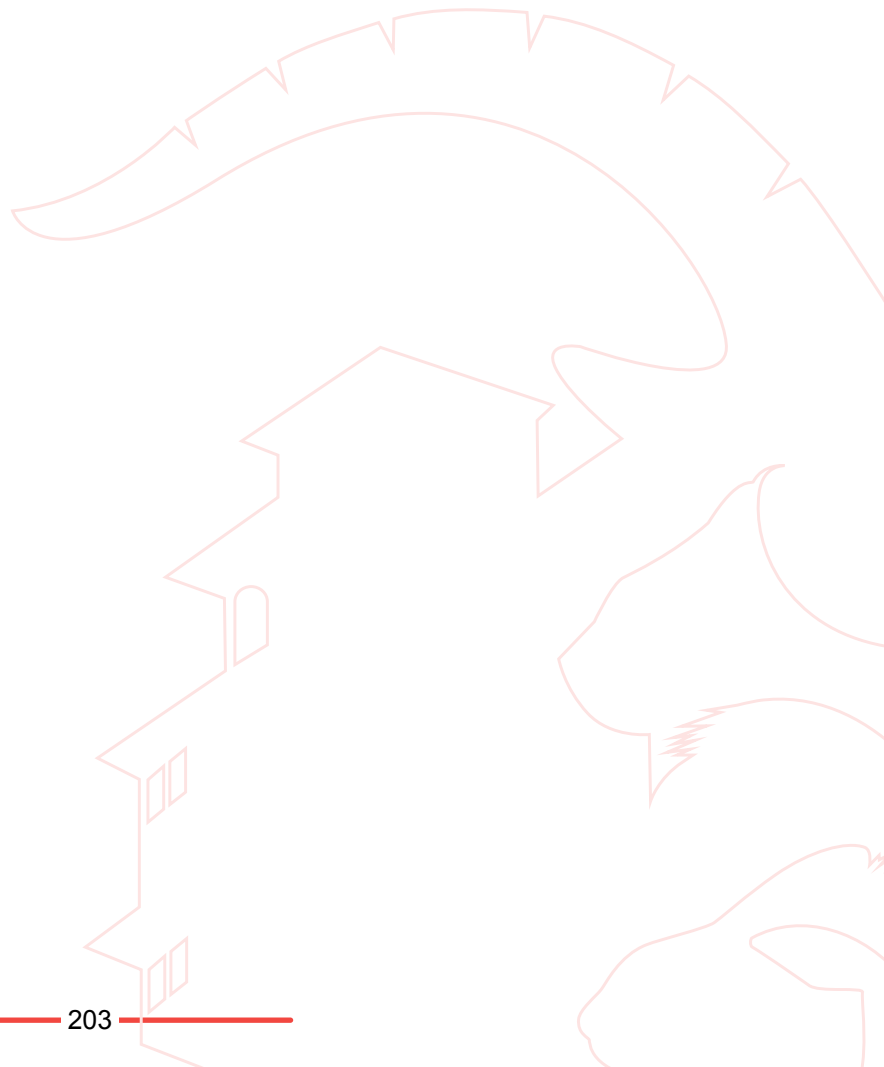
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Abstract Text

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89 VECTOR-BORNE VIRUSES IN UNGULATES IN SOUTHERN ONTARIO, CANADA: DISTRIBUTION AND ORBIVIRUS ESTABLISHMENT

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Keywords: Arbovirus, Bluetongue, Culicoides, Deer, Livestock

Abstract Text

Epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) are orbiviruses transmitted by biting midges (*Culicoides* spp.) that present an imminent threat to the health of ruminant livestock and wildlife. For some ruminant species, including wildlife, EHDV and BTV infections can result in high rates of illness and death. Information on prevalence and distribution of EHDV and BTV in Ontario, Canada are lacking, despite the likely climate change-facilitated northward spread. Our study sought to characterize the abundance and distribution of potential EHDV and BTV vectors, as well as assess for evidence of EHDV and BTV transmission to livestock and freeranging and captive cervids across Ontario. From June-October of 2017 and 2018, LED light suction traps were placed on farms and in natural areas across southern Ontario. All *Culicoides* collected were identified to species. Additionally, blood samples were collected from livestock and cervids (wild/farmed/zoo) and sera were tested for antibodies to BTV and EHDV. A total of 33,905 individual *Culicoides* spp. were collected, encompassing 14 species from seven subgenera and one species group. *Culicoides sonorensis*, a known vector of EHDV and BTV, was identified in both years. Additionally, *C. bergi* and *C. baueri* were identified in both years. These species represent new records for Ontario and Canada, and may indicate a northward expansion of their ranges. Blood samples from 349 livestock and 217 cervids were collected from 2016 to 2019. Fifteen (4.3%) livestock were seropositive for EHDV-serotype 2. Additionally, in 2017, we identified the first EHDV mortality event in wild white-tailed deer in southern Ontario, Canada. The EHDV-associated mortality in deer and seropositive cattle may represent the introduction of EHDV to Ontario through the movement of infected vectors or ruminants, and its detection in Ontario may represent the northern edge of the 2017 EHD outbreak in the eastern United States.



165 EXPERIMENTAL EVALUATION OF A PIT-TAGGING METHOD WITHOUT ANESTHETIC IN URODELES

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Keywords: Marking, Newts, PIT-Tag, Salamanders, Transponder.

Abstract Text

Amphibians are the most threatened vertebrate taxa on Earth, with over 40% of their species at risk of extinction. Therefore, there is an increasing need to monitor their health status and population trends. Capture-mark-recapture studies are an essential tool to study population and disease dynamics. Marking techniques need to be reliable, having minimal impact on the individual's survival and behavior while ensuring no tag loss. Passive Integrated Transponder (PIT) tags are a common marking method in vertebrates worldwide, including amphibians. However, the reliability of PIT-tags and marking protocols have not been evaluated for most urodele species. In this study, we assess the use of a subcutaneous PIT-tagging method without anesthesia in three species of urodeles. The method was tested on captive fire salamanders (*Salamandra salamandra*, n=18), Iberian ribbed newts (*Pleurodeles waltl*, n=12) and Pyrenean brook newts (*Calotriton asper*, n=9). All individuals were clinically healthy and kept in authorized facilities with appropriate husbandry conditions. Sterile PIT-tags (Trovan Technologies, 1.4×8mm) were injected subcutaneously in the dorsum and the site of injection was sealed with tissue adhesive. No tag rejection was observed in fire salamanders or Iberian ribbed newts, with rapid (2-3 weeks) and slightly delayed (3-4 weeks) wound healing, respectively. Conversely, we detected tag loss in Pyrenean brook newts (5/9, 55.6%), with delayed healing (> 4 weeks) and moderate inflammation at the site of injection. No death or loss of body condition was observed among individuals. The proportion of tag rejection was significantly different in Pyrenean brook newts from fire salamanders and Iberian ribbed newts (P=0.0031 and P=0.0062 respectively). These results may reflect differences in body size or ecological preferences between species, which may influence skin regeneration. Our results have implications for the future monitoring of these species and highlight the need to validate marking methods in wildlife.



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323 THE 'VICIOUS CIRCLES' OF HOST CONDITION, INFECTION SUSCEPTIBILITY AND INTENSITY MAY BE LESS COMMON THAN EXPECTED

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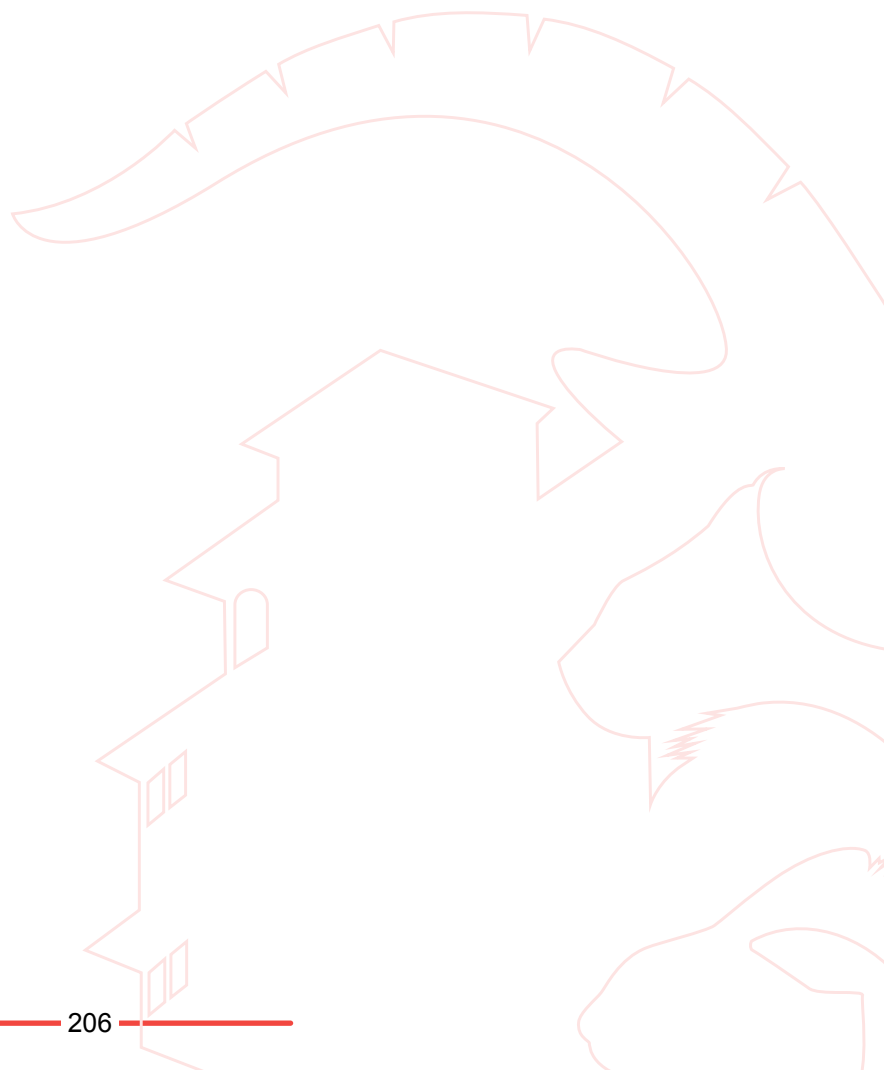
Keywords: Body Condition, Host-Pathogen Interaction, Immune Response, Resistance And Tolerance To Infection, Virulence

Abstract Text

In free-ranging wildlife populations, it is assumed that poor condition predisposes individuals to host infections, which in turn further reduces host condition, creating vicious circles. This approach is based on the concept of resistance to infection through the immune system, so hosts in poor condition have fewer resources for allocation to immune function, are more susceptible to infection, and less able to reduce the intensity or length of infection by pathogen clearance. However, poor condition is not systematically linked to an increase in pathogen susceptibility or to an intensity of infection, and host health can be not or minimally affected despite high pathogen burdens.

In this work, we discuss how “tolerance to infection”, “pathogen strategy” and the “energetic and specific nutritional requirements during infection” would explain the lack of the relationship between host condition and infection susceptibility and intensity. We performed a systematic literature research and then compared the proportion of studies detecting or not a link between host condition and infection by a Fisher's exact test. The proportion of works supporting or contradicting the idea that host condition influences susceptibility and intensity of parasite infection was similar.

The principle of tolerance, the existence of different parasite strategies, and the complex top-down and bottom-up regulations between pathogen communities and the host in the case of co-infections should be taken into account to explain observations of a lack of influence of host condition on susceptibility and intensity of infection.





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45 A NOVEL HERPESVIRUS DETECTED IN THREE DIFFERENT SPECIES IN THE ORDER TESTUDINES

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Keywords: Herpesvirus, *Stigmochelys Pardalis*, *Terrapene Alphaherpesvirus-3*, *Terrapene Mexicana Triunguis*, *Testudo [Agrionemys] Horsfieldii*

Abstract Text

Herpesviruses are important pathogens that infect all manner of taxa, and in some cases can infect across species. In testudines, herpesviruses can cause serious morbidity and mortality. To date, there are at least 22 documented alphaherpesviruses that affect testudinid species, including the fibropapilloma-associated Chelonid herpesvirus 5 and *Terrapene herpesviruses-1* and *-2* (TerHV-1, -2). Through diagnostic screening, we opportunistically identified a novel herpesvirus in three species of turtles: a captive leopard tortoise (*Stigmochelys pardalis*) in West Texas, a steppe tortoise (*Testudo [Agrionemys] horsfieldii*) found in the central Mojave Desert, California, and two three-toed box turtles (*Terrapene mexicana triunguis*) found in Forest Park, St. Louis, Missouri. Clinical signs varied across species and may be attributable to the herpesvirus, co-infecting pathogens identified in two of the individuals, or other unidentified factors. One of the three-toed box turtles displayed no clinical signs at the time of virus detection. To elucidate the phylogenetic relationship of this putative novel herpesvirus, nucleotide sequences of the highly conserved DNA polymerase gene were aligned with those of known testudinid herpesviruses. Bayesian and maximum likelihood phylogenetic analyses supported TerHV-1 as most closely related to the novel herpesvirus; therefore, we suggest the name *Terrapene alphaherpesvirus-3* (TerAHV-3). The branching order of turtle herpesviruses mirrors the divergence pattern of their hosts, consistent with codivergence. Herpesvirus infections generally show little to no clinical signs in the natural host but can cause serious disease in related hosts. This virus appears to have the ability to host-jump, which has not yet been identified with other terrapene herpesviruses. Our findings underscore the need to scrutinize instances in which non-naturally co-occurring species are placed together; e.g., the pet trade. Future screening for this herpesvirus may be useful in determining its role in testudinid disease.



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117 ANTIMICROBIAL RESISTANT *MOELLERELLA WISCONSENSIS*; A POTENTIALLY ZOOONOTIC PATHOGEN ISOLATED FROM WILD BIRDS IN GREECE

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Keywords: *Moellerella wisconsensis*, Antimicrobial Resistance, ESBL, CTX-M, Wild Birds

Abstract Text

Moellerella wisconsensis has seldom been implicated in human clinical cases, such as diarrhea, cholecystitis and peritonitis and has occasionally been isolated from environmental and animal samples. The exact distribution and the potential pathogenicity of the bacterium remain widely unknown. During 2019-2021, a total of 287 cloacal swab samples were collected from forty-three different wild bird species in Greece, in order to evaluate fecal carriage of antimicrobial resistant strains. Swabs were directly streaked on MacConkey agar and on CHROMID® ESBL agar (BioMérieux, Marcy l'Etoile, France). Identification and antimicrobial susceptibility testing of the obtained strains were performed using the Vitek-2 system (BioMérieux, Marcy l'Etoile, France), while the identity of *M. wisconsensis* isolates was additionally verified by 16S rDNA amplification. Isolates that presented resistance to 3rd generation cephalosporins were phenotypically screened for ESBL production by the double-disc synergy test and further molecularly tested for carriage of blaCTX-M. Three *M. wisconsensis* strains were obtained from one common pheasant (*Phasianus colchicus*) and two eurasian magpies (*Pica pica*). The strain isolated from a common pheasant presented resistance to polymixin B and cefalexin. The two magpie strains were resistant to polymixin B, ampicillin, cefalexin, cefalotin, cefoperazone, ceftiofur, cefquinome and tetracycline, while one of them was also resistant to gentamicin and trimethoprim/sulfamethoxazole. Both magpie strains expressed the ESBL phenotype and harbored blaCTX-M. In this study, we provide evidence of the dissemination of *M. wisconsensis* among wild birds in Greece and report ESBL production in wild birds' isolates of this bacterial species for the first time.



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302 SURVEILLANCE OF CHRONIC WASTING DISEASE IN SWEDEN

Gustav Averhed¹, Maria Noremark¹, Kaisa Sörén¹, Maria Cedersmyg², Karolina Wall², Dolores Gavier-Widén¹, Erik Ågren¹

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Keywords: Chronic Wasting Disease, Surveillance, Sweden, Epidemiology, Cervids

Abstract Text

In 2016, a case of CWD was detected in Norway in a wild reindeer and later the same year a case in moose. This led to an EU-regulated surveillance of CWD in member states with populations of reindeer and/or moose. Each country was requested to examine at least 6,000 cervids over a three-year period between 2018 and 2020.

The Swedish surveillance focuses on adult cervids at risk: those that show signs of CWD or other disease, or are found dead, including traffic killed cervids. With a financial limit of 6,000 cervids to be sampled in Sweden, healthy hunted or slaughtered animals have not been targeted, except for animals deemed unfit for human consumption. Due to regulatory issues between involved authorities, traffic killed cervids have not been accessible for sampling, despite ongoing efforts to solve this. Finding animals fulfilling the other criteria and collecting samples from them, often from remote areas, have been a logistic and educational challenge.

There have been several campaigns and efforts to inform and motivate hunters, and owners of farmed and semidomesticated cervids to submit samples for CWD surveillance, and the public to report found dead cervids. The most successful measures to obtain samples from wild cervids were communication with hunter organizations and direct personal contact with individual interested hunters.

Until now, four positive cases of CWD have been detected, all in old female moose with detectable prions in brain but not in lymph nodes. In the areas where the CWD cases were detected an intensified surveillance was conducted, which included also healthy animals from hunting and slaughter to evaluate whether there was evidence of a contagious variant of CWD. The EU-surveillance has been extended to include year 2021, as animals at risk are valuable for the surveillance results, but difficult to obtain in large numbers



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317 POSTERIOR PARALYSIS: AN OVERLOOKED CHALLENGE IN BIG CAT CONSERVATION

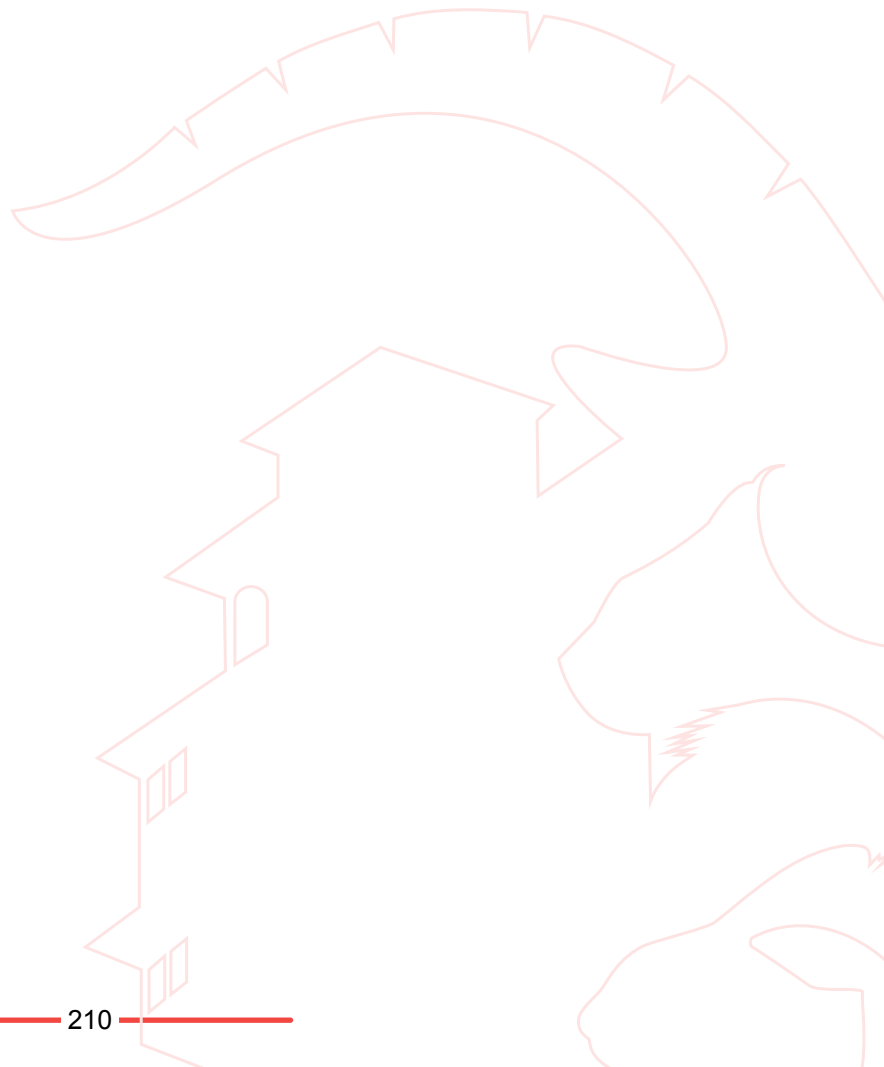
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Keywords: Big Cats, Ex- Situ Conservation, Paraplegia, Paresis, Posterior Paralysis

Abstract Text

Posterior paralysis is a fatal and often overlooked condition prevalent among both wild and captive large felids. In contrast, a retrospective study on the prevalence of posterior paralysis among Asiatic lions and other captive big cats in Indian zoos and wild populations from 1990 to 2021 was done by means of extensive literature survey through published research articles, case studies, mortality records, and newspaper articles. Additionally medical records and necropsy reports were collected from 3 Asiatic Lions suffering from hind limb paralysis in the state of Kerala. The study investigates big cats (Lions, Tigers, Leopards, Cheetahs, Snow leopards) mortality in zoos and in the wild and found large numbers ($n > 20$) of big cats that died due to posterior paralysis, which may be associated with various aetiologies like cranial malformation, nutritional deficiency, degenerative spinal disorders, incidence of viral diseases like Canine Distemper, Feline Infectious Peritonitis, Feline Immunodeficiency virus, Feline Panleukopenia virus etc. Asiatic lions are the most affected species in the study group with incidence of paralysis reported in the wild population. Immediate serosurvey & epidemiological study should be conducted to aid disease mitigation strategies as high magnitude seroprevalence of important viral diseases that can cause posterior paralysis are known to be present in captive as well as wild populations. The study discusses various effective diseases surveillance strategies, diagnosis methods, and treatments aspects.





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149 A FRAMEWORK FOR MORE CONSISTENT REPORTING OF WILDLIFE-LIVESTOCK CONTACT DATA

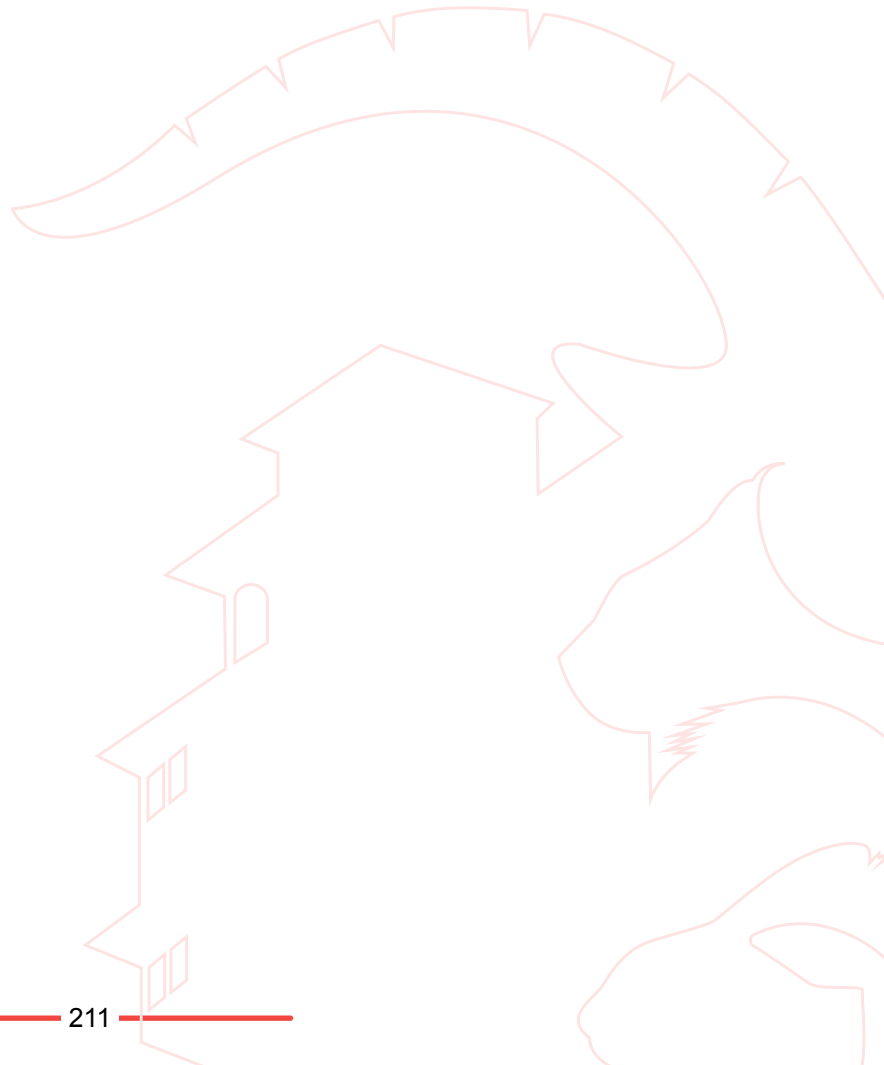
Sonny A. Bacigalupo¹, Linda K. Dixon², Simon Gubbins², Adam J. Kucharski³, Julian A. Drewe¹

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Keywords: Contact, Definition, Framework, Interaction, Wildlife-Livestock

Abstract Text

The transmission of pathogens between wild animals and livestock threatens ecosystem health, causes human-wildlife conflicts, often incurs large costs and can threaten human health. Knowledge of the types of contacts that occur between wildlife and livestock, and the rates at which these contacts occur, is necessary to identify risk factors for potential pathogen transmission and to implement and improve mitigation strategies to reduce disease risks. What constitutes a relevant contact between wildlife and livestock is, however, highly variable because it depends on the host species, the pathogen and the environment. Further variation arises from the wide variety of methods used to detect contacts. As a result, there is a lack of consistency in the terminology used to report such contacts which makes it difficult (if not impossible) to meaningfully compare studies. We will demonstrate a novel unified framework to promote consistent definitions and reporting of wildlife-livestock contacts (both direct and indirect) that is flexible and applicable to different contexts, species and diseases. It considers variation in two main components: space and time. Our framework arose from the findings of a systematic review of over 30,000 papers published from 1980 to 2019. We use a range of empirical examples from studies identified in this review to demonstrate the utility of the framework. The framework helps standardise the collection and reporting of contact data and is a valuable step towards being able to compare the efficacy of observation methods used to monitor wildlife-livestock contacts. This is important since these methods often have low detection rates and many such studies have low power. In doing so, use of the framework may aid the development of better disease transmission models and improve the design and effectiveness of interventions to reduce or prevent disease transmission between livestock and wildlife.





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125 WATER SPORTS COULD CONTRIBUTE TO THE TRANSLOCATION OF RANAVIRUSES

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Keywords: Batrachochytrium Dendrobatidis, Batrachochytrium Salamandrivorans, Boat, QPCR, Ranavirus

Abstract Text

Ranaviruses have been identified as the cause of explosive disease outbreaks in amphibians worldwide and can be transmitted between hosts both via direct and indirect contact, in which humans might contribute to the translocation of contaminated material. The aim of this study was to evaluate the possible role of water sports in the human translocation of ranavirus, *Batrachochytrium dendrobatidis* (Bd), and *B. salamandrivorans* (Bsal).

A total of 234 boats were sampled during the spring Spanish Canoe Championship which took place in Pontillón de Castro, a reservoir with a history of ranaviruses, in May 2017. Boats were tested for the presence of ranavirus and *Batrachochytrium* spp. DNA, using quantitative real-time polymerase chain reaction techniques (qPCR).

A total of 22 swabs (22/234, 9.40%) yielded qPCR-positive results for Ranavirus DNA while Bd or Bsal were not detected in any of the samples.

This research demonstrates for the first time how water-related sports such as kayaking can be a source of pathogen pollution for amphibians. Other human activities such as fishing and swimming could be additional sources through contaminated equipment, and needs to be investigated. Our results provide justification for public disinfecting stations in key areas where human traffic from water sports is high.

The study was partially supported by a grant from the Principado de Asturias, PCTI 2018–220 (GRUPIN: IDI2018-000237 and FEDER) and by the Xunta de Galicia (with the financial support of EAFRD). We are indebted to the Galician Canoeing Federation for their help



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177 TICK RISK IN ROE DEER FAWNS: WHAT LINKS WITH ENVIRONMENT AND INDIVIDUAL CHARACTERISTICS?

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Keywords: Capreolus Capreolus, Ixodes Ricinus, Climatic Variability, Density, Individual Characteristics

Abstract Text

Ticks are important vectors of many pathogens, threatening both human and animal health. Among ticks, *Ixodes ricinus* is the most common species in Central Europe, known to transmit major pathogens to domestic and wild animals and humans such as *Babesia* spp., *Borrelia* spp., *Anaplasma* spp. or Tick-Borne Encephalitis virus.

During the early 20th century, its abundance and distribution have increased in the continent, as a consequence of global environmental changes. In fact, as ticks spend most of their life in the environment, their activity and the completion of their life cycle are highly dependent of environmental conditions. For instance, increasing of wild ungulate populations, and particularly roe deer (*Capreolus capreolus*), in recent years, have allowed tick populations to grow and spread through Europe. In addition, climate change has allowed the settlement of *Ixodes ricinus* at higher latitude and altitude during last decades.

The tick risks on newborns wild ungulates is poorly documented. However, as newborns have an immature and naïve immune system, they are considered more sensitive to tick bites and risk of pathogen transmission. Thus, knowing how host itself or environment influence tick burden on newborn individuals is essential to better understand their health risks.

Based on a long-term monitoring of the roe deer fawns in Trois-Fontaines (France) from 1992 to 2020, we assessed the influence of individual phenotypic attributes, meteorological conditions and population density on tick burden of 1048 fawns.

Firstly, tick burden was positively correlated with body surface area and age of fawns, with significantly more ticks on older and larger individuals. Roe deer abundance and environmental factors seem also to influence the tick risks on newborn fawns in this population.



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313 INFECTIOUS DISEASE SURVEILLANCE AT THE WILDLIFE–DOMESTIC INTERFACE OF A PARTRIDGE FARM

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Keywords: Avian Avulavirus 1, Avian Influenza Virus, Partridges, Passeriformes, Salmonella Typhimurium

Abstract Text

Studies about the epidemiology of avian influenza virus (AIV) and other pathogens at the wildlife–domestic interface are still scarce but necessary. Here we present preliminary results from a partridge farm located in Northern Spain that is part of a study that integrates the prevalence and dynamics of AIV and other pathogens in poultry and gamebird farms and wildlife, with the ecology of wild peri-domestic species, to characterize their epidemiology at the wildlife–domestic interface. We collected samples from farmed birds on five occasions (during spring and autumn migration, wintering and breeding) during 2019 and captured small mammals and wild Passeriformes on the farm and in its surroundings. Cloacal and oropharyngeal swabs were collected from partridges and Passeriformes, and tissue samples were taken from small mammals. Samples were tested for AIV, avian avulavirus 1 (AA1), and Salmonella typhimurium by real-time RT-PCR/PCR. Seroprevalence of AIV and AA1 was determined, using commercial ELISA kits. Low pathogenic AIV were identified in oropharyngeal swab from 2.3% (4/173) of the Passeriformes and 1.0% (2/193) of the partridges. AIV prevalence was highest during autumn migration 7.0% (5/71) ($p=0.0014$) although it was also detected during wintering (1.2%, 1/86). Antibodies against AIV were detected in 5.8% (10/193) ($p=0.0553$) of the partridges and 0.8% (1/126) of the Passeriformes, with the highest prevalence detected during wintering 5.1% (4/78) and spring migration 4.6% (6/130) ($p=0.3705$). However, antibodies against AAV1 were only detected in Passeriformes (6.6% (5/76), $p=0.0016$) during autumn migration and wintering. *S. typhimurium* was detected in small mammals (3.9%, 2/51) and partridges (3.3, 5/152), but not in Passeriformes ($p=0.0525$). Detection of the same pathogens in different animal species at the wildlife–domestic interface, suggests a shared transmission. Further studies are needed to better characterize the sanitary risks related to wildlife–domestic birds interaction.



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159 EXPLORING EPIGENETICS IN ENDANGERED CETACEANS

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Keywords: Aging, Cetacean, Endangered Species, Epigenetics, Methylation

Abstract Text

Estimation of age in wild cetaceans is pivotal for conservation, enabling understanding of population demographics and survival probability. The Lahille's bottlenose dolphin (*Tursiops truncatus gephyreus*)(Tg) is an endangered cetacean, found in two geographically isolated subpopulations from Southern Brazil to Argentina. With approximately 600 individuals remaining and an estimated 360 capable of reproducing, the population is at high risk of extinction.

Epigenetics, specifically DNA methylation, provides an opportunity to develop a remote sampling diagnostic aging tool, utilising DNA extracted from skin biopsy samples. DNA methylation is the addition of methyl groups to cytosine-phosphate-guanine (CpG) sites and occurs systematically with age, therefore methylation assessment can provide a chronological age estimate. Additional CpG sites can become methylated due to biological changes and can indicate health status or biological age. Age acceleration occurs when a biological age is higher than the chronological age.

We established an epigenetic aging clock in 33 known age bottlenose dolphins (*Tursiops truncatus*) identifying 44 CpG sites from 37,491 assessed, associated with chronological aging ($R = 0.96$). In addition, known health status enabled assessment of biological age at different CpG sites providing an indication of age acceleration. Remote biopsy skin samples have been collected from 60 Tg dolphins in Brazil, to enable DNA extraction and application of this newly established bottlenose dolphin aging clock to estimate the individuals' ages.

In endangered species conservation, knowledge of population demographics can aid interpretation of biological health data influencing conservation medicine approaches, management decisions, and the development of species recovery plans.



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233 FIRST REPORT OF GI.2 IN A CAPE HARE (*LEPUS CAPENSIS*) FROM AFRICA

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Keywords: Hare, Lagovirus Europaeus/GI.2, Lepus Capensis, RHDV2, Tunisia Wildlife

Abstract Text

Rabbit hemorrhagic disease was identified for the first time in 1984 in China. The disease is caused by the rabbit hemorrhagic disease virus (RHDV), a member of the Lagovirus genus, Caliciviridae family. RHDV (genotype GI.1) was described as restricted to its natural host, the European rabbit (*Oryctolagus cuniculus*), causing a fatal acute hepatitis in adult farmed and wild rabbits, with high mortality and morbidity rate. In 2010, a newly emerged RHDV related virus called RHDV2/b or Lagovirus europaeus/GI.2 was identified in France, and then spread throughout the world replacing older circulating strains and causing extended outbreaks in most rabbit populations. In Tunisia, GI.2 was first detected in 2015 and was responsible for considerable economic losses in rabbitries.

Compared to GI.1, GI.2 has distinctive phenotypic traits, causing atypical outbreaks in rabbits of all age groups, with a higher frequency of occurrence of subacute/chronic forms. In addition, GI.2 overcame the species barrier, since it causes disease in several hare species including the European brown hare (*Lepus europaeus*), Cape hare (*Lepus capensis* subsp. *mediterraneus*), Corsican hare (*Lepus corsicanus*) and mountain hare (*Lepus timidus*).

Here we report for the first time the identification of GI.2 in a Cape hare (*Lepus capensis*) found dead in 2020 in a forest area located in the northeast of Tunisia (36°54'58.22"N 11° 4'38.89"E). Post mortem examination of the carcass revealed hemorrhagic lesions in different organs including the liver, lungs and spleen, suggestive of a pathogenic lagovirus infection. Molecular analysis by RT-PCR further confirmed infection with GI.2. As this genotype has been circulating in Tunisia since 2015, it is possible that GI.2 infection of the Cape hare resulted from a spillover event from rabbit outbreaks in neighboring areas, highlighting the need of virus surveillance at the interface between wild and domestic leporids.



207 BEAK AND FEATHER DISEASE VIRUS DETECTION AND LOAD IN MULTIPLE TISSUES AND BLOOD IN A WILD PARROT POPULATION

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Keywords: BFDV, Circovirus, Parrot, Virus Load, Wildlife

Abstract Text

Beak and feather disease virus (BFDV) is a circovirus that infects captive and wild psittacines, and thus a conservation concern worldwide. Infection with BFDV may cause chronic and often fatal disease, with feather dystrophy and loss, beak and claw deformity, and immunosuppression. Crimson rosellas (*Platyercus elegans*) are an abundant parrot occurring in south-eastern Australia. Previous research showed that, unlike some psittacine species, wild populations of *P. elegans* have high BFDV prevalence without apparent clinical signs, and seroconversion and clearing of the virus from blood has been observed. We hypothesised that (1) BFDV may persist in tissues after clearing from blood, as seen for similar virus infections such as porcine circovirus-2 and chicken anaemia virus, and (2) tissue virus load would be higher in younger birds.

To investigate this, we necropsied and sampled tissues from 66 wild *P. elegans* from Victoria, Australia. For each bird, virus load data was obtained for blood and 10-12 tissues by real-time qPCR, and antibodies to BFDV were detected by serology. Our results showed that virus load in tissues and blood from subadults were much higher and detected in more tissues than in adult *P. elegans* ($p < 0.001$). In addition, for subadults ($n=32$), virus load in bursa, spleen and skin were higher ($p < 0.001$) than other tissues like blood and muscle. While BFDV was detected in most tissues and blood from subadults, in adults ($n=34$) BFDV was not detected in blood but was still detected in some tissues. Antibodies to BFDV were primarily detected in adults.

This study has major implications for assessment of BFDV disease status and management in the wild, as the findings suggest that while BFDV replicates to high levels in apparently healthy subadults, some adult *P. elegans* seroconvert and have undetectable levels of virus in blood while still having low virus load detected in tissues.



273 MOLECULAR DESCRIPTION OF GASTROINTESTINAL HELMINTHS OF THE GREAT BUSTARD (*OTIS TARDA*) IN TWO AREAS OF THE IBERIAN PENINSULA.

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Keywords: Otis Tarda, Helminths, Molecular Analysis, COX, ITS

Abstract Text

The Great Bustard (*Otis tarda*) is a wild bird associated to agrarian ecosystems. Threats such as fragmentation and habitat loss have led it to the classification as a vulnerable species. The ecology and habitat selection of this species are well known but detailed studies of its gut parasites and their information in the genetic sequences databases are limited, although intestinal obstruction by cestodes has been described as one of the causes of mortality in Spain. In this work, intestinal helminths of the Great Bustard were characterized by morphology of the eggs and adults, and by sequence analysis. For this purpose, 170 droppings collected in two areas of the Iberian Peninsula were analysed by coprology. A selection of samples positive to helminths eggs in the coprology were subjected to DNA extraction and amplification by PCR. Besides, an adult proglottid and nematode L3 from faecal cultures, were employed. The internal transcriber spacer region (ITS) and Cytochrome C oxidase (COX) gene, two frequent targets employed for helminth molecular diagnosis, were amplified by PCR. Subsequently, a sequence analysis was performed. After assembling sequences from both directions, the first consensus ITS sequence of trichostrongilids affecting the Great Bustard were obtained. The sequence was 316 bp length and showed 96.2% homology with *Trichostrongylus colubriformis*, a frequent nematode of ruminants. Besides, a consensus COX sequence from the main cestode of the Great Bustard (*Otiditaenia* spp.), was also obtained, and the sequence of 368 bp showed 86.7% homology with *Taenia saginata*, a human cestode, and *Taenia omissa*, a cestode from pumas. This is the first report of these sequences, since no data from both helminths are included in the databases. With this work, knowledge on the parasitic helminths of the Great Bustard has increased, and PCR procedures as an alternative to coprology have been explored.



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101 CURRENT STATUS OF TOXOPLASMA GONDII IN FOXES (VULPES SPP.) FROM NORTHERN CANADA

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Keywords: Toxoplasma, Parasite, Arctic, Fox, Zoonoses

Abstract Text

In changing northern ecosystems, understanding the mechanisms of transmission of zoonotic pathogens, including the coccidian parasite *Toxoplasma gondii*, is essential to protect vulnerable animal and human populations living in these regions. As high-level predators and scavengers, foxes provide a sensitive indicator of the distribution and transmission of *T. gondii*, without being a source of human exposure. The objectives of our research are to generate baseline data on *T. gondii* in foxes across northern Canada and understand the trophic relationships between foxes and their prey species. Red (*Vulpes vulpes*) (n=579) and Arctic fox (*Vulpes lagopus*) carcasses (n=155) were collected by local trappers and collaborators from Labrador, Québec, northern Manitoba, Nunavut, and the Northwest Territories during winters of 2015-2019. *Toxoplasma gondii* DNA was detected in heart and brain using magnetic capture PCR. Antibodies in heart fluid were detected using enzyme-linked immunosorbent assay as evidence of previous exposure to the pathogen. We reconstituted the diet of Nunavik foxes for a year by measuring stable isotope ratios of C and N in hair and muscles to link prey with status of infection. The overall *T. gondii* tissue prevalence was 27% (n=179/662, 95% CI:24-31) in foxes, compared to a seroprevalence of 36% (n=259/717, 95% CI:33-40). Tissue prevalence in foxes from western Nunavik [51% (n=38/75; 95% CI:36-70)] was significantly higher than in eastern Nunavik [20% (n=33/165; 95% CI:14-28)], possibly due to dietary differences. Stable isotope mixing model analysis showed that infected foxes have a higher probability to consume marine food sources and snow geese (*Chen caerulescens*) compared to negative foxes. Our study sheds new light on the current status of *T. gondii* in foxes in northern Canada. Future work is needed to determine the potential impact of *T. gondii* infection on foxes, and the significance of these findings for human exposure.



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291 RNA IN SITU HYBRIDIZATION AND VIRUS CHARACTERIZATION OF SKUNK ADENOVIRUS IN NORTH AMERICAN WILDLIFE DEMONSTRATES SEVERE MULTISYSTEMIC INFECTIONS AND GENETIC VARIATION IN A BROAD HOST RANGE.

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Keywords: Skunk Adenovirus, Disease, Bronchointerstitial Pneumonia, Porcupine, Raccoon

Abstract Text

Skunk adenovirus is an emerging pathogen in North American wildlife, with a broad host range. It has been reported in two North American porcupines, a colony of African pygmy hedgehogs, a striped skunk, and a grey fox. However, the spectrum of disease caused by skunk adenovirus in wildlife species, particularly porcupines, has not yet been completely characterized. We describe and characterize the pathologic findings and tissue distribution of skunk adenovirus in 24 wildlife diagnostic cases including 16 porcupines, 3 striped skunks, and 5 raccoons, of which infection in the latter species (raccoons) has not yet been described. The most common lesion in all species was severe necrotizing bronchopneumonia with (n=12) or without (n=10) interstitial involvement. Intranuclear inclusion bodies appeared predominantly in respiratory epithelium (n=21) and less often in renal tubular (n=6) and biliary epithelium (n=1). Several cases were associated with significant secondary bacterial infections including *Bordetella bronchiseptica*, *K. pneumoniae*, *Pasteurella multocida*, *Streptococcus zooepidemicus*, and *E. coli*. RNA in situ hybridization in porcupine (n=6), raccoon (n=1), skunk (n=1), grey fox (n=1), and African pygmy hedgehog (n=1), revealed skunk adenovirus DNA in lung, trachea, turbinates, liver, kidney, lymph node, and brain in multiple cell types including epithelium, endothelium, and mesothelium; these findings were consistent across species. Preliminary comparisons of viral genomes isolated from porcupines, skunks, and raccoons demonstrated DNA point mutations in coding and noncoding regions which resulted in variations in amino acid sequences between all three virus isolates including two regions (nucleotide positions 27956 and 27992) of the fiber protein, which is important for entry into host cells. These findings describe the spectrum of disease associated with skunk adenovirus infection in 24 diagnostic cases from wildlife and suggest variation in fiber protein sequence as a possible mechanism for its ability to infect a broad host range.



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303 SUSCEPTIBILITY OF ANURANS, LIZARDS, AND FISH TO INFECTION WITH DRACUNCULUS SPECIES LARVAE AND IMPLICATIONS FOR THEIR ROLES AS PARATENIC HOSTS

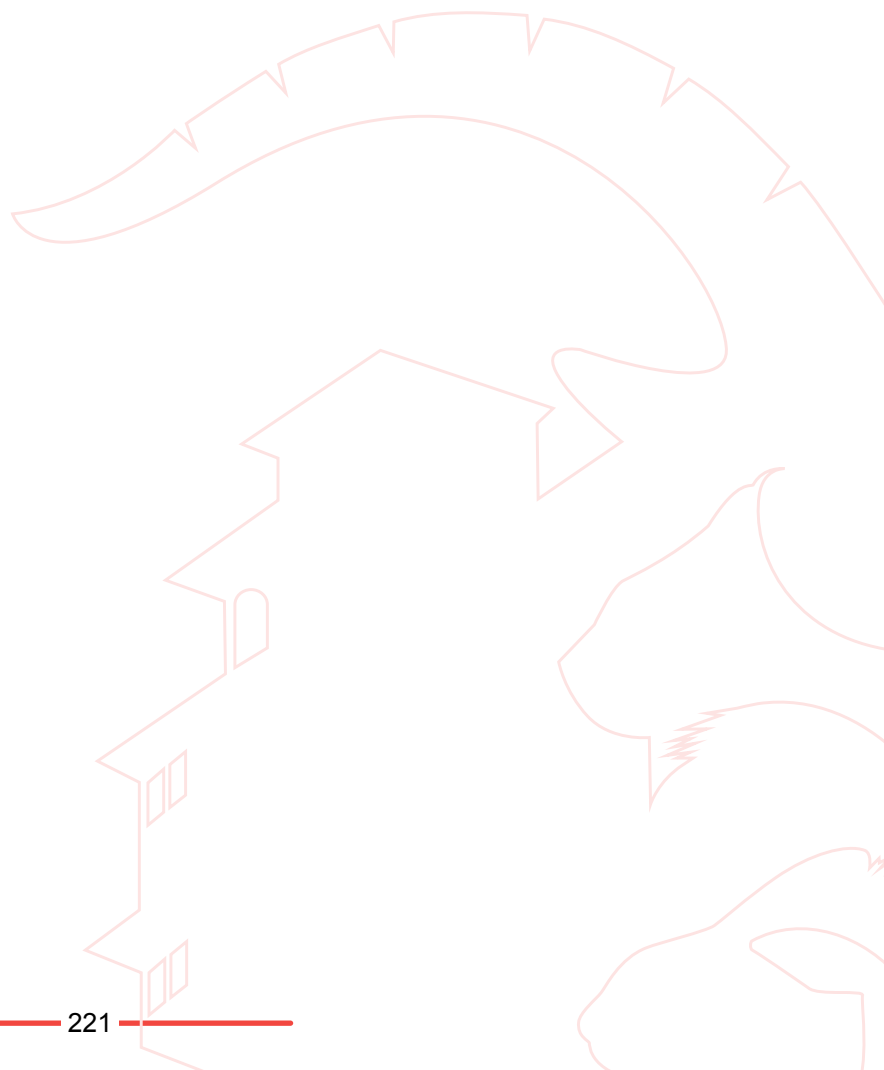
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Keywords: Life Cycle, Nematode, Parasite, Paratenic Host, Transmission

Abstract Text

Species in the genus *Dracunculus* are parasitic nematodes that infect numerous species of mammals and reptiles. The life cycles of Dracunculids are complex, and questions remain regarding the role of paratenic and transport hosts in transmission to definitive hosts. We investigated two primary objectives: 1) to assess the susceptibility of several species of anurans, lizards, and fish as paratenic hosts for *Dracunculus* species, and 2) to determine the long-term persistence of *Dracunculus* infections in African clawed frogs (*Xenopus laevis*). Animals were exposed per os to copepods containing infectious third-stage larvae (L3s) of either *Dracunculus insignis* or *Dracunculus medinensis*. *Dracunculus* L3s were recovered from four anuran species, two lizard species, and one fish species, demonstrating that Dracunculids can infect tissues of a diversity of species. In long-term persistence trials, *D. medinensis* L3s were recovered from African clawed frogs tissues up to 58 days post-infection, and *D. insignis* L3s were recovered up to 244 days post-infection. Our findings regarding the susceptibility of novel species of frogs, lizards, and fish to infection with *Dracunculus* nematodes, and the long-term persistence of L3s in paratenic hosts address pressing knowledge gaps regarding *Dracunculus* infection in paratenic hosts and may guide future research regarding the transmission of *Dracunculus* to definitive mammalian hosts.





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326 COPEPOD CONSUMPTION BY AMPHIBIANS AND FISH WITH IMPLICATIONS FOR TRANSMISSION OF DRACUNCULUS SPECIES

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Keywords: Life Cycle, Nematode, Parasite, Paratenic Host, Transport Host

Abstract Text

Parasitic nematodes in the genus *Dracunculus* have a complex life cycle that requires more than one host species in both aquatic and terrestrial habitats. The most well-studied species, *Dracunculus medinensis*, is the causative agent of human Guinea worm disease (dracunculiasis). There are several other *Dracunculus* species that infect non-human animals, primarily wildlife (reptiles and mammals). The classic route of *D. medinensis* transmission to humans is through the ingestion of water containing the intermediate host, a cyclopoid copepod, infected with third-stage larvae (L3s). However, many animal hosts (e.g., terrestrial snakes, dogs) of other *Dracunculus* sp. appear unlikely to ingest a large number of copepods while drinking. Therefore, alternative routes of infection (e.g., paratenic or transport hosts) may facilitate *Dracunculus* transmission to these species. To better understand the role of paratenic and transport hosts in *Dracunculus* transmission to animal definitive hosts, we compared copepod ingestion rates for aquatic species (fish, frogs [tadpoles and adults], and newts) which may serve as paratenic or transport hosts. We hypothesized that fish would consume more copepods than amphibians. Our findings confirm that African clawed frogs (*Xenopus laevis*) and fish consume copepods, but that fish ingest, on average, significantly higher numbers (68% [34/50]) than adult African clawed frogs (36% [18/50]) during a 24-hour time period. Our results suggest that amphibians and fish may play a role in the transmission of *Dracunculus* to definitive hosts. Still, additional research is required to determine whether, in the wild, fish or frogs are serving as paratenic or transport hosts. If so, they may facilitate *Dracunculus* transmission. However, if these animals simply act as dead-end hosts or as means of copepod population control, they may decrease *Dracunculus* transmission.



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200 RNA PATHOGEN DETECTION IN FREE-RANGING BLANDING'S TURTLES (*EMYDOIDEA BLANDINGII*)

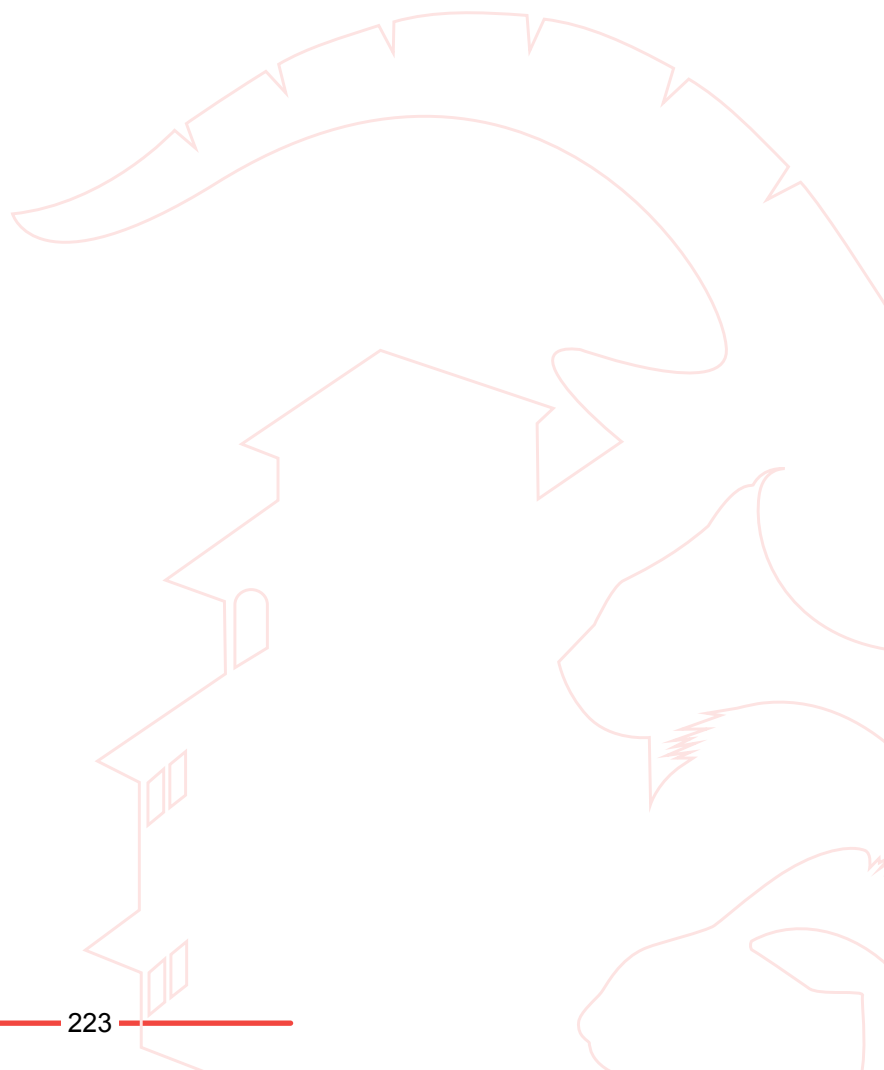
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Keywords: RNA Pathogens, Blanding's Turtles, *Emydoidea blandingii*

Abstract Text

Blanding's turtles (*Emydoidea blandingii*) are threatened throughout much of the United States and Canada. Assessment of individual and population health are critical to support successful conservation efforts. DNA viruses including herpesviruses and adenoviruses have been detected in wild Blanding's turtles, but a paucity of information regarding RNA virus prevalence exists. The objective of this study was to test for commonly reported RNA pathogens of chelonians in the Blanding's turtle. Cloacal/oral swabs were collected from 50 adult Blanding's turtles from northern Illinois during the summer of 2020 and preserved in RNALater. Out of the 50 samples, 37 were females, and 13 were males. Complimentary DNA from extracted RNA samples was tested for picornaviruses, ferlaviruses, bornaviruses, and reoviruses using existing conventional consensus PCR assays. All samples were negative for all four viruses and no clinical signs of disease were observed in any individual. Evaluating viral prevalence in other populations of Blanding's, as well as expanding RNA pathogen discovery may be useful to identify emerging threats, and support subsequent conservation and management efforts.





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70 SIZE DOESN'T MATTER, FIT DOES: MICRORNAS AS BIOMARKERS OF IMMUNOMODULATION

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Keywords: Biomarkers, Immunomodulation, MicroRNA, Migratory Shorebirds, Virome

Abstract Text

Pollutant exposure has been linked to immunosuppression and disease outbreaks in various wildlife species. Yet, our understanding of the molecular mechanisms involved in pollutant-induced immunomodulation remains limited.

Recently, microRNAs have been identified as key regulators of the immune response and important determinants of disease outcomes. MicroRNAs are a class of small noncoding RNAs that bind specific mRNA transcripts (from the host cell as well as from viruses) and prevent their translation into proteins. Alterations in microRNA expression have been found after exposure to various pollutants and pathogens (e.g. influenza virus). Recent in vitro studies have demonstrated that pollutants deregulate microRNA pathways involved in antiviral responses. MicroRNAs might therefore be a mechanistic link in our understanding of pollutant-induced immunomodulation. The presence and stability of microRNAs in blood makes them potentially interesting biomarkers of pollution-induced disease outcomes.

As part of the COAST IMPACT project, we study the potential of microRNAs as biomarkers of pollution exposure and disease in migratory shorebirds. Next-generation sequencing was used to characterise the microRNA profiles in serum from shorebirds with different avian influenza virus status. We will present potential target sequences of the identified serum microRNAs in the shorebird transcriptome and virome. Furthermore, blood pollutant concentrations will be analysed alongside microRNA profiles to investigate potential microRNA signatures of pollution exposure.

The identification of specific microRNA profiles associated with infectious disease and/or pollution exposure could (i) elucidate the molecular mechanisms inducing pollutant-induced immunomodulation, and (ii) facilitate the assessment of pollution exposure effects in free-living birds of conservation concern.



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175 THE FIRST THREE YEARS PERIOD OF EUROPEAN GOLDEN JACKAL (*CANIS AUREUS MOREOTICUS*) HEALTH SURVEILLANCE IN ITALY (2018-2021)

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Keywords: Canis Aureus, Golden Jackal, Surveillance, Wild Carnivores

Abstract Text

Golden jackal (*Canis aureus*) is a carnivore species that is naturally expanding its distribution range from Eastern Europe to north-eastern Italy and it is protected by Italian law (L157/92). Jackal populations are well established in the Friuli Venezia Giulia Region and are expanding into other Italian territories.

A total of 34 jackals (12 males, 20 females and 2 undetermined) were submitted for post-mortem examination during the period 2018-2021, after the first individual was examined in 2012. Most of animals (28) were collected following car accidents, while death circumstances of 6 individuals were unclear.

Regional health wildlife surveillance plan included rabies, canine distemper virus (CDV), trichinellosis, *Echinococcus multilocularis* (EM), leptospirosis and sarcoptic mange; further diseases or pathological conditions were investigated according to symptoms or gross lesions observed in analyzed individuals.

All jackals were negative for rabies, CDV, *Trichinella* and EM. Pathological lesions referable to sarcoptic mange and leptospirosis were not observed. The only infectious disease agent detected was parvovirus: canine parvovirus type 2 (CPV2) was evidenced in the gut of 2 jackals and 1 jackal was positive for canine parvovirus type 1 (CPV1). Besides car accidents, causes of mortality were poisoning (4), suspected predation by wolves (1) and drowning (1). Poisoning events were due to organophosphate methamidophos occurring in 2 jackals in a single episode and methaldehyde in other 2 jackals in separate occasions.

The absence of rabies, *Trichinella* and EM was in accordance with other wild carnivore's epidemiological condition. Nevertheless, CDV was widespread in 2018 and 2019 in red foxes and badgers; the contrasting CDV results may be due to jackals' massive increase occurring in the last two years, while contacts with other carnivores were maybe previously infrequent. Italian jackals populations appear to be in a general good health condition, car accidents and poisoning representing main threats.



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304 PASSIVE AND TARGETED HEALTH SURVEILLANCE OF WILD BOAR (*SUS SCROFA*) POPULATIONS IN NORTH-EASTERN ITALY

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Keywords: African Swine Fever, Aujeszky's Disease, *Sus Scrofa*, Surveillance, Wild Boar

Abstract Text

Wild boar (*Sus scrofa*) populations' management in the Friuli Venezia Giulia Region (north-eastern Italy) includes traditional hunting, selected hunting and demographic control accordingly to different geographical areas. Wildlife surveillance program prioritised important diseases at the wildlife-livestock-human interface: African Swine Fever (ASF), Classical Swine Fever (CSF), Aujeszky's Disease (AD), Trichinellosis, Tuberculosis, Brucellosis and Salmonellosis. Passive surveillance was the main framework for the early detection of most of these diseases examined according defined suspected cases. ASF virus was searched from spleen or marrow bones of each carcass using a PCR method. AD and Trichinellosis were monitored by active collection of hunted wild boars' samples. Tonsils and trigeminal ganglia were analysed for the search of AD virus by means of PCR and meat juice was obtained for the detection of AD antibodies; *Trichinella* spp. was tested according to the EC Regulation 1375/15.

Since the activation of the regional wildlife surveillance plan in 2018, 103 dead/road killed wild boars and 13.535 samples from hunted/killed wild boars were analysed. Most of carcasses were collected in consequence of car accidents. ASFV and *Trichinella* were never detected and CSFV suspect cases were not recorded. We did not observe tubercular lesions but submandibular lymphadenitis and abscesses along the isolation of *Streptococcus porcinus* (27,2%). The only one suspect of brucellosis was not confirmed by culture analysis. AD virus was detected from the tonsils of 8 wild boars (3,9%) and AD antibodies were revealed in meat juice samples (11,6%). *Salmonella Choleraesuis* was isolated from viscera of 10 wild boars (9,7%) and *Salmonella Typhimurium* from 2 individuals (1,9%).

Results confirm previous knowledge on regional epidemiological condition for the diseases under survey.

Further actions will be enhanced in order to improve the surveillance network capacity to detect dead wild boars in natural environment and thus expand the early detection system.



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221 DEVELOPING NEXT-GENERATION SEQUENCING TOOLS FOR HEALTH SURVEILLANCE AT THE WILDLIFE-LIVESTOCK INTERFACE.

Stephanie Brien¹, Melissa Marr¹, Marie Petretto², Ouled Ahmed Hatem³, Erhan Yalcindag¹, Mark Bronsvort¹, Rob Ogden¹

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Keywords: Haemoparasites, Health Surveillance, Nanopore Sequencing, Wildlife-Livestock Interface, Wild Ungulates

Abstract Text

Background

Portable, next-generation nanopore sequencing devices enable health surveillance to be performed in the field in near real-time for both diagnostic and conservation applications. They can be used to identify emerging infections and provide information about co-infections. Protocols for using these tools at the wildlife-livestock interface could greatly increase the scope of health surveillance and improve understanding of transmission dynamics in multi-host systems.

Goals

- (i) To design a nanopore sequencing pipeline for use in health surveillance at the wildlife-livestock interface.
- (ii) To design universal primers that enable comprehensive pathogen screening.

Methods

We developed molecular and bioinformatic pipelines for use with a Flongle nanopore sequencer. We validated the pipelines using livestock samples containing a range of haemopathogens diagnosed with Illumina sequencing. We then used the pipeline to assess samples from wild ungulate-livestock interfaces in Africa. Universal primers for haemoparasites and viruses are currently under development.

Results

Sequences obtained from nanopore and Illumina sequencing were comparable. The nanopore pipeline was able to accurately identify a range of haemoparasites in livestock and wildlife.

Conclusions

The nanopore sequencing pipeline is able to accurately identify infectious agents in livestock and wild ungulates.



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220 HEALTH SURVEILLANCE TO IMPROVE UNDERSTANDING OF WILDLIFE-LIVESTOCK DISEASE TRANSMISSION RISKS AND GUIDE DECISION-MAKING IN ANTELOPE CONSERVATION REINTRODUCTIONS

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Keywords: Antelope, Haemoparasites, Land-Sharing, Reintroduction, Wildlife-Livestock Interface

Abstract Text

Background

Endangered desert antelope such as scimitar-horned oryx (*Oryx dammah*) and addax (*Addax nasomaculatus*), are being reintroduced to the Sahelo-Sahara region as part of broader programmes to restore arid land biodiversity. To be sustainable, such programmes require land-sharing between antelope and livestock. This carries a risk of inter-species disease transmission, heightened by the shared evolutionary relationships and similar infection susceptibility profile of different ungulate species. Such diseases pose a threat to wildlife, livestock and humans.

Goals

- (i) To improve understanding of the infection status of endangered antelope populations involved in conservation reintroductions.
- (ii) To identify infections that could pose a risk at the wildlife-livestock interface.

Methods

We screened blood samples collected from endangered antelope involved in reintroduction programmes in Tunisia and Chad for haemoparasites using PCR and sequencing.

Results

We identified a range of haemoparasite genera that cause infections in livestock, including *Anaplasma*, *Ehrlichia* and *Theileria*. There is also evidence of bacteraemia associated with novel, poorly characterised bacterial families that have been identified as a cause of emerging infectious disease in wildlife and humans.

Conclusions

Haemoparasite infections are common in Sahelo-Saharan antelope scheduled for release and could present a risk at the wildlife-livestock interface due to potential differences in pathogenicity between species and altered transmission dynamics. Future work is planned to (i) assess infection status more broadly using next-generation sequencing approaches with more universal primers, (ii) compare the infection status of antelope with and without livestock contact, and (iii) assess how infection status impacts on health.



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238 THE WORST AVIAN INFLUENZA (HPAI-H5N8 AND H5N5) SEASON EVER IN WILD BIRDS AND POULTRY IN SWEDEN

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Keywords: Avian Influenza, H5N5/H5N8, HPAI, Poultry, Wild Birds

Abstract Text

Highly pathogenic avian influenza (HPAI) viruses H5N8 and H5N5 have caused numerous disease outbreaks across Europe during fall and winter 2020/2021. In Sweden, this is the most severe avian influenza season so far when considering the number of wild birds and poultry affected. Over 900 dead free-living wild birds were reported between November 2020 and April 2021 and a sample of these (n=526) were tested for avian influenza virus (AIV). All suspected poultry cases were tested for AIV. Virus was detected and typed from tissue samples and swabs (cloacal/pharyngeal) by Real-Time qPCR methods based on European Union Reference Laboratory (EURL) recommended methods and additional published protocols. Post-mortem examination, microscopy, and immunohistochemistry were performed. In total, 87 wild birds tested positive for AIV-H5 (H5N8, H5N5 or H5NX). Virus was detected in 21 different wild bird species, such as eagle owls (*Bubo bubo*), common buzzards (*Buteo buteo*), barnacle geese (*Branta leucopsis*), mute swans (*Cygnus olor*), peregrine falcons (*Falco peregrinus*), northern goshawks (*Accipiter gentilis*), Canada geese (*Branta canadensis*), and whooper swans (*Cygnus cygnus*). Outbreaks occurred on 24 poultry farms in layers (n=7, barn or organic), meat turkeys (n=4), broiler parents (n=2), backyard poultry (n=7, chickens, peafowl, domestic ducks and geese) and one each in pullets, organic broilers, game pheasants and a zoo. Multiple flocks were affected and over 2.2 million poultry died or were euthanized. Both H5N8 and H5N5 were identified among poultry. Gross lesions varied from inconspicuous to widespread congestion, hemorrhage, and acute parenchymal lesions. Microscopically, acute necroses were observed in many tissues, including brain, and virus was broadly detected by immunohistochemistry. The N-type was not identifiable in all wild bird cases possibly because ct-values were generally higher than in poultry. Compared to previous HPAI-outbreaks, cases were distributed further north and westward. Moreover, the species range was broader.



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334 COMPARISON OF TRAP-BIAS AND HEALTH OUTCOMES BETWEEN TWO SMALL RODENT LIVE-TRAPS IN WISCONSIN, UNITED STATES

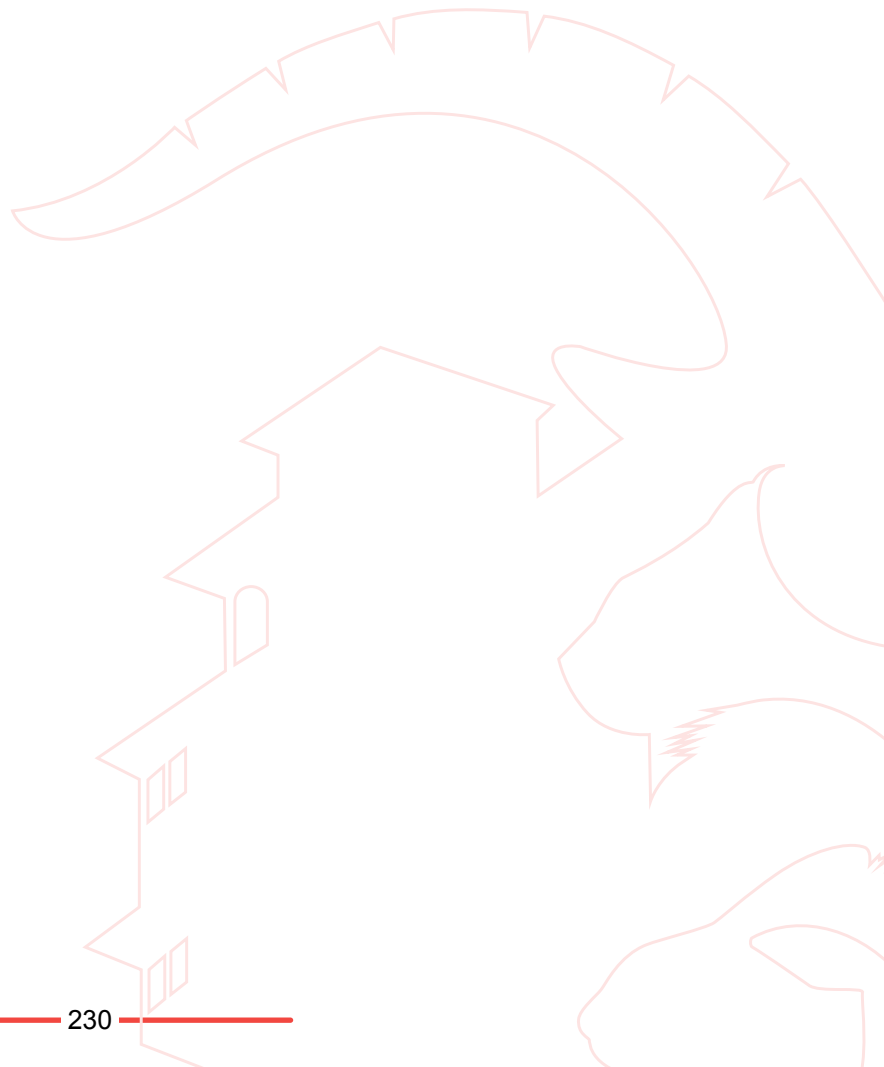
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Keywords: Animal Welfare, Small Mammal Trapping, Shrews, Sorex

Abstract Text

Small rodent trapping is a very common practice in wildlife, forest and ecology research and education. Since their establishment in the 1960s, Institutional Animal Care and Use Committees have greatly improved handling and sampling procedures to better protect small mammals captured during field studies. However, traps commonly used in small mammal studies have changed very little during this time period and can be considered sub-optimal. The objective of this study was to compare 1) rodent health and 2) capture biases for two live-trap types: the Sherman live-trap and the Heslinga live-trap. We hypothesized that the elevated nesting chamber and gravity-fed door of the Heslinga trap would improve animal health indicators (alertness, turgor, condition of fur, injuries) and survival compared to the conventional Sherman trap. Conversely, the larger entrance of the Sherman trap would allow for the capture of more rodent species (richness). In a paired study design, small rodents were trapped from July to September 2019 in a mixed forest in Northcentral Wisconsin. Heslinga traps were more likely to capture shrews (*Sorex* spp.) compared to Sherman traps (20 shrews in 727 trap nights versus 1 shrew in 731 trap nights). There was no significant difference in *Peromyscus* spp. captures and both traps caught five small mammal species. Failed trap events were caused by triggered doors without a small rodent capture in Heslinga traps and insensitive / stuck treadles in Sherman traps. Most captured animals were active, dry and well-hydrated. We showed the importance of utilizing different trap types to assess rodent communities and explored a quick health scoring system that can be universally utilized to evaluate and adjust trap conditions to improve small mammal trap protocols.





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65 FERAL CATS COLONIES AS CARRIERS OF SALMONELLA SPP. WITH IMPACT ON PUBLIC HEALTH.

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Keywords: Feral Cats, Public Health, Salmonella Enterica, Serotypes.

Abstract Text

Cats have been identified as a potential risk factor of infection in humans by Salmonella. In fact, the contact with clinically ill cats and with shelter cats has been linked to outbreaks in humans by this bacterium. Public administrations control the overpopulation of these animals in the cities through the development and implementation of different control programs for stray cat colonies (TNR method: Trap-Neuter-Return). The control of the health status of these animals has a direct impact on public health by reducing the risks to health and transmission of zoonotic diseases. Due the lack of knowledge of the health status of these animals as possible healthy carriers in their faeces of Salmonella spp., we have considered as objective of this study to determine whether they carry Salmonella spp. For this study, one hundred rectal swabs were taken for culturing between November 2018 and January 2019. All these feral cats were from the TNR campaigns from Gran Canaria island. The samples were processed using Rappaport Vassiliadis as an enrichment media to 42 °C during 24 hours. All Salmonella spp. isolates were serotyped at the Central Veterinary Laboratory of Algete (Spain). In our geographic area, from the total of feral cats studied, we obtained a 19% of positives to Salmonella spp. All strains (19) were identified as Salmonella enterica subsp. enterica and they belonged to five different serovars: 11 S. Nima 28:y:1,5 (57.89%), 3 S. Bredeney 4,12:1,v:1,7 (15.78%), 2 S. Grancanaria 16:z39:- (10.52%), 2 S. Florida 6,14,25:d:1,7 (10.52%) and 1 strain of S. Kottbus 6,8:e,h:1,5 (5.26%). In conclusion, feral cats carry different serotypes of Salmonella enterica subsp. enterica with impact on Public Health.



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381 THE BIRD, THE PARASITE, AND THE VIRUS: CO-INFECTION OF FREE-LIVING RED-LEGGED PARTRIDGES (*ALECTORIS RUFA*) WITH BAGAZA VIRUS AND AVIAN MALARIA

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Keywords: Avian Malaria, Plasmodium Relictum, Bagaza Virus, Co-Infection, Avian Host.

Abstract Text

Avian malaria parasites and Flaviviruses such as West Nile (WNV), Usutu (USUV) and Bagaza (BAGV) virus are pathogens that cycle naturally between birds and mosquito vectors. Temporal and spatial co-circulation and co-infection of avian malaria parasites, and West Nile virus has been documented in several geographic regions, both in birds and mosquito vectors. Also, WNV, USUV and BAGV have been found to co-circulate regionally. Less is known however about the interaction of the three viruses and malaria parasites during potential consecutive or co-infections of an avian host.

Here we report on the co-infection of free-living red-legged partridges in a hunting estate in Southern Spain with *Plasmodium relictum* and BAGV in a small-scale temporal mortality event. Partridge mortality due to BAGV had occurred in the area in 2010 and since then co-circulation of WNV, BAGV and USUV had been confirmed on several occasions.

Partridges in fair to poor body condition were found dead in early October. All birds had mottled locally pale pectoral muscles, enlarged, congestive greenish-black tinged livers and enlarged kidneys. All birds had widespread inflammatory and congestive microscopic lesions and phanerozoites were present in numerous tissues including the liver, spleen, kidneys and skin. Molecular testing and sequencing allowed for detection of both, *P. relictum* and BAGV in several different tissues of the partridges, and immunohistochemistry confirmed the presence and co-localisation of both pathogens in organs such as the liver and spleen. Our findings are the first account of a mortality caused by the co-infection with these two avian pathogens which

is of concern both for red legged partridges that seem highly susceptible but also for other endangered species in the region.



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40 MOLECULAR DETECTION OF KOBUVIRUSES IN DOMESTIC AND WILD ANIMALS IN NORTHWESTERN ITALY

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Keywords: Kobuviruses (KoVs), Northwestern Italian Alps, Domestic And Wild Ungulates

Abstract Text

Kobuviruses (KoVs) are non-enveloped viruses, with a single-stranded, positive-sense RNA, representing a distinct genus in the family Picornaviridae. Based on their genomic organization KoVs are currently classified into six species, Aichivirus A to F and display a wide host range worldwide, including humans, dogs, cats, pigs, cattle, goats, sheep, bats, rats, and mice. Several evidence indicate that genetically closely related strains circulate in both domestic and wild species, suggesting a limited host-species restriction for these viruses. In the landscape of the Northwestern Italian Alps wildlife and extensive farming livestock can encounter and share the same environment, allowing the sharing and spread of pathogens. The aim of this study was to investigate the circulation and the genetic diversity of KoVs infecting domestic and wild ungulates, with special attention to the wildlife/livestock interface. During 2017-2019 a total of 483 enteric samples (stool and rectal swabs) was collected in the Valle d'Aosta and Piemonte regions from 128 sheep, 167 goats, 30 deer (*Cervus elaphus*), 36 roe deer (European roe deer), 43 chamois (*Rupicapra rupicapra*), 16 Alpine ibex (*Capra ibex*) and 63 wild boars (*Sus scrofa*). By using either broadly reactive primer pairs UNIV-kobu-F/UNIV-kobu-R or specific Aichivirus B primers, both targeting a fragment of the polymerase region (RdRp), KoV RNA was detected in 1.2% (2/167) of samples collected from goats, 4.7% (2/43) from chamois and 3.2% (2/63) from wild boars. Sequence and phylogenetic analyses based on the RdRp region and on the complete VP1 gene, obtained for three strains detected in goats and in a chamois, revealed the circulation in the geographical setting assessed of at least two species of KoVs, Aichivirus B in wild and domestic ruminants and Aichivirus C in wild boars. Understanding the role of the different wild and domestic species in spreading and maintaining KoV infections deserves further epidemiological studies.



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251 THE SPATIOTEMPORAL DYNAMICS OF EXPOSURE OF WILD UNGULATES TO FLAVIVIRUS SHAPES THE PATTERNS OF WEST NILE VIRUS OUTBREAKS IN SPAIN

Laia Casades Martí¹, Raúl Cuadrado Matías¹, Roxana Triguero Ocaña^{1,2}, Patricia Barroso¹, Saúl Jiménez Ruiz^{1,3}, Pablo Palencia¹, Eduardo Laguna¹, Alfonso Peralbo Moreno¹, Sara Baz Flores¹, Yolanda Fierro⁴, Francisco Ruiz Fons¹

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Keywords: Emerging Zoonosis, Epidemiology, Flavivirus, Pathogen Dynamics, Vector-Borne Diseases

Abstract Text

West Nile virus (WNV) is a neuropathic virus for humans, horses and birds transmitted by mosquitoes. The recent increase of clinical cases in Spain shows the need to better understand the ecology of this Flavivirus, not only in urban areas, but also where birds, WNV and mosquitoes interact with wild ungulates, to better predict/prevent WNV outbreaks. We analysed the dynamics of exposure of wild ungulates to Flavivirus along 15 years (2005-2019) in a south-to-north gradient in 5 areas where WNV cases occur since 2007. Sera of 2,418 wild ungulates (*Cervus elaphus* & *Sus scrofa*) from Doñana National Park (A1), Western Sierra Morena (A2), Central Sierra Morena (A3), Guadiana river Valley (A4) and Toledo Mounts (A5) were analysed with a blocking ELISA highly specific for WNV. Weather conditions were gathered from two climatically and environmentally contrasting areas: i) A1, a thermo-Mediterranean wetland; and ii) A4, a Mediterranean continental forest/shrubland. The risk of Flavivirus exposure of ungulates was modelled with weather covariates (average winter/spring/summer temperatures and annual/winter-spring/spring/summer rainfall) by logistic binary regression. The proportion of exposed ungulates was higher in A1 (33.5%) and A2 (35.3%) than in A3 (18.7%), A4 (20.3%) and A5 (18.7%), shaping the contrasting reported incidence of WNV outbreaks in southern (n=189) and south-central (n=2) Spain. The annual patterns of exposure of ungulates also shaped the temporal emergence of WNV outbreaks. Higher winter temperature associated positively to the risk of exposure in A1 whereas in A4 the risk increased with annual rainfall whereas it decreased with increasing spring precipitation. These preliminary results point out that whereas in wetlands, where water is abundant, smoother winter temperatures better predict WNV circulation, annual rainfall seems to be a better predictor for WNV infection risk in dry continental Mediterranean areas. Wild ungulates additionally prove to be efficient predictors for Flavivirus spatiotemporal dynamics.



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367 ESTIMATING INTERACTIONS BETWEEN LIVESTOCK AND WILDLIFE IN THE SELVA LACANDONA, MEXICO.

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Keywords: Interactions, Lacandona, Forest, Livestock, Mexico Wildlife

Abstract Text

Lacandona Forest is one of the most important rainforests of southeastern Mexico. Its biodiversity is currently threatened by deforestation, land use changes, intentional forest burning, timber extraction and wildlife overexploitation. Forest fragmentation has increased the frequency of contacts between wildlife and livestock, and this has been deemed as an important driver of transmission of shared diseases at the wildlife-livestock interface. This study focuses on determining the types of wildlife-livestock contact in this Forest. Thirty-eight farmers from 2 villages (Marques de Comillas), were personally interviewed to estimate contact types and frequencies. Direct contacts, distance between individuals, the type of resources shared, and the timing of interactions were the subject of interviews. The reporting of a wild animal (in the absence of cattle) using a resource that cattle also exploit was considered as an indirect contact. Farmers reported the wild species passing by cattle grasslands and the frequency with which these were observed. According to interviews, the highest frequency of direct contacts occurred between cattle and white-tailed deer (*Odocoileus virginianus*) (57.9%), collared peccary (*Pecari tajacu*) (42.1%), coati (*Nasuanarica*) (23.6%), lowland paca (*Cuniculus paca*) (18.4%) and Guatemalan black howler (*Alouatta pigra*) (15.7%). The resources shared between these species were: mineral salt, grass, water and tree leaves. The shortest distance of a direct contact was one meter and the largest was 12 meters. Indirect contacts were frequent with white-tailed deer (81.5%), collared peccary (65.7%), coati (44.7%), raccoon (*Procyon lotor*) (21%), eastern cottontail (*Sylvilagus floridanus*) (42.1%), black howler (34.2%) and Virginia opossum (*Didelphis virginiana*) (23.6%). Two additional endangered species, the Baird's tapir (*Tapirus bairdii*) (18.4%) and jaguar (*Panthera onca*) (3%) were reported as indirectly interacting with cattle. These results are unique in Lacandona Forest and essential to estimating risks of shared diseases transmission in addition to applying control measures for infectious diseases.



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364 STUDY OF TOXOPLASMA GONDII IN WILD AND DOMESTIC LAGOMORPHS IN SPAIN

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Keywords: Lagomorphs, Oe Health, Seroprevalence, Toxoplasma Gondii, Zoonosis.

Abstract Text

Toxoplasmosis is a zoonosis caused by the protozoa *Toxoplasma gondii* which infects warm-blooded species worldwide, including humans. Wild rabbits and hares are very important small game species in Spain and demand for their meat for human consumption is increasing. In addition, these species are the most important food for the endangered Iberian Lynx (*Lynx pardinus*), which is a definitive host of *T. gondii* and can close the parasite cycle. Although infections in lagomorphs are documented to be mainly subclinical, fatal acute toxoplasmosis and clinical outcomes has been previously reported. A total of 1,127 serum samples from wild and domestic lagomorphs were collected in 16 provinces of Spain between 2018 and 2021 and were assayed for antibodies against *T. gondii* by the modified agglutination test (MAT, cut-off 1:25). Antibodies against *T. gondii* were detected in 50 of 1,127 animals (4.4%; 95%CI: 3.2-5.6) and antibody titres of 1:25, 1:50, 1:100 and $\geq 1:500$ were found in 33 (66.0%), 12 (24.0%), 4 (8.0%) and 1 (2.0%) individuals, respectively. By species, the frequency of positives was 10.9% (5/46) in Iberian hare (*Lepus granatensis*), 4.8% (43/898) in wild rabbit (*Oryctolagus cuniculus*), 1.1% (2/178) in domestic pet rabbit (*Oryctolagus cuniculus domesticus*) and 0.0% (0/5) in European hare (*Lepus europaeus*). At least one *T. gondii* seropositive animal was detected in 33.7% (30/89) of the analyzed hunting states. No statistically significant differences were observed by age, sex or sampling area, although significantly higher seroprevalence was observed in wild lagomorphs (5.1%; 95%CI: 3.7-6.5) compared to domestic ones (1.1%; 95%CI: 0.0-2.7) ($P = 0.046$). The results obtained indicate a limited and moderate *T. gondii* exposure in domestic and wild lagomorphs, respectively. However, the high hunting state prevalence, indicates widespread circulation of this parasite among wild lagomorphs in Spain, with may pose a potential risk for humans if consumed undercook meat.



357 CAUSE OF DEATH IN FLORIDA FARMED WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) DURING 2017–2020 AND THEIR USE AS SENTINELS TO MONITOR HEMORRHAGIC DISEASES OUTBREAKS

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Keywords: Cause Of Death, Epizootic Hemorrhagic Disease, *Escherichia Coli*, *Odocoileus Virginianus*, *Trueperella Pyogenes*

Abstract Text

White-tailed deer (*Odocoileus virginianus*) farming is an emerging agricultural industry in Florida. Bacterial infections and viral hemorrhagic diseases cause high mortality in fawn and yearling deer. Before health and management can be improved and properly implemented, the cause of death must be determined. The University of Florida Cervidae Health Research Initiative (CHeRI) provides a diagnostic service to Florida deer farmers to determine and monitor the causes of death in farmed white-tailed deer. From 2017 to 2020, participating Florida deer farms provided recently deceased white-tailed deer for necropsy or shipped tissues for analysis by the CHeRI diagnostic program. Sampled tissues were tested for hemorrhagic disease and were subjected to additional microbial culture, histopathology analysis, and parasite identification as necessary to determine a probable cause of death. Furthermore, diagnostic results allow us to effectively use farmed white-tailed deer as a sentinel to detect and monitor hemorrhagic disease outbreaks and recurring seasonal cycles in Florida.

Our results show that bacterial infection was the most frequent cause of death (57%) among deer aged 1-90 days. Viral hemorrhagic disease due to epizootic hemorrhagic disease virus and bluetongue virus was the most frequent cause of death (69%) in deer aged 4-12 months. In adult deer aged 13+ months, the most frequent cause of death was a combination of hemorrhagic disease (41%) and bacterial infections (34%). The overall percentage for all categories analyzed together confirms that hemorrhagic diseases and bacterial infections account for 80% of deaths. *Escherichia coli*, *Trueperella pyogenes*, and *Pseudomonas aeruginosa* were the most frequently isolated bacterial pathogens. These data provide valuable information to improve preventive health measurements and clinical treatment of Florida white-tailed deer. In addition, farmed white-tailed deer have proved to be an effective sentinel for monitoring hemorrhagic disease outbreaks in Florida.



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147 THE SALMONELLA DYNAMICS OF AMERICAN WHITE IBIS (*EUDOCIMUS ALBUS*) NESTLINGS

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Keywords: Disease, Ibis, Nestling, Salmonella, Urbanization

Abstract Text

Salmonella can cause disease in young aquatic birds and is influenced by habitat use. We studied Salmonella epidemiology in adult American white ibis (*Eudocimus albus*), a wading bird that recently began breeding in urban areas. We found that ibis 1) shed Salmonella at a high prevalence (~26%) and at higher rates in urban-foraging populations, 2) are colonized by diverse serotypes, 3) are reservoirs for Salmonella genotypes found in people. Here, we investigate the epidemiology of Salmonella in young ibis. We 1) monitored a captive colony of wild-caught nestlings for Salmonella, 2) experimentally infected those nestlings, and 3) sampled free-living nestlings in urban and natural colonies weekly for the first weeks of life.

Fifty-eight percent of wild-caught nestlings (n=24) raised in captivity shed Salmonella at the time of collection (two serotypes), but after group housing, the prevalence increased to 70% for 5 weeks. By 18 weeks of age, no birds were shedding Salmonella. At 26 weeks of age, 20 nestlings were inoculated with an oral suspension of 106S. typhimurium. Post-inoculation, 3 birds shed at DPI1, one of which developed clinical disease, from which it recovered, and 1 at DPI5. Among urban free-living nestlings, 81% (n=36) shed Salmonella during the course of sampling (3 weeks; 17 serotypes). Ten birds tested positive for multiple consecutive weeks, and shedding time varied between individuals. The prevalence decreased with age, (from 54% (n=37) in birds <7 days old to 42% (n=26) in birds >15 days). Similar data for nestlings in natural colonies is pending analysis.

Aside from studies on the domestic chicken, these studies provide the most complete age-specific findings of Salmonella epidemiology in an avian species. Although clinical disease is rare, wild ibis nestlings are commonly infected with Salmonella which reflects their diet, and early infection may provide immunity to older nestlings.



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148 AVIAN INFLUENZA VIRUS DYNAMICS IN URBAN NESTLING AND JUVENILE AMERICAN WHITE IBIS (*EUDOCIMUS ALBUS*)

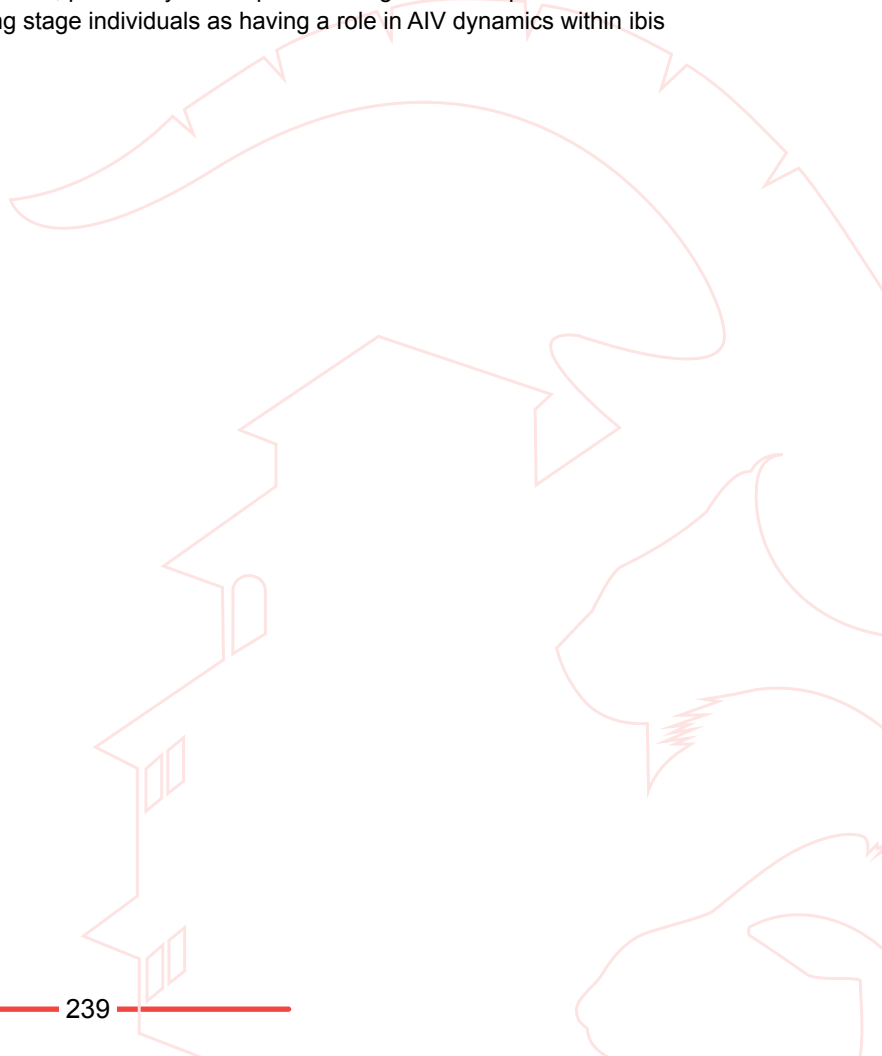
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Keywords: Avian Influenza, Antibodies, Ibis, Urban, Wildlife

Abstract Text

The epidemiology of pathogens in wild bird species is impacted by multiple biological and environmental factors that are often complex to untangle. To better understand how these pressures affect birds pushed into anthropogenic zones by habitat loss, multiple studies were done on the dynamics of avian influenza virus (AIV) in the American white ibis (*Eudocimus albus*). We found that experimentally infected ibis are competent hosts for multiple influenza subtypes, shedding virus for 5-6 days, and that adult ibis in natural populations are commonly exposed to AIV and seroconvert (70% average antibody prevalence). However, we have yet to isolate AIV from a free-living white ibis, leaving the mechanisms of transmission and the timing of infection unclear.

To better understand the age-specific AIV dynamics of ibis, we sampled nestlings from an urban breeding colony over two breeding seasons, capturing nestlings weekly from hatching until capture was no longer possible (~3 weeks; n=36). We collected choana-cloacal swabs for rRT-PCR and virus isolation, and plasma to screen for maternal AIV antibodies using a commercial bELISA. We also collected fecal samples from urban juvenile ibis during the winter between the two breeding seasons. AIV was not detected in any individual at any time by rRT-PCR or virus isolation, but we detected maternal antibodies to AIV in all nestlings. Antibody levels in individuals decreased over time, consistent with decay of maternal antibodies, but the rate of this catabolism varied, with many nestlings remaining antibody-positive to at least 24 days old. These results confirm that adult ibis are commonly exposed to AIV and provide evidence that nestlings in breeding colonies may have some degree of protection, potentially due to pre-breeding season exposure to IAV in nesting females and pointing us towards post-nestling stage individuals as having a role in AIV dynamics within ibis populations.





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107 THE RISK FROM SARS-COV-2 TO BAT SPECIES IN ENGLAND

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Keywords: Bats, Chiroptera, Fieldworkers, Risk Assessment, SARS-CoV-2

Abstract Text

SARS-CoV-2, the coronavirus responsible for the Covid-19 pandemic, has been associated with infection and disease in numerous captive wild animal species. Fruit bats of the Chiroptera order are susceptible to experimental infection, and the susceptibility of other bat species is unknown. Numerous conservation fieldwork activities are undertaken across the United Kingdom enabling close contact between bats and potentially infected humans. In this study we analysed the risks associated with SARS-CoV-2 to free-living bat species in England through fieldworkers undertaking conservation activities and ecological survey work. A qualitative, transparent method devised for assessing threats of disease to free-living wild animals was used.

Results of the exposure assessment estimated that the probability of bats being exposed to SARS-CoV-2 ranged from negligible to high, depending on the conservation activity undertaken and the proximity between bats and fieldworkers during the activity. The likelihood of infection after exposure was estimated to be high and the probability of dissemination of the virus through bat populations medium. Clinical disease associated with SARS-CoV-2 has not been reported in bats, although minimal research exists. Therefore, the likelihood of disease in free-living bats in England was estimated to be low, and associated ecological, economic and environmental consequences also predicted to be low. The overall risk estimation was low and, as such, mitigation measures are advisable to reduce this risk. The authors suggest disease risk management measures, including the use of personal protective equipment, good hand hygiene and following existing government advice.

There is limited available evidence regarding the pathogenicity of SARS-CoV-2 in bats and, therefore, considerable uncertainty in the risk estimation. The disease risk analysis should therefore be updated as understanding of the epidemiology of SARS-CoV-2 and related viruses in bats improves. Health surveillance of free-living bats may also inform any re-analysis performed in future.



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168 A SPECIES INDEPENDENT DOUBLE-ANTIGEN ELISA ALLOWING FOR CCHFV ANTIBODY DETECTION IN WILDLIFE

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Keywords: CCHF, ELISA, Multi Species

Abstract Text

Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne disease caused by the Crimean-Congo hemorrhagic fever virus (CCHFV), which is a Bunyavirus belonging to the family Nairoviridae. CCHFV is present in many wildlife animals and transmitted to humans by tick bites, crushing of ticks and exposure to blood, tissues or bodily fluids of viremic livestock or infected patients. The virus causes an often-fatal hemorrhagic illness in humans, while animals do not develop clinical symptoms upon infection. The detection of anti-CCHFV antibodies in domestic and wildlife samples is therefore used to reveal CCHFV infection risk areas.

Materials and methods

This work presents the development and validation on wildlife samples of a CCHF double antigen (CCHFDA) ELISA for the detection of anti-CCHFV nucleoprotein (NP) antibodies. As the ELISA is based on recombinant protein it can be run under standard biosafety conditions.

Due to lack of wildlife positive samples, sensitivity could be assessed only with domestic samples: 271 sera from animals from CCHF endemic regions (origin: Albania, Cameroon, Kosovo, Macedonia, Turkey...) served as a CCHFV positive reference serum panel (confirmed by three serological assays) (FLI-inhouse ELISA, species adapted VectorBest ELISA and Euroimmune IFA). 2136 negative domestic and wildlife samples from non-endemic zone (Germany and France) served as negative panel. Moreover, sera from chamois, isard, roe deer, alpine ibexes, mouflons, foxes, pigs, raccoons, raccoon dogs, hares, rats, dogs, camels and ferrets were tested to determine the suitability of this ELISA for these species.

Results and discussion

All negative reference sera were confirmed by the CCHFDA ELISA indicating a specificity of 100% (CI 95%: 99.8% - 100%) regardless of the species tested. 268 of 271 positive reference sera were tested positive for CCHFV-specific antibodies which means a sensitivity of 98.9% (CI 95%: 96.8% - 99.8%). Part of this work was done within the EU-funded grant FP7 (EDENext).



241 THE COST OF SYNURBIZATION FOR WILD BOARS IN BARCELONA, SPAIN

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Keywords: Synurbization, Trade-Off, Urban Wild Boar, Human-Wildlife Conflict

Abstract Text

Wild boar (WB, *Sus scrofa*) synurbization is not only favoured by the great behavioural plasticity of this mammal but also by the high availability of anthropogenic food resources in urban areas. Recent research indicates that wild boar from urban environments grow faster than their counterparts living in the wild. However, it is unclear whether urban areas act as refuge favouring wild boar survival, or are acting as sinks with consequences for the fitness of boars.

Between 2015 and 2018, 860 wild boars were either hunted in Collserola Natural Park (n=255) or captured and euthanized in the urban area of Barcelona (n=605), and subsequently necropsied. Sex, age, location, body mass and biometrical measurements were recorded. Post-mortem lesions were registered and those non-attributable to the capture method were classified using a Severity Score (SS) according to individual health and welfare assessment as follows: without pathological findings (SS=1, 55%, n=463), presenting minor to moderate lesions (SS=2, 37%, n=314), and presenting serious to lethal lesions (SS=3, 8%, n=70). Hierarchical Clustering on a Principal Components Analysis was used to analyse the effect of sex, age, body condition and urban environment proximity on WB SS.

Four clusters were identified according to SS, age, proximity to the urban environment and body condition. Rural piglets and juveniles had the lower SS, followed by rural and urban adults, while urban piglets and juveniles had the highest SS. Urban adults had higher body condition than rural ones.

WB exploring the urban environment had a higher SS, mostly attributable to anthropogenic disturbances such as vehicle collisions and dog attacks. Moreover, SS turned out to be higher in piglets and juveniles exploring the urban environment than in urban adults. Hence, the trade-off of exploiting the urban environment for WB has welfare and health drawbacks to the higher food supply.





155 RICKETS-LIKE SYNDROME IN TWO FREE-RANGING IBERIAN LINX (*LINX PARDINUS*) KITTENS

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Keywords: Rickets, Iberian Linx, Linx Pardinus

Abstract Text

The Iberian lynx is one of the most endangered felids in the world. Although the population has experienced a steady growth due to conservation efforts, anthropogenic pressures, low genetic diversity, prey declining and habitat loss may still put the species at risk.

In 2018 and 2020, during routine lynx surveillance, two wild-born Iberian lynx kittens presenting skeletal disorders were brought in the wildlife rehabilitation center of Ciudad Real (Spain).

The first case, a 4-month-old male was retrieved from the field after it was killed by the litter's sire. According to camera data, this kitten showed delayed growth relative to its siblings.

The second case, a 4-month-old male, from the same area, was found alive presenting multiple fractures, deficient body condition and delayed growth. After one month of treatment and due to poor prognosis, euthanasia was indicated.

In both cases necropsy revealed skeletal development disorders: low mineralization, growth plates ossification, pathologic fractures and teething alterations.

The most relevant abnormalities observed in a serum biochemistry panel obtained from the second kitten included: low Vit D [56 mmol/L (reference range: 126-163)], low ionized calcium [1.26 mmol/L; (1.4-1.8)] and hyperphosphatemia [2.3 mmol/L; (0.8-1.19)].

Several compatible disorders including Ca/P ratio imbalanced, secondary hyperparathyroidism, renal osteodystrophy, malabsorption syndrome due to high endoparasites loads, osteogenesis imperfecta, or vitamin D absorption impairment due to lead toxicosis, were ruled out based in the clinical pathology or histopathology. Therefore, a genetic origin of this syndrome could be considered.

Vitamin D dependent hereditary rickets Type I has been described in domestic cats and a genetic study of these kittens is being investigated.

To our knowledge, these are the first descriptions of a rickets-like syndrome in free ranging Iberian lynx. Genetic studies must be carried out to ensure the viability in this population nuclei.



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330 THE SPATIOTEMPORAL DYNAMICS OF CRIMEAN-CONGO HAEMORRHAGIC FEVER VIRUS IN ENZOOTIC IBERIAN SCENARIOS.

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Keywords: Dynamics, Hyalomma, Prevention, Tick, Zoonosis

Abstract Text

Crimean-Congo haemorrhagic fever (CCHF) is a highly lethal zoonosis caused by an Orthonairovirus that is mainly transmitted through the bite of *Hyalomma* spp. ticks. CCHF is an emerging human disease in Spain, where it has caused 8 cases with 3 deaths since 2016 (43% case fatality rate). Since the first detection of CCHF virus (CCHFV) in *H. lusitanicum* ticks of red deer (*Cervus elaphus*) in 2010, this wild ungulate proved to be an excellent indicator of virus circulation. This study seeks to better understand the long-term spatiotemporal dynamics of CCHFV along a south-to-north gradient with 6,178 red deer sampled in 21 years (1999-2020) to aid in better predicting virus exposure risks and modulating environmental factors. A retrospective annual cross-sectional survey was designed for 8 study areas on the basis of findings of a previous cross-sectional survey of red deer. The presence of specific CCHFV antibodies in sera was estimated using a commercial ELISA (ID Screen® CCHF Double Antigen Multi-species, IDvet, France). The overall seroprevalence was 72.3% (CI95%:71.2-73.4). The prevalence of anti-CCHFV antibodies was very high and similar in the 6 areas located in the southern half of mainland Spain (72.9-87.5%), whereas it was lower in central (47.2%) and northern (30.6%) areas of the country. Within-area CCHFV exposure displayed a varying pattern that was related to annual temperature and rainfall in a preliminary statistical modelling of data from two areas. These findings show the widespread circulation of CCHFV across mainland Spain and further support previous findings suggesting that the virus is enzootic in the country. Being enzootic, the question is why CCHF did not emerge before. A detailed and thorough analysis of the environmental drivers of exposure variation will provide insights to better predict and prevent transmission of CCHFV to humans.



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231 SCREENING OF VECTOR-BORNE PATHOGENS IN ICELANDIC ARCTIC FOXES, *VULPES LAGOPUS*

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Keywords: Arctic Fox, Iceland, Vector-Borne Pathogens, *Vulpes Lagopus*

Abstract Text

The current accelerated climate and landscape changes can influence the occurrence and spread of pathogens. This is especially true for vector-borne pathogens spreading towards the arctic habitats. During the last 30 years, average temperature has increased in Iceland, supporting more favorable conditions for ticks and other arthropod vectors. Accordingly, questing *Ixodes ricinus* ticks have been reported in Iceland, implying potentially new threats posed by tick-borne diseases both for animal (wildlife and domestic) and human populations. The aim of this study was to screen the arctic fox, the only native terrestrial mammal in Iceland, for vector-borne pathogens. Liver samples collected from 60 individuals in 2011-2012 were tested for vector-borne protozoan parasites (*Trypanosomatidae*, *Babesia*, *Theileria*, *Hepatozoon*) and bacteria (*Anaplasma*, *Bartonella*, *Borrelia*, *Ehrlichia*, hemotropic *Mycoplasma*, *Rickettsia*) by PCRs targeting the 18S, 16S rRNA, *msp2*, flagellin and *gltA* genes, respectively. None of the pathogens were detected with the exception of an adult female fox from coastal ecotype being positive for *Anaplasma phagocytophilum*. Our results provide baseline evidence about the low prevalence of vector-borne pathogens in Icelandic arctic foxes; in light of the climate changes the geographic distribution of these pathogens might change, which require continuous monitoring in the arctic ecosystems, including both sedentary and migratory species.



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244 MOLECULAR ANALYSIS SUGGESTS THAT NAMIBIAN CHEETAHS (*ACINONYX JUBATUS*) ARE DEFINITIVE HOSTS OF A YET UNKNOWN *BESNOITIA* SPECIES

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Keywords: *Besnoitia* Spp., Namibia, Real-Time PCR, Phylogeny, *Acinonyx Jubatus*

Abstract Text

Besnoitia darlingi, *B. neotomofelis* and *B. oryctofelisi* are closely related coccidian parasites with cats as definitive hosts. These parasites use a large variety of species as intermediate hosts. While opossums (*Didelphis virginiana*) are intermediate hosts of *B. darlingi*, *B. neotomofelis* has been described in Southern plains woodrats (*Neotoma micropus*) and *B. oryctofelisi* in domestic rabbits (*Oryctolagus cuniculus*) as intermediate hosts. Based on conserved regions in the Internal Transcribed Spacer 1 (ITS-1) sequence of the ribosomal DNA (rDNA) of these *Besnoitia* spp., a real-time PCR for sensitive detection of these parasites in tissues of intermediate and in faeces of definitive hosts has recently been established. Based on available sequence data, species such as *B. acodoni* and *B. jellisoni* are also expected to be covered by this assay. It was hypothesized that additional *Besnoitia* spp. closely related to *B. darlingi*, *B. neotomofelis*, *B. oryctofelisi*, *B. acodoni* or *B. jellisoni* exist worldwide. Faecal samples from two free-ranging cheetahs (*Acinonyx jubatus*) from Namibia which previously tested positive for coccidian parasites by coproscopy were used for this study. PCR and sequencing methods were used to clarify the identity of these coccidian parasites. One of these samples tested positive for *B. darlingi*/*neotomofelis*/*oryctofelisi*-like parasites by real-time PCR, while both samples tested negative for other coccidian parasites including *Toxoplasma gondii*, *Hammondia hammondi*, *H. heydorni*, *B. besnoiti* and *Neospora caninum*. The rDNA of the *B. darlingi*/*neotomofelis*/*oryctofelisi*-like parasite was sequenced. Comparison with existing sequences in Genbank revealed a close relationship to other *Besnoitia* spp., but also clear divergences. These results suggest that a yet unknown *Besnoitia* sp. may exist in Namibian wildlife, which is closely related to *B. darlingi*, *B. neotomofelis*, or *B. oryctofelisi*. The cheetah (*Acinonyx jubatus*) can be considered the definitive host of this newly discovered parasite and its prey species may act as intermediate hosts.



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237 IN SICKNESS AND IN HEALTH: PLASMA PROTEOMICS OF HIBERNATING EUROPEAN AND NORTH AMERICAN MYOTID BATS

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Keywords: Bat, Hibernation, Myotis Spp., Proteomics, Pseudogymnascus Destructans

Abstract Text

Emerging fungal diseases have become challenges for wildlife health and conservation. North American hibernating bat species are threatened by the psychrophilic fungus *Pseudogymnascus destructans* (Pd) causing the disease called white-nose syndrome with unprecedented mortality rates. The fungus is widespread in North America and Europe, however, the disease is not manifested in European bats. Differences in epidemiology and pathology indicate an evolution of resistance or tolerance towards Pd in European bats. We compared the proteomic profile of blood plasma in asymptomatic and Pd colonized European *Myotis myotis* and North American *Myotis lucifugus* in order to identify pathophysiological changes associated with Pd colonization, which might also explain the differences in survival. Additionally, in order to better understand the molecular mechanisms associated with hibernation, we investigated the plasma proteomic profile of European *M. myotis* and hibernation-associated changes between torpid and active individuals. Expression analyses of plasma proteins revealed no significant differences between asymptomatic and Pd colonized *M. myotis* whereas in *M. lucifugus* differential expression was detected. We could identify differentially expressed proteins for acute phase response, constitutive and adaptive immunity, oxidative stress defence, metabolism, and structural proteins of exosomes and desmosomes suggesting a systemic response against Pd in North American bats. The differences in plasma proteomic profiles between European and North American bat species colonized by Pd suggest European bats have evolved tolerance towards the fungus. When comparing torpid and active *M. myotis*, results revealed an alternation of proteins involved in transport, fuel switching, innate immunity, and blood coagulation between the two physiological states, which is similar to previous changes described in other hibernators. Further characterization of the proteomic plasma profile identified transport proteins, coagulation proteins, and complements factors and detected a high abundance of alpha-fetoprotein. Our results demonstrate the utility of proteomics in bats in both eco-physiological and pathological studies.



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199 HEMATOLOGY, PLASMA BIOCHEMISTRY, AND PATHOGEN DISCOVERY IN ILLINOIS HEADSTARTED AND WILD-REARED POPULATIONS OF BLANDING'S TURTLES (*EMYDOIDEA BLANDINGII*) IN TWO NORTHERN ILLINOIS COUNTIES

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Keywords: Blanding's Turtle, Conservation Intervention, Emydoidea Blandingii, Headstarting, Release Health

Abstract Text

Blanding's turtles (*Emydoidea blandingii*) are state endangered in Illinois and of conservation concern across their entire range from the eastern United States to Southern Canada. Headstarting is a common conservation technique in chelonians, but rarely has health been systematically investigated during these efforts. We assessed head-started turtle health pre- and post-release (minimum of 4 weeks after release) using physical examination, hematology, plasma biochemistries, and pathogen detection, and compared to juvenile wild counterparts. Two hundred fifty-three assessments from one hundred ninety-eight juveniles and sub-adults were included. All individuals were negative for pathogens before release, while 3% were positive for adenovirus and 1.5% were positive for *Emydomyces testavorans* after release and 8% wild-reared were positive for adenovirus and 1% for *Mycoplasma* sp. Pre-release turtles had higher packed cell volume (PCV), total solids (TS), monocytes, heterophil:lymphocyte ratio (H:L), phosphorous, albumin:globulin ratio (AGR), and all protein electrophoresis fraction concentrations compared to post-release turtles, while post-release turtles had higher erythrocyte sedimentation rate (ESR) and calcium:phosphorous ratios (Ca:P). Wild turtles had higher total leukocyte counts (WBC), lymphocytes, monocytes, basophils, creatine kinase (CK), aspartate aminotransferase (AST), glutamate dehydrogenase (GLDH), and gamma globulins compared to headstarts, and lower H:L and alpha 1 globulins. Overall, rearing conditions in juvenile Blanding's have a profound impact on health assessment parameters. Future studies should evaluate long-term impacts on morbidity and mortality to aid in improving health of all populations of Blanding's turtles.



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124 LARGE-SCALE SURVEY FOR CANINE VECTOR-BORNE PARASITES IN DIFFERENT BIOCLIMATIC REGIONS OF CHILE: FIRST DESCRIPTION OF BABESIA IN DOGS AND HEPATOOZON IN FOXES

Sophia Di Cataldo¹, Aitor Cevidanes¹, Claudia Ulloa-Contreras², Javier Cabello³, Delia Gambino⁴, Valeria Gargano⁴, Constanza Napolitano⁵, Irene Sacristán¹, Nicole Sallaberry-Pincheira¹, Juliana Vianna⁶, Gerardo Acosta-Jamett⁷, Domenico Vicari⁴, Domenico Otranto⁸, Javier Millán⁹

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Keywords: Protozoan, Piroplasmida, Nematode, Culpeo, Chilla

Abstract Text

Chile is a large country that presents a range of climates that makes it an ideal scenario for the study of vector-borne parasites. The presence of Hepatozoon, piroplasmids and nematodes was studied in blood samples of 774 free-ranging rural dogs, 154 Andean foxes (*Lycalopex culpaeus*), and 91 South American grey foxes (*L. griseus*) from six bioclimatic regions across 3000 km in Chile through molecular and serological methods. We found a prevalence of 43% of Hepatozoon spp. DNA in foxes. All sequences in Andean fox were phylogenetically associated with *H. felis*. In grey foxes, all belonged to the *H. americanum* clade, except for one, that showed 100% identity with *H. canis*. Risk factor assessment identified juvenile age associated with higher probability of Hepatozoon infection in foxes. All dogs were negative for Hepatozoon DNA. DNA of Piroplasmida was found in 0.7% of the dogs, and in no fox. Antibodies against *Babesia* sp. were detected in 24% of the dogs and 25% of the foxes. A positive association between the presence of antibodies against *Babesia* and high *Rhipicephalus sanguineus* burden in dogs was observed. *Acanthocheilonema reconditum* was the only nematode detected in blood, being present in 1.5% of the dogs and in no fox. Our study presents the first description of *Babesia* in dogs and of Hepatozoon in foxes from Chile. The seroprevalence of *Babesia* among all the assessed bioclimatic regions suggested an underestimated molecular prevalence of this agent in dogs of the country. Possible host preference among foxes was detected for Hepatozoon species. The presence of vector-borne parasites that were not reported in Chile before, is essential to the achieve correct diagnosis in domestic dogs, improving control measures that can further beneficiate sympatric wild canids conservation plans.



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38 A PREVALENT CRYPTIC BACTERIUM IN THE ENDANGERED DARWIN'S FOX: GENETIC DIVERSITY, RISK FACTOR ASSESSMENT AND EFFECTS OF INFECTION

Sophia Di Cataldo¹, Aitor Cevidanes¹, Ezequiel Hidalgo-Hermoso², Irene Sacristán¹, Constanza Napolitano³, Claudia Hernández⁴, Fernando Esperón⁵, Darío Moreira-Arce⁶, Javier Cabello⁷, Javier Millán⁸

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Keywords: Canidae, Lycalopex, Mycoplasma, Risk Factors, South America

Abstract Text

Mycoplasma haemocanis (Mhc) is prevalent in the endangered Darwin's fox (*Lycalopex fulvipes*) in its main stronghold, Chiloé Island (Chile). The origin of the infection, its dynamics, its presence in other fox populations and the potential consequences for fox health remain unexplored.

During eight years, 82 foxes in Chiloé and other two fox populations and 250 free-ranging dogs from Chiloé were sampled, and the presence of hemoplasmal DNA screened and characterized.

The prevalence of Mhc in foxes was similar to that previously described, and coinfection with *Candidatus Mycoplasma haematoparvum* was confirmed in 30% of the foxes. Both hemoplasma species were detected in the two mainland fox populations and in Chiloé dogs. Mhc was significantly more prevalent and more genetically diverse in foxes than in dogs. Two of the seven Mhc haplotypes identified were shared between these species. Network analyses did not show genetic structure either by species (foxes vs. dogs), geographic (island vs. mainland populations), or temporal (years of study) factors. Models showed that the probability of infection with Mhc increased with fox age but was not associated with sex, season, or degree of anthropization of individual fox habitats. Intra-specific Mhc fox transmission appears to be predominant. Some foxes recaptured with years of difference were infected with the same haplotype in both events and no hematological alterations were associated with hemoplasma infection, suggesting tolerance to the infection. Nevertheless, such a prevalent pathogen in a threatened species represents a concern that must be considered in conservation actions.



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333 MERCURY EXPOSURE AND RISK ASSESSMENT FOR EURASIAN OTTERS (*LUTRA LUTRA*) IN DENMARK

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Keywords: Ecotoxicology, Eurasian Otter, *Lutra Lutra*, Mercury, Stable Isotopes

Abstract Text

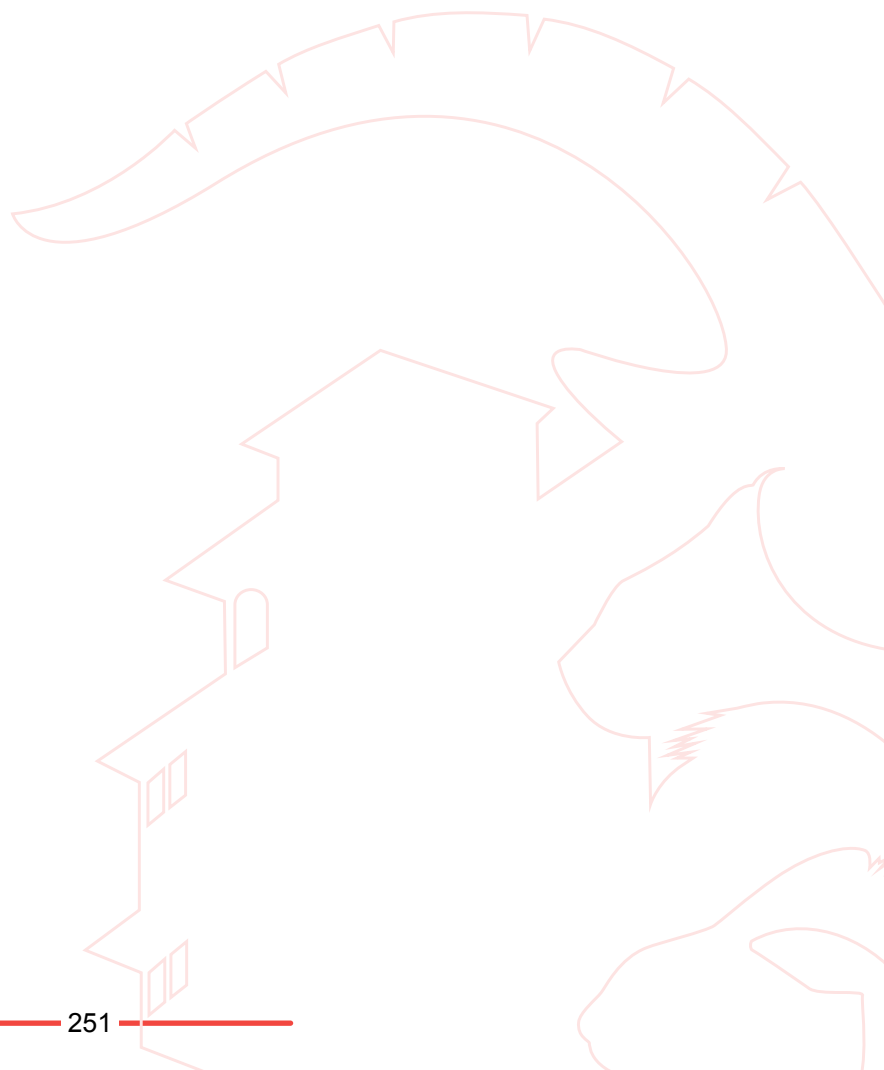
Mercury (Hg) pollution is widespread in aquatic environments, and exposure may cause a wide range of adverse effects in mammals. A piscivorous apex predator such as the Eurasian otter (*Lutra lutra*) may accumulate pollutants such as Hg. This study investigates the Hg concentrations in liver and fur samples from Danish otters between 2011-2019. The Hg concentrations will be compared to age, sex, trophic position, and habitat.

Hg concentrations were determined in liver and fur samples. The sex and age of the individuals were investigated. The stable isotope imprint of ¹³C and ¹⁵N in muscle tissue was used to determine the habitat and the trophic position, respectively.

The correlations among variables were determined, and an analysis of variance was conducted among age groups, males and females. A general linear modelling (GLM) was used in order to characterize the Hg exposure.

The results are generally low Hg concentrations (0.015-10.12 mg kg⁻¹ in liver), indicating a low or no threat of clinical Hg toxicity to the Danish population of otters.

However, a significant proportion of the Hg concentrations in liver tissue exceed the lowest-observed-effect-level (LOEL), where changes in central nervous system biomarkers have been described. The statistical analyses indicate that Hg concentrations are correlated to the age and the foraging habitat, but not to the sex and the trophic position. Hg concentrations increase with age and towards freshwater environments.





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102 BUTORPHANOL COMBINATIONS FOR ANESTHESIA OF DOMESTIC GOATS: MODELS FOR SMALL WILD RUMINANTS

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Keywords: Anesthesia, Butorphanol, Goat, Monitoring, Narcotics Small Ruminants Wildlife

Abstract Text

Current drug availability for use in small wild ruminants is changing from reliance on high potency narcotics. A variety of drug combinations using lower potency narcotics like butorphanol are becoming common, but data on patient stability is not always readily available.

The Idaho Department of Fish and Game used domestic goats as models for teaching chemical immobilization for 20 years. Numerous drug combinations were used to simulate results that could be anticipated in small wild ruminants. Pack goats (n=5-6 per year) were used annually for 4-5 years and then replaced with other animals. Goats were randomly selected for drug combinations and dosages. Animals were fasted for 24 hr prior to drug administration by hand injection under physical restraint. Animals were observed during induction and monitored for heart and respiratory rate, rectal temperature, capillary refill time, and mucus membrane color at 5-8 min intervals throughout anesthesia. Oxygen saturation was determined using a Nelcor pulse oximeter sensor placed on the tongue, lip, ear or teat.

Carfentanil-Xylazine (C-X), Etorphine-Xylazine (E-T), Thiafentanil-Xylazine (T-X), Butorphanol-Medetomidine (BM), Butorphanol-Azaperone-Medetomidine (BAM), Butorphanol x 2-Azaperone-Medetomidine 1/2 (BAM2), Butorphanol-Midazolam-Medetomidine (BMM), Butorphanol-Midazolam-Xylazine (BMX) and others were used in animals multiple times over multiple years.

A summary of drug combinations used with anesthetic monitoring parameters for comparisons will be presented. Most parameters were considered adequate under most drug combinations. Pulse oximeter readings were generally acceptable when using high potency narcotics. Drug combinations with Medetomidine routinely resulted in low O₂ saturation, with BAM, BAM2, BMX and BMM showing progressive improvements in patient stability. Pulse oximeter readings averaged 82.6, 86.7, 88.1, 88.5, 91.9, for BAM, BAM2, BMM, BM, and BMX, respectively compared to 87.6, 89.5, and 91.8 for C-X, E-X and T-X, respectively.

Drug combinations containing Medetomidine produced profound hypoxemia, especially BAM. All animals given Medetomidine combinations should be provided oxygen supplementation.



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167 INFLUENZA A VIRUS INFECTION IN URBAN AND RURAL POPULATIONS OF WILD BOARS IN SPAIN

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Keywords: Influenza A Virus, Synurbic Wild Boar, Urban Wildlife, Zoonotic Hazard

Abstract Text

The World Organization for Animal Health (OIE) recognizes Spain as a priority region for the surveillance of swine influenza A virus (IAV). Currently, Spain is the largest pig producer in Europe, holding a domestic pig population of around 30 million. The wild boar (*Sus scrofa*) is a domestic pig conspecific, hence susceptible to swine IAV. Wild boar populations are growing in number and geographic range all over Europe, and are increasingly in contact with free-ranging pigs and other domestic and wild animals. Moreover, the expanding use of urban environments by wild boars creates new opportunities for interactions with humans. Since transmission events leading to the introduction of human IAV into pigs can occur, there is a likelihood for the emergence of human-pig influenza recombinant viruses with potential to infect humans back.

In this study, we aim to investigate risk factors determining the epizootiology of influenza infection in rural and urban populations of wild boar in Spain. Serum samples from extensively-reared Iberian pigs (south-western Spain), rural wild boars (Sierra Nevada Natural Space and south western Spain) and urban wild boars (Barcelona) were analysed for antibodies against influenza A virus. The viral subtype profile was further characterized.

The seroprevalence against IAV was higher in domestic pigs than in wild boars, but also higher in the urban wild boars as compared to the rural ones. Furthermore, virus subtype profile differed significantly between rural and urban wild boars, most probably because of transmissions of viruses from human origin to the synurbic wild boars.



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140 SEROPREVALENCE OF CRIMEAN-CONGO HAEMORRHAGIC FEVER IN WILD UNGULATES FROM NORTH-EASTERN SPAIN

Johan Espunyes^{1,2}, Oscar Cabezón^{1,3}, Lola Pailler⁴, Andrea Dias-Alves¹, Lourdes Lobato-Bailón^{1,2}, Ignasi Marco¹, Maria Puig Ribas^{1,2}, Sebastian Napp⁴

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Keywords: Crimean-Congo Haemorrhagic Fever, Emerging Disease, Tick-Borne Disease, Zoonosis

Abstract Text

Crimean-Congo haemorrhagic fever is an emerging tick-borne disease caused by the arbovirus Crimean–Congo haemorrhagic fever virus (CCHFV). In humans, the disease can be severe and even fatal in up to 40% of cases, but the infection is usually subclinical in wild and domestic animals. CCHFV is endemic in several African, Asian and eastern European countries, but has recently emerged in Western Europe when it was detected in ticks from central Spain. Since 2016, four human cases have been reported in Spain. Surveys on ticks, humans and animals have evidenced the circulation of CCHFV in several regions from central and south-western Spain. With the aim of determining the possible circulation of CCHFV in north-eastern Spain (Catalonia), we carried out a serosurvey for the detection of CCHFV antibodies in different wild ungulates species.

We tested serum samples from 173 red deer (*Cervus elaphus*), 66 Iberian ibexes (*Capra pyrenaica*), 79 roe deer (*Capreolus capreolus*), 24 wild boars (*Sus scrofa*) and 4 fallow deer (*Dama dama*) for the presence of CCHFV antibodies using the CCHF Double Antigen Multi-species ELISA kit (IDvet, Montpellier, France). The samples were collected between 2016 and 2020, within the framework of the wildlife surveillance program of Catalonia.

We detected antibodies against CCHFV in 72/346 animals, including Iberian ibexes (66/66), roe deer (1/79) and wild boars (5/24). All positives belonged to the same area in Southern Catalonia, located at less than 5 kilometres from the Ebro Delta, an important wetland in Spain and a key stopover for birds migrating from Africa to Europe. This area was identified as a key “hot-spot” for the arrival and establishment of *Hyalomma* ticks, potentially infected with CCHFV. Therefore, the hypothesis of introduction via infected ticks transported by migrating birds seems likely.



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141 ARE GRIFFON VULTURES (*GYPS FULVUS*) SPREADERS OF ANTIMICROBIAL RESISTANT ENTEROPATHOGENS?

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Keywords: Antimicrobial Resistance, *Campylobacter*, *Escherichia Coli*, Griffon Vulture, *Salmonella*

Abstract Text

The emergence and spread of antimicrobial resistance (AMR) is one of the greatest threats to human medicine and public health. While the occurrence of AMR in livestock has been broadly studied, the role of wild animal species in the maintenance and transmission of resistance is still poorly understood. Vultures are particularly exposed to AMR food-borne pathogens due to the frequent consumption of infected livestock carcasses in supplementary feeding sites and organic waste in landfills. As so, they can be potential carriers and spreaders of AMR bacteria. In this study, we sampled a population of griffon vultures (*Gyps fulvus*) from north-eastern Spain and assessed the occurrence of ceftriaxone-resistant (CR-) *Escherichia coli*, *Salmonella* spp. and *Campylobacter* spp. Minimal inhibitory concentration was performed to determine AMR profiles. Out of the 220 individuals sampled between June 2019 and February 2020, 86 (39.1%) were positive for CR-*E. coli*, 19 (8.6%) for *Salmonella* spp. (particularly monophasic *Salmonella* Typhimurium) and 11 (5.0%) for *Campylobacter lari*. Among the CR-*E. coli*, 100% showed resistance to cefotaxime and ampicillin, 95.3% to ciprofloxacin, 91.9% to ceftazidime, 84.9% to sulfamethoxazole, 87.2% to tetracycline, 83.7% to trimethoprim, 70.9% to nalidixic acid, 69.8% to chloramphenicol, 39.5% to gentamicin and 1.2% to tigecycline. Among *Salmonella* isolates, we detected resistances to tetracycline (52%) and ampicillin (48%), followed by trimethoprim (10.5%), ciprofloxacin (5.2%), nalidixic acid (5.2%), chloramphenicol (5.2%) and gentamicin (5.2%). *Campylobacter* isolates presented resistance to ciprofloxacin (54.5%). The present study demonstrates that griffon vultures in NE-Spain are important carriers of AMR zoonotic enteropathogens. In order to mitigate the further spread of AMR, the monitoring and control of antimicrobial resistances in farms and landfills should be a priority.



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128 PATHOGENS OF COMMON PALM CIVETS (PARADOXURUS PHILIPPINENSIS, JOURDAN 1837), DOMESTIC CATS (FELIS CATUS L.), AND DOMESTIC DOGS (CANIS FAMILIARIS L.) IN MT. MAKILING FOREST RESERVE, LUZON ISLAND, PHILIPPINES

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Keywords: Serological Detection, Canine Parvovirus, Canine Distemper Virus, Feline Coronavirus, Toxoplasma Gondii

Abstract Text

The pathogens of common palm civets, domestic cats, and domestic dogs were studied using rapid diagnostic testing from July 2019 to February 2020 in Mt. Makiling Forest Reserve (MMFR), Luzon Island, Philippines. Blood, fecal, and nasal swab samples from two (2) civets, seven (7) domestic cats and four (4) domestic dogs underwent serological detection for canine parvovirus, canine distemper virus, feline coronavirus, and Toxoplasma gondii. Canine parvovirus was detected in an adult male common palm civet, a sub-adult female domestic dog, and a sub-adult male domestic dog. Feline coronavirus was detected in two (2) male adult cats. Canine distemper virus and Toxoplasmosis gondii were not detected in any individuals. It is possible that the isolated animal population in MMFR have not yet been infected with these diseases or perhaps those that have been infected died of the disease before infecting other individuals. This study represents the first research on the serological detection of pathogens in wild common palm civets in the Philippines and highlights the importance of closely monitoring infectious disease prevalence in domestic cats, domestic dogs, civets, and other wildlife in protected areas such as MMFR. In order to regulate the population of domestic cats and dogs, which are not native to the area, a spay/neuter, vaccination, and pet registration system should be put in place.



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335 ARE WILD UNGULATES IN CLOSE CONTACT TO HUMANS EXPOSED TO SARS-COV-2?

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Keywords: Anthropic Contact, Coronavirus, ELISA, Iberian Red Deer, Wild Boar

Abstract Text

Starting in December 2019 in Wuhan (China), a human respiratory disease caused by SARS-CoV-2, a beta-coronavirus of zoonotic origin, spread through human-to-human transmission to be declared a pandemic by the World Health Organisation in March 2020. Human-to-animal spill-back transmission has since been reported, and the potential role of domestic and wild animals in SARS-CoV-2 epidemiology remains a matter of discussion and concern. Close contact between wildlife and humans can favour bidirectional transmission of pathogens. Therefore, the study of wildlife exposed to humans can provide information on the role of these species as potential indicators or hosts. The aim of this study is to investigate the exposure to SARS-CoV-2 of farmed red deer (*Cervus elaphus*) and urban wild boar (*Sus scrofa*) in close contact with humans.

To achieve this objective, 285 serum samples from a farmed red deer population and 282 serum samples from a peri-urban wild boar population in Spain were collected in 2019, prior to the first European COVID-19 cases, and in 2020, during the ongoing pandemic. The sera were analysed through enzyme-linked immunosorbent assays (ELISA) for antibodies against the SARS-CoV-2 nucleocapsid protein (N), spike protein (S), and spike Receptor Binding Domain (RBD).

Antibody detection was more frequent in 2020, although the lack of test specificity rendered positive sera for both species also in 2019, particularly for the N ELISA. Thus, only four red deer and three wild boar sera with an ELISA% value >300 to the RBD or the S were considered positive. These seven sera were re-tested through competitive serum neutralization, resulting negative.

The results do neither confirm nor discard that red deer and wild boar populations in close contact with humans may be exposed to SARS-CoV-2. However, since experimental SARS-CoV-2 infection resulted in intraspecific transmission in white-tailed deer (*Odocoileus virginianus*), our results warrant further investigation.



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355 SUSPECTED BRUCELLA-ASSOCIATED ABORTION IN A HAWAIIAN MONK SEAL (*NEOMONACHUS SCHAUINSLANDI*)

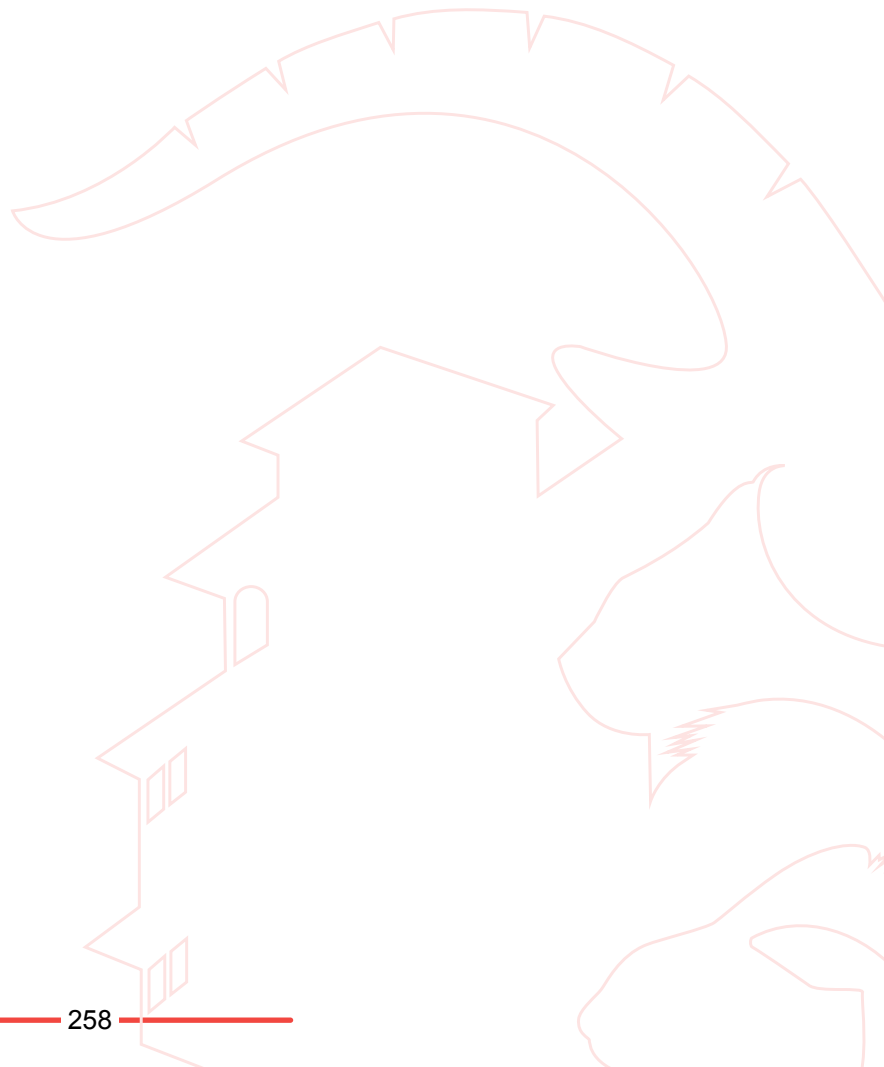
Cara Lisa Field¹, Gregg Levine¹, Megan Mcginnis¹, Kathleen Colegrove², Karen Terio², Andrea Packham³, Tracey Goldstein³, Claudia Cedillo⁴, Michelle Barbieri⁴

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Keywords: Abortion, Brucella, Hawaiian Monk Seal, Neomonachus Schauinslandi

Abstract Text

An eleven year-old adult female multiparous Hawaiian monk seal (*Neomonachus schauinslandi*), resident to Hawaii Island, was floating in a shallow lagoon in Waikoloa, HI for several days. She was presumed pregnant with a projected parturition date of April 4, 2020 based on previous parturition timing. On February 29, 2020, a large plume of bloody discharge consistent with fetal expulsion was noted while in shallow water, though no fetus was observed. She appeared agitated and uncomfortable on land; her genital region was notably swollen with bloody discharge, thus she was admitted into rehabilitation on March 3. On physical examination, the seal was in excellent nutritional condition and had mixed sanguinous and caseous vaginal discharge. Ultrasound showed right uterine horn enlargement with intraluminal material of mixed echogenicity. Vaginal cytology had marked neutrophilic inflammation with intracellular bacteria. Treatment with ceftiofur crystalline was initiated. Serology was strongly positive for *Brucella* spp. (Delta mP 176.8; Fluorescence Polarization Assay). Indirect immunofluorescence assay for *Toxoplasma gondii* was weakly positive at 1:640 and negative for *Sarcocystis* and *Neospora*. The vaginal discharge sample was positive for marine *Brucella* spp. and negative for *T. gondii* by PCR. Multilocus sequence typing of the *Brucella* sample was most consistent with the ST 26 genotype of *B. ceti*. The seal was released on March 18 as she appeared clinically normal. Her presentation and findings are most consistent with *Brucella*- associated abortion. The seal has been frequently re-sighted exhibiting normal behavior and in robust body condition; attention to reproductive status is on-going.





97 FEEDING HABITS OF CORMORANT IN THE PROVINCE OF TRENTO (ITALY) AND ITS ROLE AS VECTOR OF FISH VIRUSES

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Keywords: Cormorant, Ichthyophagous Birds, Feeding Habits, Viral Vector

Abstract Text

The cormorants (*Phalacrocorax carbo lucidus*) are elements of negative interference with fish species of high naturalistic value and several studies have shown that ichthyophagous birds can act as vectors for various fish diseases, both bacterial and viral. The Autonomous Province of Trento has been implementing a plan for the containment and prevention of damage from cormorants since 2010, with disturbance actions and culling in the feeding areas of greatest value for fish.

During the study period, from December 2015 to March 2020, five cormorant culling plans were conducted along the main rivers of the Trentino region, in the North-East of Italy. The aim of the work hereinafter described was to define cormorants' feeding habits and assess their potential role in spreading fish viruses of salmonids and cyprinids.

The crop and stomach of 196 cormorants were examined and the fish species found inside them were identified macroscopically and/or using biomolecular methods. A cloacal swab was performed to search VHSV (Viral Hemorrhagic Septicemia Virus) and IHNV (Infectious Hemorrhagic Necrosis Virus) from each cormorant; moreover, the search for IPNV (Infectious Pancreatic Necrosis Virus) was added only in 2017-2018 season. Organs from ingested salmonids were tested for VHSV, IHNV and IPNV, while cyprinids were tested for CyHV (Cyprinid Herpesvirus).

Fish were found in 39.3% of the cormorants. The ingested fish belonged to more than a dozen different species. The most represented fish families were cyprinid (43.5%), percid (34.1%) and salmonid (18.8%).

All cormorants and fish tested negative for viral diseases, with the exception of organs from two cyprinids found positive for CyHV in the 2015-2016 season.

The present study showed that in the ichthyofauna present in the digestive system of cormorants and in the cormorants themselves, important fish viruses like VHSV, IHNV, IPNV and CyHV were not detected.



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208 *EMYDOMYCES TESTAVORANS* SURVEILLANCE IN MULTIPLE FREE-RANGING TERRESTRIAL AND AQUATIC CHELONIAN SPECIES IN ILLINOIS

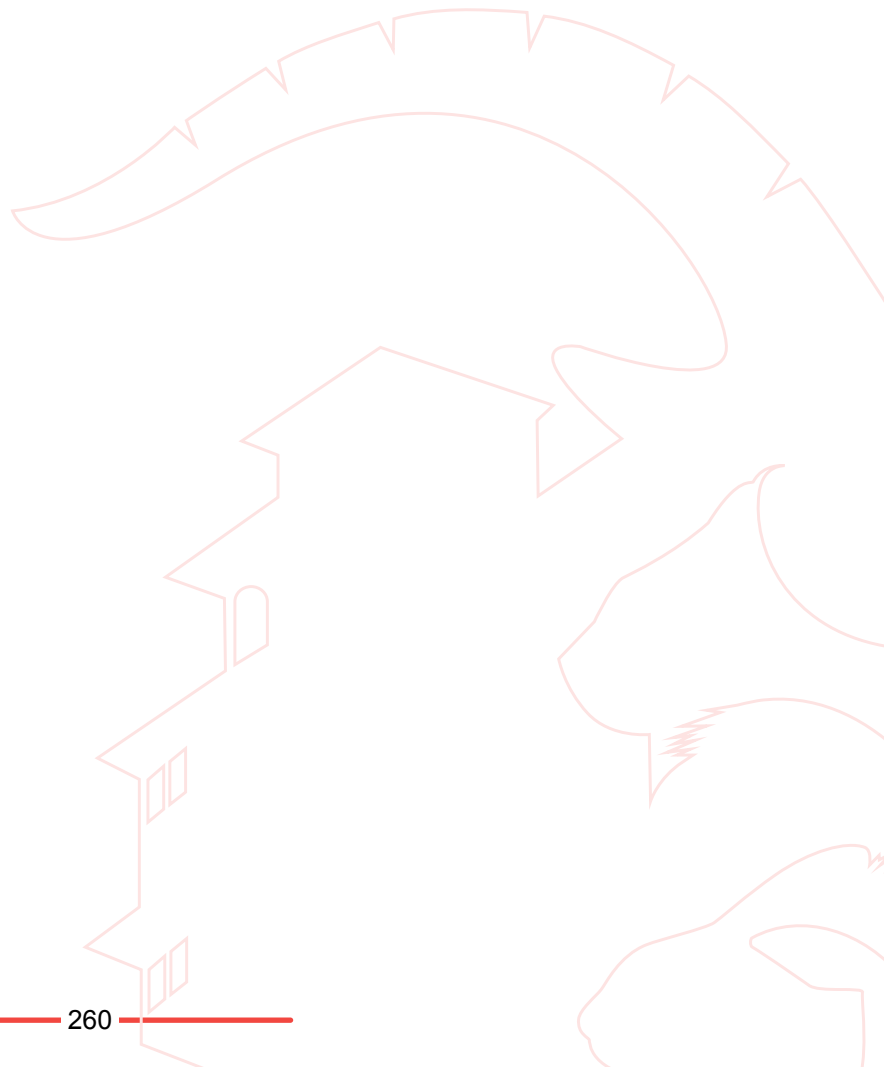
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Keywords: Blanding's Turtle, Chelonians, *Emydoidea blandingii*, *Emydomyces Testavorans*, Shell Fungus

Abstract Text

The order Onygenales contains multiple fungal pathogens that affect free-ranging and captive reptilian species. *Emydomyces testavorans*, an emerging Onygenalean fungus associated with skin and shell disease, has been sporadically detected in aquatic chelonians. Due to the recent discovery of this pathogen, little is known about its prevalence in free-ranging chelonians. The objective of this study was to determine the prevalence of *E. testavorans* in six free-ranging aquatic and terrestrial chelonian species in Illinois: Blanding's turtles (*Emydoidea blandingii*), painted turtles (*Chrysemys picta*), common snapping turtles (*Chelydra serpentina*), red eared sliders (RES, *Trachemys scripta elegans*), eastern box turtles (EBTs, *Terrapene carolina carolina*) and ornate box turtles (OBTs, *Terrapene carolina ornata*). In the 2019 and 2020 field seasons, combined cloacal-oral swabs (COS) were collected from free-ranging Blanding's (n=515), painted (n=171), and RES (n=40) turtles and tested for *E. testavorans* using TaqMan quantitative PCR. Shell swabs (n=204) were also collected from 181 free-ranging adults of all six species in the 2020 field season and subsequently tested. *E. testavorans* was detected in chelonians during both 2019 (n=3, 1.5%) and 2020 (n=3, 1.7%). All positive samples were from adult and juvenile Blanding's turtles, 66.7% of positive samples were from COS and 33.3% were from shell swabs. Shell lesions consistent with *E. testavorans* were present in 83.3% of the positive turtles. These results represent the first reported detection of *E. testavorans* in Blanding's turtles. Additional studies should determine this pathogen's impact on individuals and clarify its impacts on conservation efforts for Blanding's turtles.





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153 NECROPSY FINDINGS IN WILDLIFE VEHICLE COLLISIONS: COMPARISON OF MORTAL LESIONS IN MAMMALS AND BIRDS

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Keywords: Collision, Portugal, Roadkill, Wildlife, Trauma

Abstract Text

One of the major causes of wildlife deaths worldwide is vehicle collisions. The aim of this work was to identify and systematize injuries resulting from traffic accidents involving wild animals over a ten-year period in the Northern region of Portugal. In order to characterize pathologic lesions sustained by wild animals injured due to vehicle collisions, the reports of 170 wild animals' necropsies performed between January 2010 and June 2019 were evaluated. One hundred seventy wild animals were included in the study, 45 belonged to the class Aves (26.5%) and 125 in the Mammalia class (73.5%), being 81 females and 89 males, mostly adults (n=150). The most commonly affected body areas were abdomen and pelvis injuries in mammals (80.8%) and coelomic cavity in birds (80.0%). Musculoskeletal injuries were most commonly found in birds and organ injuries in mammals. Necropsy of wildlife vehicle collisions, although not generally critical for the diagnosis of the cause of death, may provide important data to increase knowledge in this area of pathology. The evaluation and systematization of fatal injuries caused by motor vehicle collisions could contribute to other studies comparing with other causes of traumatic death. On the other hand, may be of additional importance for facilitating treatment and predicting the effects of run-over lesions in wildlife



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154 OUTCOMES, MORTALITY CAUSES AND PATHOLOGICAL FINDINGS IN EUROPEAN HEDGEHOGS (*ERINACEUS EUROPEUS*, LINNAEUS 1758): A SEVENTEEN-YEAR RETROSPECTIVE ANALYSIS ON THE NORTH OF PORTUGAL

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Keywords: *Erinaceus Europaeus*, Hedgehog, Portugal, Mortality, Trauma

Abstract Text

This study aimed to analyze the admission causes, outcomes, primary causes of death and main lesion observed in the post mortem exam of Western European hedgehog *Erinaceus europaeus* (Linnaeus, 1758) in the north of Portugal. The data was obtained by consulting the records from the two main wildlife rehabilitation centers located at the north of Portugal (Wildlife Rehabilitation Centre of Parque Biológico de Gaia and the Wildlife Rehabilitation Centre of the University of Trás-os-Montes and Alto Douro). Over 17 years (2002-2019) a total of 740 animals were admitted. Most of the animals were juveniles, with the highest number of admissions occurring during summer (36.8%) and spring (33.2%). Main reasons for admission were debilitated (30.7%) and random find (28.4%). Of the total number of individuals admitted to these centers, 66.6% were released successfully back into the wild. The most relevant causes of death were trauma of unknown origin (32.7%), non-trauma of unknown origin (26.6%) and nutritional disorders (20.2%). The main lesions observed were related to trauma, with skeletal and skin lesions (fractures, hemorrhages, wounds) and organ damage, particularly lungs and liver. The hedgehog is a highly resilient and adaptable animal. The urban environment has many benefits for hedgehogs, yet, the human presence can be harmful. In the future, the public needs to become even more involved in the activities of the wildlife centres, which will make a positive difference for these populations.



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83 A PRELIMINARY STUDY OF ENDOPARASITES IN LIVE LOGGERHEAD SEA TURTLES

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Keywords: Apicomplexa, *Caretta caretta*, In Vivo Diagnosis, Mediterranean Sea, Trematoda

Abstract Text

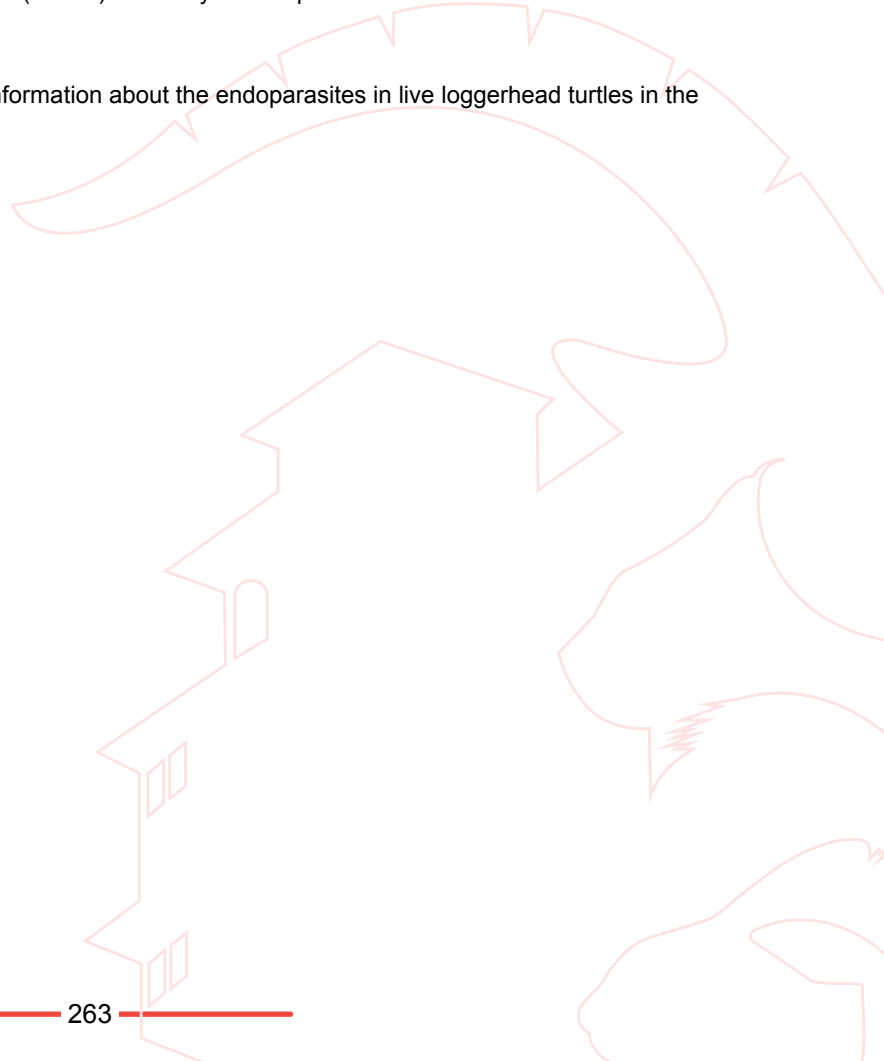
The loggerhead sea turtle (*Caretta caretta*) is the most abundant turtle species in the Mediterranean Sea. This chelonian has two main nesting areas; one is located off Florida shores from which young exemplars travel to the other, the Alboran Sea. Their population is mostly growing here because of the increasing nutrition chances for not fully developed turtles.

Parasites play strongly as a regularly primary factor of natural milieu *Caretta caretta* and a deep impact is likely to be caused by it on birth rate potential, migration span changes, or even increases in mortality.

Recent surveys have been conducted mainly following post-mortem techniques and a few have been done in vivo research. That is a paramount reason for us to start this new approach. This project has assessed the parasitic forms in 25 exemplars, using the coproparasitological diagnosis through sedimentation-flotation. The exemplars came from different areas of the Valencian Community coast after they had been stranded or captured due to anthropogenic reasons related to extractive fishing. This practice though becoming more and more a grievous menace for these animals has been the main source of samples for our study.

The total prevalence was 32%, similar to previous studies in other areas of the Mediterranean Sea. From the living animals, only Trematoda (75%) and Apicomplexa (25%) were found. The species identified were: *Enodiotrema megachondrus* (62.5%) and *Orchidasma amphiorchis* (12.5%). The only found species of coccidian was *Eimeria caretta* (25%).

This is the first research in vivo providing baseline information about the endoparasites in live loggerhead turtles in the western Mediterranean Sea.





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308 SURVEILLANCE FOR ECHINOCOCCUS SPECIES INFECTIONS AMONG WILD CANIDS IN PENNSYLVANIA, USA.

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Keywords: Echinococcus Multilocularis, Echinococcus Granulosus (Canadensis), Wild Canids, Prevalence, Parasite

Abstract Text

Echinococcus species are tapeworms (family Taeniidae, class Cestoda) of veterinary and medical concern, and can cause disease in their intermediate hosts (either cystic or alveolar echinococcosis depending on the species). Two species of interest in North America are *E. multilocularis* and *E. granulosus/E. canadensis*. The primary wildlife definitive hosts for *E. multilocularis* and *E. granulosus/E. canadensis* are red foxes (*Vulpes vulpes*), gray foxes (*Urocyon cinereoargenteus*), coyotes (*Canis latrans*), and wolves (*Canis lupus*). The typical intermediate hosts for *E. multilocularis* and *E. granulosus/E. canadensis* are rodents and artiodactylids, retrospectively. Although historically absent in the eastern United States, *E. multilocularis* was recently reported in a domestic dog in Virginia and a human in Vermont, while *E. granulosus/E. canadensis* has been reported in coyotes in Maine and translocated elk (*Cervus canadensis*) in Tennessee. These recent reports highlight the need for surveillance to determine the prevalence and distribution of Echinococcus in the eastern US. This study focused on samples from Pennsylvania. During 2019-2020, gastrointestinal tracts (GIT) were collected from wild canids that were euthanized or found dead. Heart and/or blood samples were also collected for future testing for selected vector-borne pathogens. To date, 472 GITs have been collected and 67 have been examined, with 3% (2/67) positive for Echinococcus canadensis (genotype G8) which were confirmed by analysis of partial cox1 gene sequences. Both positive individuals were coyotes (2/31) from the northeastern region of Pennsylvania, close to New York; none of the foxes examined to date (32 red fox and 4 gray fox) were positive. Our data show that Echinococcus canadensis is present in wild canids in Pennsylvania and highlights the need for further study and surveillance of this pathogen in the eastern United States.



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321 EVALUATION OF CHLAMYDIACEAE IN WILD BLACK-HEADED VULTURE (*CORAGYPS ATRATUS*)

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Keywords: Cathartidae, Chlamydiaceae, Chlamydiosis, Public Health, Scavengers' Birds.

Abstract Text

The black-headed Vulture (*Coragyps atratus*) is a Cathartidae specie widely distributed in Central and South America. Due to their scavengers feeding habit, they play an important role in the ecosystem, being known as the “environment cleaners”. Even though they rarely show clinical signs of disease, due to adaptations that gives them more resistance to pathogens present in the carcasses, little is known about their role as reservoirs of these microorganisms. In view of their co-living in the cities, close to humans and domestic animals, a better understanding of their interaction with pathogens is necessary to evaluate their role as a risk factor to public health and to domestic and wild animals' health.

The Chlamydiaceae is a Family of intracellular bacteria. This Family contains 11 species, including the zoonotic *C. psittaci*, and others with impact in domestic animal production. The most common found in birds is the *C. psittaci*. However, there is already evidences of their infection with *C. avium*, *C. gallinacea*, *C. abortus*, *C. pecorum*, *C. suis* and *C. muridarum*.

In this study, we analyzed the occurrence of Chlamydiaceae in the cloacal swab of 141 wild adult *C. atratus* capture in de city of São Paulo, Brazil, using the PCR technique. As result, we found 33 positive samples (23.40%) for Chlamdia sp. All positive samples were tested using a specific PCR showing negative results for *C. psittaci*.

These results reveal that the other species from Chlamydiaceae are present in this population of vulture. The chlamydial specie present in this population still needing to be clarified, also considering the epidemiological relationships of vultures with other wild and domestic animals and the urban environment. Further studies are necessary to understand the epidemiology and importance of new species of Chlamydia in birds.



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301 ARE ZOO MAMMALS POTENTIAL SENTINELS FOR ZONOTIC FLAVIVIRUSES MONITORING?

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Keywords: West Nile, Usutu, Tick-Borne Encephalitis, Sentinel, Public Health

Abstract Text

Flaviviruses are important emerging and re-emerging zoonotic vector-borne pathogens. During the last decade, flaviviruses have widely spread in Europe, representing an increasing threat for public and animal health. The aim of the present study was to assess emerging flavivirus exposure in zoo mammals in Spain and to determine the kinetics of seropositivity in species longitudinally surveyed during the study period. Serum samples from 570 zoo animals belonging to 120 mammal species were collected in ten zoos (A-J) from Spain between 2002 and 2019. In addition, twenty-one of these animals were longitudinally sampled in four of the zoos during the study period. Nineteen (3.3%; 95%CI: 2.0-5.2) out of the 570 animals analyzed presented antigenically-related flavivirus antibodies using bELISA. Seropositivity was observed in ten (8.3%) of the 120 species tested. Five (23.8%) of the 21 animals sampled more than once showed seropositivity at all samplings whereas one seroconversion was detected in white rhinoceros (*Ceratotherium simum*). Flavivirus antibodies were found in six of the ten sampled zoos and in consecutive years between 2008 and 2018. Virus neutralization tests confirmed West Nile virus (WNV), Usutu virus (USUV) and tick-borne encephalitis virus (TBEV) infection in ten (1.8%; 95%CI: 0.7-2.8), five (0.9%; 95%CI: 0.1-1.6) and one (0.2%; 95%CI: 0.0-0.5) animal, respectively. The results demonstrate WNV, USUV and TBEV exposure in zoo mammals, which may be of public health and conservation concerns. Seropositivity to WNV and USUV was detected in regions where these viruses have not been previously reported. Anti-WNV antibodies found in zoo animals sampled in 2009 point to WNV circulation at least one year before the first outbreaks were reported in horses and humans in Spain. Our findings indicate that zoo mammals could be useful sentinel species for monitoring emerging flaviviruses activity in urban areas.



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360 FRESHNESS MIGHT DETERMINE THE OUTCOME OF WILDLIFE HEALTH SURVEILLANCE BASED ON COPROLOGY

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Keywords: Endoparasites, Coprological Examination, Faecal Samples, Population Monitoring

Abstract Text

Coprology of faecal samples collected during field surveys is fast gaining popularity in wildlife health surveillance programmes worldwide. A high endoparasite burden is usually interpreted as a signal of poor health status of the target population. Though fresh faecal samples are necessary to conduct coprological analysis, little is known about the impact of the time elapsed from defecation on the technique. On the other hand, there is no criteria to determine the freshness of faecal samples by the visual observation of dungs.

In this work, we performed an experiment using a sample of freshly faeces from a herd of sheep with high parasite burdens to assess the impact of the method of preservation and the time from collection on the number of nematode eggs, coccidian oocysts, nematode larvae per gram. The initial sample mixed and split into five treatments (e.g., in a fridge at 4°C, outside exposed to light and in the shade, and in a greenhouse at light and in the shade). We performed a coprology of a sample from each treatment during 15 days. Just four days of exposition, the number of nematode eggs/gr decreased in more than 50% of the initial burden, in particular in samples exposed to high temperatures. Along the same lines, coccidian burden also from day four and nematode larvae increased due to egg hatching. The visual aspect of faeces was also correlated to their freshness but raining might easily lead to a confusion. Based on our findings, we recommend collecting dark and glossy faecal samples with 1 to 2 days post defecation to avoid spurious low parasite burdens. Glossy and dark pellets collected on a sunny and dry day are a proxy of freshness and ideal to perform health surveillance of wildlife based on environmental samples.



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257 INTRAOCULAR PRESSURE REFERENCE VALUES IN ADULT BONELLI'S EAGLES (*AQUILA FASCIATA*)

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Keywords: Tonometry, Ophthalmology, Bonelli's Eagle, Wildlife

Abstract Text

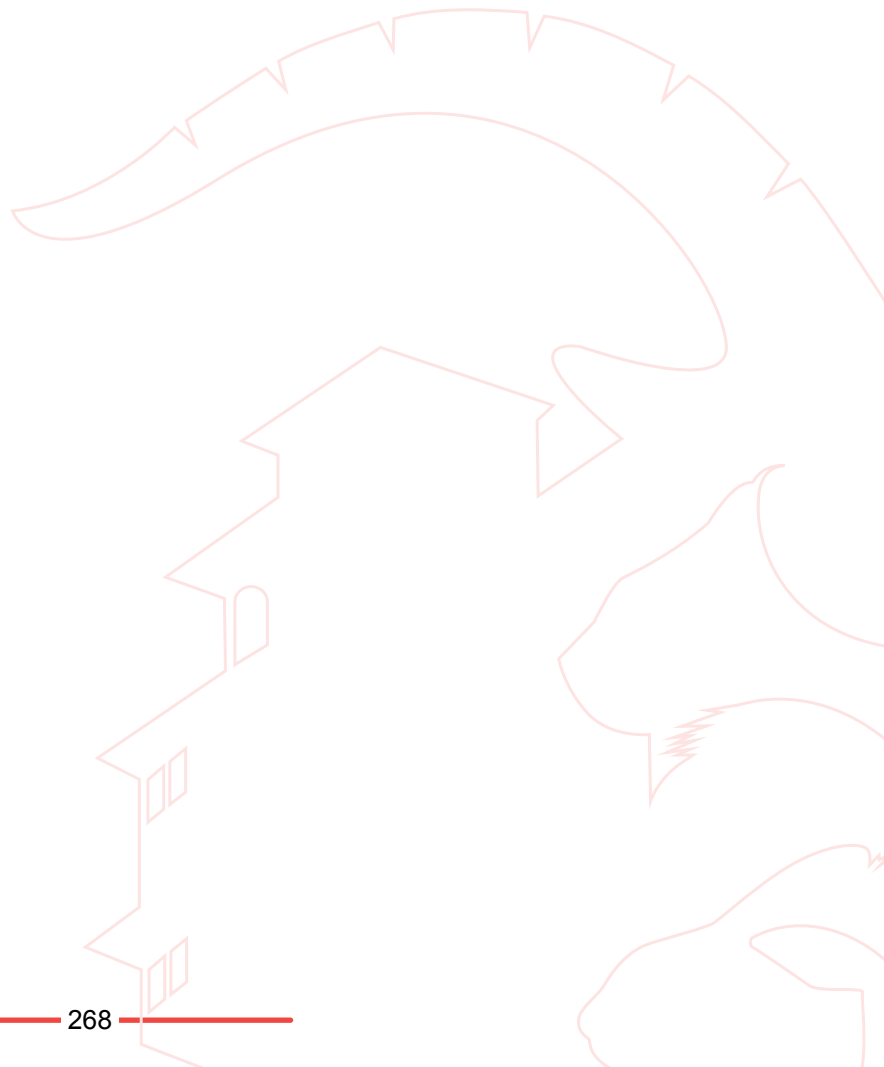
The presence of eye lesions in free-living raptors admitted to wildlife rescue centers is quite common due to different accidents, such as trauma. Full recovery of the vision capacity is essential for these animals to be released into the wild, therefore a complete ophthalmological examination must be done.

Tonometry is a common procedure in ophthalmological examination of wild birds to determine intraocular pressure (IOP). However, IOP has been reported to be different between avian species. The aim of this study was to determine IOP reference values in adults Bonelli's eagles (*Aquila fasciata*) and its relationship with gender and eye side.

Tonometry was performed in 52 eyes, right and left, of 26 Bonelli's eagles (*Aquila fasciata*) using a tonometer based on a rebound measuring principle (Icare® Tonovet) in a wildlife hospital in Spain. A complete physical and ophthalmological examination with PanOptic™ ophthalmoscope was performed, confirming the healthy state of all birds and the absence of ocular lesions.

Results showed mean IOP values (mmHg ± SD) of 38.27 ± 8.18 (52 eyes). A statistical analysis of the data and its relationship with gender and eye side was performed and no significant differences were found between genders or between left and right eyes.

These results show that rebound tonometry is useful in measuring IOP in adults Bonelli's eagles as a tool for the diagnosis of ocular pathologies.





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328 SEVOFLURANE ANAESTHESIA IN COMMON KESTREL (*FALCO TINNUNCULUS*)

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Keywords: Anesthesia, Falco Tinnunculus, Sevoflurane

Abstract Text

The use of inhalant anesthesia is very frequent in wildlife bird medicine. Since these birds are highly sensitive to stress due to manipulation, it represents a common resource for the execution of determined procedures that require immobilization. Inhalant anesthetic agents are the most used due to their safety, but there exists a relatively high perianesthetic mortality. An apparently safer alternative to isoflurane, the reference drug in avian medicine, is sevoflurane, but there is currently no report regarding the common kestrel (*Falco tinnunculus*). The aim of this study is to establish a preliminary approach to the anesthetic profile of sevoflurane in *Falco tinnunculus*.

Sevoflurane was administered (induction with mask at 8%; maintenance under intubation at 3-5%) to common kestrels (n=6). Different physiologic parameters were monitored during anesthesia, as well as the times for analyzing induction and recovery. These times were based on different events: onset of delivery of sevoflurane, intubation, discontinuation of delivery of sevoflurane, extubation, bird being able to hold its head up and tracking. A descriptive and inferential statistical analysis has been carried out (ANOVA repeated measures and Friedman's test); normality was evaluated through the Shapiro-Wilks' test. No variations in temperature, heart rate (HR), respiratory rate (RR) and end tidal CO₂ pressure during anesthesia were observed. Times of induction and extubation were short (123.33 ± 49.33 s and 63.33 ± 29.70 s, respectively). Tracking was not useful to evaluate recovery in this species because it was not present in all animals.

The use of sevoflurane in *Falco tinnunculus*, apparently, does not produce any variations in the HR or RR during anesthesia. This suggests its stability at cardiac and respiratory levels, although it should be evaluated in birds with different diseases. Besides, its rapid induction and recovery could be beneficial, especially in debilitated animals and when there appear complications



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283 PREVALENCE AND GENOTYPING OF ENTERIC PROTIST PARASITES IN WILD UNGULATES IN SPAIN.

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Keywords: Wild Ungulate, Enteric Protist Parasites, PCR, Sequencing

Abstract Text

Wild ungulates may act as suitable hosts for a wide range of parasitic and commensal protist species. Molecular epidemiological studies assessing the frequency and molecular diversity of enteric protists in wild animal populations are scarce. This cross-sectional epidemiological study aims to determine the diversity and frequency of the main species/genotypes of diarrhoea-causing protists in wild ungulates (Artiodactyla) in Spain, and their role as potential disease reservoirs for both domestic animals and humans.

Faecal samples were collected from four wild ungulate species legally hunted (2014–2019) and additionally from semi-extensively farmed red deer (2012–2014). Enteric protists occurrence was investigated by molecular (PCR and Sanger sequencing) methods.

Giardia duodenalis was the most prevalent protist found in mouflon (11.11%, 1/9), followed by wild boar (*Sus scrofa*) (5.03%, 14/278), fallow deer (4.70%, 4/85) and red deer (4.10%, 24/587). *Cryptosporidium* spp. and *Blastocystis* sp. were more prevalently detected in wild boar (8.27%, 23/278; 9.35%, 26/278) followed by deer (1.87%, 11/587; 6.13%, 36/587). These protists were not detected in fallow deer and mouflon. *Enterocytozoon bieneusi* was found in red deer (11.92%, 70/587) and wild boar (1.08%, 3/278), but not in fallow deer and mouflon. *Balantioides coli* was detected in wild boar only (3.24%, 9/278). None of the *G. duodenalis* isolates could be genotyped. *Cryptosporidium ryanae* and *C. parvum* were identified in deer and wild boar, *C. suis* in red deer and *C. scrofarum* and *C. fragile* in wild boar. *Blastocystis* ST1, ST5, ST10, ST12, ST13, ST14, ST21, and ST24 were detected in red deer and ST2 and ST5 in wild boar. Within *E. bieneusi*, known (EbPA, N1A1, S5, HLJD-V, BEB6, BEB17, Wildboar3, NCF2, Type IV) and novel genotypes were detected in red deer and wild boar.

Our results indicate that infections by enteric protists, some of them zoonotic, are relatively frequent in the species/hosts screened.



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91 NOVEL APPROACHES FOR DIAGNOSING TUBERCULOSIS IN WILDLIFE IN RESOURCE-POOR COUNTRIES.

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Keywords: GeneXpert MTB/RIF Ultra, Mycobacterial Culture, Mycobacterium Tuberculosis Complex, TiKa, Wildlife

Abstract Text

Globally, the health of managed and free-ranging wildlife populations is threatened by tuberculosis, a chronic progressive disease caused by infection with members of the Mycobacterium tuberculosis complex (MTBC)^{1,2}. Since most infected wildlife remain asymptomatic until disease is advanced, diagnosis can be difficult and interventions to prevent transmission are often delayed³. The definitive diagnosis of TB remains the direct isolation and identification of the specific pathogen through mycobacterial culture⁴. However, this involves harsh decontamination treatments prior to culturing, destroying an order of bacilli present, resulting in suboptimal sensitivity and long incubation periods (6-8 weeks).

The application of a new qPCR, the GeneXpert MTB/RIF Ultra (Ultra) and a modified mycobacterial culture technique, called the TiKa MGIT platform (TiKa), have both previously shown major potential in diagnosing TB in humans and livestock⁴. Recently, in wildlife, we have further shown their utility for the rapid detection of MTBC DNA and promoting mycobacterial growth from clinical paucibacillary antemortem and postmortem wildlife specimens. Overall, the Ultra produced a mean sensitivity of 92% and specificity of 83% in clinical respiratory and tissue samples from African buffaloes, elephants, and rhinoceros⁵. Using oral swabs collected in-field from known *M. bovis* infected buffaloes, stabilised in a novel sterilizing molecular transport medium, the Ultra produced a sensitivity of 81%⁶. Lastly, improved MTBC recovery by culture was observed when using TiKa with a 95% sensitivity compared to 44% when using conventional culture and an overall reduction of time to detection of 6.5 days. Both techniques are species non-specific, with the Ultra already utilized in reference human TB laboratories with culture capabilities in important wildlife range countries like South Africa, Botswana, and Zimbabwe⁷.

Therefore, this presentation will describe the utility of Ultra and TiKa for TB detection in wildlife species which may be performed in zoos, clinical, or laboratories throughout the world.



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126 FIRST REPORT OF CANINE CIRCOVIRUS AND CANINE PARVOVIRUS IN RED FOXES OF NORTH-EASTERN ITALY

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Keywords: Aleutian Mink Disease Virus, Canine Circovirus, Canine Parvovirus, Phylogenesis, Red Foxes

Abstract Text

Wild foxes have been proven to host several viral pathogens of both human and veterinary interest. Besides the obvious implication for fox population health, they can represent a threat for endangered wild species, as well as livestock and companion animals. Significantly, single-stranded DNA viruses typically targeting other hosts, like Carnivore protoparvovirus 1, particularly Canine parvovirus (CPV) and Feline parvovirus, Canine circovirus (CanineCV) and Aleutian mink disease virus (AMDV) have all been reported in foxes.

Nevertheless, the epidemiology of these viruses in wild foxes is poorly understood and few research data are available. Italy makes no exception in this sense. Aiming to fill this gap, we investigated the presence of these viruses in Northern Italy red foxes populations.

A total of 117 spleens were collected from foxes during hunting season or passive surveillance activities in North-Eastern Italy, Belluno Province, from 2017 to 2020.

All samples were tested by qPCR for CanineCV, CPV and AMDV and, when possible, positive samples were amplified and sequenced for further phylogenetic analysis.

CanineCV DNA was detected in 5/117 (4.3%) spleens, CPV in 6/117 (5.1%), whilst no one tested positive per AMDV. Positive specimens showed low viral titer and no coinfection between the tested pathogens was detected. One partial CanineCV sequence could be obtained, which did not demonstrate any close association with other strains (minimum p-distance of 3.3% with a Norwegian red fox strain). Similarly, one partial Carnivore protoparvovirus sequences was obtained and allowed the strain characterization as CPV. However, the limited sequence size impeded further inferences.

The prevalence of both CanineCV and CPV was low but not negligible, suggesting a promising topic for further studies on the host-virus interaction and coevolution.



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100 THE IMPORTANCE OF MANGE DIAGNOSTICS AND SOME UNUSUAL CLINICAL CASES IN WILDLIFE

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Keywords: Mange, Mites, Diagnostics, Epidemiology, Parasites

Abstract Text

Mange refers to skin disease caused by different parasitic mite species. Animals with mange may have minimal lesions that resolve or may develop severe disease with hair loss, severe itching, and crusty skin that can result in mortality. Mange can likely occur in any domestic and wild mammalian species and can be caused by numerous mite genera. Accurate morphologic examinations, and sometimes molecular techniques, are imperative for correctly identifying the causative agents and documenting the epidemiology of this disease in wildlife. In the United States, some of the more commonly detected types of mange in wildlife include sarcoptic mange (caused by *Sarcoptes scabiei*) in American black bears (*Ursus americanus*), red foxes (*Vulpes vulpes*), coyotes (*Canis latrans*), and gray wolves (*Canis lupus*); demodectic mange (*Demodex* spp.) in cervids and black bears; psoroptic mange (*Psoroptes* spp.) in white-tailed deer (*Odocoileus virginianus*); and notoedric mange (*Notoedres* spp.) in bobcats (*Lynx rufus*), squirrels (*Sciurus* spp.) and bats. In this “what’s your diagnosis” presentation we discuss four mange cases in American black bears from Georgia and Massachusetts, a porcupine (*Erethizon dorsatum*) from Pennsylvania, and an eastern cottontail (*Sylvilagus floridanus*) from Florida. Their diagnosis and importance will be discussed. Although mange cases generally involve individual animals within a population, the mange cases in cottontail rabbits from Florida were unusual in that at least five rabbits were reported sick or dead at this site during 2020, but only this one was submitted. These cases represent unusual mite species detections or expanded distribution reports which emphasize that mange is a syndrome and not an etiologic diagnosis, so careful examination of mites is critical to best understand their ecology and assist in management. Furthermore, there are numerous causes of hair loss and skin lesions in wildlife that are unrelated to mites, so ancillary tests may be needed.



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41 TREATMENT OF *BATRACHOCHYTRIUM DENDROBATIDIS* IN EASTERN HELLBENDERS (*CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS*) WITH TERBINAFINE

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Keywords: *Batrachochytrium Dendrobatidis*, *Cryptobranchus Alleganiensis Alleganiensis*, Eastern Hellbender, Lamisil, Terbinafine

Abstract Text

Two wild-caught, adult female Eastern hellbenders (*Cryptobranchus alleganiensis alleganiensis*) were examined and swabbed individually for chytrid testing via quantitative polymerase chain reaction (qPCR). Both females were positive for *Batrachochytrium dendrobatidis* (Bd). Infection was subclinical, as both hellbenders had no abnormal findings on physical exam. A course of terbinafine hydrochloride (HCL) in alcohol (LamisilAT® Spray) given topically via treatment baths, was initiated once daily, over five days, five minutes per session. Both animals were individually retested one week, three weeks and one-month post treatment using PCR. All post treatment samples were negative for Bd in both females. These cases represent the first successful treatment with terbinafine HCL in alcohol to eliminate chytrid infection in Eastern Hellbenders. This case underlines the importance of routine and pre-shipment testing for chytridiomycosis in amphibians being transferred to different facilities as a means to minimize risk of disease introduction via a carrier species into a new collection.



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158 BLOOD MERCURY IN THREE POPULATIONS OF ENDANGERED WHOOPING CRANE (*GRUS AMERICANA*)

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Keywords: Whooping Crane, Blood Mercury, Exposure Risk, Biomonitoring

Abstract Text

The Whooping Crane (*Grus americana*) is an iconic endangered species believed to be at risk from environmental contamination. This study documented Hg exposure among three extant populations. Blood samples were analyzed for total mercury (THg) using an adaptation of the CDC NHANES Laboratory method for avian blood and inductively-coupled plasma mass spectrometry. Blood THg was greater in cranes reintroduced during 2001-2008 that range in the eastern US (mean = 0.36 ug/g ww, n = 17) than both wild cranes in central North America (mean = 0.12 ug/g ww, n = 21) and from captivity (mean = 0.01 ug/g ww, n = 10). The mean THg levels in the two free-ranging populations of Whooping Cranes were low compared to reproductive toxic thresholds suggested for other large bird species, but one crane sampled (6% of samples from the reintroduced population) had blood THg = 1.04 ug/g ww. There were no significant differences in THg concentrations between female and male Whooping Cranes in any population. These results likely reflect variable dietary Hg exposure among these populations, but the singular elevated result in our study's small sample suggests some eastern migratory cranes may approach risk thresholds for Hg toxic effects at critical times of the year. Future studies should expand biomonitoring to discern risk of greater Hg exposure nearer to the time of breeding and potential effects on productivity.



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263 SURVEILLANCE FOR *BATRACHOCHYTRIUM DENDROBATIDIS* AND POSSIBLE ASSOCIATION WITH SKIN KERATIN ABUNDANCE IN RED-SPOTTED NEWTS (*NOTOPHTHALMUS VIRIDESCENS VIRIDESCENS*) AND MOLE SALAMANDERS (*AMBYSTOMA TALPOIDEUM*)

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Keywords: *Batrachochytrium Dendrobatidis*, Skin Keratin Abundance, *Notophthalmus*, *Ambystoma*, Caudate

Abstract Text

Surveillance for *Batrachochytrium dendrobatidis* (Bd) in amphibians and understanding risk factors associated with detection and infection are necessary for mitigating the potential detrimental impacts. The Bd prevalence at two sites in Georgia, USA (Whitehall Experimental Forest in the Piedmont region and Sandhills Wildlife Management Area in the Upper Coastal Plain region) were investigated from September 2020–April 2021. The potential association between Bd prevalence and skin keratin abundance between two focal species, red-spotted newt (*Notophthalmus viridescens viridescens*) and mole salamander (*Ambystoma talpoideum*), was also investigated. Bd was detected in at least one species at all study ponds at both study sites. The prevalence of Bd varied by season, location, male sexual characteristics, and species sampled. The overall prevalence of Bd detection was 30.5% (n=393) with the highest prevalence in adult red-spotted newts (42.9%, n=191) and paedomorphic mole salamanders (28.4%, n=81). Marked seasonality was noted from a low in September 2020 (0%, n=4) to a peak in December 2020 (39.0%, n=82). The skin keratin abundance was scored (scale 0-3) based on microscopic examination of skin samples from the caudal abdominal cavity and hindlimbs. Keratin abundance was higher in adult red-spotted newts (score=1.65) compared to paedomorphic mole salamanders (score=0). The relatively high prevalence of Bd in mole salamanders yet lack of detected keratin in the stratum corneum indicate that there is not an interactive effect between Bd prevalence and skin keratin abundance, although there may be sufficient keratin in other body regions to maintain Bd infection. These data support the purported role of red-spotted newts as a reservoir of Bd and previously reported seasonality in this region. Additional research is needed on mole salamanders as the relatively high Bd prevalence, which is a novel finding, suggests they may be reservoirs but they may also suffer morbidity/mortality that has not been previously detected.



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72 ASSESSING THE NATIONAL PROGRAMME FOR GENERAL WILDLIFE HEALTH SURVEILLANCE IN SWITZERLAND

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Keywords: Wildlife, Health, Surveillance, Survey

Abstract Text

Wildlife health surveillance continuously gains importance worldwide, as pathogen transmissions among wildlife, domestic animals and humans raise increasing health, conservation and economic concerns. In Switzerland, the Centre for Fish and Wildlife Health (FIWI) carries out the governmentally mandated general wildlife health surveillance programme. A marked increase in the number of case submissions for post-mortem investigation over the past twenty years motivated this study. As the FIWI faces financial constraints, the aim was to assess whether the current surveillance system should be maintained as it is, potentially with more resources invested, or could improve in efficiency instead.

We assessed the following critical points using different methods: (1) A retrospective analysis of the diagnostic data from 2002-2019, to identify potential causes for the increased case load; (2) Telephone interviews of programme partners, to clarify the needs concerning wildlife health investigations; (3) Online questionnaires for game wardens and hunters, to understand current decision criteria for case selection in the field and to identify potential for improvement; (4) In-house time recordings of post-mortem investigations, to document current time requirements per case and assess the potential for more time efficient workflows.

We found that (1) case increase was mainly due to infectious diseases and population growth of protected species; (2) programme partners were overall satisfied with the services offered by the FIWI, the provided information and communication regarding wildlife diseases; (3) case selection in the field was carried out wisely and (4) time-consuming cases were mainly monitored protected carnivores and those including histology.

In conclusion, our preliminary results suggest that wildlife health surveillance in Switzerland is already on a high standard. However, restricted laboratory capacities and required selection in the field cause an information gap regarding disease occurrence information.

Next steps include comparisons with other European wildlife health surveillance programmes.



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188 PATHOGENS OF ZONOTIC AND CONSERVATION CONCERN IN LOS ANGELES COUNTY, CALIFORNIA

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Keywords: Leptospira, Mammals, Pathogens, Urban

Abstract Text

Many pathogens carried by urban wildlife can be transmitted to humans and domestic pets, but much remains unknown about the abundance, population dynamics and pathogen loads of the urban mammals inhabiting many large metropolises. To address these existing knowledge gaps in Los Angeles County, we are finalizing a 4-year pathogen survey of five common mammal species (coyotes, raccoons, striped skunks, Virginia opossums and fox squirrels) that may carry zoonoses (e.g. *Leptospira*, *Giardia* and *Cryptosporidium* spp.) or pathogens of conservation concern (e.g. canine distemper virus – CDV). To assess fecal pathogens in raccoons (n=151), skunks (n=16) and coyotes (n=64), we analyzed feces for pathogen DNA using polymerase chain reaction (PCR), with positive results for CDV (n=110), *Salmonella* (n=22), *Cryptosporidium* (n=37) and *Giardia* (n=4). In all five species, we assessed prior *Leptospira* exposure via microscopic agglutination testing (MAT; n=353) and active infections using *Leptospira* PCR (n=375). Prior *Leptospira* exposure was detected in 13/54 coyotes (24%), 30/88 raccoons (34%), 60/102 fox squirrels (59%), 5/20 striped skunks (25%) and 4/89 Virginia opossum (5%), and MAT cross-reactivity patterns suggest multiple *Leptospira* serovars may be circulating in the Los Angeles area. Active *Leptospira* infections were detected by PCR in 2/77 coyotes (3%), 8/96 raccoons (8%), 5/21 striped skunks (22%) and 1/89 opossums (1%). Intriguingly, despite their high exposure prevalence, all of the fox squirrels have been negative (0/92). By mapping pathogen occurrence in relation to indices of urbanization, we gain a qualitative understanding of factors governing pathogen distribution across this urban landscape. This study provides an initial assessment of pathogens of zoonotic and conservation concern in L.A. County mammals across an urbanization gradient. When considered with paired host genetic samples, these results will increase our knowledge of connectivity, pathogen occurrence and transmission potential in these urban mammals.



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366 PATTERNS OF BARTONELLA INFECTION IN SMALL MAMMAL FROM INTENSIVE FARMLANDS, NW SPAIN

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Keywords: Apodemus Sylvaticus, Co-infection Patterns, Crocidura Russula, Mus Spretus, Zoonotic Pathogen

Abstract Text

Small mammals act as wild reservoirs of Bartonella species. In intensive farmlands of NW Spain, *Microtus arvalis* harbour five Bartonella spp. whose prevalence is higher during winter and varies with host (vole, mice) density. *Microtus arvalis* undergoes cyclic fluctuations in abundance, and sympatric hosts (mice, shrew) have annual, seasonal dynamics. This study aimed to investigate Bartonella diversity and prevalence in the sympatric small mammal guild during a *M. arvalis* fluctuation. We also studied how prevalence varied seasonally and depending on the sex of the alternative hosts. To detect Bartonella species, DNA extracted from a mix of liver and spleen was tested using a real-time PCR. Positive samples were amplified by conventional PCR and subsequently screened by reverse line blotting for species-level identification. We sampled 341 small mammals (*Apodemus sylvaticus* = 225, *Mus spretus* = 65, *Crocidura russula* = 51) and identified ten different Bartonella species. The zoonotic *B. grahamii* was shared by all small mammal hosts (including *M. arvalis*), *B. taylorii* was only detected in rodents, and *B. elisabethae* was present in alternative hosts to *M. arvalis*. Mixed infections (>1 Bartonella spp.) reached 78.9% of all Bartonella-positive hosts, with higher variability in mice. Bartonella prevalence was higher in *M. spretus* (63.1%) and *A. sylvaticus* (47.1%) than in *C. russula* (17.7%). Only males were Bartonella-positive in *C. russula*, but similar infection rates in both sexes were found in *A. sylvaticus* and *M. spretus*. We found seasonal differences in Bartonella prevalence in *A. sylvaticus*, and an influence of vole cycles on prevalence in mice, which was higher during *M. arvalis* population peaks. We conclude that *B. grahamii*, the most relevant in terms of zoonotic potential, is the commonest Bartonella species harboured by all the studied small mammals, and that rodent fluctuations should be taken into account to understand Bartonella spp. infection among sympatric competent hosts.



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173 GIARDIA SPP. IN WILD RODENTS FROM A LANDSCAPE DOMINATED BY EXOTIC PLANTATIONS IN CHILE

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Keywords: Giardia, Rodents, Zoonosis, Land-Use Change

Abstract Text

Land conversion for forestry/agricultural activities may modify transmission of zoonotic parasites in wildlife hosts, sometimes creating conditions that increase human exposure to zoonotic pathogens. In Chile, one of the most important land-use change is the replacement of native forests by exotic Monterey pine (*Pinus radiata*) plantations, which modifies the abundance and composition of wildlife, which in turn, may also modify transmission of parasites. The aim of this study was to determine the prevalence of *Giardia* spp. in fecal samples from wild rodents in a coastal area of the Maule Region, and to compare the prevalence between three habitat types (3 replicates for each): (1) native forest, (2) adult Monterey pine plantations, and (3) young pine plantations. In each habitat type, trapping was undertaken for four consecutive nights, using a 7 × 10 grid of Sherman traps, during all four season in 2017. Fecal samples were collected and *Giardia* spp. cysts were detected using the modified Telemann method. 505 fecal samples from 4 rodent species were analyzed. All rodent species had positive samples and *Giardia* cysts were present across all habitat types. The total prevalence of *Giardia* spp. was 23.56%. Using Generalized linear models with binomial distribution, we found that the probability of *Giardia* occurrence in rodent feces was significantly higher in winter and spring, and also in young pine plantations (prevalence 31.66%) compared to the native forest and adult pine plantations (prevalence 10.93% and 9.1%, respectively). Our findings highlight the increase of *Giardia* shedding in rodents inhabiting the exotic pine plantations, which could potentially increase transmission risks to humans. Further research should include molecular analysis of *Giardia* cysts, in order to identify potential zoonotic species of this parasite that may circulate in rodents from this geographic area.



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356 MODELLING DENSITY WILD BOAR POPULATIONS IN EUROPE FOR WILDLIFE DISEASE CONTROL

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Keywords: Hunting Bags, Density Model, Downscaling, Wild Boar

Abstract Text

Wild boar populations have had a sharp growth and are nowadays a huge concern, due to a high risk of transmission diseases to humans and domestic animals (g.e. African swine fever). Moreover, recently, there have been some outbreaks of African swine fever in central Europe, reason why some sanitary controls are being made to reduce the risk of disease transmission.

For this reason there is a huge interest to know where wild boars concentrate more, and European countries are making a big effort to model its abundance. However, species abundance models made until now failed in quantified species abundance when a downscaling approach was made at a 2x2km grid. Our aim was to improve results of previous models avoiding overprediction when downscaling.

We obtained 55844 hunting yield (HY) data for 31 countries from the ENETWILD consortium. Data with different resolution scale (NUTS2, NUTS3 or hunting ground scale) were transformed to densities (i.e. HY data divided by surface) and used as response variable. Climatic, land cover, and area were used as environmental predictors and 4 bioclimatic zones and NUTS level were used as factor environmental variables. All of them were used as explanatory variables. We construct a negative binomial generalized lineal model and an intrinsic Conditional Auto-Regressive model (iCAR) to account for spatial autocorrelation. Model predictions were downscaled to 2x2km grid and aggregated at country level to compare density predictions with an external dataset.

Our results were able to detect spatial variation and showed a similar geographical pattern as previous wild boar abundance models. Our density spatial distribution model downscaled at 2x2km did not show overprediction, improving previous model predictions. This close-fitting result could help in wildlife disease transmission management to define an interface with livestock, to focus the effort in controlling wildlife populations to decrease the risk of disease transmission.



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260 LIVER PARASITE *PSEUDAMPHISTOMUM TRUNCATUM* INFECTS MAINLY SUBADULT BALTIC RINGED SEALS

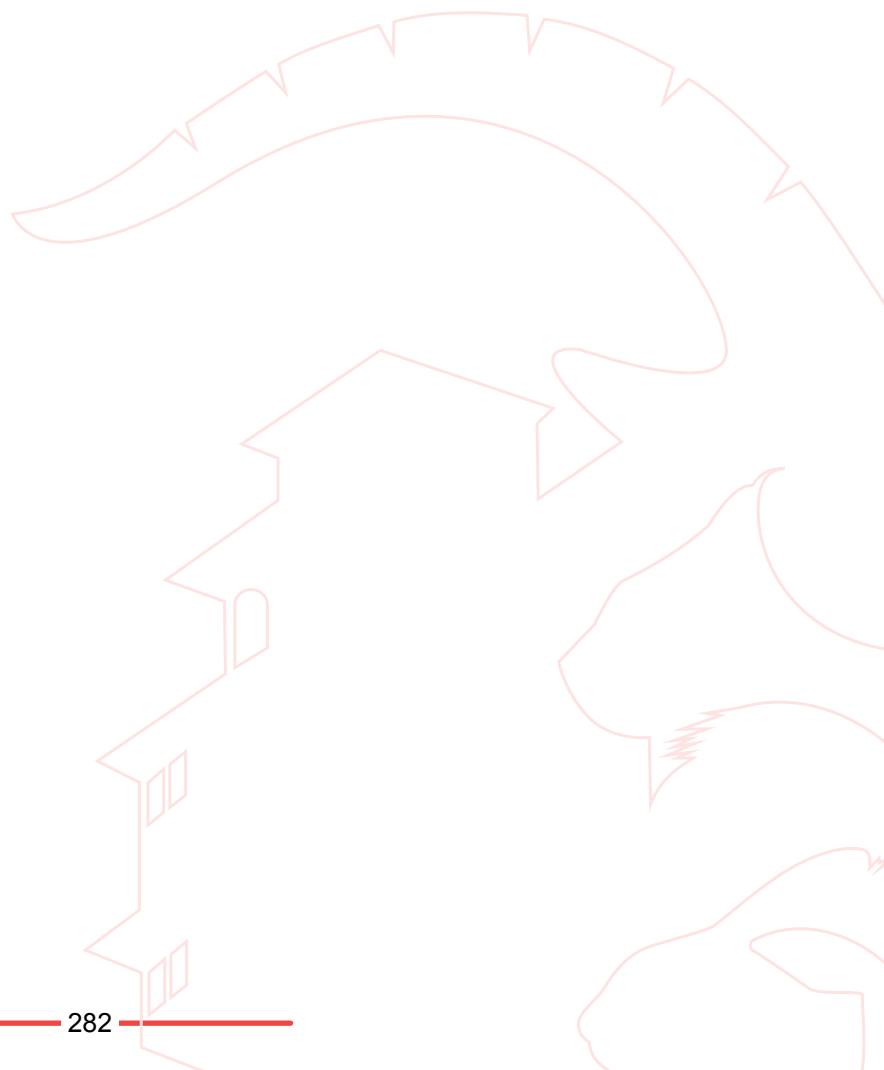
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Keywords: Baltic Ringed Seal, Parasite, Prevalence, *Pseudamphistomum Truncatum*

Abstract Text

The Baltic ringed seal *Pusa hispida botnica* inhabits the northern part of the Baltic Sea, mainly the Bothnian Bay. The Baltic Sea environment is and has been heavily influenced by human activities. The ringed seal population suffered from excessive hunting and environmental contaminants in the 20th century but has recovered especially in the Bothnian Bay during the past decade. Seals are exposed to the biliary trematode *Pseudamphistomum truncatum* when eating cyprinid fish infected with the larvae of the parasite. This zoonotic parasite has recently become more prevalent in the Baltic grey seal *Halichoerus grypus* suggesting changes in the Baltic marine environment. To assess the occurrence of *P. truncatum* in the Baltic ringed seal, we examined livers from hunted seals collected in April-May in 2015-2020 (N = 590). In total, 6.3% of the ringed seals were found positive for the trematode. There was no discernible temporal trend in the occurrence. None of the pups (2-3 months old) were infected. The highest prevalences were found in age classes 1-2-year-old (15.2%) and 3-4-year-old (27.3%). In male seals, the prevalence was high already at 1-2 years of age (23.3%) compared to females of the same age (8.2%). The prevalence in ringed seals older than 4 years (breeding population) was notably lower than in the younger age classes, only 4.1%. In addition, a whole carcass of a Baltic ringed seal found dead was examined pathologically for which the cause of death was determined as liver failure due to severe parasitic cholangiohepatitis caused by *P. truncatum*. The seal was a juvenile female, approximately one year old. The pattern of occurrence of *P. truncatum* in the Baltic ringed seal may stem from e.g. parasite-induced immunity or mortality or age-related dietary differences. *P. truncatum* can cause serious disease in the Baltic ringed seal.





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146 METAGENOMIC SURVEILLANCE OF FOODBORNE PATHOGENS AND PHENOTYPIC CHARACTERIZATION OF ANTIBIOTIC RESISTANCE OF ESCHERICHIA COLI ISOLATED FROM FARM DWELLING RODENT PESTS

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Keywords: Agriculture, Rodent, 16S Amplicon Sequencing, Metagenomics, Antibiotic Resistance

Abstract Text

The effective control of rodent populations on farms is a critical component of food- safety, as rodents are reservoirs and vectors for many foodborne pathogens (e.g., *Salmonella* spp., *E. coli* O157, etc.). The functional role of rodents in the amplification and transmission of foodborne pathogens is likely underappreciated in the United States. Clear links have been identified between rodent and outbreaks of foodborne pathogens throughout Europe and Asia, however, comparatively little research has been devoted to studying this rodent-agricultural interface in the USA, particularly across the Midwest. Here, we address this existing knowledge gap by characterizing the metagenomic communities of rodent pests collected from Minnesota and Wisconsin food animal farms. We leveraged the Oxford Nanopore MinION sequencer to provide a rapid real-time survey of the putative food-borne pathogens. Rodents (mice and rats) were live trapped from three food animal farms. Tissues and fecal samples were collected from all rodents and DNA extraction was performed on 90 rodent colons. Full-length 16S amplicon sequencing was performed with the MinION. Our data suggests the presence of pathogenic strains of *Salmonella* spp., *Campylobacter* spp., *Clostridium* spp., and *Escherichia coli* O157, along with many important mastitis pathogens. A critically important observation is that we discovered these pathogens within five species of rodents (*Microtus pennsylvanicus*, *Mus musculus*, *Peromyscus leucopus*, *Peromyscus maniculatus*, and *Rattus norvegicus*). In addition, we phenotypically characterized antibiotic resistance patterns of *E. coli* isolated from the rodent feces using traditional culture techniques. We observed that the most common drug resistance was for Tetracycline (49%), followed by Streptomycin (42%), and Ampicillin (30%). Furthermore, multidrug resistance (MDR) was obtained for 45% of the isolates. Data generated from our study will likely result in the identification of new reservoirs for food-borne pathogens and bring insights on antibiotic resistance carried by the rodent pests.



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161 MULTIPLE STRAINS OF A NOVEL HANTAVIRUS IN VOLES IN CONTINENTAL EUROPE

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Keywords: Hantavirus, Rodent, Microtus, Germany, Lithuania

Abstract Text

Human cases of haemorrhagic fever with renal syndrome in Europe are mainly caused by Puumala orthohantavirus, Dobrava-Belgrade orthohantavirus and Seoul orthohantavirus. Only few cases were caused by Tula orthohantavirus (TULV) infection. Tatenale orthohantavirus (TATV) is a new orthohantavirus with unknown zoonotic potential, found in field voles (*Microtus agrestis*) in England.

Here, we describe a reverse-transcription-polymerase chain reaction (RT-PCR) based hantavirus screening of different voles, namely the common vole (*Microtus arvalis*), the field vole (*M. agrestis*) and the root vole (*M. oeconomus*) in Germany and Lithuania. In Germany 126 field voles and 13 common voles were trapped and sampled, while in Lithuania at 17 trapping locations 46 field voles, 109 common voles and 79 root voles were collected.

TULV-RNA was detected in two field voles and one common vole in Germany. In one additional field vole a new hantavirus, Traemmersee hantavirus (TRAV), was detected. In Lithuania, we failed to detect TULV-RNA, but detected a new hantavirus, Rusne orthohantavirus (RUSV), at one location over several years in the root vole population.

Phylogenetic analyses of the complete coding sequences of RUSV and TRAV showed highest similarity to each other as well as to TATV. Further analysis revealed that TRAV and RUSV belong to the putative species "Tatenale orthohantavirus". A recombinant RUSV nucleocapsid antigen was generated in yeast and allowed the ELISA detection of RUSV-specific antibodies in four of seven positive-tested root voles.

In conclusion, we detected two strains of TATV for the first time in Continental Europe. In comparison to field vole-associated TATV and TRAV, we identified the root vole as a new reservoir of the RUSV strain of this virus species. Future studies need to examine the geographic distribution of this virus species and its strains, its reservoir(s) as well as the zoonotic potential of this new agent.



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292 INTEGRATED CONTROL OF TUBERCULOSIS AT THE WILDLIFE-LIVESTOCK INTERFACE IN OUTDOOR IBERIAN PIG FARMS IN SPAIN

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Keywords: Biosecurity Measures, Outdoor Production Systems, Risk Of Interaction, Shared Infections, Wildlife-Livestock Interface.

Abstract Text

Interactions between wild ungulates and extensively raised livestock are expected to facilitate the maintenance and spread of shared infections that impact animal health, productions, conservation and even public health. However, a holistic approach for disease control has been rarely assessed at this interface. The aim of this study was to develop an integrated program for animal tuberculosis (TB) control in pigs and wild ungulates from outdoor Iberian pig farms in south-western Spain. Between 2017-2019, a TB surveillance (based on serological and molecular methods) and on-farm wildlife risk audits were simultaneously carried out in 18 farms, providing a technical report for risk mitigation to each farmer. Additionally, the occurrence of interspecific interactions was monitored at specific risk points (n=36) in six of the farms using photo-trapping. Active circulation of Mycobacterium tuberculosis complex (MTC) was detected in 88.9% (16/18) of pig farms and a non-free status of TB was recorded in cattle in 3 out of 13 (23.1%) that were mixed. MTC circulation was also found in wild ungulates in 87.5% (7/8) of farming enclosures sampled. The risk of interaction was significantly higher at growing and fattening farms compared to breeding-weaning ones, and at water sites than in feeding points or buildings. MTC seropositivity tended to be higher in farms with higher interaction rates, being the ponds the more concurred points. On average, a total of 50.8 (10-100) risk mitigation actions were suggested per study farm and 2.7 (0-5) per risk point. However, the implementation of the proposed program was limited to the sanitary surveillance (externally funded) and the low-cost biosecurity measures. It is imperative to aware outdoor pig farmers about the need to be enrolled in integrated disease control programs that target the wildlife-livestock interface, especially keeping in mind the threat of diseases as severe as African swine fever.



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219 CHARACTERIZATION OF ERYTHROCYTE SEDIMENTATION RATE IN SOUTH AMERICAN SEA LIONS (OTARIA BYRONIA) AS AN INDICATOR OF INFLAMMATION

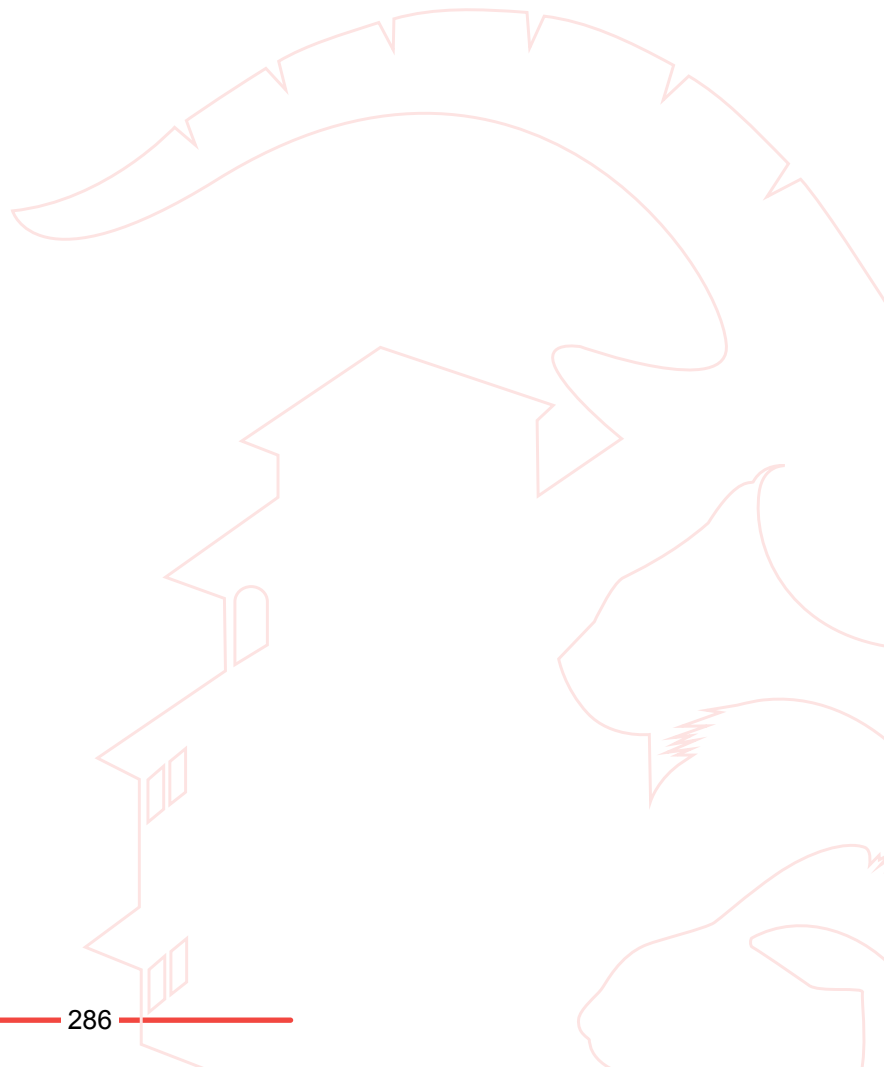
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Keywords: Erythrocyte Sedimentation Rate, Inflammation, Otaria Byronia, Pinniped, Sea Lion

Abstract Text

Erythrocyte sedimentation rate (ESR) is an established nonspecific measure of acute inflammatory response in multiple species. As part of an ongoing population health evaluation, ESR was investigated in the locally threatened Peruvian population of South American sea lions (SASL; *Otaria byronia*) as an additional measure of health. Hematologic parameters including complete blood counts, serum chemistries, and ESR were measured in six adult SASL and 32 pups in April 2018 within the marine protected area of Punta San Juan, Peru. ESR was measured using the Wintrobe method from a commercially available kit (Winpette, Guest Scientific AG, Switzerland). ESRs ranged from 0-64 mm with a median value of 12 and 10-90th percentile of 1-37. Adults (median: 35 mm/hr) had significantly higher ESRs compared to pups (median: 6.5 mm/hr; $p=0.003$). Twenty-two individuals were noted to have active or healing wounds and/or cutaneous ulcerations on their flippers and genitalia. There was no significant difference in ESR for those with active versus inactive lesions ($p=0.626$). However, analysis of the pups alone revealed significantly higher ESR in animals with active lesions (median: 14 mm/hr) compared to those with inactive lesions (median: 3.5 mm/hr) ($p=0.014$). A positive correlation was also detected between ESR and total white blood cell counts ($R=0.325$, $p=0.046$), as well as total protein ($R=0.571$, $p<0.0001$). These correlations with known inflammatory markers, suggest ESR can provide information on acute inflammation and animal health in challenging field environments where testing of fibrinogen and acute phase proteins may not be possible.





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81 APPLICABILITY OF ULTRASONOGRAPHY IN THE CLINICAL MANAGEMENT OF CYSTIC ECHINOCOCCOSIS IN CAPTIVE LANGURS OF THE GENERA TRACHYPITHECUS AND PYGATHRIX

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Keywords: Cystic Echinococcosis, PAIR, Pygathrix Sp, Trachypithecus Sp, Ultrasonography

Abstract Text

The Endangered Primate Rescue Center located in Northern Vietnam houses one of the largest captive populations of endangered and critically endangered langurs of the genera *Trachypithecus* and *Pygathrix*. Cystic Echinococcosis due to *Echinococcus ortleppi* is the most identified cause of morbidity and mortality, with cysts commonly located in the liver and the lungs. Until recently, Echinococcosis was an incidental postmortem finding by reason of its asymptomatic presentation until acute to peracute mortality. Ultrasonographical examination of 32 individuals was performed in conjunction with physical examination, complete blood count, biochemistry, radiographs, and serology when possible. Parasitic cysts of all stages (WHO Informal Working Group) were diagnosed and measured in 21 of the langurs by abdominal and thoracic ultrasound (Esaote MyLab One Vet-13-4 MHz Linear Transducer). The course of treatment was designed based on the cystic number, size, location, and stage. Additionally, coexisting ultrasonographical findings such as aerophagia, increased left ventricular and gallbladder wall thickness, hepatic heterogeneity and ascites contributed to the severity assessment of the disease but also to the therapeutic protocol. Treatment approaches included 10mg/kg albendazole BID in four weeks cycles at 14-day intervals with or without 20mg/kg praziquantel SID (chemotherapeutic doses), percutaneous ultrasound guided puncture aspiration, injection and reaspiration (PAIR) for active hepatic cysts that did not resolve with chemotherapy, no treatment for inactive cysts and euthanasia in severe pulmonary hydatidosis. Moreover, ultrasonography was used to evaluate the treatment efficacy by remeasuring the cysts and repeating their staging. In conclusion, ultrasonography has been valuable for the management of cystic Echinococcosis in langurs, as it is a non-invasive, highly sensitive and specific diagnostic tool, provides a minimally invasive therapeutic possibility and permits an objective assessment of treatment response.

Acknowledgments: The authors would like to thank Cuc Phuong National Park and Leipzig Zoo for their support with the current project.



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75 GROSS EVALUATION AND SUSPECTED CAUSE OF MORTALITY IN INDIAN ELEPHANTS (*ELEPHANT MAXIMUS INDICUS*) IN SOUTHERN INDIA

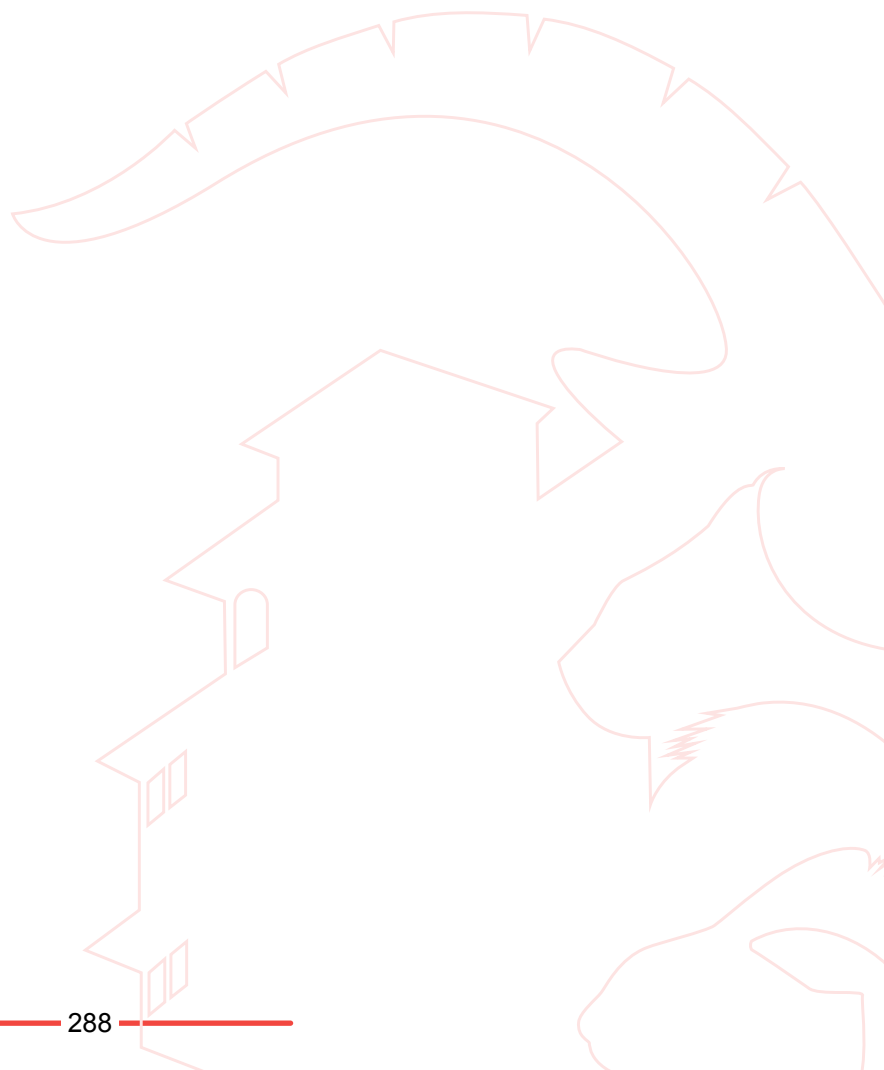
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Keywords: *Elephas Maximus Indicus*, Indian Elephants, Mortality, Seasonality.

Abstract Text

Studies in wild elephants are invaluable tools for investigating diseases, determining anthropogenic threats, and investigating environmental impacts. The main purpose of this study was to review reliable post-mortem reports of 63 wild Indian elephants (*Elephas maximus indicus*) from an elephant reserve in Southern India from 2013 to 2018. Suspected causes of mortality are described and are compared by age, sex, and seasonality. Among the reviewed post-mortem reports, the primary cause of death was related to the musculoskeletal system (28.5%), followed by the integumentary system (14.2%), gastrointestinal system (12.7%), respiratory system (11.1%), and cardiovascular system (6.34%). Integumentary and gastrointestinal causes may occur more frequently in sexually mature elephants, while respiratory and musculoskeletal (trauma) disease occur more frequently in infant elephants. There was significant correlation between age and mortality ($P = 0.0284$). There was no significant correlation between sex and mortality ($P = 0.3176$) and between seasonality and mortality ($P = 0.4434$). Identifying causes of mortality in wild elephants will help wildlife managers with the decision-making process involved in the protection and conservation for this endangered species.





171 SUBCUTANEOUS CYSTICERCOSIS OF TAENIA CRASSICEPS IN RED FOXES (*VULPES VULPES*)

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Keywords: *Taenia Crassiceps*, Cysticercosis, Red Fox, Canine Distemper Virus

Abstract Text

Taenia crassiceps is a widely distributed cestode in the northern hemisphere and often found as a large but harmless tapeworm in the intestine of its definitive carnivore hosts. Natural intermediate hosts are mainly rodents, in which larva encyst as cysticerci in the subcutis, muscles, and abdominal cavity.

Within three years, two red foxes (*Vulpes vulpes*) were presented at the Centre for Fish and Wildlife Health (FIWI), Switzerland, for disease investigation after being shot by local game wardens due to obvious weakness and a highly distended chest. In both animals, the subcutis around the thorax and proximal abdomen was highly expanded by large multilobular fluctuant masses composed of myriads of cysts consistent with cysticerci. Based on morphological and molecular (PCR/DNA-sequencing) criteria, the cysts were identified as *Cysticercus longicollis*, the larval stage of *Taenia crassiceps*. Adults of *T. crassiceps* were found in the intestinal content of one fox. In the other case, concurrent canine distemper virus (CDV) infection was demonstrated by PCR and histopathology.

Cysticercosis by *C. longicollis* is sporadically reported in aberrant hosts such as humans, non-human primates, dogs, and red foxes, often associated with immunodeficiencies. Concurrent CDV infection may have resulted in immunosuppression in one fox. In the second case, no specific cause for immunodeficiency could be demonstrated, but the simultaneous occurrence of both adult and larval stages of *T. crassiceps* in the same host is considered a rare event. In central Europe, red foxes are major drivers of the parasite cycle due to high population densities and high *T. crassiceps* prevalence.

Considering their widespread urban and rural occurrence, environmental contamination with *T. crassiceps* is not only a threat to humans but could also affect domestic dogs and wildlife species, especially with the recent CDV emergence affecting carnivore hosts. Such findings highlight the importance of general health surveillance in wildlife.



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95 UNCOVERING TUBERCULOSIS IN SOUTH AFRICAN WILDLIFE – WHAT ANTE-MORTEM DIAGNOSTIC TOOLS ARE OUT THERE?

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Keywords: Bovine Tuberculosis, BTB Diagnosis, Immunological Assays, Mycobacterium Bovis, South African Wildlife

Abstract Text

Infectious diseases, such as bovine tuberculosis (bTB) caused by *Mycobacterium bovis* (*M. bovis*), pose a threat to wildlife populations globally. To date, *M. bovis* infection has been detected in 24 South African wildlife species. The detection of *M. bovis* infection in wildlife species is essential to limit its dispersal, and manage bTB disease in wildlife and neighbouring livestock species. The main challenges influencing the management of bTB in wildlife populations is firstly that typically only animals with advanced disease show clinical manifestations, and secondly, there is a lack of ante-mortem diagnostic assays available for the detection of bTB in wildlife. With the continuous development of novel reagents and technologies, our research over the last several years has focused on the development of tools which are able to identify *M. bovis* infection in South African wildlife. These species-compatible cytokine assays, including ELISA (IFN- γ and IP-10) and gene expression assays (IFN- γ CXCL9, CXCL10, CXCL11), are used in combination with the QuantiFERON®-TB Gold Plus tubes for TB specific antigen stimulation. Species for which cytokine release assays have successfully been developed include African buffalo (*Syncerus caffer*), African wild dogs (*Lycaon pictus*), African lions (*Panthera leo*) cheetahs (*Acinonyx jubatus*), leopards (*Panthera pardus*), black and white rhinoceros (*Diceros bicornis*; *Ceratotherium simum*), common warthogs (*Phacochoerus africanus*), spotted hyenas (*Crocuta crocuta*) and various antelope species. Serological assays that detect antibodies specific to mycobacterial antigens have also shown value in testing species for bTB including African elephants (*Loxodonta africana*), common warthogs, cheetah, rhinoceros, and hippopotamus (*Hippopotamus amphibius*). The aim of this presentation is therefore to highlight what ante-mortem diagnostic tools are currently out there for uncovering bTB in various South African wildlife and how these tests will contribute to improving the diagnosis and management of bTB in not only South African wildlife, but other wildlife species as well.



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96 RUMINANT INTERFERON-GAMMA RELEASE ASSAY (IGRA) SHOWS POTENTIAL FOR DETECTION OF MYCOBACTERIUM BOVIS INFECTION IN ANTELOPE SPECIES.

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Keywords: Bovine Tuberculosis, BTB Diagnosis, IFN- γ Release Assay, Mycobacterium Bovis

Abstract Text

Infectious diseases, such as bovine tuberculosis (bTB) caused by *Mycobacterium bovis* (*M. bovis*), pose a threat to wildlife populations globally. Maintenance hosts, including African buffaloes (*Syncerus caffer*) and greater kudu (*Tragelaphus strepsiceros*) are considered important sources of bTB, with many carnivore species (spillover hosts) including African lions (*Panthera leo*) and African wild dogs (*Lycaon pictus*) contracting *M. bovis* through the consumption of infected carcasses. One of the confounding factors influencing the management of bTB in wildlife populations is the lack of ante-mortem diagnostic assays available for the detection of *M. bovis* infection. The goal of this study was to determine whether a commercially available interferon-gamma release assay (IGRA) developed and optimized for detection of ruminant interferon-gamma (IFN- γ) can be used to detect immune sensitization in various antelope species from the Kruger National Park, South Africa. New diagnostic tests are essential for advancing our understanding of bTB in susceptible species, especially for surveillance, diagnosis, and prevention strategies. A pilot study using mitogen-stimulated whole blood has shown that the Indical Bioscience cattletype® IFN- γ ELISA is able to detect immune responses in greater kudu, nyala (*T. angasii*), bushbuck (*T. scriptus*), sable antelope (*Hippotragus niger*), waterbuck (*Kobus ellipsiprymnus*) and impala (*Aepyceros melampus*). In addition, antigen-specific IFN- γ release was able to identify a culture-confirmed *M. bovis*-infected bushbuck (n=1) and greater kudu (n=1). This commercial ruminant IFN- γ release assay shows promise as a screening assay for *M. bovis* infection in antelope species.



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135 TOXINS FROM HARMFUL ALGAE IN FISH FROM SCOTTISH COASTAL WATERS

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Keywords: Domoic Acid, Paralytic Shellfish Toxins, Risk Assessment, Chronic Exposure, Top Predators

Abstract Text

The number of harmful algal bloom events is increasing in various water bodies around the world with significant economic impacts on the aquaculture, fishing and tourism industries. As well as their potential impacts on human health, toxin exposure from harmful algal blooms (HABs) has resulted in widespread morbidity and mortality in marine life, including top marine predators. There is therefore a need for an improved understanding of the trophic transfer, and persistence of toxins in marine food webs. For the first time, the concentrations of two toxin groups of commercial and environmental importance, domoic acid (DA) and saxitoxin (including Paralytic Shellfish Toxin (PST) analogues), were measured in the viscera of 40 different fish species caught in Scotland between February and November, 2012 to 2019.

Overall, fish had higher concentrations of DA compared to PSTs, with a peak in the summer / autumn months. Whole fish concentrations were highest in pelagic species including Atlantic mackerel and herring, key forage fish for marine predators including seals, cetaceans and seabirds. The highest DA concentrations were measured along the east coast of Scotland and in Orkney. PSTs showed highest concentrations in early summer, consistent with phytoplankton bloom timings. The detection of multiple toxins in such a range of demersal, pelagic and benthic fish prey species suggests that both the fish, and by extension, piscivorous marine predators, experience multiple routes of toxin exposure.

Risk assessment models to understand the impacts of exposure to HAB toxins on marine predators therefore need to consider how chronic, low-dose exposure as well as acute exposure during a bloom could lead to mortalities. The potential synergistic, neurotoxic and physiological effects of multiple toxins require investigation in order to appropriately assess the risks of HAB toxin exposure on fish species as well as their predators.



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3 ADIPOSE TISSUE ESTIMATION IN GREEN TURTLES (*CHELONIA MYDAS*) USING DEEP LEARNING, DIAGNOSTIC IMAGING AND BIOELECTRICAL IMPEDANCE ANALYSIS

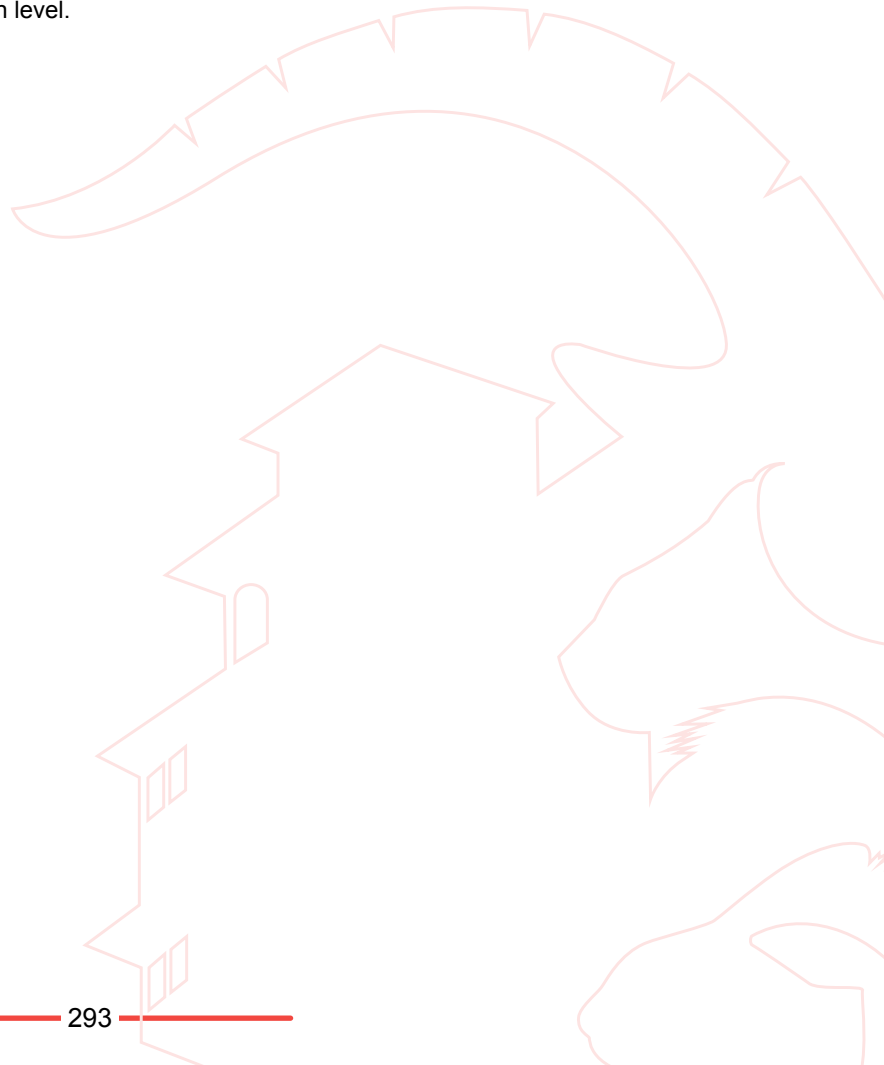
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Keywords: Body Composition, Calibration, Computed Tomography Scans, Field Techniques, Validation

Abstract Text

Sea turtle populations are endangered worldwide due to anthropogenic impacts. The loss of fat reserves (adipose tissue) in individual turtles is linked to environmental stress and diseases, and is considered an indicator of health status. Bioelectrical Impedance Analysis (BIA) has emerged as a portable technology that accurately estimates adipose tissue in fishes and humans, showing potential for field-based studies. We determined device reliability, quantified the impacts of potential confounders, and calibrated BIA measurements using computed tomography (CT) scans in green turtles (*Chelonia mydas*). The effects of temperature (20-30°C), digestive state, and dry-docking time on impedance parameters (R_0 , R_{50} and R_{inf}) were measured on 35 juvenile turtles using multi-frequency BIA. Impedance measurements were used to calculate adipose tissue mass. Adipose tissue calculations (mass) were compared to those determined from CT scans on 50 additional turtles. A deep learning model, based on convolutional neural networks, was trained for CT image processing. Results showed that BIA measurements were reproducible. The impedance parameters did not significantly alter with digestive state, but were inversely correlated with body temperatures. A temperature correction algorithm was therefore developed to enable field BIA use between 20-30°C. Calculations of adipose tissue correlated well between BIA and CT techniques. We present the first BIA calibration study in sea turtles, and our standardised protocol provides an accurate estimation of adipose tissue in green turtles. This valuable information on individual health status can inform conservation management decisions on a population level.





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295 EDWARDSIELLA TARDA SEPTICEMIA IN AN ADULT STRIPED DOLPHIN (*STENELLA COERULEOALBA*)

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LABOCEA, Ploufragan, France

Keywords: Edwardsiella Tarda, Septicemia, Striped Dolphin

Abstract Text

An adult male striped dolphin (*Stenella coeruleoalba*) stranded on the north coast of Brittany was submitted for a complete necropsy to the Departemental Laboratory followed by bacteriology and histopathology on major organs and organs with lesions.

Main gross lesions were emaciation, cutaneous ulcerations, a gingivitis with many worn teeth, an ulcerative glossitis, a gastric ulceration, a verminous bronchopneumonia, lymphadenomegaly, hepatomegaly, splenomegaly and edema of the brain. Bacteriological analyses (culture followed by identification of colonies by MALDI-TOF MS) revealed the presence of *Edwardsiella tarda* in the intestine, spleen, heart, lung, lymph nodes and brain. *Clostridium perfringens* was also identified, in smaller amounts, in the intestine, liver, kidney and lymph nodes. Microscopic examination confirmed macroscopic lesions of the skin, gingiva, tongue, lungs and revealed a neutrophilic lymphadenitis, an acute hepatitis with leucostasis and an acute neutrophilic adrenalitis.

Marine animals are an important reservoir of *E. tarda* as being part of their microbiota. This bacterium from the family Enterobacteriaceae can also be the etiological agent of several infectious diseases of freshwater and marine fish (Mohanty et al., 2007). In marine mammals, it has been described in Steller's sea lions, harbor porpoise, California sea lions, but considered as an opportunistic invader in otherwise sick or injured animals (Coles et al., 1978; Stroud et al., 1979). It has also been described and associated to a sepsis in a sperm whale (Cools et al., 2013). In our case, *E. tarda* was associated with acute and suppurative lesions and could be considered as the possible cause of death of the animal. This dolphin was old and emaciated with a gingivitis with worn teeth and a chronic gastric ulcer, thus probably immunodeficient. Moreover, other causes of immunodeficiency such as a morbillivirus infection and toxicants (heavy metals and organochlorines) may coexist and are under investigations.



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79 DETECTION OF A NOVEL MYCOPLASMA GALLISEPTICUM-LIKE SPECIES IN COMMON STARLING (*STURNUS VULGARIS*) AROUND POULTRY FARMS IN FRANCE

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Keywords: Mycoplasma Gallisepticum, Poultry, Starling, Wild Birds, Wildlife-Livestock Interface

Abstract Text

Recent outbreaks of highly pathogenic avian influenza in South-West France have questioned the role of commensal wild birds in introduction and dissemination of pathogens in poultry farms. To assess possible infectious contacts at the wild-domestic bird interface, the presence of *Mycoplasma gallisepticum* (MG) was studied in the two sympatric compartments in South-West France.

Among various peridomestic wild birds (n=385), usual PCR primers targeting 16S rRNA of MG showed a high apparent prevalence (up to 45%) in cloacal swabs of common starlings (*Sturnus vulgaris*, n=108), while MG-specific *mgc2* gene was not detected. No tracheal swab of these birds came out positive, and no clinical sign was observed in positive birds, suggesting commensalism in digestive tract of starlings. A mycoplasma strain was then isolated from a starling swab and its whole genome was sequenced using Illumina and Nanopore technologies. Phylogenetic analysis showed its close relativity with MG and *M. tullyi*, although it was a distinct species.

A pair of specific PCR primers targeting the *mgc2*-like gene of this MG-like strain was designed and used to screen again the same avian populations and a wintering urban population of starlings (n=50). Previous PCR results obtained in starlings were confirmed to be mostly due to this new strain (20/22 positive pools). On the contrary, it was not detected in fresh faeces of urban starlings. Furthermore, it was detected in 1 tracheal pool of cattle egrets and 1 cloacal pool of white wagtails, suggesting infectious transmissions between synanthropic birds of similar feeding behaviour. As the new starling mycoplasma was not detected in ducks (n=80) in close contact with positive starlings, nor in backyard (n=320) and commercial (n=720) chickens of the area, it might not be infectious to poultry. However, it could be involved in mycoplasma horizontal gene transfer in such multi-species contexts.



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363 MOLECULAR IDENTIFICATION OF BETACORONAVIRUS IN BATS FROM SARDINIA (ITALY): FIRST DETECTION AND PHYLOGENY

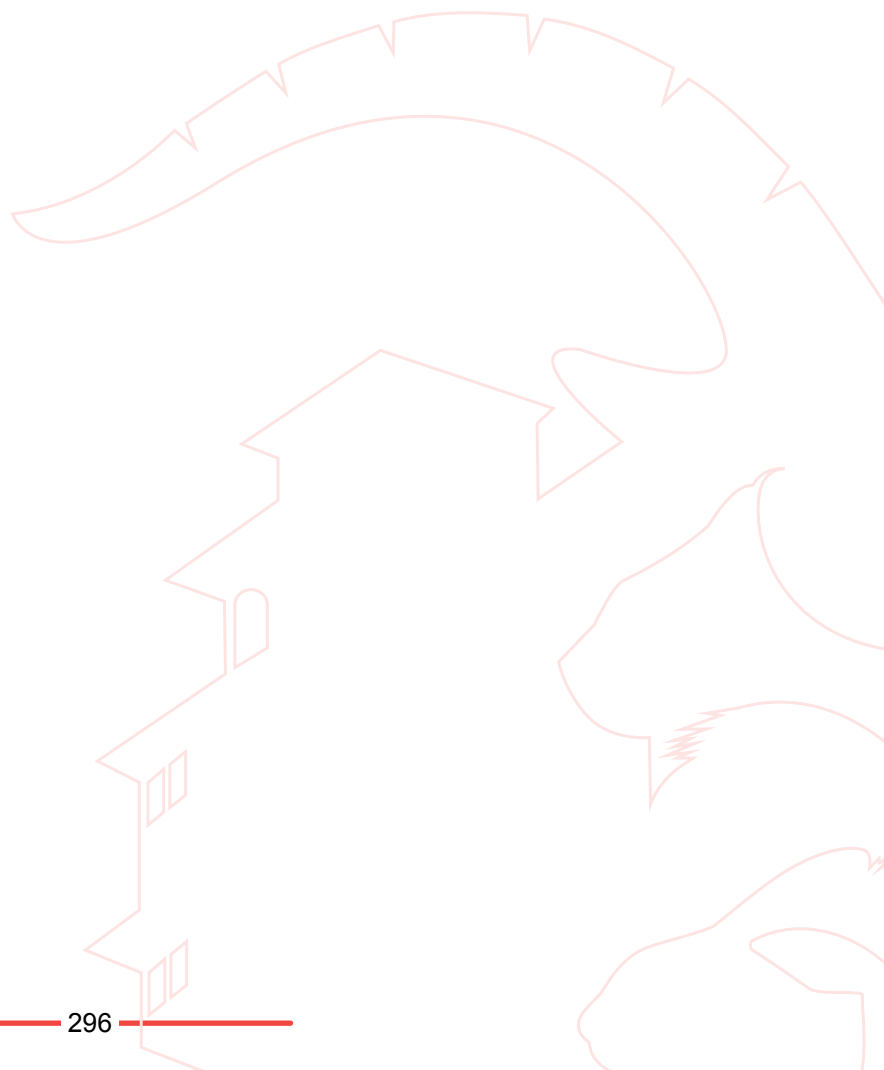
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Keywords: Bats, Coronavirus, RNA-Dependent RNA Polymerase, Sardinia

Abstract Text

Bats may be natural reservoirs for a large variety of emerging viruses, including mammalian coronaviruses (CoV). The Covid19 current pandemic and the recent emergence of severe acute respiratory syndrome-associated coronaviruses (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) in humans, with evidence that these viruses may have their ancestry in bats, highlights the importance of virus surveillance in bat populations. Here, we report the identification and molecular characterization of a bat β -Coronavirus, detected during a viral survey carried out on different bat species in the island of Sardinia (Italy). Cutaneous, oral swabs, and faecal samples were collected from 46 bats, belonging to 15 different species, and tested for viral presence. Coronavirus RNA was detected in faecal samples from three different species: the greater horseshoe bat (*Rhinolophus ferrumequinum*), the brown long-eared bat (*Plecotus auritus*), and the European free-tailed bat (*Tadarida teniotis*). Phylogenetic analyses based on RNA-dependent RNA polymerase (RdRp) sequences assigned the detected CoV to clade 2b within betacoronaviruses, clustering with SARS-like bat CoVs previously reported. These findings point to the need for continued surveillance of bat CoV circulating in Sardinian bats, and extend the current knowledge on CoV ecology with novel sequences detected in bat species not previously described as β -Coronavirus hosts.





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110 DETECTION OF A NOVEL SPECIES OF COVIRUS IN A TAWNY OWL (*STRIX ALUCO*) IN SOUTHERN ITALY

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Keywords: Birds Of Prey, Tawny Owl, Circovirus, Virology, Rodent

Abstract Text

Since its establishment in the 1990s, the virus family Circoviridae, comprising viruses with circular ssDNA genomes, has undergone an intensive research activity. Particularly, the genus Circovirus recognizes 43 species found in a broad host range including mammals, fishes and birds.

This project aimed to assess the possible circulation of circoviruses in birds of prey. Totally, 61 liver and 13 spleen samples were collected during necropsy of birds of prey of 10 different species, both diurnal and nocturnal, performed at the wildlife rescue centre Federico II in Naples (Southern Italy).

The samples were analysed by PCR with a published set of degenerate primers. All subjects tested negative, except one spleen sample from a tawny owl (*Strix aluco*). The complete genome was subsequently sequenced by primer walking.

According to the official demarcation criteria, this “tawny owl-associated circovirus” qualifies as a new species. Its 1745 nt-long genome displayed the ambisense organization typical of circoviruses, with two ORFs found on different strands and encoding for a capsid (Cap) and a replication-associated (Rep) protein.

Phylogenetically, the detected virus clustered with mammalian rather than avian circoviruses, and was closely related to a rodent circovirus. It may be therefore hypothesized that the original host was a micro-mammal, especially since the tawny owl was fed with rodent meat during the rehabilitation period. Several detections of circoviruses in unconventional hosts have been explained with an alimentary transmission without replication, although they primarily occurred in fecal samples. The mechanism by which the virus may have reached the bird's spleen would therefore need further study.

Alternatively, an actual host jump could have occurred, likely favoured by the continuous exposure due to predation.

Further investigations are currently ongoing both in birds of prey and rodents, to identify the natural host of the discovered circovirus and define its epidemiological features and possible disease associations.



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296 META-TRANSCRIPTOMIC PROFILES OF RODENTS AT THE RODENT-AGRICULTURAL INTERFACE

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Keywords: Babesia, Listeria, Pasteurella, Pathogens Discovery, RNASeq

Abstract Text

Rodents commonly occur in and around farm and agricultural settings. Biosecurity measures often are implemented to control and mitigate the presence of commensal rodents on farms; however, certain measures are not always successful, and rodents can establish resident populations that cost farmers billions of dollars annually. Understanding how pathogens circulate in farm settings is a key component to successfully implementing biosecurity measures at the rodent-agricultural interface. In the summer and winter of 2019, we collected and sampled native and invasive species of rodents from a medium-sized mixed animal (dairy cattle, pigs) farm in Minnesota. Meta-transcriptomic profiles of liver or spleen were generated using the RNASeq method on the Illumina platform for *Rattus norvegicus*, *Mus musculus*, *Peromyscus* spp., and *Microtus pennsylvanicus*. Host RNA was filtered out and remaining RNA was used to characterize the community (bacterial, viral, and eukaryota). Preliminary results show that *Mus musculus* harbors *Listeria monocytogenes*, and all rodent species contained *Pasteurella multocida*. In ruminants, *Listeria* can cause encephalitis and uterine infections that can lead to spontaneous abortion; and *Pasteurella multocida* can cause bovine respiratory disease in cattle. *Babesia bovis*, a parasite that causes Texas cattle fever, was found to be associated with *Microtus pennsylvanicus*. Additional analyses are underway to further characterize apicomplexan sequences discovered in all four rodent species. The study presented herein helps to better understand rodent-associated zoonoses circulating within a farm landscape and underscores the importance of farm-level rodent biosecurity measures.



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113 INVASION PATHWAYS AND PUBLIC HEALTH RISKS OF THE RACCOON AND ITS ROUNDWORM BAYLISASCARIS PROCYONIS IN THE NETHERLANDS

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Keywords: Procyon Lotor, Baylisascaris Procyonis, Zoonoses, Epidemiology, Public Health

Abstract Text

The geographic range of the zoonotic raccoon roundworm (*Baylisascaris procyonis*) is expanding together with the range of its host, the raccoon (*Procyon lotor*). This creates a new public health risk in parts of Europe where this parasite was previously absent. In the Netherlands, a raccoon population is becoming established and incidental findings of *B. procyonis* have been reported. To assess the risk to public health, the prevalence of *B. procyonis* was determined in the province of Limburg, where currently the largest Dutch raccoon population is present. Furthermore, genetic methods were employed to assess invasion pathways of both the raccoon and *B. procyonis* to aid in the development of control measures.

Macroscopic analysis of intestinal content and testing of faecal samples were performed to detect *B. procyonis* adults and eggs. The population genetics of both *B. procyonis* and its raccoon host were analysed using samples from central and northwestern Europe.

B. procyonis was found in 14/23 (61%, 95% C.I. 41-78%) raccoons from the province of Limburg. Genetic analyses showed that the majority of the Dutch raccoons and their roundworms were introduced through ex-captive individuals. As long as free-living raccoon populations originate from captivity, population control methods may be pursued. However, natural dispersal from the border regions will complicate prolonged population control. To reduce the public health risk posed by *B. procyonis*, public education to increase awareness and adapt behaviour towards raccoons is key.



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174 MYCOPLASMA OVIPNEUMONIAE IN YUKON: SURVEILLANCE AND THE DOMESTIC-WILDLIFE INTERFACE

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Keywords: Livestock-Wildlife Interface, Mycoplasma Ovipneumoniae, Pneumonia, Thinhorn Sheep, Wildlife Disease Surveillance

Abstract Text

Pneumonia outbreaks in bighorn sheep have been reported in British Columbia, Canada and the western United States. The bacterium *Mycoplasma ovipneumoniae* (*M. ovi*), which can be carried undetected by domestic sheep and goats, has been implicated as a key pathogen in those outbreaks. *M. ovi* is a pathogen of concern for the thinhorn sheep and mountain goat populations in Yukon.

Currently, a five-year Yukon government control order under the Animal Health Act is in effect in Yukon. Owners of small ruminants must meet containment requirements and have their animals tested for *M. ovi*. Animals that test positive are destroyed or removed from the population and the owners are compensated for their losses. Additional requirements include individual animal identification, record keeping and import permits. In 2019, prevalence of *M. ovi* was 44% (101/232) in domestic sheep and 16% (27/176) in domestic goats in Yukon. In 2020, the prevalence of *M. ovi* was 0% (0/179) in domestic sheep and 9% (17/186) in domestic goats. Strain typing on positive samples is underway and results may further contribute to our knowledge of management at the livestock-wildlife interface.

Since 2015, over 450 nasal swab samples have been collected from free-ranging thinhorn sheep and mountain goats throughout Yukon. Given detection of *M. ovi* in caribou, moose and thinhorn sheep in Alaska, USA, surveillance in Yukon wildlife was broadened to include more ungulates in 2018. Since then, over 300 caribou, moose, deer, elk and muskox samples have been tested for *M. ovi*. One swab collected in 2018 from a caribou near the border with Alaska tested positive for *M. ovi*. To date, no outbreaks of pneumonia have been detected in thinhorn sheep or mountain goats in Yukon and surveillance is ongoing.



250 *YERSINIA PSEUDOTUBERCULOSIS* OUTBREAK IN EURASIAN BLACKCAP (*SYLVIA ATRICAPILLA*) IN EBRO DELTA, SPAIN

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Keywords: European Blackcap, *Sylvia atricapilla*, Yersiniosis, *Yersinia pseudotuberculosis*, Wild Birds

Abstract Text

Yersinia pseudotuberculosis is a ubiquitous Enterobacteriaceae frequently isolated from many captive and free-ranging wildlife. Rodents and birds are regarded as reservoir hosts and may show mild clinical signs or even be asymptomatic, but sporadically cases of disease are reported in several mammal and bird species. Most infections are seen in wintertime in Europe. Between early March and early April 2021, 14 Eurasian blackcaps (*Sylvia atricapilla*) were found dead in two localities 14 km apart in the Ebro Delta, north-eastern Spain. Postmortem examinations were performed on nine birds (five males and four females). Body weight ranged from 8.5 to 18.0 g, and animals were considered in regular to low body condition according to pectoral muscle mass and body fat reserves. Gross and histological lesions were indicative of acute to subacute fatal septicaemia. Splenomegaly and hepatomegaly with pale yellow foci, up to 1 mm in diameter, were the most consistent findings during the gross examination. Microscopically, these foci consisted of caseous necrosis with large irregular dense bacterial colonies. These necrotic foci were also seen in the kidneys, lungs, and serosal surface of the intestines. An additional finding was that five out of the nine birds had up to nine filiform worms in the thoracic and abdominal air sacs identified morphologically as *Diplotriaeana* sp. Bacterial cultures in MacConkey agar (37°C, 24-48h, aerobiosis) from different organs were performed from all nine necropsied animals. Lactose-negative colonies were identified biochemically (Vitek®2 system, bioMérieux) as *Yersinia pseudotuberculosis*. This report describes the diagnostic evaluation and pathology associated with an outbreak of *Y. pseudotuberculosis* septicemia that specifically affected Eurasian blackcaps and underlies the need for further studies on ecological and host conditions that favor these outbreaks. A continuous monitorization of wildlife is needed to assess the frequency and trends of these presumably endemic diseases.



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116 TOXIGENIC *CORYNEBACTERIUM ULCERANS* EMERGES FROM WIDESPREAD HEDGEHOG (*ERINACEUS EUROPAEUS*) DISEASE

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Keywords: *Corynebacterium Ulcerans*, *Erinaceus Europaeus*, Diphtheria

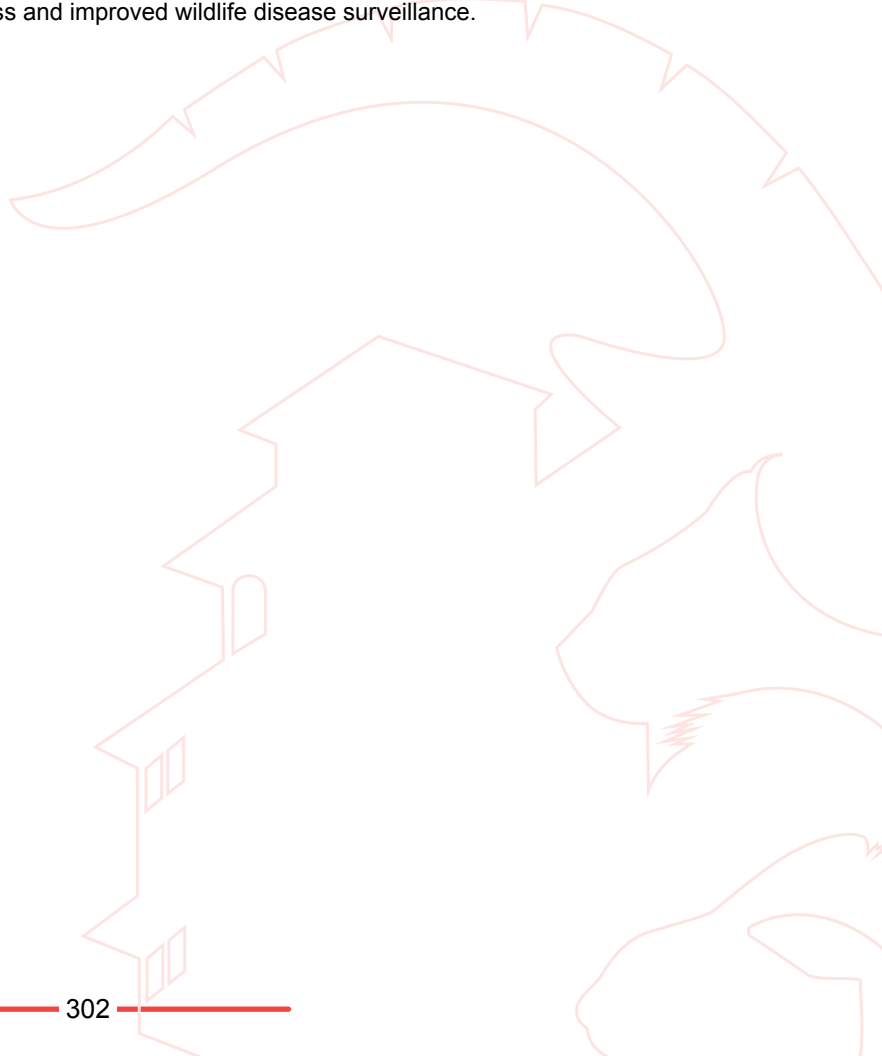
Abstract Text

During May and June 2020, we obtained 60 isolates of *Corynebacterium ulcerans* from 81 hedgehogs (*Erinaceus europaeus*) that were presented with ulcerative skin lesions by the public to four animal rescue centers across northern Belgium. The bacterium was isolated from ulcers or abscesses on the head or limbs of 53 out of 81 investigated hedgehogs, all of them being adult males. The isolates were identified on species level using MALDI-TOF MS and sequencing of the *rpoB* gene and were typed by analysis of infrared spectra. The isolates grouped with *C. ulcerans* strains from humans and other animals (hedgehogs and red foxes (*Vulpes vulpes*) from Germany) and clustered in three sublineages. The pronounced strain diversity suggests emergence from an endemic situation.

Distribution of minimal inhibitory concentration values of 11 antimicrobials determined by epsilometer (E-TEST, bioMérieux, Marcy l'Etoile, France) showed limited evidence of acquired antimicrobial resistance against enrofloxacin (4 isolates) and spiramycin (1 isolate).

Presence and expression of toxicity were evaluated by detection of the diphtheria toxin gene (*toxE*) using a duplex PCR and the Elek test. Results showed the presence of the *toxE* gene in 50 isolates and a positive or weak positive Elek test in 26 and 16 isolates, respectively.

The high number of hedgehogs presented with this important human diphtheria organism in a short timeframe prompts identifying causative factors, raising public awareness and improved wildlife disease surveillance.





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137 FELINE LEUKAEMIA VIRUS IN FREE-RANGING EURASIAN LYNX (*LYNX LYNX*) – A PATHOGEN TO KEEP AN EYE ON

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Keywords: Eurasian Lynx, Feline Leukaemia Virus, In-Situ Surveillance, Mortality, Provirus

Abstract Text

Feline leukaemia virus (FeLV) occurs in domestic cats and closely related wild felids worldwide. FeLV outbreaks with associated mortality in free-ranging Florida panthers (*Puma concolor*) and Iberian lynx (*Lynx pardinus*) raised concerns regarding the potential disease impact on wildlife. Eurasian lynx (*Lynx lynx*) populations in Switzerland have been investigated for this pathogen since the 1980ies without its detection. Yet, in 2019 an adult male was found positive for FeLV provirus in the framework of a translocation programme. The lynx showed no clinical signs of disease and tested negative for FeLV antigen and feline immunodeficiency virus antibodies. FeLV provirus burden was low, while serology revealed a high antibody level against FeLV. These findings are compatible with a regressive FeLV infection. Considering both clinical and laboratory findings, the risk of disease development and pathogen transmission was considered unacceptable for translocation but low enough for repatriation in the animal's original territory. The lynx was released and monitored by radiotelemetry and regular visual checks. No signs of disease were noted throughout two years. Simultaneously, two FeLV positive lynx were reported from distinct populations in Germany: A juvenile in a rehabilitation centre (Bohemian-Bavarian-Austrian population) and a free-ranging subadult (Harz population). Both were antigenemic. The captive juvenile was found to shed virus via saliva and faeces and showed a rapid clinical deterioration after an asymptomatic period. Both animals died within a few months.

The three cases demonstrate the susceptibility of Eurasian lynx to FeLV. The two reported outcomes, corresponding to a regressive and progressive course, respectively, correlate to two known infection outcomes in the domestic cat. The apparent FeLV emergence in three distinct lynx populations might result from exposure to infected domestic cats or European wildcats (*Felis silvestris*). Our observations highlight the importance of veterinary examinations in context of wildlife translocations and releases of rehabilitated wildlife.



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346 DIFFUSE LARGE B CELL LYMPHOMA AND A NOVEL GAMMAHERPESVIRUS IN TWO NORTHERN ELEPHANT SEALS

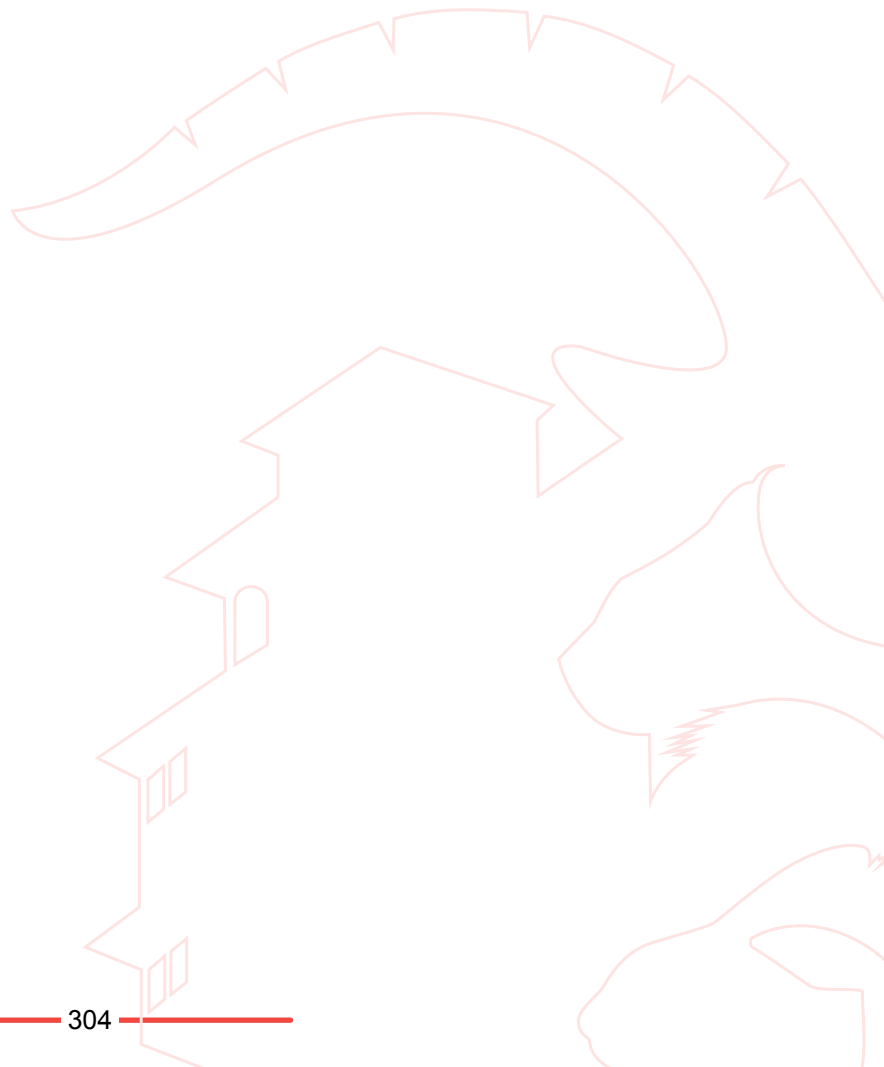
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Keywords: Lymphoma, Gammaherpesvirus, Northern Elephant Seal, B Cell

Abstract Text

Within a year, two malnourished male northern elephant seal (NES) pups were admitted to The Marine Mammal Center (Sausalito, CA) for rehabilitation. Complete blood count showed rapid progression of marked leukocytosis characterized by a predominance of large mononuclear cells suggestive of lymphoid origin with flower-shaped nuclei. The seals were euthanized due to suspected neoplasia. At necropsy, most lymph nodes were markedly enlarged and intestinal mucosae were thickened. One of the two cases also had an enlarged thymus, spleen, and thickened urinary bladder musosae. On histopathology, the lymph nodes were effaced by sheets of neoplastic round cells. Individual neoplastic round cells had little cytoplasm and a single nucleus 2x the diameter of an erythrocyte. Similar neoplastic cells expanded other affected organs such as the intestines. Immunohistochemistry revealed most of the pleomorphic round cells had CD20, CD79a, and variable PAX5 labeling. PCR and phylogenetic analysis identified a novel gamma-herpesvirus from affected tissues from the first case, with similar analysis pending for the second and two control animals. Based on the canine World Health Organization (WHO) classification system, this neoplasm was diagnosed as a diffuse large B cell lymphoma-immunoblastic subtype. This is the first description of B cell lymphoma with leukemic manifestation and detection of a novel gammaherpesvirus in free-living NES. Further research regarding the prevalence of this new gammaherpesvirus and its association with pathology in NESs is ongoing as this may represent a newly identified or emerging disease.





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258 ANTIMICROBIAL RESISTANT ESCHERICHIA COLI IN BONELLI'S EAGLE (AQUILA FASCIATA) IN SPAIN AND FRANCE

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Keywords: Antimicrobial Resistance, Bonelli's Eagle, Escherichia Coli.

Abstract Text

Antimicrobial resistance is a global problem with consequences for public health, animal health and the environment. The assessment of the presence of resistant bacteria in birds of prey gives an insight of its impact in the natural environment. Thus, the aim of this study was to evaluate the occurrence of *Escherichia coli* and its antimicrobial resistances in Bonelli's eagles (*Aquila fasciata*) from Spain and France. This study is included in the context of the AQUILA a-LIFE project.

Bonelli's eagles ($n = 83$) were sampled, including wild nestlings ($n = 54$), nestlings born in captivity ($n = 24$), and wild adults ($n = 5$). Cloacal samples were cultured on MacConkey agar. Antimicrobial susceptibility test was performed in the *E. coli* isolates following the Kirby-Bauer method to evaluate 15 antimicrobials. *E. coli* was recovered in 59 of 83 analyzed samples (71%). The recovery of *E. coli* showed statistical differences regarding living condition: captivity vs. wild ($p = 0.001$). The 28.8% of isolates were resistant, at least, to one antibiotic, and 8.5% were multidrug-resistant. Ampicillin/ticarcillin were the antibiotics with the highest percentage of resistance (20.3% each), followed by tetracyclines, quinolones and potentiated sulfonamides. This result mirrors the use of these antibiotic groups in Spain.

In conclusion, this study highlights the role of Bonelli's eagles as carriers of antimicrobial resistant *E. coli*. Isolates from captive-born nestlings presented a higher number of resistances than those from wild nestlings ($p = 3 \times 10^{-4}$); this must be taken into account if subsequent reintroduction into the wild is considered.



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259 ANTIMICROBIAL RESISTANT SALMONELLA ISOLATED FROM CHELONIANS ADMITTED TO A WILDLIFE RESCUE CENTER IN CENTRAL SPAIN

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Keywords: Salmonella, Antimicrobial Resistance, Multi-Drug Resistance, Chelonians, Testudo

Abstract Text

The exponential development of antimicrobial resistance has become a serious global health problem. Salmonella is an enterobacteria of great importance in both public and veterinary health, with a wide range of hosts and high persistence in the environment. In recent years, numerous resistance to different antimicrobials have been detected in the genus Salmonella. The present study aims to determine the prevalence of Salmonella spp. in native chelonians and to study the presence of antimicrobial resistance to assess the potential of these species as reservoirs of both Salmonella and antimicrobial resistance.

From August 2015 to September 2015, a total of 78 chelonians admitted to the GREFA Wildlife Hospital were examined and sampled. After a complete veterinary examination, a cloacal swab was taken from each individual prior to any treatment administration. In addition, a bath water sample was collected also when possible. All the samples were processed regarding the ISO 6579:2002 recommendations (Annex D) for the detection of Salmonella spp. Isolated strains were serotyped by agglutination with specific antisera following the White-Kauffman-Le Minor scheme. Finally, an antimicrobial susceptibility test was performed to each isolated strain by disk diffusion test according to the Kirby-Bauer method.

Results showed 19.2% of the individuals positive to Salmonella spp., all of them young tortoises belonging to the genus Testudo bred in particular gardens. Serotypes detected were Salmonella enterica enterica Abony (73.3%), S. Postdam (13.3%), S. Kenya (6.7%) and one Salmonella enterica salamae serovar 9,12 : z29 . 1,5. Finally, 80% of the isolated strains presented resistance to different antimicrobials, mainly: gentamicine (40%), cefotaxime (33.3%), ceftazidime (26.7%), azithromycin (13.3%) and ciprofloxacin (6.7%).

Due to the viability of Salmonella on the environment and the ability to transmit resistant genes through plasmids to other bacteria, tortoises reintroduced from captive breeding can be an important spreading reservoir for Salmonella and antimicrobial resistance.



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262 MULTI-DRUG RESISTANT *E. COLI* ISOLATED FROM FREE-LIVING GRIFFON VULTURES (*GYPS FULVUS*) AND CINEREOUS VULTURE (*AEGYPIUS MONACHUS*) FROM CENTRAL SPAIN

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Keywords: Escherichia Coli, Griffon Vulture, Cinereous Vulture, Antimicrobial Resistance

Abstract Text

Antimicrobial resistance (AMR) is one of the most important threats of 21st century. Wildlife has been described as reservoir of different species of resistant bacteria. The presence of AMR bacteria in the human-animal-environmental interface is a clear example of the One Health medicine. In this context, *Escherichia coli* is a good indicator for AMR research due to the wide range of hosts it can colonize and its survival rate on the environment. Also, colibacillosis is one of the most common infection in human and animal medicine, and the illness caused by *E. coli* resistant strains would be more difficult to treat. Vultures are scavenger birds included on the top of the food chain in all the ecosystems, so they are exposed to more pathogens and toxics than other animals. In this framework, the aim of this study was to evaluate the presence of AMR in *E. coli* isolated from free-living vultures in Central Spain.

A total of 20 vultures were included on the study: 10 cinereous vultures and 10 griffon vultures. A cloacal swab was collected from each animal and preserved on Cary Blair transport medium. *E. coli* detection was performed by culture on MacConkey agar. Antimicrobial susceptibility test of the strains was performed with the Vitek2® system, using AST-N243 cards, which include 20 different antimicrobials from 7 different families. 75% of the strains were resistant to at least one antimicrobial, while 33.3% were considered multidrug-resistant (MDR). MDR patterns were: AMX-AMP-CIP-STX-NAL (13.33%); AMX-AMP-CIP-GEN-STX-NAL (13.33%); AMX-AMP-STX-NAL (6.67%). The most common antimicrobial resistance founds was to AMX (73.3%), AMP (73.3%), STX (73.3%), followed by NAL (53.3%), CIP (33.3%) and GEN (20%). No ESBL-producing strains were detected.

Results highlight the need for AMR surveillance on the wildlife interface and the role of vultures as suitable sentinels for AMR epidemiology studies.



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351 SEROLOGICAL AND MOLECULAR DETECTION OF ANAPLASMA SPECIES IN DOMESTIC AND WILD RUMINANTS FROM EASTERN SPAIN.

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Keywords: Anaplasma Spp., Vector-Borne Diseases, Wild Ruminants,

Abstract Text

Vector-borne diseases are increasingly recognized as a cause of disorder in several mammalian species, including humans worldwide. Ticks play important role in maintenance and transmission. Wild ruminants in Europe are suggested to serve as reservoir hosts of these diseases. In the present study, serological and molecular assays were used to investigate the occurrence of Anaplasma spp in a population of wild ruminants from the Comunitat Valenciana (Eastern Spain)

From 2017 to 2020, an indirect ELISA test was performed in 259 serums from four wild ruminant species including mouflon (*Ovis orientalis musimon*), Spanish ibex (*Capra pyrenaica*), deer (*Cervus elaphus*), and fallow deer (*Dama dama*). In addition, sera from 54 domestic goats that shared grazing areas with the sampled animals were analyzed. Also, 106 spleen samples from wild ruminants were analyzed by PCR of the 16rRNA gene marker.

Global seroprevalence of Anaplasma sp. was 52.5%. There were significant differences between the sampled species. Domestic goats showed more risk to be seropositive (OR=3.33 CI95%1,70 -6,50) than wild ruminants. There were no differences between the seroprevalence between species in wild ruminants ($p>0,05$). However, the results of PCR showed a significant risk for mouflon to be infected by Anaplasma sp. (OR=2.44 CI95%1,11 -1,30), despite global prevalence values were similar to those of the ELISA, 55,8%.

Sequencing of the 16rRNA gen showed that the majority of the isolated corresponded to *Anaplasma ovis* (85.7%). One isolate was identified as *Anaplasma centrale* (7,1%) and the other isolate was *Anaplasma platys* (7,1%).

Results showed a wide presence of Anaplasma in ruminant populations, mainly *A. ovis*, at Valencian Community where domestic goats had a higher prevalence than wild ruminants. Mouflon was especially prone to the infection in these areas shared with domestic ruminants. The herd behavior of the species, similar to domestic animals, could influence the differences observed.



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374 MOLECULAR EVIDENCE OF PIROPLASMID INFECTIONS IN SPANISH WILD RUMINANTS FROM VALENCIAN COMMUNITY, (EASTERN SPAIN).

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Keywords: Mouflon, Theileria Spp., Tick-Borne Pathogens, Wild Ruminants.

Abstract Text

Wildlife can act as a reservoir of different vector-borne diseases of veterinary and zoonotic importance. There have been several studies on the prevalence of tick-borne pathogens in wild ungulates in Europe, but very few studies are documented in wild ruminants in Spain. The objective of this research was to study the piroplasm infections in wild ruminants at Valencian Community.

From 2017 to 2020 a total of 111 spleen samples from 71 mouflons (*Ovis orientalis musimon*), 21 Spanish ibex (*Capra pyrenaica*), 10 fallow deer (*Dama dama*), and 9 red deer (*Cervus elaphus*), were tested by PCR for DNA *Babesia* and *Theileria* species targeting the 18sRNA gene and were identified by Sanger sequencing.

Global prevalence of piroplasms was 70.8%. Factors significantly associated with the infection were ruminant species since mouflons showed between 1.12 and 2.04 more likely to be parasitized than other species, and spring season, when animals presented a higher risk of being infected (OR 5.12; IC95% 1.4, 18.3).

From positive samples, 23 amplicons were selected for posterior identification. Four different piroplasms were identified: *Theileria ovis* clone AWT (43.5%), *T. ovis* isolate D5 (34.8%). *T. capreoli* isolate Tr/Th889 was detected in 17.4% of samples, and one isolate (4.3 %) was identified as *T. capreoli* isolate BAB1164. Species of *T. ovis* were isolated from mouflons whereas *T. capreoli* was from Cervidae. No *Babesia* species were identified.

Wild ruminants, particularly mouflons, act as a reservoir of *Theileria* species at the Eastern Iberian Peninsula, playing an important role as reservoir of *T. ovis* for the livestock.



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230 NON-INVASIVE INVESTIGATIONS OF THE MICROBIOME AND ANTIMICROBIAL RESISTANCE PATTERNS IN CETACEANS: A ONE HEALTH APPROACH TO ECOLOGICAL HEALTH IN HONG KONG

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Keywords: Cetacean, Dolphin, Porpoise, Microbiome, Antimicrobial Resistance

Abstract Text

Abstract

Among all the known cetacean species worldwide, only two species occur all year-round in Hong Kong waters: the Indo-Pacific humpback dolphin (or Chinese white dolphin) (*Sousa chinensis*) and the Indo-Pacific finless porpoise (*Neophocaena phocaenoides*). Both these species are listed as vulnerable on the IUCN red list and are facing multiple threats. Among those threats, anthropogenic microbial pollution is being investigated, as Hong Kong is a highly urbanised, densely populated territory. Within the dolphins and porpoise's habitat, marine bacterial pollution occurs through human activities such as sewage and waste discharge of material of human and domestic animal origin or from freshwater runoff.

It has been shown in other species that both the microbial community and the parasites harboured by the host are central to the host's health status, in particular their immune system function and neonatal health. This is extremely important given that neonates and young of the year represent a large proportion of the mortalities observed in the declining population of Indo-Pacific humpback dolphins in Hong Kong.

Next generation sequencing (NGS) is used here to describe the bacterial communities of cetaceans and their antibiotic sensitivity and resistance patterns, this being carried out through non-invasive collection methods, by sampling material from stranded dolphins and porpoises.

This project emphasizes the role of marine species as sentinels of the marine ecological health. This novel approach, within the One-Health concept which examines jointly human, marine species and ecological health is essential to enhance cetacean conservation in the Pearl River Estuary. Firstly, this provides insights on ecology and evolution of microbiome in relation to their hosts and their health. Secondly, our study provides a better understanding on anthropogenic threats, such as marine bacterial pollution and antimicrobial resistance, in order to guide future decisions in relation to prioritisation of conservation actions.



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217 EFFECTS OF LOW SALINITY EXPOSURE ON BOTTLENOSE DOLPHINS (*TURSIOPS TRUNCATUS*)

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Keywords: Dolphin, Freshwater, Pathophysiology, Salinity, Skin

Abstract Text

Bottlenose dolphins (*Tursiops truncatus*) have a worldwide distribution and often inhabit estuarine environments, indicating their ability to maintain homeostasis in low salinity for limited periods of time. Understanding the physiological changes and limits of low salinity and exposure duration is critical for dolphin conservation, as evidenced by multiple recent mortality events caused by significant decreases in environmental salinity, as well as increasing concern over anthropologically-driven salinity changes.

Stranding data has provided some knowledge about epidermal and biochemical changes associated with wild dolphins' low salinity exposure; however, the exposure duration and salinity level are often unknown or estimated. A retrospective analysis of medical records from 46 managed dolphins in the U.S. Navy Marine Mammal Program and blood results from 43 Navy dolphins exposed to a variety of salinity levels during deployments for different durations covering 43 years (1967-2010) was performed to assess epidermal, biochemical and hormonal changes. Blood samples collected during low salinity exposure (0-30 parts per thousand; ppt) were compared to samples collected while the same dolphins were in seawater (31-35 ppt).

Epidermal changes were observed in 35% of dolphins in the low salinity exposure cohort, with the prevalence inversely proportional to the salinity level. Significant decreases in serum sodium, chloride, and calculated serum osmolality and significant increases in blood urea nitrogen and aldosterone were observed during low salinity exposure. An improved understanding of the homeostatic limits of exposure duration and salinity level in dolphins will allow for enhanced animal care and conservation management decisions during low salinity mortality events.



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99 CHARACTERIZING EPIDEMIOLOGICAL AND GENOTYPIC FEATURES OF MYCOBACTERIUM BOVIS INFECTION IN WILD DOGS (LYCAON PICTUS)

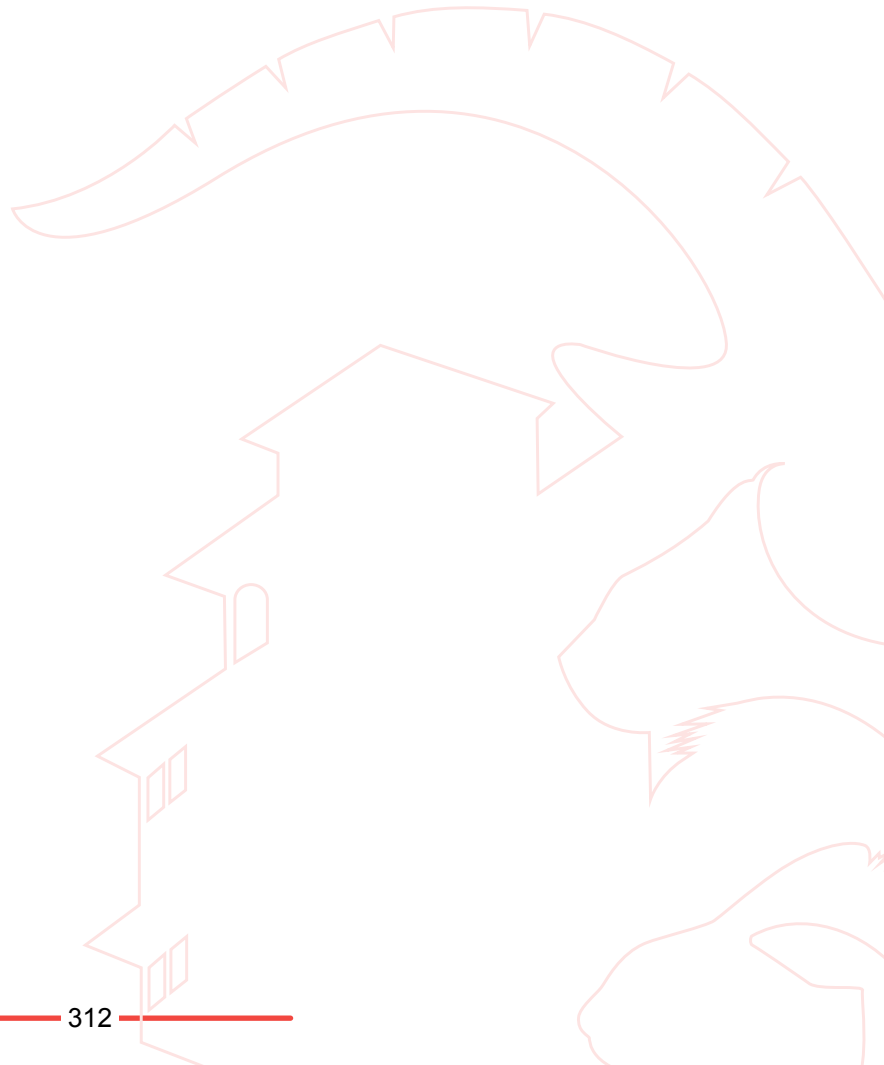
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Keywords: African Wild Dog, Bovine Tuberculosis, Mycobacterium Bovis, Spoligotyping, Whole Genome Sequencing

Abstract Text

Mycobacterium bovis (*M. bovis*) infects a wide range of wildlife species and has recently been discovered in the endangered African wild dog (*Lycaon pictus*). This study aimed to characterize the epidemiology of tuberculosis (TB) in wild dogs in endemic areas of South Africa. We describe 12 TB cases in wild dogs from Kruger National Park (KNP), Hluhluwe-iMfolozi Park (HiP), and a private facility in Hoedspruit from 2015 to 2017. Spoligotyping was used to identify the disease-causing *M. bovis* strain in these cases and whole genome sequencing was performed on 5 *M. bovis* isolates (KNP = 2 and HiP = 3) to investigate genomic diversity as well as the relationship to other isolates found in these geographical areas. Three distinct strain types were responsible for the *M. bovis* infections in this species. The SB0121 strain was observed in wild dogs from KNP, whereas SB0130 was responsible for infection in wild dogs from HiP. A novel strain, SB2681, was also identified in the HiP wild dogs. Whole genome sequence analysis suggests that different infection sources exist among these wild dogs and that inter-species transmission most likely occurred between wildlife predators and prey located within shared geographical areas. This study highlights the importance of regular disease surveillance to identify and characterize potential threats for successful control of infection and protection of endangered species.





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39 EASTERN EQUINE ENCEPHALITIS OUTBREAK IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) IN MICHIGAN, USA, 2019 TO 2020.

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Keywords: Eastern Equine Encephalitis, Michigan, White-Tailed Deer

Abstract Text

Eastern equine encephalitis (EEE) is a rare arbovirus that can cause severe disease with high mortality in horses and humans. In 2005, Michigan experienced a die-off of eight free-ranging white-tailed deer (*Odocoileus virginianus*), which at the time was the only known die-off in the United States involving multiple white-tailed deer. This die-off occurred in a three-county area in the southwest portion of the state. While there have been sporadic mortalities in white-tailed deer in the state attributable to EEE since that time, most have involved single animals. From late summer of 2019 through fall of 2020, EEE was diagnosed in 16 white-tailed deer. Fourteen of these cases occurred in 2019 across ten counties, representing historic EEE mortality in Michigan white-tailed deer with a much greater geographic distribution than the previous die-off. Nearly all deer (88%) were displaying clinical signs including lack of fear of humans, wandering, circling, stumbling, inability to stand, and/or drooling or foaming at the mouth. On histopathological examination, mild, moderate, or severe lymphoplasmacytic meningoencephalitis was observed in fixed brain tissue from all deer and confirmed as EEE viral infection on polymerase chain reaction, using 2 separate assays. During the same time period, EEE was detected in five wild birds: three ruffed grouse, one bald eagle, and one mute swan, and in seventy domestic mammals with mortality rates of nearly 100%. The virus also infected thirteen Michigan residents resulting in seven fatalities. These findings emphasize the importance of wildlife mortality investigations in the detection of zoonotic diseases, particularly in areas where vector monitoring may be lacking.



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196 CROSS-SECTIONAL SEROLOGICAL SURVEY OF AUJESZKY'S DISEASE VIRUS AND CLASSICAL SWINE FEVER VIRUS IN WHITE-LIPPED PECCARY (*TAYASSU PECARI*) AND COLLARED PECCARY (*PECARI TAJACU*) IN THE PERUVIAN AMAZON

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Keywords: Amazonia, Conservation, Aujeszky's Disease Virus, Classical Swine Fever Virus, Serology.

Abstract Text

The Amazon is a highly biodiverse region and home of indigenous communities, where wild meat represents a significant source of animal protein. The white-lipped peccary (*Tayassu pecari*) and collared peccary (*Pecari tajacu*) are the most frequently hunted species, contributing up to 70% in term of biomass consumed. The decrease and disappearance of entire populations of peccaries has been widely reported in Amazonia, and the influence of infectious diseases have been proposed. Several high-impact viruses have emerged in the global swine population in recent decades, including Aujeszky's disease virus (ADV) and classical swine fever virus (CSFV), which represent a serious constraint to health in swine species by affecting growth, reproduction, and mortality. Given logistic constrains, the knowledge of the impact of infectious diseases in wildlife in the Amazon is limited. In order to evaluate the possible factors in the disappearance of peccaries in the Amazon, we carried out a cross-sectional serosurvey for the detection of ADV and CSFV antibodies in two peccary species. Sera from 78 peccaries (n=45 *Tayassu pecari*; n=33 *Pecari tajacu*) were tested for the presence of ADV and CSFV antibodies using the ID Screen Aujeszky gB Competition ELISA kit and ID Screen Classical Swine Fever E2 Competition ELISA kit, (IDvet, Montpellier, France) respectively. During 2019 and 2020, blood samples were collected taking advantage of subsistence hunting conducted by local people from a remote and poorly disturbed area on the border between Peru and Brazil. Antibodies against ADV were detected in 2 out of 45 white-lipped peccaries (4.44%; CI95% 1.23% - 14.83%), but not in collared peccaries. Sera from both species tested negative for antibodies against CSFV. Our results highlight the presence of ADV infection in free-ranging white-lipped peccaries. However, further studies are needed to evaluate the impact of ADV and CSFV infections on peccaries' populations dynamics.



240 PREVALENCE OF GASTROINTESTINAL PARASITES IN WILD CARNIVORE SPECIES FROM CENTRAL SPAIN

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Keywords: Intestinal Parasites, Prevalence, Epidemiology, Wildlife, Carnivores

Abstract Text

Wild carnivores can act as reservoirs of parasites that affect wild (affecting protected species) and domestic animals, and even humans. Due to their diet, movements and habits, they may contribute (to an unknown extent) to the spread of parasites in the area they inhabit. At present, little information is available on the occurrence of gastrointestinal parasitic infections in wild carnivores in Spain, the magnitude of environmental contamination by parasites in defecations, or the risks they may pose to domestic animals and humans.

In this ongoing epidemiological survey, a total of 163 individual and fresh fecal samples were collected from *Neovison vison* (n=2), *Meles meles* (n=26), *Genetta genetta* (n=4), *Lynx pardinus* (n=13), *Martes foina* (n=11), *Herpestes ichneumon* (n=6), *Lutra lutra* (n=16), *Mustela putorius* (n=5), *Vulpes vulpes* (n=77), *Mustela nivalis* (n=1) *Canis lupus* (n=2); were obtained from roadkill carcasses (n=32) and tracking techniques (n=131) during the period from 2019 to 2021. The investigated specimens were collected in three Spanish autonomous communities, including Castilla-La Mancha (n=22), Castilla y León (n=72) and Madrid (n=64).

A total of 163 faecal samples were analysed by conventional coprological (Teleman and Baermann) and molecular methods for *Cryptosporidium* spp. (n=76) and *Giardia duodenalis*. The intestinal parasites detected were helminths species belonging to the phylum Acanthocephala (*Acanthocephalus* spp. 10%), Cestoda (*Taenidae*: 2%), Nematoda (*Ancylostomatidae*: 18%, *Capillaria* spp.: 2%, *Spiruridae*: 1%, *Toxascaris leonina*: 29%, *Toxocara cati*: 6%, *Trichuris vulpis*: 4%), and Trematoda (6%). Among the protozoa, *Cystoisospora* spp. (27%), *Eimeria* spp. (6%), *Cryptosporidium* spp. (1%) and *G. duodenalis* (6%) were found.

A great diversity of gastrointestinal parasites, especially helminths, was observed in the Spanish carnivore population surveyed. Some of them have zoonotic potential, which should be further investigated using molecular (PCR and Sanger sequencing) tools to aim the relevance of this data in One Health approach.



300 A CASE STUDY OF WILD BOAR AND TB: GIVING UP THE RESERVOIR ROLE?

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Keywords: Maintenance Host, Reservoir, Surveillance, Tuberculosis, Wild Boar

Abstract Text

In 2004, we detected the first high-prevalence focus of tuberculosis (TB) in a free-ranging wild boar population from northern Spain (Ports de Tortosa i Beseit, Catalonia). TB eradication in sympatric cattle and intensive wild boar harvesting contributed to decrease TB prevalence in wild boar from values over 75% in 2004 to 35% (9/26, 95% CI: 19-54%) in 2012, when intensive management measures stopped. From then on, monitoring of this focus decreased in intensity due to its integration in the Catalan wildlife health surveillance programme, which displays lower spatial resolution, largely relies on hunters for samples collection and is mostly based on serology. This resulted in uncertainty on the evolution of the focus, despite the seroprevalence values observed from 2013 to 2017 showed an apparent temporal decreasing trend at the region scale.

To shed light on this, 37 adult wild boars were harvested in the focus area from September 2018 to June 2019. Cervical lymph node samples were analysed by histopathology, Ziehl-Neelsen stain and PCR, and serum samples by ELISA. A single wild boar displayed tuberculosis-like lesions and positive results to PCR and ELISA, whereas a second one was positive by ELISA.

Altogether, the TB prevalence was 5.6% (2/37, 95% CI: 1.5-18%), lower than the 35% recorded in 2012 in the focus area, as well as below the values observed in 2013-2017 at the regional scale, hence confirming the decreasing trend of TB prevalence. Concurrently, the cattle stock grazing in the focus area has not been diagnosed with TB reinfections in this time-frame. Our results suggest that wild boar may not be able to maintain high prevalence TB in this region in the mid-term independently of livestock. However, continued surveillance will be necessary to fully assess the evolution of TB and the epidemiological role of the wild boar in this region.



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254 RICKETTSIA AESCHLIMANNII IN HYALOMMA MARGINATUM AND H. RUFIPES TICKS FROM TRANS-SAHARAN MIGRATORY PASSERINES IN SPAIN

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Keywords: Crimean Congo Hemorrhagic Fever Virus, Migratory Birds, Rickettsias, Ticks-Borne Pathogens

Abstract Text

This study reports the detection of tick-borne pathogens such as Rickettsias spp. Crimean-Congo hemorrhagic fever virus, Anaplasma spp. and Babesias spp. and Theileria spp. in Hyalomma marginatum and H. rufipes ticks collected from trans-Saharan migratory Eurasian reed warblers (*Acrocephalus scirpaceus*) in the spring of 2019 in Spain.

Rickettsial zoonoses are among the oldest-known vector-borne diseases. Crimean-Congo hemorrhagic fever virus (CCHFv) is a human emerging pathogen in Spain, so currently there's an important gap in epidemiological knowledge to understanding the pathways of CCHFv spread over the country. Other tick-borne pathogens, e.g. Anaplasma spp., Babesia spp. and Theileria spp. may also be exchanged spatially by ticks on migratory birds.

Amplification of the different genetic markers of Rickettsia spp., Anaplasma spp. 16S rRNA gene, and 18S rRNA gene of Babesia/Theileria spp. was carried out by conventional PCRs whereas the S segment of CCHFv was analysed by a nested RT-PCR. Ticks were identified by amplifying the 16S rDNA gene. Rickettsia spp. positive samples were further characterized by targeting specific genes: 16S rRNA, OmpA, OmpB, AtpA, GltA) and RecA. The molecular identification of the 5 immature ticks collected confirmed three nymphs as H. marginatum, and the other nymph and the larva as H. rufipes. All samples were negative to the other tick-borne pathogens. A ML phylogenetic tree was built using the AtpA, OmpB and RecA sequences to compare with reference sequences in NCBI database to confirm the molecular identification of the species.

Reed warblers cross the Sahara Desert in autumn to winter in sub-Saharan tropical region countries. The presence of H. rufipes immatures on the reed warbler shows that it was migrating from Africa because H. rufipes has not stable populations in Europe. These results corroborate that migratory birds act as vehicles whereby ticks and their pathogens are spread out between Europe and Africa.





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264 BLOOD MICROBIAL 16S RRNA METATAXONOMIC ANALYSIS REVEALS INFECTIOUS RISKS CARRIED BY WILD BLACK AND BROWN BEARS

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Keywords: Anaplasma, Bears, Borrelia, Microbiome, Wolbachia

Abstract Text

In Japan, two different bear species exist, the Hokkaido brown bear (*Ursus arctos yesoensis*) and the Japanese black bear (*Ursus thibetanus japonicus*). Hokkaido brown bears live only in the northern island of Japan, while Japanese black bears are widely distributed in Honshu and Shikoku Islands. Although both bear species are the apex predators in Japan, their potential role in transmitting infectious agents is not fully described. Hence, detecting the bacterial composition of blood in bears can help understanding the disease risks in bears and the associated zoonosis.

Here, we aimed to identify the bacterial composition in the blood of bears in relation to the associated demographics and ecological factors. We amplified a fragment of the 16S rRNA gene of all possible bacteria in the blood of black (n = 92) and brown (n = 50) bears. The resulted amplicons were sequenced using next generation sequencing (NGS) technology. A total of 6,605,500 reads were obtained from MiSeq and 1,215,555 remained after quality filtering and denoising consisting of 12,029 features. All alpha and beta diversity metrics were significantly variable between black and brown bear blood samples ($p < 0.001$) as tested by Kruskal-Wallis and Pairwise permanova, respectively. The PCoA plots detected overlapping between the samples from different age, or sex. The taxonomic analysis showed that two *Wolbachiaspp.* were the highly abundant (22.5%) and was detected in 79.6% (113/142) of the bears, with one unique *Wolbachia sp.* in each bear species. In addition, the prevalence of *Anaplasma bovis*, *Borrelia sp.* and *Ehrlichia sp.* was 22.5% (32/142), 2.8% (4/142) and 0.7% (1/142), respectively. We detected several other potentially pathogenic bacteria such as *Mycoplasma haemofelis* (16.2%) and one brown bear was infected with a *Yersinia* species. The results of this study provide an opportunity to better understanding the disease risks associated with bears in Japan.



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252 REDUCE THE RISK OF DISEASE EMERGENCE AND PROTECT WILDLIFE HEALTH BY ADOPTING THE ONE HEALTH APPROACH.

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Keywords: Disease, OIE, One Health, Surveillance, Wildlife

Abstract Text

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

The World Organisation for Animal Health's (OIE's) mandate as the leading international organisation on animal Health, and in representing the interests of National Veterinary Services in 182 Member Countries, recognises that animal health, balanced ecosystems, and biodiversity contribute to achieving One Health.

Through a collaborative effort involving contributions from OIE staff, OIE Wildlife Working Group, international partners, OIE Delegates and National Focal Points for Wildlife, a comprehensive OIE Wildlife Health Framework was developed in 2020 to better integrate wildlife health into the OIE's core activities and reinforce One Health strategies. The resulting framework integrated the views and expectations of OIE Members collected through a survey and two global webinars attended by over 350 stakeholders.

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



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121 MODELLING FELINE LEUKEMIA VIRUS IN THE IBERIAN LYNX (*LYNX PARDINUS*) FROM AN OUTBREAK: APPLICATIONS FOR DISEASE MANAGEMENT IN REINTRODUCTION PROGRAMS

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Keywords: Feline Leukaemia Virus, Iberian Lynx, Lynx Pardinus, Outbreak, Reintroduction

Abstract Text

By 2007, the critically endangered Iberian lynx (*Lynx pardinus*) comprised less than 250 individuals secluded in two nuclei: Doñana and Sierra Morena (Andalusia, Spain). The small and inbred Doñana nucleus suffered devastating consequences from a feline leukaemia virus (FeLV) outbreak that year. The effects of infectious diseases seemed to have a profound impact in the survival of that nucleus at that time. Beginning in 2002, conservation measures included habitat and prey management, decrease of mortality, genetic management, and reintroductions. To manage the risks associated with disease and reduce the impact that an outbreak of FeLV could have during the establishment of reintroduced lynx populations, we created a mathematical model based on data available from the scientific literature regarding the 2007 FeLV outbreak. The aims of this model were to investigate the disease transmission, and the basic reproduction number (R_0), to finally, explore the critical vaccination level to achieve herd immunity threshold considering the outbreak's demographic and temporal features. We developed a Susceptible-Infected-Recovered/Dead model. We also included a Quarantine compartment, since during the outbreak management measures, lynxes were isolated to avoid infection spread. Model results express that, in this case, FeLV transmission was more aggressive than that occurring in domestic cats, resulting in a $R_0 \approx 2.15$. This may be explained due to the Doñana population traits at that time, where a low genetic diversity and high inbreeding rate could have led to a compromised immunocompetence that would have facilitated disease spread. Based in this model, a critical vaccination level of 54% of the population would be enough to achieve herd immunity threshold. Although more genetically diverse reintroduced lynxes are vaccinated prior to release, this vaccination coverage could be considered in reintroduction programs to avoid FeLV dissemination in case of an outbreak emergence in this newly established populations.



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129 A WEBGIS TO SUPPORT THE EPIDEMIOLOGICAL SURVEILLANCE OF TRICHINELLOSIS IN NORTH-EAST ITALY

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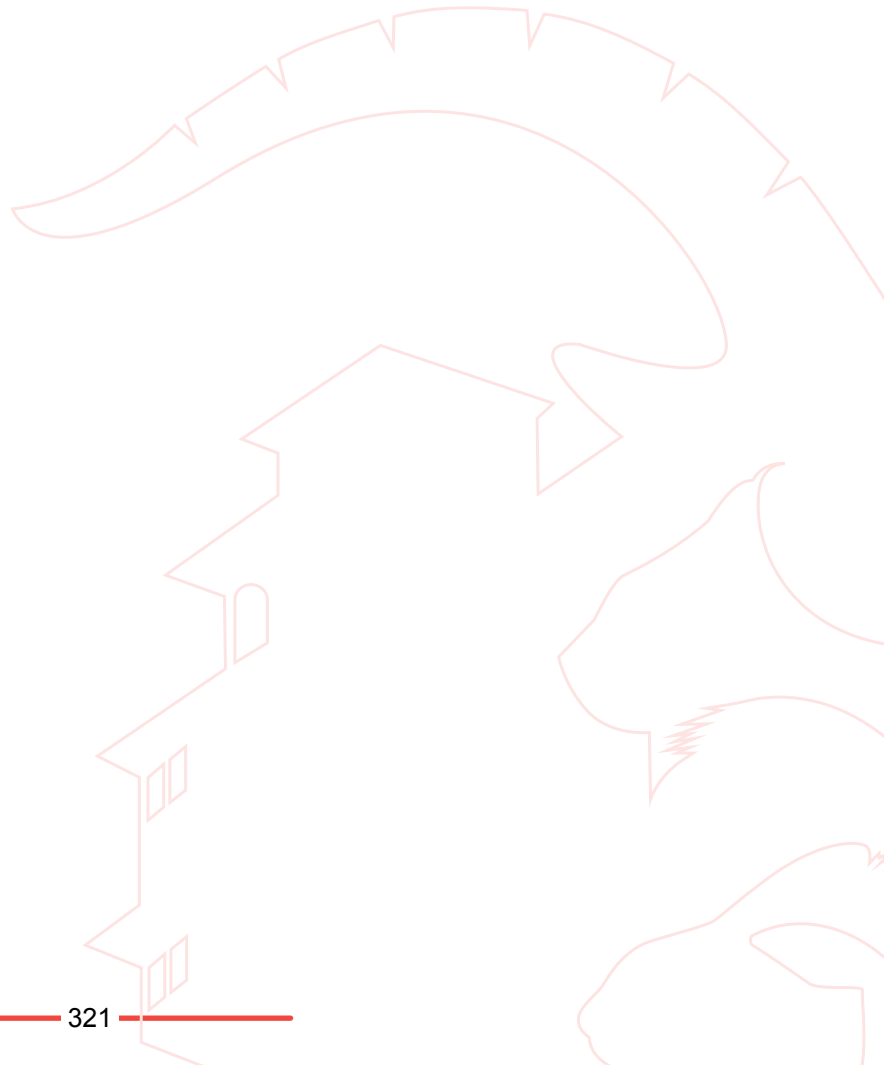
Keywords: Red Fox, Surveillance, Trichinella Spp, WebGIS, Wild Carnivores

Abstract Text

Trichinella spp. has dramatically lowered its prevalence, becoming sporadic in North-Eastern Italy in the last decades. Controls in meat from livestock (pigs, equines) and wild boar remain necessary for the consumer's safety, but are not aimed at understanding its ecology and epidemiology. For this purpose a surveillance plan should consider instead the reservoir hosts, in particular the red fox (*Vulpes vulpes*). To support the surveillance in this area, a WebGIS has been developed for spatial localization and visualization of foxes and other wild carnivores. The aim is the creation of a framework to collect passive surveillance data and sampling for *Trichinella* spp. according to the EC Regulation 1375/15 and Directive 2003/99/EC. The WebGIS uses Java developed language combined with JavaScript and a set of spatial extensions such as OpenLayers3. The web application is published through the Tomcat 7 application server in a dedicated Linux server in IZSve.

Currently, more than 10000 foxes and other wild carnivores, from 2005 to 2020, are uploaded: among these, 10 red foxes in which *Trichinella britovi* was found. Preliminary spatial analysis was performed to identify possible *Trichinella* clusters, thus defining a surveillance strategy and introducing a risk-based component.

Our results did not highlight representative clusters to target a more intensive surveillance aimed at identifying risk factors for the presence and maintenance of this parasite. In the future, we plan to use the WebGIS to plan active surveillance on a local scale where the parasite had been identified in the past, to increase the likelihood of its detection and estimate a maximum possible prevalence.





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249 FIRST REPORT OF SUGGESTED SEPTICAEMIA IN A EUROPEAN OTTER (*LUTRA LUTRA*) CAUSED BY THE FISH PATHOGEN *YERSINIA RUCKERI*

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Keywords: Enteric Redmouth Disease, European Otter (*Lutra Lutra*), Fish, Septicaemia, *Yersinia Ruckeri*

Abstract Text

An adult, male European otter (*Lutra lutra*) was found dead in dam in the north of Sweden. At necropsy, the spleen was found to be enlarged with a prominent follicular pattern. Furthermore, the liver was pale with ruptures and adhering blood clots, and the abdomen was filled with 60 mL of blood. Hence, the cause of death was suggested to be blunt force trauma, possibly from a car collision. To rule out underlying disease, the spleen was sent for bacterial cultivation and tissues were sampled for histopathology.

Yersinia ruckeri was isolated in pure culture after aerobic cultivation at 37°C. In fish, *Y. ruckeri* is a notifiable disease being the causative agent for enteric redmouth disease (ERM). To confirm the bacteria as a fish pathogen, an additional, successful cultivation at 20°C was done.

At histologic evaluation, the spleen showed moderately hyperplastic follicles with accumulation of eosinophilic material and necrosis of follicle centres. Widening of follicle mantle zones with infiltration of neutrophils in the mantle zone and the red pulp was noted. In the liver, sinusoids and periportal areas had moderate accumulations of degenerative neutrophils, and there was scattered single cell necrosis of hepatocytes. In the right ventricle, a focal necrosis of myocardial fibres was seen, with infiltration of neutrophils.

The presented otter had signs of disseminated acute inflammation and splenomegaly, consistent with toxemia or septicaemia. At bacteriologic cultivation, the only demonstrated bacteria was *Yersinia*, hence it is suggested to be the causative agent of the lesions. No previous publication of *Y. ruckeri* as a pathogen for otters exist, prompting the need for more surveillance of this bacterium in otters. As the bacteria could be cultured under fish-like conditions, it could suggest that otters can be a carrier of this important pathogenic bacterium of fish.



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44 HEALTH STATUS OF THE ALPINE IBEX IN THE NORTHWESTERN ITALIAN ALPS

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Keywords: Alpine Ibex, Infectious Diseases, Northwestern Italian Alps

Abstract Text

Aim of this work is to evaluate the presence of infective agents among Alpine ibex (*Capra ibex ibex*). We considered four key areas in northwestern Alps: Gran Paradiso National Park, Aosta Valley (areas other than the Park), Alpi Cozie Parks, Alpi Marittime Park. Between May 2018 and December 2019 we have considered 148 captured animals. In the frame of the monitoring plan established by WP3 Interreg ALCOTRA LEMED-IBEX serological, bacteriological and molecular analyses were used to detect a number of infectious diseases. All animals were negative for *Brucella abortus/melitensis*, *Coxiella burnetii*, *Borrelia burgdorferi*, *Neospora*, *Chlamydiaceae*, *Leptospira*, BTV, Schmallenberg virus, Respiratory syncytial virus, Bovine Herpes virus type I, Kobuvirus. Assuming that the tested animals may be considered as a representative sample of the four areas, with a 95% confidence level, the results are compatible with a maximum possible prevalence for the listed diseases of 3.3%. Seropositivity was found for *Brucella ovis* (3.6% - 95% CI 1.2-8.1), CAEV (8.6% - 95% CI 2.9-19.0), MAP (2.8% - 95% CI 0.8-6.9), PI3 virus (2.3% - 95% CI 0.3-8.1), *Salmonella abortus ovis-abortus equi* (67.4% - 95% CI 59.1-74.9; titres from 1:20 to 1:160), Border disease virus (9.0% - 95% CI 4.9-14.9), *Besnoitia* (0.7% - 95% CI 0.02-3.9), *Toxoplasma* (0.7% - 95% CI 0.02-3.9). The molecular analysis showed the following prevalence: BVDV-1, st 1a (0.7% - 95% CI 0.02-3.9), *Mycoplasma conjunctivae* (2.3% - 95% CI 0.5-6.5), *Yersinia enterocolitica* (0.8% - 95% CI 0.02-4.4). Bacteriological examination revealed three cases of *Corynebacterium pseudotuberculosis* (subcutaneous abscess). The analyses on Alpine ibex from four areas of the NW Italian Alps suggest that currently a number of commonly reported diseases have a low probability to be circulating. Only *Salmonella abortus ovis-abortus equi* is widely detected, whereas a few diseases show low prevalence that may deserve targeted interventions.



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132 EXTERNAL EVALUATION AND IMPROVEMENTS OF THE EPIDEMIOLOGICAL SURVEILLANCE OF AMPHIBIANS IN FRENCH NATIONAL PARKS

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Keywords: Amphibian, Epidemiology, Evaluation, OASIS, Surveillance

Abstract Text

Ranaviruses and chytridiomycosis are known to cause mortality in French protected areas. Consequently, amphibian populations are monitored in National Parks for disease-associated mass mortality.

This study aimed at evaluating the surveillance network of amphibian mortality in French National Parks using the OASIS method. It consists in semi-directive interviews of field agents and network leaders allowing the fulfilment and analysis of an evaluation grid.

The main strengths of the network revealed by the evaluation are: (i) active participation of most of the field agents of National Parks enabling the investigation of many mortality events, (ii) a strong will of supervisors to implement effective monitoring and management of amphibian populations.

However, limitations narrow the efficiency of the surveillance, including the absence of national coordination which decreases the sustainability of the network. The insufficient number of lab agents delays the possibility of adequate communication and management actions. Furthermore, the lack of standardised protocols and dedicated work-time for field agents prevent the detection of mortalities in cryptic and small-sized populations.

Those observations resulted in recommendations for the surveillance of amphibian populations and in a proposition for update of surveillance protocols in National Parks. These encompass the inclusion of amphibian discussion time and experts to existing steering committees (locally and nationally), the reinforcement of laboratory capacity alongside with the setting-up of macroscopic pathology and histology techniques, the use of e-DNA monitoring and active surveillance of endangered species.

This study also highlighted the importance of evaluation of epidemiological surveillance networks to ensure their efficiency and durability



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282 MULTI-SPECIES CLOSTRIDIAL OUTBREAKS IN NEONATAL, JUVENILE AND ADULT GREATER SAGE GROUSE (*CENTROCERCUS UROPHASIANUS*) IN A CONSERVATION BREEDING PROGRAM

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Keywords: *Centrocercus*, *Clostridium*, *C. Difficile*, *C. Perfringens*, Sage Grouse

Abstract Text

The greater sage grouse (*Centrocercus urophasianus*) is an endangered Canadian grassland species that has exhibited precipitous population declines across its former range, with only 150-222 wild individuals left in Canada. Since 2014, the Calgary Zoo has maintained a conservation breeding flock of greater sage grouse with annual releases to the wild since 2018.

The control and management of disease in endangered species breeding programs is critical to their success. In 2019 and 2020, enteritis-associated deaths occurred in multiple age classes (52 neonates, 60 juveniles, 4 adults). In neonates (1-12 days of age), clinical signs included rapid onset of lethargy, squinting, diarrhea, drooping wings, decreased appetite, weight loss, and sudden death. Gross pathologic findings included severe segmental hemorrhagic enterotyphlocolitis, coelomic effusion, and muscle pallor. Histologic examination confirmed a hemorrhagic enteritis with rare areas of superficial necrosis including rare 'volcano' lesions. Subsequent culture and enterotoxin PCR identified *Clostridium difficile* elaborating both A and B toxins. Treatment of clinical cases was mostly unsuccessful. Potential sources considered for the *C. difficile* included food sources, the environment, and human caretakers.

In older birds (4-12 week old and adults), clinical signs included diarrhea, drooping wings, lethargy, decreased appetite, and sudden death. Gross necropsies identified severe diffuse fibrinonecrotic enteritis of the duodenum/jejunum, coelomic effusion, pericardial effusion, pulmonary edema, dehydration, and muscle pallor. Histologic lesions were classical for necrotic enteritis as described in other galliformes. Clostridial culture and enterotoxin PCR was positive for *Clostridium perfringens* producing alpha toxin. Flock treatment with lincomycin resulted in resolution of this outbreak



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52 TOXOPLASMA GONDII SERO-PREVALENCE IN WILD CERVIDS IN DENMARK

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Keywords: Denmark, Sero-Prevalence, Toxoplasma Gondii, Wild Cervids

Abstract Text

Toxoplasma gondii is a protozoan parasite and the causative agent of toxoplasmosis in humans. Felines is the only definitive host, excreting oocysts to the environment, while possibly all warm-blooded animals can be intermediate hosts. In the intermediate hosts, *T. gondii* can form tissue cysts in the muscles. Humans can get infection by ingesting undercooked or raw meat containing tissue cysts. Several cases of *T. gondii* infections in humans had been reported in association with ingesting uncooked or undercooked venison. In this study, we aim to assess the seroprevalence of *T. gondii* in the Danish population of wild cervids by sampling carcasses that were intended for human consumption. In total, 428 cervids were screened for antibodies against *T. gondii* by ID Screen® Toxoplasmosis Indirect Multi-species ELISA kit. Blood samples were collected from 87 fallow deer (*Dama dama*), 272 red deer (*Cervus elaphus*), 66 roe deer (*Capreolus capreolus*) and 14 sika deer (*Cervus Nippon*) shot during hunting season October to January 2017/2018. Of the tested cervids, 105 (24.5%) were sero-positive for *T. gondii*. Of these, 12 (13.8%) were fallow deer, 74 (27.2%) were red deer, 18 (32.7%) roe deer and 1 (7.1%) sika deer. The prevalence was significantly different between the cervid species ($p < 0.0086$). The odds of sero-positivity was 7.6 times higher in roe deer than sika deer, and 5.1 times higher in red deer than in sika deer. The prevalence was significantly different between the age groups ($p < 0.0001$). The odds of sero-positivity in adults (3-5 years) was 9.3 times higher than in calves (<1 year), and 2.7 times higher than in yearlings (1-2 years). Cervids from Denmark should be considered a significant source of human toxoplasmosis. However, the risk of infected meat depends on the age of the animal and the cervid species.



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80 PATTERNS AND PATHOGEN INFECTION OF DEER KEDS (DIPTERA: HIPPOBOSCIDAE) AND TICKS (IXODIDA: IXODIDAE) FOUND ON WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS) IN THE EASTERN UNITED STATES

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Keywords: Deer Ked, Tick, Tick-Borne Pathogens, White-Tailed Deer

Abstract Text

White-tailed deer (*Odocoileus virginianus*) host several ectoparasites in the eastern United States, most notably various species of ticks and deer keds. Ticks transmit pathogens to humans and animals, but little is known about pathogen transmission by deer keds. On-host localization and pathogen infection of ticks and deer keds on white-tailed deer were thus evaluated in different geographical regions to determine how their spatial relationship on the host impacts co-feeding acquisition of pathogens.

Ticks and deer keds were collected from hunter-harvested white-tailed deer from six states in the eastern United States. Differences in mean ectoparasite counts across body sections and states were evaluated. Molecular assays were used to detect *Bartonella* spp., family Anaplasmataceae spp., *Rickettsia* spp., and *Borrelia* spp. in blacklegged ticks and deer keds.

Ticks were collected from all states, with *I. scapularis* being predominant. Mean *I. scapularis* counts from the head and front sections were greater than from the rear section. Keds from Pennsylvania (*Lipoptena cervi*) were found on all body sections of deer, but keds from Alabama or Tennessee (*L. mazamae*) were more often found in the rear body section. Bacteria detected in *I. scapularis* were not detected in *L. cervi* infesting the same deer. This is the first evidence of possible niche partitioning of ticks and two geographically distinct deer ked species (*L. cervi* in the northeast and *L. mazamae* in the southeast) on white-tailed deer. Preliminary molecular results indicate that *I. scapularis* and *L. cervi* that co-parasitize a host do not acquire the same bacteria, which may reflect the relatively short time deer keds spend feeding. These differences in tick and deer ked spatial distributions on white-tailed deer and pathogen infection status may have implications for transmission rates of vector-borne pathogens and warrant further study over a wider geographic range and longer time frame.



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306 HPAI H5N1 OUTBREAK INVESTIGATION IN WILD BIRDS, CAMBODIA 2021

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Keywords: Asian Openbill Stork, Avian Influenza, H5N1, HPAI, Wild Bird

Abstract Text

In March of 2021, a wild bird mass mortality event was detected by government rangers and community members in Prey Veng province, Cambodia. A network of multisectoral stakeholders was notified with support from WildHealthNet, an initiative to strengthen wildlife health surveillance in the region, funded by DTRA BTRP. An investigation involving environment and animal health agencies, conservation organizations, and local authorities was conducted to determine the cause of the mortality event and assess the utility of environmental samples in detecting the causative agent.

During the investigation, oral and cloacal swabs from 8 Asian openbill stork carcasses and a live domestic duck were collected and tested for avian influenza at the national laboratory. Following the initial investigation, water and sediment samples from 5 locations around the lake were also collected and tested for avian influenza. Oral/cloacal swabs from wild bird carcasses were collected to confirm the cause of mortality. Once mortalities were no longer reported, wild bird fecal samples were collected, tested for avian influenza, and positives barcoded to confirm bird species.

Between March 17-April 17, the total number of dead birds recorded was 2009, of which the majority (n=2002) were Asian openbill storks. Juveniles represented 78% of mortalities. Oral/cloacal swabs (3/3) collected during the initial investigation were positive for HPAI H5N1. Tissue from the domestic duck and unfiltered water samples were negative for avian influenza. Additional swab, sediment, and fecal sample results are pending.

This investigation confirms the first detection of HPAI H5N1 in free-ranging wild birds in Cambodia. The origin and how the virus was introduced into the wild bird population is still unknown. Unfiltered water samples did not successfully detect avian influenza in the environment during an outbreak. A structured network of stakeholders is essential for efficient communication and a coordinated response during an outbreak investigation.



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288 DETECTION OF AFRICAN SWINE FEVER VIRUS IN WILD BOAR IN SOUTHEAST ASIA

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Keywords: African Swine Fever, ASF, Southeast Asia, Wild Boar

Abstract Text

African Swine Fever (ASF), a highly contagious and fatal swine disease, was first detected in Southeast Asia in early 2019, and has since spread rapidly throughout the region. Although significant efforts have been made to track and diagnose the disease in domestic pigs, little is known about ASF in wild boar in the region. Investigations were conducted in Cambodia, Laos, and Vietnam to 1) describe the interface between domestic pigs and wild boar, 2) assess the risk of ASFV transmission at the domestic/wild pig interface, and 3) detect the presence of ASFV in wild boar.

Investigative teams visited areas with confirmed ASF outbreaks or large domestic pig mortalities from 2019-2020 to interview villagers and document evidence of wild boar presence. Passive reporting of wild boar carcasses was facilitated by engagement with a network of villagers, hunters, rangers, and government officers. Wild boar carcasses, tissue/meat, feces, and environmental samples were collected and sent to the respective country's national laboratory for ASFV testing via RT-PCR.

Many opportunities for wild/domestic pig interaction were documented in each country, suggesting a high-risk interface for ASFV transmission. Wild boar carcasses were detected in all three countries through passive reporting. Tissue samples in Laos and Cambodia, and tissue, feces, and environmental samples in Vietnam were confirmed positive for ASFV. These investigations were supported through WildHealthNet, a regional initiative funded by DTRA BTRP, to strengthen wildlife health surveillance. They document the first cases of ASFV in wild boar in Southeast Asia, likely due to spillover from domestic pigs. These investigations highlight the importance of early and ongoing surveillance in wild boar and implementation of biosecurity measures to prevent and control ASF in the region.



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385 LEPTOSPIRA IN CALIFORNIA SEA LIONS (*ZALOPHUS CALIFORNIANUS*): CLIMATE-ASSOCIATED FADEOUT AND RE-EMERGENCE OF AN ENDEMIC PATHOGEN IN A WILDLIFE HOST

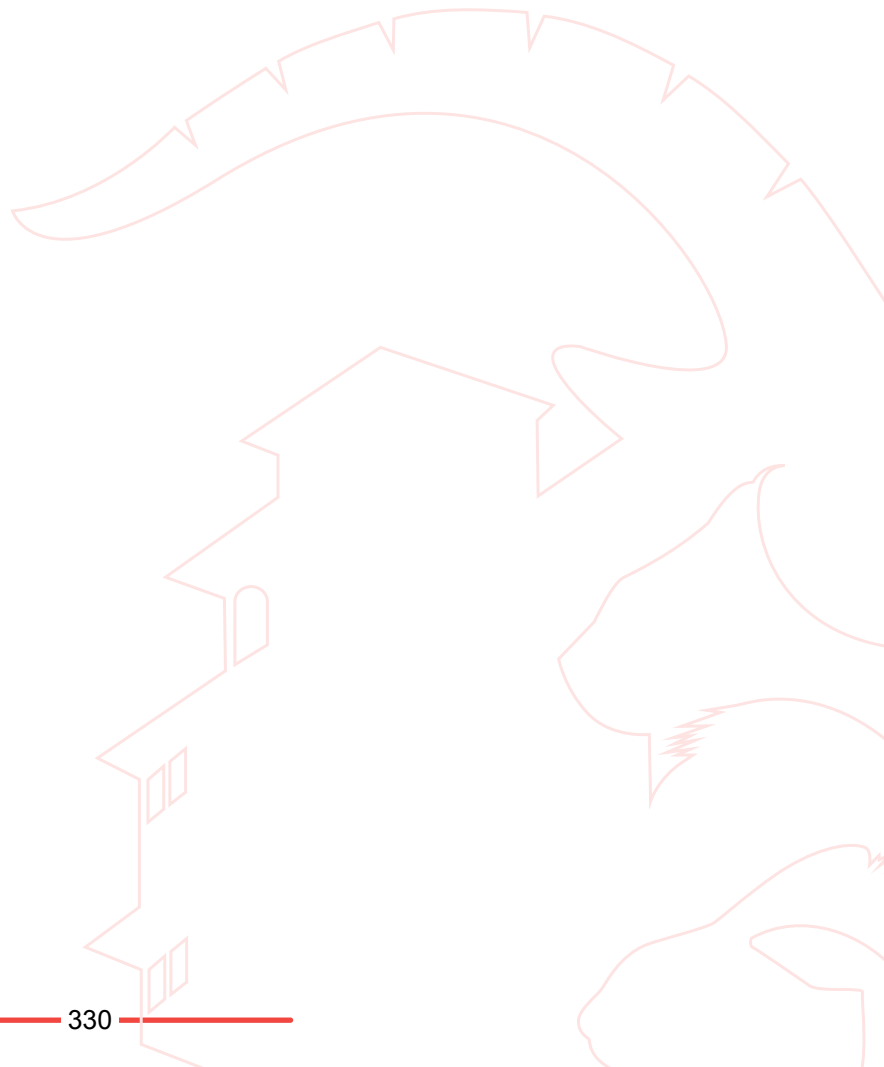
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Keywords: Leptospira, California Sea Lion, Climate, Pathogen Fadeout

Abstract Textf

Leptospira interrogans serovar Pomona has been circulating endemically in the California sea lion (*Zalophus californianus*) population since at least the mid-1980s, causing yearly, seasonal outbreaks of varying magnitude. Using serologic, molecular, demographic and ecological data and samples collected between 2010-19 we show that *L. interrogans* serovar Pomona disappeared from the California sea lion population in 2013 and re-emerged in 2017. We provide multiple lines of evidence that perturbations in both host demography and seasonal movement patterns – driven by oceanographic anomalies – caused pathogen fadeout in the system and facilitated re-emergence. This is the first recorded example of spontaneous fadeout of an endemically circulating pathogen from a large, robust, host population. In a future where greater fluctuations in global climatic variables are predicted, and the impacts of zoonoses on wildlife and human populations are increasingly of concern, our study provides novel insights into how climatic and intrinsic host factors may interact to influence pathogen transmission and persistence in a natural system.





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378 CYTOPATHIC EFFECTS OF TRICHOMONAS GALLINAE ON CELL CULTURE AFTER ENVIRONMENTAL PERSISTENCE TRIALS

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Keywords: Trichomonas, Virulence, Persistence, Cell Culture

Abstract Text

Through investigation of the role of shared water sources in outbreaks, the deadly avian parasite *Trichomonas gallinae* has been shown to persist in simulated bird baths in various environmental conditions, including the addition of organic material, alteration of dissolved oxygen, and exposure to UV light. Although persistence has been established, the effect of persistence on parasite virulence has not been investigated. We aimed to determine any effects persistence trials may have on trichomonad virulence to assess whether persistent trichomonads retained the capability to cause disease and death in birds. We used cell culture to measure cytopathic effect (CPE) of trichomonads maintained in parasite-specific culture (or non-persistence (NP)) versus parasites that persisted after different time points in simulated environmental conditions. We documented a broad-winged hawk (BWAH) trichomonad isolate exposed to UV light for 2 and 4 hours in clean, distilled bird baths produced an increased CPE than that of NP BWAH. In an organic material bird bath, BWAH and Cooper's hawk (COHA) persistence isolates did not show statistically different changes in CPE than NP isolates indicating less effect of these conditions on trichomonad virulence. We have shown that trichomonad virulence can be affected by persistence in bird baths. This discovery can change our understanding of the role of bird baths and shared water sources in the transmission of *T. gallinae*. By improving our knowledge of the relationship of trichomonad virulence and bird baths, we can suggest strategies to help mitigate outbreaks and decrease transmission.



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205 DETECTION OF HERPESVIRUSES IN WILD BIRD CASUALTIES IN SLOVENIA

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Keywords: Avian, Herpesvirus, PCR, Phylogenetic, Slovenia

Abstract Text

Avian HV have been isolated from diseased as well as healthy appearing but latently infected wild, captive, and domestic birds. Clinical signs are usually nonspecific with general depression of common behavioural traits, however sudden death may be the only sign in many species of birds. The complete host range of HVs in free-living birds is unknown and information about nucleotide sequences are available in limited cases. The aim of the study was to detect the presence of HV in wild birds and to gain more information about their phylogenetic relationship. Oropharyngeal and cloacal swabs of 462 wild birds from 15 different orders presented as wildlife casualties, were examined for HV presence. For the detection of HV's, a nested PCR that target a region of the HV DNA polymerase gene was used. HV was detected in oropharyngeal and/or cloacal swabs in 43 (9.3%) birds. HV was detected in 15 species from six different avian orders: Accipitriformes, Charadriiformes, Columbiformes, Falconiformes, Passeriformes, and Strigiformes. The phylogenetic results show that different HV's sequences are present in free-living bird population and that HV's are related to bird species. However, identical HV sequences were detected in Ural owl (*Strix uralensis*), and in long-eared owl (*Asio otus*), which confirms findings that HV are not always restricted to species specific host. Moreover, it seems that some bird species, such as Eurasian eagle owl (*Bubo bubo*), and common kestrel (*Falco tinnunculus*) are susceptible for infection with different HV's. In this study we report the detection of known as well as novel HV's in different wild bird species. Some of the detected HV's could be prey related, as others could coexist within its bird host, but this should be explored more in future.



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226 SEROLOGICAL INVESTIGATION OF SELECTED VECTOR-BORNE VIRUSES IN MIGRATORY FREE-LIVING PASSERINE BIRDS CAPTURED DURING AUTUMN MIGRATION IN SLOVENIA

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Keywords: Autumn Migration, Passerines, Serology, Slovenia, Vector-Borne Viruses

Abstract Text

Migratory birds are involved in the geographic spread of West Nile virus (WNV), Usutu virus (USUV), Tick borne encephalitis virus (TBEV), and Sindbis virus (SINDV). However, whether birds can transmit the Chikungunya virus (CHIKV) and Zika virus (ZIKV) over long distances is still unknown. In our study, passerine birds were captured with mist nets during autumn migration in 2017 in Slovenia. Each bird was banded and clinically examined. A total of 221 blood samples from 20 different species were collected from the jugular vein and placed in collection tubes (BD Microtainer®). The blood was centrifuged and the separated plasma was stored at -20 °C until analysis. The plasma of the birds was tested for antibodies to WNV, USUV, TBEV, SINV, ZIKV and CHIKV by an indirect immunofluorescence assay (IIF) using anti-bird IgG conjugate (Bethyl Laboratories Inc., Montgomery, TX, USA). No cross-reactivity was observed between antigens in the IIF. Antibodies against WNV, SINV, ZIKV and CHIKV were detected in 2 (0.9 %), 2 (0.9 %), 2 (0.9 %) and 5 (2 %) of 221 passerine birds, respectively. All samples were negative for TBE and USUV. For ZIKV, 2 of 98 (2 %) Eurasian Blackcaps (*Sylvia atricapilla*) were serologically positive. In addition, 2 out of 98 (2 %) Eurasian Blackcaps were positive for WNV and 2 of 98 (2 %) were positive for SINV. Specific antibodies against CHIKV were present in 2 out of 39 (5 %) European Robins (*Eritacus rubecula*), 2 out of 15 (13 %) Great Tits (*Parus major*) and 1 out of 2 (50 %) Red-Backed Shrikes (*Lanius collurio*). We conclude that vector-borne viruses are circulating in migratory passerine birds in Europe. Furthermore, our results support that further efforts should be made to investigate the role of birds in the biology of ZIKV and CHIKV.



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138 LIMITED EVIDENCE FOR DETRIMENTAL EFFECTS OF LEUCOCYTOZOON INFECTIONS AMONG EMPEROR GEESE (*ANSER CANAGICUS*) BREEDING ON THE YUKON-KUSKOKWIM DELTA, ALASKA

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Keywords: Haemosporidian, Mass, Leucocytozoon, Parasite, Survival

Abstract Text

Emperor geese (*Anser canagicus*) have a geographically limited distribution, are subject to subsistence and sport harvest, and have been identified as harboring diverse viruses and parasites associated with avian disease. To better assess if disease represents a vulnerability for emperor geese breeding on the Yukon-Kuskokwim Delta, Alaska, we evaluated if haemosporidian parasites were associated with decreased mass or survival among adult female nesting birds captured during 2006–2016. Through molecular analyses, we detected genetically diverse *Leucocytozoon*, *Haemoproteus*, and *Plasmodium* parasites in 28%, 1%, and 1% of 607 blood samples screened in triplicate, respectively. Using regression analysis, we found evidence for a small but significant effect of *Leucocytozoon* infection on the mass of incubating adult female emperor geese with estimated mass of infected individuals approximately 43 g (95% CI: 20–67 g) less than uninfected birds when captured during the second half of incubation (days 10–25). We did not find support, however, for an effect of *Leucocytozoon* infection on survival of adult female nesting emperor geese using a multi-state hidden Markov framework to analyze mark-resight and recapture data. Through genetic characterization of parasite mitochondrial DNA sequences, we identified 23 haplotypes among infected emperor geese, including *Leucocytozoon* haplotypes that clustered into three phylogenetically supported clades designated as 'L. simondi clade A', 'L. simondi clade B', and 'other *Leucocytozoon*'. We did not find evidence that parasites assigned to any of these clades were associated with differential mass measures among infected adult female nesting emperor geese. Collectively, our results provide limited evidence for *Leucocytozoon* parasites as causing detrimental effects to adult female emperor geese breeding on the Yukon-Kuskokwim Delta. However, our results do not preclude potential effects of haemosporidian parasites to other age/sex cohorts, birds infected with these parasites under adverse ecological conditions, or potential fitness consequences of less common parasite genera and haplotypes.



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109 ADIASPIROMYCOSES IN ALPINE WILD RODENTS FROM PYRENEES, CATALONIA (NORTH-EASTERN SPAIN)

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Keywords: Adiaspiromycosis, *Emmonsia Crecens*, Wild Rodents

Abstract Text

Adiaspiromycoses are non-transmissible infectious pulmonary diseases caused by the inhalation of propagules from thermally dimorphic fungal species belonging to the Ajellomicetaceae family, like *Emmonsia crescens*. *Emmonsia crescens* has a universal distribution, growing as a mycelial saprobic form in soil within a temperature range of 6–30°C, while at 33–39°C its propagules transform into large thick-walled spherical structures called “adiaspores”.

Adiaspiromycoses caused by *E. crescens* have been recorded in 120 species worldwide, spanning 7 mammal orders and 22 families, with small burrowing mammals being considered the main hosts for this environmental pathogen. Since the review on *E. crescens* infections in wildlife by Jaroslav Dvořák and collaborators (1973), only a handful of works on adiaspiromycosis in European wildlife have been published, most of them being case reports of accidental necropsy findings.

The objective of the present study is to assess the presence of adiaspiromycosis in wild rodent populations of high-mountain ecosystems.

We captured and euthanized wild mice (n1=53) and voles (n2=18) in the central Pyrenees (Catalonia, NE Spain) during Autumn 2020, within the framework of the project EFA357/19/INNOTUB. Their lungs were preserved in formaldehyde during field necropsies and later screened by histopathology for the presence of adiaspores. Pulmonary adiaspiromycosis by putative *E. crescens* infection was present in 12.6 % of all individuals (CI95%: [5.63, 21.13] %) corresponding to 16.67 % (CI95%: [0.00, 33.33] %) of voles and 11.32 % (CI95%: [3.77, 20.75]) of mice. These results show that the infection is present in wild rodents from the Spanish Pyrenees, with similar prevalence to that of other continental European countries. Although the impact of this infection on non-endangered species is probably mild, in critically endangered species it might contribute significantly to genetic diversity loss, as illustrated by the death of 1% of wild northern hairy-nosed wombats due to pulmonary adiaspiromycosis in Australia in 2012.



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84 PROTIST DIVERSITY OF CULEX QUINQUEFASCIATUS MOSQUITOES IN GRENADA

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Keywords: Protista, Culex Quinquefasciatus, Metagenomics

Abstract Text

The metagenome of a mosquito consists of three elements: the insect itself, microbes that are part of the mosquito's normal flora, and microbes found in the blood and plant material the mosquito feeds on. Metagenomic studies have revealed that mosquitoes harbor a highly diverse microbiome, comprising those latter two categories. This study analyzed the protist microbiome of *Culex quinquefasciatus*, an abundant mosquito species in Grenada. A total of 300 mosquitoes collected between January 2018 and December 2018 using BG-Sentinel traps from six semi-rural locations in St. George Parish. After RNA extraction, shotgun metagenomic sequencing was conducted using the Illumina HiSeq 1500 deep sequencing platform. The metagenomic analysis showed a distribution of the most significant protist families in decreasing order of abundance as follows: Trypanosomatidae; Albuginaceae; Bodonidae; Plasmodiidae; and Dinophysiaceae. Trypanosomatids are widespread, single-celled, flagellated protozoa, many of which are devastating animal and human parasites; specifically, *Paratrypanosoma confusum* (an insect parasite), *Trypanosomaspp.*, and *Leishmania naiffi* (a causative agent of human mucocutaneous leishmaniasis) were identified here. *Albugo laibachii* (an oomycetous plant pathogen in the Family Albuginaceae) and unidentified microbes in the Bodonidae family (a relative to the parasitic trypanosomes) were also reported in abundance. *Plasmodium relictum*, in particular, is a parasite that is the most common cause of malaria in birds and was found in our analysis; species of *Plasmodium* (Family Plasmodiidae) are distributed globally. Insect hosts are most frequently mosquitoes of the genera *Culex* and *Anopheles*. Vertebrate hosts for *Plasmodium* include reptiles, birds, and mammals, all of which are feed grounds for *Culex*, as demonstrated in our previous studies. *Dinophysis fortii* (Family Dinophysiaceae), a dinoflagellate species responsible for diarrhetic shellfish poisoning, was found as well. Further studies will be needed to determine the source of these protists and their impact in *Culex* life cycle and vectorial capacity.



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78 ASSESSMENT OF URETHRAL CATHETERIZATION FOR SEMEN COLLECTION AND CHARACTERIZATION OF NORMATIVE SEMINAL TRAITS IN WILD OCELOTS (*LEOPARDUS PARDALIS*) AND BOBCATS (*LYNX RUFUS*) IN SOUTH TEXAS

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Keywords: Ocelot, Reproduction, Semen

Abstract Text

Recent studies of wild felid populations have shown loss of genetic variability over time, including in South Texas, where signs of decreased genetic diversity and inbreeding depression have been documented in ocelot populations. Inbreeding depression may cause reduced semen quality of male felids, ultimately decreasing reproductive success. Assisted reproductive techniques (ARTs), including semen collection and analysis, can enable detailed assessments of reproductive traits for individuals and populations, but may require technique modification for practical field use.

Traditionally, semen has been collected via electroejaculation for most feline species. A new method was recently developed using alpha-2 agonists to induce direct sperm release into the urethra, allowing collection by catheterization and decreasing the need for specialized electroejaculation equipment and training. The goal of this study was to assess the effectiveness of urethral catheterization and characterize normative seminal traits of wild ocelot and bobcat populations in South Texas. For semen collection, urethral catheterization was conducted ~30 minutes after medetomidine injection, an alpha-2 agonist, and assessed for percent sperm motility and rate of forward progression, concentration, ejaculate volume, morphology, percent intact acrosomes, and testicular volume.

In the first year, semen collection was attempted with six adult felids (n=3 ocelot; n=3 bobcats). Semen collection was successful in two of three ocelots and two of three bobcats. Overall, ocelots exhibited a greater percentage of normal sperm morphology, progressive motility, and larger testicular volume in comparison to bobcats. However, these parameters were decreased as compared to ocelots managed within zoos, a more genetically diverse population. Future collections will allow for more in-depth assessment of seminal traits and their possible association with inbreeding depression in wild felids. These initial results suggest that urethral catheterization represents a practical method for semen collection in free-ranging wild cats and may facilitate broader application of ART for felid conservation efforts.



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225 OUTBREAKS OF DIGITAL NECROBACILLOSIS IN WILD REINDEER IN NORWAY

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Keywords: Fusobacterium Necrophorum, Necrobacillosis, Pathology, Rangifer Tarandus

Abstract Text

In the last decade, digital necrobacillosis has presented as an emerging disease, with high mortality amongst the wild reindeer (*Rangifer tarandus*) in the fragmented mountain areas of Norway. The disease is also well-known as footrot, and is likely driven by the obligate anaerobe, Gram-negative bacterium *Fusobacterium necrophorum* (FN). Today, digital necrobacillosis has been diagnosed in nine of the 24 wild reindeer management areas, and in 2019 there were large disease outbreaks in several of these areas. The losses were large, and especially among calves. Warmer and wetter climate, narrowing of habitats and hence more contact between individuals in the herds have been proposed as contributing factors as to why the infection spreads. However, much is unknown regarding the time of infection, which factors that are required for infection and whether or not infected animals can heal.

The bacterium is believed to enter the skin through abrasions or wounds, and causes a purulent dermatitis that often involves deeper structures like joints, tendons and bone, which is unlikely to heal. Consequently, animals end up severely lame and struggle to follow the gregarious herd. If the reindeer survive the initial phase, they may develop chronic tendinitis, arthritis and osteomyelitis.

We have examined reindeer legs with suspected digital necrobacillosis submitted to The Norwegian Veterinary Institute by hunters after the annual reindeer hunt in the autumn. In addition, wildlife managers from the Norwegian Nature Inspectorate have culled severely afflicted animals outside of the hunting season due to welfare reasons. Our study shows that a majority of the legs have lesions consistent with digital necrobacillosis. The pathological lesions have been described, and bacterial isolates of FN were acquired for further analysis. In addition, X-rays of affected legs have made it possible to examine the pathological changes in greater detail. Preliminary results will be presented.



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53 OVERVIEW OF POST-MORTEM LESIONS IN FREE-RANGING RED FOXES (*VULPES VULPES*) IN NORTHERN BELGIUM IN 2018-2020

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Keywords: Disease Surveillance, Red Fox, Necropsy, Rabies, Flanders

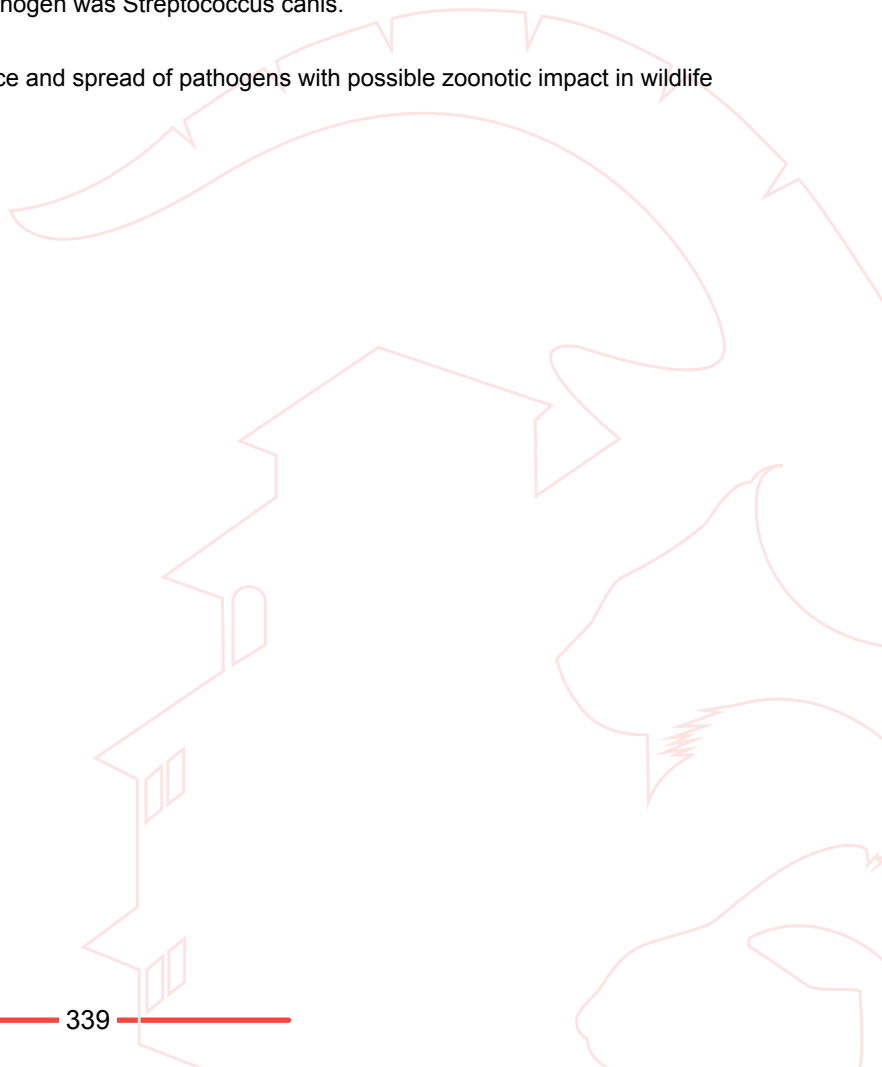
Abstract Text

In northern Belgium (i.e. Flanders) a spectacular increase occurred in the distribution and density of the Red fox in the period 1980-2000. This resulted in the presence of foxes over the whole territory of Flanders (Vervaeke et al., 2003). Since foxes may be infected by Rabies lyssavirus, *Echinococcus multilocularis*, *Trichinella spiralis*, and other pathogens with possible zoonotic impact, the Agency for Nature and Forests performs a disease surveillance in the Red fox population in northern Belgium. This surveillance is conducted in cooperation with DGZ, Sciensano, hunting associations and Wildlife rescue centres.

This study reports a retrospective analysis of the necropsy data of red foxes in northern Belgium with an overview of the causes of mortality and detection of pathogens.

From July 2018 until December 2020, fifty-six dead foxes were collected in northern Belgium as found dead animals without visible death cause (i.e. no signs of hunting or road casualty). The carcasses were admitted for necropsy, rabies screening and histopathological analysis. The most common lesions visible on necropsy included pneumonia, hemothorax, hemo-abdomen and pulmonary helminth infestation. All foxes tested negative for the Rabies lyssavirus. Non-infectious conditions were also common and included suspected coumarin intoxication, fractures related to trauma and rarely a metabolic disorder (chronic kidney disease). One animal died due to starvation and another due to suspected drowning. The most common isolated pathogen was *Streptococcus canis*.

This study contributes to the knowledge of occurrence and spread of pathogens with possible zoonotic impact in wildlife populations in Belgium.





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112 ASSESSING THE EURASIAN OTTER (*LUTRA LUTRA*) POPULATION HEALTH IN SCHLESWIG-HOLSTEIN, GERMANY – PRELIMINARY RESULTS FROM 2015-20

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Keywords: Eurasian Otter, Monitoring, Population, Health, Necropsy

Abstract Text

The Eurasian otter (*Lutra lutra*) population in Germany is currently recovering from serious declines in the past century. Numbers are rising and strictly protected otters are recapturing former habitat especially in northern and eastern Federal states, such as Schleswig-Holstein. Growing numbers of otters also indicate more human wildlife conflicts, e.g. with local fisheries, as roadkill accidents, via infectious diseases etc. Therefore, it is essential to investigate the health status of Schleswig-Holstein's otter population in the light of future management options. Systematic health investigations have been conducted since 2019 in order to establish a monitoring program.

All otters found dead were collected by a diverse network of collaborators and were brought to the ITAW in BÜsum. All carcasses underwent standardized necropsies following a specific protocol, including assessment of biometric data. Various organ samples were collected for a tissue bank and cementum ageing was performed. Further, histological, bacteriological, virological and parasitological investigations are ongoing.

A total of 92 otters from the years 2015-2020 were dissected. Finding locations concentrated along the Continental region. Males (n=53) dominated over females (n=38) and most otters were younger than 3,5 years. Most otters displayed a good nutritional status. Pathogens detected so far include amongst others various Streptococci, Clostridium perfringens, Vagococcus lutrae, ticks, Sarcocystis lutrae, Corynosoma spp., further data is still pending. Four males displayed nephrolithiasis or urolithiasis. Placental scars occurred in four females, another was pregnant. 14 males displayed cysts on the vas deferens.

The major causes of death was roadkill (n=74), besides unclear cause (n=12) and disease or other (n=5). Our findings are similar to other European studies on otters and represent a population with male bias and so far few infectious diseases. Further investigations on contaminant loads and related pathologies need to be conducted to get full insight into the health status of the population.



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179 MOLECULAR IDENTIFICATION OF BOT FLIES (*CUTEREBRA BAERI*) INFESTING GREY-LEGGED NIGHT MONKEYS (*AOTUS GRISEIMEMBRA*) AND HOWLER MONKEYS (*ALOUATTA SENICULUS*) IN COLOMBIA

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Keywords: Alouatta, Aotus, Bot Flies, Colombia, Cuterebra

Abstract Text

Myiasis is a neglected parasitosis caused by infection with the larval stages of some fly species. In neotropical non-human primates (NHP) three bot fly species causing cutaneous myiasis have been reported: *Cuterebra baeri* in *Alouatta belzebul*, *Aotus trivirgatus*, *Alouatta seniculus*, and *Alouatta palliata* (Guimarães, 1971; De Thoisy et al. 2001; Cristobal-Azkarate et al. 2012), *Cochliomyia hominivorax* in *A. seniculus* and *Pithecia pithecia* (Vie & Richard-Hansen, 1997), and *Dermatobia hominis* in *A. palliata* and *Saguinus mystax* (Smith, 1977; Herrera & Heyman, 1998), along with *Dermatobia* sp. parasitizing *Aotus* sp. (Tantalean et al. 1990). Studies on myiasis in NHP are scarce and mainly based on larval morphological identification, while molecular approaches have been barely used. In Colombia, *Cuterebra* sp. has been morphologically identified in *Aotus vociferans* and *Aotus nancymae*, in the Amazon region (Roncancio et al. 2018). This study aimed to molecularly identify bot flies parasitizing two free-ranging primate species living sympatrically in central Colombia.

Sampling was conducted in a lowland rainforest fragment in Santander, Colombia. Four bot fly larvae were collected from two grey-legged night monkeys (*Aotus griseimembra*) and one from a howler monkey (*Alouatta seniculus*). Larvae were measured and photographed, and subsequent DNA extraction and PCR amplification of a partial *cox1* mitochondrial region were performed (Cavallero et al. 2017). All PCR products were visualized on an agarose gel and good quality amplicons were sequenced. Sequences were manually edited and used for BLAST search and alignment.

All specimens were identified as *Cuterebra baeri*, according to the best match in BLAST showing 98% of identity (accession number AF497777 corresponding to specimens characterized in monkeys from Panama, Otranto et al. 2003). This is the first molecular identification of bot flies infesting NHP in Colombia, and the first record at the species level for *A. seniculus* and *A. griseimembra* in the country.



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43 A FOCUS ON TEN YEARS OF WILDLIFE SURVEILLANCE IN EMILIA-ROMAGNA REGION (ITALY)

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Keywords: Surveillance, Wild Animals, Trichinella, Wild Boar, Fox

Abstract Text

In recent years, wildlife surveillance has received growing attention worldwide, due to the increased awareness of its role in zoonotic and livestock infections.

Since 2010 the Italian region Emilia Romagna (RER) has applied a specific plan for wildlife health surveillance, in order to early detect the introduction of notifiable and zoonotic diseases, some of which may have a serious economic impact. The plan consists of a passive and an active surveillance system.

In this work, we share the last decade of surveillance data on Trichinellosis, Brucellosis, African and Classical Swine Fever (ASF and CSF), Aujeszky's disease (AD) and Swine Vesicular Disease (SVD), recorded in RER.

Trichinella sp. was searched for in shot foxes, in found-dead wolves and mustelids, which are considered targeted species. All the hunted wild boars were also examined, as they represent a hazard for the Public Health.

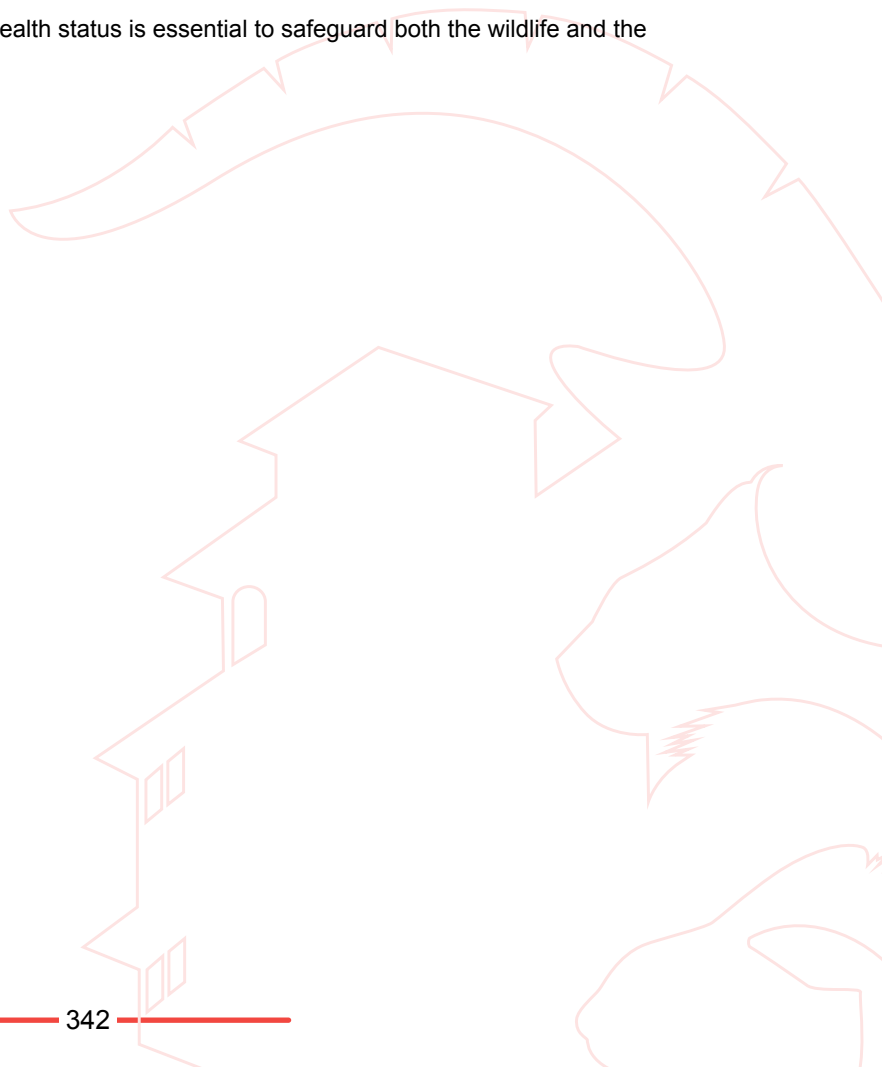
Since 2010, only 14 animals out of 179.171 examined, scored positive for Trichinella spp.: *T. britovi* was detected in 5 foxes, 3 wolves, and 2 wild boars; *T. pseudospiralis* was detected in one wild boar. For the first time in Italian wildlife, *T. spiralis* was found in 3 foxes. Trichinella sp. has never been found in domestic pigs.

Brucella strains, all serotyped as *B. suis*, were isolated from 41 out of the 7.294 examined wild boars.

From 2010, ASF, SVD or CSF have never been detected in the wild boar population.

Within the last decade, every year about 30% of the examined wild boars scored seropositive for AD, unlike the domestic pigs, in which the herd prevalence decreased from 15% to less than 1%, suggesting a segregation of the two populations.

Our results show that a monitoring of wild animals' health status is essential to safeguard both the wildlife and the livestock.





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42 USUTU VIRUS SURVEILLANCE IN WILD BIRDS OF EMILIA-ROMAGNA REGION, NORTH ITALY

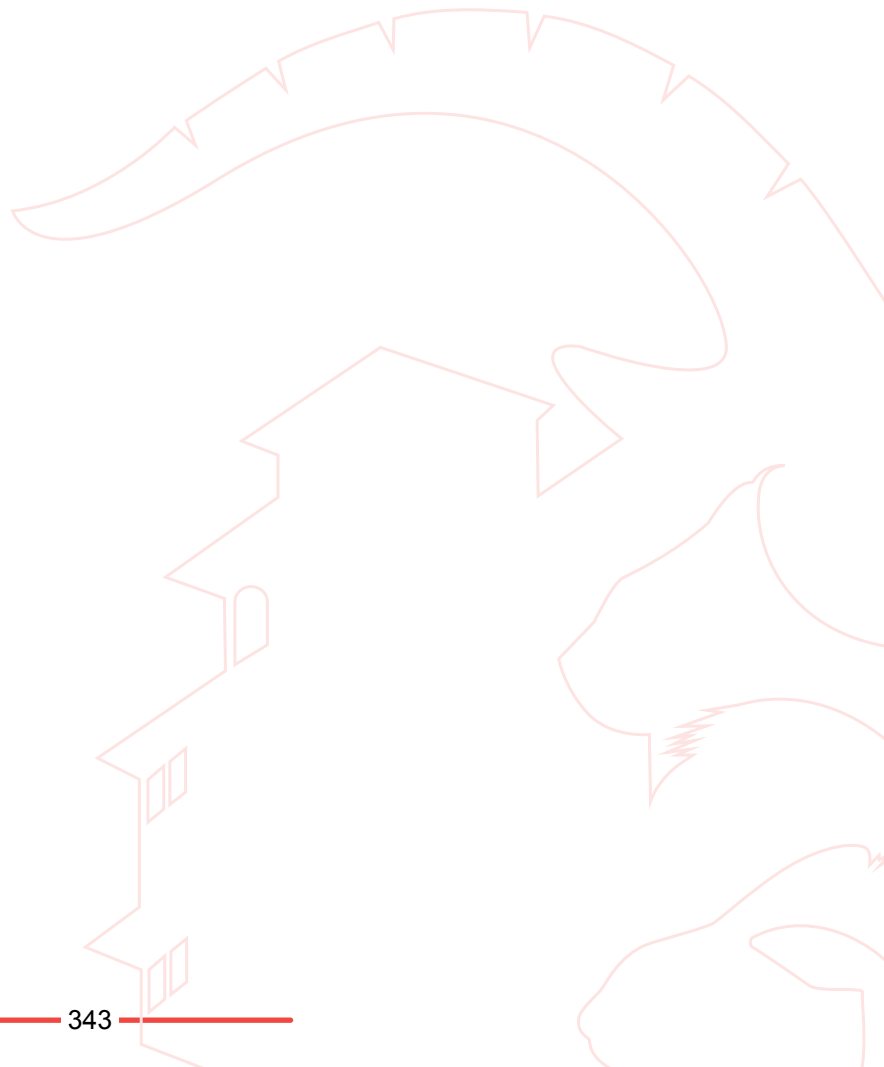
Alessandra Lauriano, Annalisa Santi, Paolo Bonilauri, Elena Carra, Arianna Rossi, Gabriele Casadei, Giorgio Galletti, Marco Tamba

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Keywords: Usutu Virus, Integrated Surveillance, Wild Birds, Reservoir.

Abstract Text

Usutu virus (USUV) is a zoonotic Flavivirus closely related to West Nile virus (WNV). Its life cycle involves ornitophilic mosquitoes as vectors and sylvatic birds as amplifying hosts. Humans and horses may act as accidental hosts. USUV and WNV undergo surveillance programs in endemic areas, in order to reduce their risk of transmission to humans. The Italian National Integrated Surveillance for West Nile and Usutu viruses combines entomological, veterinary and human surveys. The National program is adapted to the local situation by the Regional Authorities. In Emilia-Romagna, Northern Italy, the Regional Surveillance program specifies that the entomological survey consists of the partitioning of the region in 11x11 Km-quadrants where mosquito CO₂-baited traps are homogeneously distributed. The veterinary survey consists of an active and a passive sampling of targeted bird species (Passeriformes, Strigiformes, Caradriformes, Ciconiformes, Falconiformes) during the period of mosquito vectors activity (May-October). Both these surveys concurrently follow a biweekly calendar. Entomological and veterinary samples are processed in order to detect the presence of WNV and/or USUV by PCR. In this study, we report the results of the surveillance carried out on wild birds from 2013 to 2019. A total of 15,731 birds were sampled: 11,504 within the active and 3,867 within the passive surveillance. We detected 336 (2.1%) positive samples, of which 125 (1.1%) and 211 (5.5%) from the active and the passive surveillance, respectively. The results show that USUV has been circulating from 2013 to 2019 in the survey area within the wild birds population and is frequently detected in dead birds. The highest prevalence was recorded in August. However, we also found that birds tested positive in months when vectors are not active suggesting a possible role as virus reservoir.





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106 PERSECUTION OF BIRDS OF PREY IN FLANDERS BETWEEN 2011-2019: A RETROSPECTIVE STUDY

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Keywords: Birds Of Prey, Illegal Killing, Intoxication

Abstract Text

For decades birds of prey have been under the protection of European law, but deliberate or unintentional killing is still a large scale problem in Europe.

In an effort to monitor illegal practices in Belgium, the Agency of Nature and Forests (ANF) of the Flemish government established several bird of prey hotlines in 2006. Whenever a suspicious dead bird of prey is encountered by the general public, foresters and inspectors of the ANF through passive surveillance, the carcass is necropsied to assess whether the death is from an illegal cause.

If shooting was suspected, carcasses were screened for the presence of metallic objects and accompanying lesions using radiographic images. If intoxication was suspected, samples were further sent for toxicological investigation. The presence of cholinesterase inhibitors, strychnine, anticoagulants was investigated qualitatively.

In total, 315 birds of prey, of which 260 were common buzzards, were collected between January 2011 and December 2019. As the ANF occasionally collected more than one bird at the same location, these 315 birds were comprised in 226 suspicious mortality events. In 36.7% (83/226) of all mortality events, an illegal cause of death was found, with poisoning being demonstrated in 32.3% (73/226), shooting in 4% (9/226) and entrapment 0.01% (2/226) of all cases. Cholinesterase inhibitors were the most commonly used toxins, being detected in 84.9% of the toxicological cases. With 116 individual, common buzzards were the species most involved in illegal practices.

In conclusion, birds of prey are still frequent victims of illegal practices, with the common buzzard having the highest number of individuals being killed through illegal practices. Whenever the presence of toxins was demonstrated, cholinesterase-inhibitors were the most commonly used toxic substances.



86 MONITORING OF ALOPECIA IN WILD CARNIVORES USING CAMERA-TRAPPING: INSIGHTS FOR THE STUDY OF SARCOPTIC MANGE

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Keywords: Camera-Trapping, Canis Lupus, Iberian Peninsula, Sarcoptic Mange, Vulpes Vulpes

Abstract Text

Sarcoptes scabiei mite is the aetiological agent of sarcoptic mange, an infectious and contagious disease characterized by skin lesions, like alopecia and crusts. Non-invasive diagnosis and monitoring of this zoonosis are particularly valuable in wildlife. Photographic detection methods, such as camera-trapping, can be applied to identify mange-compatible lesions, and for investigating the dynamics of the disease and related behavioural modifications. We aimed to study sarcoptic mange epidemiology in two species of wild canids by using camera-traps to identify seasonal patterns in prevalence and differences in the activity of alopecic animals.

Camera-traps were distributed over ~40 km² in Northwestern Portugal, between May 2018 and October 2019. All photographic records were analysed for the presence of the target species (Iberian wolf *Canis lupus signatus* and red fox *Vulpes vulpes*), number of individuals detected, and number of alopecic individuals. Altogether, 518 detections of the target species were obtained, of which 441 were classifiable, allowing the inspection for alopecic lesions. Variable degrees of alopecic lesions were shown in 15% (IC95% 8.8-25.3%; N=72) of wolf detections and in 9% (IC95% 6.4-12.3%; N=369) of fox detections. Higher proportions of detections of alopecic animals were observed from February to July, ranging from 11.8% to 27.3%, with a peak in April. The alopecic wolves tended to be more active than the non-allopecic ones (difference=0.16, p=0.21), whereas in the foxes the opposite was observed (difference=-0.06, p=0.58), although non-significantly in both species. The activity pattern of the alopecic animals was uniform throughout the day (significantly on foxes, p<0.05), demonstrating a tendency to be more diurnal compared to non-allopecic conspecifics.

This non-invasive method has potential in studying the epidemiology and activity pattern of mange-infected animals. However, it cannot identify the aetiology of skin lesions, and mild cases of mange may be undetected, therefore future research assessing its performance is needed.



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338 SPATIAL REPRESENTATION OF THE INTERFACES BETWEEN WILD AND DOMESTIC UNGULATES IN SPAIN: POTENTIAL USE FOR THE CONTROL OF SHARED DISEASES

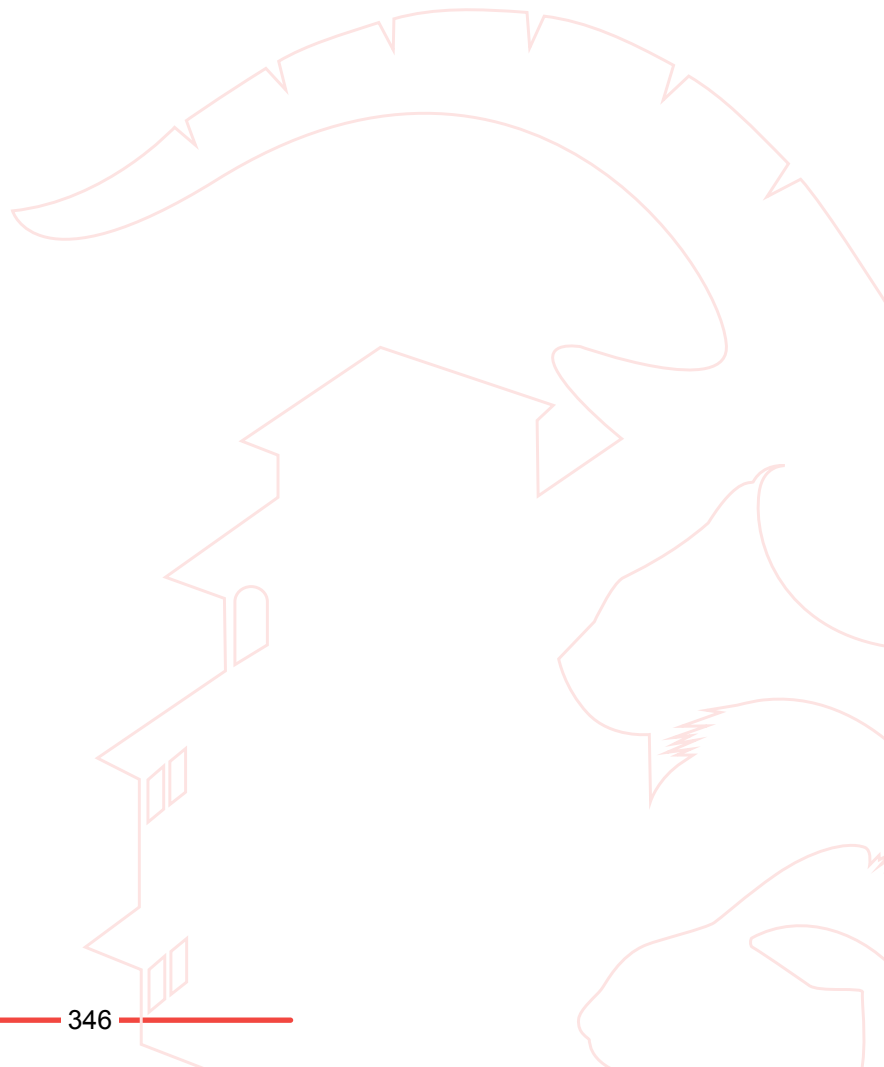
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Keywords: Wild Ungulates, Spatial Modelling, Shared Diseases, Risk Analyses

Abstract Text

Wildlife is nowadays one of the most important elements in animal health surveillance. Monitoring of diseases affecting wildlife is essential at the wildlife/livestock interface areas, where there can be a high risk of pathogen transmission between compartments. This interface is an essential interplay among host species where disease spill-over is largely under-reported, often even zoonosis. Large-scale data availability on wildlife and livestock distribution and abundance may help to depict the interface, and to describe different scenarios to evaluate broad-scale risks associated to disease spread and maintenance at such interface. To date, Spain has a wildlife disease surveillance plan based on the sampling of different wildlife species and diagnosis of diseases of interest. However, the so-called denominator information (population data) is not always available to interpret wildlife disease surveillance data, so as to evaluate the risks of disease transmission at the interface with wild ungulates. We used high-resolution data on wild ungulates (hunting ground level) and livestock farms (discriminating farming systems, i.e., intensive indoor vs extensive outdoor) to depict the interface (areas of maximum spatial overlapping of respective abundances) between wild ungulates and livestock in Spain mainland. We describe the observed patterns, discuss the different scenarios and the potential application of this broad-scale approach to evaluate and control risks at the interface. This study evidences the need for better, harmonized and standardized data in both the wild and domestic compartments, for which we propose future steps in data collection.





340 ORAL YEASTS AND LESIONS IN CINEREOUS VULTURE (*AEGYPIUS MONACHUS*) NESTLINGS: RISK FACTORS AND IMPORTANCE

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Keywords: Cinereous Vulture, Oral Lesions, Oral Yeasts, Antibiotics, Supplementary Feeding

Abstract Text

Vultures as obligate scavengers provide important ecosystem services through the removal of carcasses. Many vulture populations are threatened and for species like the cinereous vulture, catalogued vulnerable by the IUCN, Spain with 90% of European vulture populations is the remaining stronghold. While use of livestock carcasses as supplementary food supply in “vulture restaurants” is controversial, locally cinereous vultures have also started to exploit solid urban residue landfills due to a human-induced decline in naturally available food in the past. Both could expose vultures to residues of toxic substances or antibiotics that could have negative effects on the vulture’s digestive tract microbiota.

Here we investigate the prevalence, importance, cause, and risk factors of oral lesions in cinereous vulture nestlings from a large colony in a protected area, the adults of which, at least occasionally forage on a landfill. We registered presence and number of lesions, cultured oral yeasts, and tested the presence of antibiotic residues and vitamins in plasma from nestlings.

While 89% of the nestlings had oral yeasts, only 31.9% had compatible lesions. Yeasts most frequently detected were: *Candida albicans*, *Rhodotorula mucilaginosa*, *Lodderomyces elongisporus* and *Candida catenulata*. Presence of oral lesions did not affect body condition of the nestlings; residues of commonly used antibiotics were absent in the plasma of the nestlings and the detection of lesions was not related to the presence of a specific yeast. Tendencies of slightly higher prevalence of *Rhodotorula mucilaginosa* and reduced plasma Lutein/Zeaxanthin were detected but not statistically significant. However, nestlings with oral lesions had a less diverse community of oral yeasts than those with no lesions. The latter suggests that changes in the oral microbiota could favour the appearance of lesions, albeit risk factors are yet to be found. Also, oral lesions seem not to pose a significant problem to the nestlings.



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279 A PRELIMINARY STUDY OF VIRAL AND BACTERIAL PATHOGENS PRESENT IN SPANISH BATS: IDENTIFICATION OF NEW TICK-BORNE PATHOGEN GENETIC VARIANTS.

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Keywords: Bats, Coronavirus, Nairovirus, Rickettsiales, Tick-Borne Pathogens

Abstract Text

Chiroptera order is one of the most abundant, diverse, and widespread groups of mammals, comprising about 1,200 species and representing almost 25% of the class Mammalia. Thirty-five species for this order are autochthonous of Iberian Peninsula. In recent years, bats have been of particular interest not only for their ecological interest, but also for public health reasons, as they are considered to play an important role in the emergence and transmission of zoonotic agents. In fact, these animals act as a natural reservoir for a wide range of pathogens. Twenty-two species were sampled and analysed in this study, collecting oral swabs and blood samples from four different regions of Spain. The study focused on detection and identification of pathogens belonging to virus families Coronaviridae and Nairoviridae (Crimean Congo Hemorrhagic Fever virus, CCHFv), and to the bacterial orders Rickettsiales and Piroplasmida. These groups, *Rickettsia* spp., *Anaplasma* spp., *Babesia* spp., *Theileria* spp. and Nairovirus, are tick-borne pathogens and, along with Coronavirus, are pathogens causing relevant emerging diseases for the human and wild/domestic animals. Amplification of the different genetic markers for *Rickettsia* spp. (16S rRNA, OmpA, OmpB, AtpA, GltA and RecA genes), *Anaplasma* spp. (16S rRNA, RpoB, GltA and Msp5 genes), and *Babesia/Theileria* spp. (18S rRNA gene) was carried out by conventional PCR, whereas Nairovirus (S segment of CCHFv) were analysed by a nested RT-PCR. A generic qRT-PCR and a specific qRT-PCR for SARS-CoV-2 designed by CDC were used to identify different coronavirus. The study detected positive samples for Nairovirus (CCHFv), Coronavirus (universal RT-PCR for the genus Coronavirus), *Anaplasma phagocytophilum* and *Babesia vesperuginis*.



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341 ANAPLASMA AND PIROPLASM CO-INFECTION IN SMALL RUMINANTS FROM PORTUGAL

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Keywords: Anaplasma, Domestic Animals, Theileria, Tick-Borne Pathogens, Wild Animals

Abstract Text

The incidence and the range of tick-borne diseases is increasing worldwide, affecting wild and domestic animals, and humans. This work aims to evaluate the prevalence of tick-borne pathogens, in particular, bacteria belonging to genus *Anaplasma* and protists to order Piroplasmida and know the presence of animal co-infection by both pathogens and how they could be shared between wildlife and domestic animals. To achieve this proposal, the study included ticks collected from wild animals, such as red deer (*Cervus elaphus*), mouflons (*Ovis musimon*) and fallow deer (*Dama dama*) from two regions (Cáceres and Badajoz) of Spain near the border with Portugal, and blood samples collected from domestic hosts, sheep (*Ovis aries*) and goats (*Capra hircus*), from regions in Portoalegre (Portugal) close to the border with Spain, originating from farms with various production systems and breeds. The identification and characterization at species level was carried out by molecular diagnosis and phylogenetic analysis of obtained sequences to reach a consensus.

A total of 290 blood samples from 180 sheep and 110 goats, and 178 *Hyalomma lusitanicum* ticks collected from red deer, mouflons and fallow deer were analysed. Samples were tested with different primer sets. *Anaplasma* identification and characterization was analysed using 16SrRNA and molecular markers for specific genes, and Piroplasmida identification was carried out targeting 18SrRNA gene. The results showed a coinfection prevalence of 11% in domestic animals and 14% in ticks collected from wildlife. Some of the tick-borne pathogen species detected in co-infection were present in both domestic and ticks from wild animals.

Findings indicate the presence of these zoonotic pathogens both in the domestic and wild host sampled, and the sharing among them possibly due to vectors such as ticks. The results show new genetic variants, so suitable surveillance and further analyses of other hosts and areas are required.



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352 SELECTION OF SAMPLES TO DETERMINE THE PREVALENCE OF SALMONELLA SPP. IN FREE-LIVING TRACHEMYS SCRIPTA TURTLES

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Keywords: Prevalence, Salmonella Spp., Sampling, Trachemys Scripta,

Abstract Text

Trachemys scripta is an invasive species that has been established in wet areas along the Valencian Community. Its presence supposes an important risk for endangered native turtles, such as Spanish pond turtle *Mauremys leprosa* and European pond turtle *Emys orbicularis*, not only by competition for trophic resources but also by pathogen transmission. Stands out for its importance *Salmonella* genus, a zoonotic bacteria which foreign aquatic turtles can act as a reservoir in the wild.

The objective of this study was to determine the prevalence of *Salmonella* spp. in free-living *Trachemys scripta* turtles in the Valencian Community comparing two sources of samples, cloacal swab and intestinal fragment.

A total of 68 turtles trapped by local authorities were sampled taking two samples of each one, a cloacal swab and a fragment of the intestine, making a total of 136 samples. Following the recommendations of the UNE-EN ISO 6579 Standard, the pre-enriched samples were inoculated in the Rappaport- Vassiliadis semi-solid medium (MSRV). Positive cultures were grown on XLD Agar. Black colonies, suspicious for positive, were transferred to Chromogenic Agar specific to *Salmonella* spp. to confirm the positive.

The global prevalence of *Salmonella* spp. in introduced turtles was 58,8% (40/68). Of the 40 positive animals, the bacteria was isolated from cloacal samples in 87,5% (35/40) of the cases whereas 60% (24/40) were isolated from the intestinal samples. The pathogen was isolated from both samples only in 47,5% of the positive animals (19/40). The differences in the results between both samples were statistically significant ($p < 0.05$), with a weak correlation between both samples ($\kappa = 0.388$).

Cloacal swabs are a good sampling option to monitor the presence of *Salmonella* in wild populations of *Trachemys scripta*, as they can be a major problem for Public Health.



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55 NORTH AMERICAN CO-INVADERS? SEROVARS OF *SALMONELLA ENTERICA* CARRIED BY THE INVASIVE CALIFORNIA KINGSNAKE (*LAMPROPELTIS CALIFORNIAE*) IN GRAN CANARIA, SPAIN

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Keywords: Invasive Species, Salmonella, Zoonoses

Abstract Text

Invasive species not only present a threat to biodiversity, but also humans, as they can carry important zoonotic pathogens such as *Salmonella* spp. The California kingsnake (*Lampropeltis californiae*) has emerged as a serious pest in Gran Canaria with thousands of snakes captured annually as part of an eradication program. The reptiles are reported entering houses on a near daily basis, making the wildlife-human interface, either accidentally or via workers of the control program, as close as its pet trade origin. Non-typhoidal salmonellosis has emerged as an important neglected tropical disease. Clusters of cases of systemic illness, mainly in children and immunosuppressed individuals dictates an urgent need to understand the presence of zoonotic pathogens to better inform preventive measures.

In 2019, 72 faecal samples collected from 36 apparently healthy snakes, corresponding to two periods (June (A) and October (B)), were investigated for *Salmonella* spp. *Salmonella* strains were isolated and identified using conventional culture methods and biochemical tests. Serotypes were determined by the National Reference Laboratory of Animal Health (Algete, Madrid, Spain).

Seven serotypes of *Salmonella enterica* were identified in 15/72 samples. All positive samples were from group B (October). These serotypes are the first to be described in the California kingsnake, as well as new serotypes for the Canary Islands. None of the serotypes previously isolated from the endemic reptile (*Gallotia stehlini*) were found in the snakes, suggesting its foreign nature, and little cross infection between reptile species. More variables should be evaluated to understand the relevance of the difference between the two sampling periods. The current epidemiological situation of *Salmonella* cases in Gran Canaria needs to be updated, to enlighten the actual role of these animals in non-typhoidal cases of human salmonellosis.



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56 COPROLOGICAL APPROACH TO PARASITES OF THE CALIFORNIA KINGSLAKE (*LAMPROPELTIS CALIFORNIAE*); AN INVASIVE SPECIES IN GRAN CANARIA, SPAIN

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Keywords: Invasive Species, Macaronesia, Snake, Parasitology.

Abstract Text

The worldwide demand for novel, more exotic species of companion animal has also led to growth in the illegal release of invasive species into non-native ecosystems. Whilst the animals themselves can cause significant imbalances to biodiversity, the pathogens they can carry to their new habitats are less well documented. The California kingsnake (*Lampropeltis californiae*), native to south-western North America, has emerged as a significant ecological problem on the island of Gran Canaria, Spain, and its control has proved challenging. The snake preys on endemic reptile species and current data supports the threat of extinction for some of these animals.

Between 2016 and 2020, in order to assess the possible introduction of foreign parasites which could pose an additional risk to local biodiversity, faecal samples from this snake species were analysed at the Laboratory of Parasitology, Faculty of Veterinary Sciences, University of Las Palmas de Gran Canaria. Faeces extracted from dead and frozen animals (A) were tested using NaCl flotation and formol-ether sedimentation, and freshly collected material from live snakes (B) with sugar centrifugal flotation.

In total, 118 samples were analysed, with true parasites identified in only three snakes (2.5%): *Serpentirhabdias* sp., *Eimeria lampropeltis* and *Caryospora* sp., one in each of three samples (0.8% each). Parasites from the snakes prey species were also present, including disrupted eggs of oxiurids (5.1%), tapeworms (2.5%) and *Adelina tribolii* (3.4%). *Sarcocystis* sp. were also found in eight animals (6.8%), but due the poor state of preservation, it was not possible to determine if they were proper parasites, or those from prey.

This is the first report of *Adelina tribolii* (coccidia from beetles) in the Canary Islands. No known zoonotic or parasites important to ecosystem conservation were found in the faeces, however this needs to be further monitored through ongoing post-mortem and coprological examinations.



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57 A POTENTIAL CONSERVATION THREAT TO MACARONESIAN RAPTORS: FIRST DOCUMENTED CASE OF FATAL VIRAL HEPATITIS IN A CANARY ISLANDS KESTREL (*FALCO TINNUNCULUS CANARIENSIS*).

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Keywords: Canary Islands, Herpesvirus, Kestrel, Parasitology.

Abstract Text

The Canary Islands kestrel (*Falco tinnulculus canariensis*) is an endemic subspecies of the common kestrel, found only in the western Canary Islands (Spain) and Madeira (Portugal). It has a varied diet based on birds, micromammals, small lizards and insects. Whilst threats to kestrels from human activity are well documented, information on natural infections and associated pathologies in this subspecies are poorly understood.

A young female Canary Islands kestrel (*Falco tinnulculus canariensis*) was found dead in the field and submitted to the Parasitology Laboratory of the Faculty of Veterinary Sciences of the University of Las Palmas de Gran Canaria for post-mortem and parasitological examination. The animal was heavily infested with mites (*Ornithonyssus bursa*) and with severe multifocal necrotizing hepatosplenitis with large intranuclear eosinophilic inclusion bodies. Other parasites were found in the upper digestive tract (adults and larvae of *Synhimantus (Dispharynx) nasuta*) and the intestine (*Centrorhynchus* sp. and *Caryospora falconis*). Lice were also recorded (*Degeeriella fusca*). These findings were typical of Falcon Inclusion Body disease, previously unreported in the Canary Islands and only the second record in Spanish raptors. Further molecular work is being performed to confirm the herpesviral ethiology (Columbid herpesvirus-1 (CoHV-1))

Currently, the virulence and epidemiology of CoHV-1 in birds of prey is not fully understood. Antibodies to this virus have been found in different raptors with low prevalence, which suggests an underestimation of the disease, as experimental infection almost always leads to sudden death. The finding of a presumed fatal herpesviral infection in an endemic raptor suggests a potential threat to the conservation of several endangered Macaronesian raptors. Surveillance of suitable subclinical and asymptomatic hosts should be performed to further understand this potential threat.

This communication also constitutes the first report of parasites from kestrels in Canary Islands



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58 SUBCUTANEOUS MITES FROM AN ENDEMIC LAUREL PIGEON (*COLUMBA JUNONIAE*), AN ENDANGERED REINTRODUCED SPECIES IN GRAN CANARIA, SPAIN

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Keywords: Acari, Endemic Species, Molecular Biology, Parasitology.

Abstract Text

The laurel pigeon (*Columba junoniae*) is one of the two endemic species of columbids that inhabit the Canary Islands. Destruction of its unique laurel forest (*laurisilva*) habitat and predation by feral cats and rats led to the bird's extinction on Gran Canaria. However, thanks to a captive breeding program, it has been successfully reintroduced to areas of replanted and protected laurel forest on the island.

In June 2019, a laurel pigeon was brought to the Laboratory of Parasitology, Faculty of Veterinary Sciences, University of Las Palmas de Gran Canaria for post-mortem examination. Examination revealed multiple fractures of both femurs and tibiotarsi, necrotizing hepatitis and suppurative pneumonia, with septic shock the likely cause of death. Tiny (1-2mm) "rice-shaped" white structures were noted in the connective tissue and subcutis over the pectoral muscles and were identified as nymphal stages of *Hypodectes propus* (Acarina: Hypoderatidae). A 240 bp fragment of the ribosomal DNA was amplified by PCR and sequenced. BLAST analyses showed 92.04% identify with *Hypodectes* sp. (GenBank n° JQ000124).

The taxonomy of the parasite is based on the morphology of immature stages, hence molecular methods should be used to determine if laurel pigeons and other known hosts carry their own endemic species of mites, as has been shown for other endemic bird species of the Canary Islands. Indeed, given the endangered nature of the laurel pigeon a greater understanding of the role of the mite as a possible threat to re-introduction programs is required.

This constitutes the first record of *Hypodectes propus* in Spain, and a new host species for this mite.



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59 A PASSENGER FROM A LONG-DISTANCE TRAVELER? STORY OF LUTZTREMA ATTENUATUM (DIGENEA: DICROCOELIIDAE) CARRIED BY A BLACKBIRD (TURDUS MERULA).

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Keywords: Migratory Birds, Trematoda, Veterinary Pathology.

Abstract Text

The life cycle and associated pathology of liver fluke infestation in livestock and humans are well characterised, unlike those from birds where even accurate taxonomical positioning of many species remains uncertain. Furthermore, no detailed descriptions of the possible role of these parasites as a cause of death in passerines are available.

In July 2019, a young male blackbird (*Turdus merula*) which died naturally while at the Wildlife Recovery Center of Tafira, Gran Canaria was submitted to the Laboratory of Parasitology of the Faculty of Veterinary Sciences of the University of Las Palmas de Gran Canaria, for post-mortem and parasitological examination. Death was most likely due to multiple cerebral infarctions caused by emboli of gram-negative bacteria. The source of the bacteria was presumed to be pneumonia and fibrino-suppurative pleuritis in the left lung, which extended to the intercostal muscles and subcutaneous space. Although penetrating injury was thought a likely aetiology, no obvious fractures or scarring were found. Histopathological examination of the liver revealed intraductal trematodes with haematin and abundant cellular debris. The walls of the ducts were enlarged and mildly fibrotic. The flukes were identified as *Lutztrema attenuatum*.

As *L. attenuatum* has not been previously identified in Spain, its presence in a bird in the Canary Islands raises the question of the origin of this blackbird. Blackbirds migrate from northern and western Europe to winter in southern Europe and North Africa, and it is well recognized that small numbers overwinter in the Canary Islands. *L. attenuatum* has a wide distribution in central Europe, and the finding of this parasite in a blackbird from Gran Canaria suggest migratory passerine birds may act as vectors of exotic parasites to the islands to which endemic species may have little resistance. Further studies on parasites in native/endemic passerines is warranted.



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104 LONG-TERM DETERMINANTS OF THE SEROPREVALENCE OF THE BLUETONGUE VIRUS IN DEER SPECIES IN SOUTHERN SPAIN

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Keywords: Vector-Borne Diseases, FAST Diseases, Doñana National Park, Deer, Shared Infection

Abstract Text

Bluetongue is a vector-borne disease affecting domestic and wild ruminants, with a major socioeconomic impact. Endemic circulation of the bluetongue virus serotype 4 (BTV-4) and BTV-1 have occurred in Spain since 2004 and 2007, respectively. However, epidemiological studies have seldom been approached from a long-term perspective in wild ruminants. 881 deer were necropsied as part of the DNP health-monitoring program. Serum samples were tested for antibodies against BTV. We assessed the main drivers of BTV maintenance in the wild ruminant hosts of Doñana National Park using generalised linear mixed models. Red deer displayed statistically significant higher seroprevalences of BTV (SBT; 78.6%) than fallow deer (53.1%). The detection of BTV-1 and BTV-4 by the serum neutralization test in calves suggested the circulation of both serotypes for the study period. For red deer, wet years together with high densities could associate to most suitable conditions for vector borne BTV transmission. Moreover, proximity to permanent pasturelands was associated with higher SBT, which may be mediated by the higher suitability of this habitat to Culicoides. The differences in the ecology and behaviour of deer species influencing the exposure to the vectors could determine the differences found in the SBT patterns. This study evidences the role that deer species may play in the maintenance of BTV in host communities. However, elucidating the epidemiological role deserves further research.



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105 LONG-TERM DETERMINANTS OF THE SEROPREVALENCE OF THE HEPATITIS E VIRUS IN WILD BOAR (SUS SCROFA)

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Keywords: Hepatitis E Virus, Long-Term, Public Health, Shared Infection, Wild Boar

Abstract Text

The hepatitis E virus (HEV) is an emerging zoonotic pathogen whose main reservoir is suids. Most of the ecological and epidemiological aspects of its sylvatic cycle remain unknown. We therefore studied the drivers of HEV exposure in the wild boar population of Doñana National Park (DNP, southwest Spain) operating in the medium and long-term (2005-2018). Anti-HEV antibodies were widely distributed throughout the wild boar ($46.7 \pm 3.8\%$, 327 out of 700 sampled), showing a statistically significant age-increasing pattern. The temporal pattern displayed important interannual fluctuations. This could be mediated by marked variations in the population control of the wild boar, and subsequent changes in abundance rates, and its interplay with climatic conditions; as wet years together with a low abundance of wild boar led to the lowest seroprevalence. The fact that seroprevalence was high during conditions of high abundance, and not affected by rainfall level, was probably due to the increased interactions among the animals, and possibly, the subsequent higher environmental contamination with HEV particles. The proximity to the marshland (the main water body of the study area) was associated with a higher risk of testing positive, which is probably mediated by the preferential use of this area during the dry season and the favourable environmental conditions for the survival of HEV particles. A deeper understanding of the epidemiology of HEV in host communities deserves future research concerning other susceptible species. Most importantly, wild boar population control remains a challenge at the international level and an increase of shared pathogen-related conflicts associated with this species is expected, as exemplified by HEV. Therefore, surveillance of wild boar diseases, including integrated population monitoring and sustainable population control programmes will be essential to control the associated risks.



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66 ESTIMATING THE PREVALENCE OF A GLOBALLY-EMERGED PATHOGEN IN A CHILEAN AMPHIBIAN ASSEMBLAGE: EFFECTS OF IMPERFECT PATHOGEN DETECTION AND INDIVIDUAL PSEUDOREPLICATION

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Keywords: Amphibian Chytridiomycosis, Batrachochytrium Dendrobatidis, Darwin'S Frog, False-Negative Errors, Uncertainty

Abstract Text

Accurate estimation of disease parameters is essential to enable effective wildlife disease surveillance. However, wildlife systems are imperfectly observed and key epidemiological parameters such as the prevalence of infection can be significantly biased if observational uncertainty is not taken into account. Here, we adjust for the combined effects of individual pseudoreplication (due to animals not individually identifiable being repeat-sampled by researchers) and imperfect pathogen detection to provide a more reliable estimate of *Batrachochytrium dendrobatidis* (Bd) infection period prevalence in a Chilean amphibian assemblage. We individually-identified amphibians using photography to eliminate pseudoreplication. We took duplicate skin swabs over the same areas of skin, analyzed DNA extracted from each swab twice using quantitative Polymerase Chain Reactions (qPCR) and fitted a recently-developed hierarchical model to our data to quantify and adjust for false-negative error rates arising from both sampling and diagnostic testing. We also illustrate how the definition of a positive case of infection affects the estimation of prevalence and its corrections. Our results show that the prevalence of Bd infection could be underestimated by over 110% if individual identities and false negatives were not considered. As chytridiomycosis threatens many amphibians (including the southern Darwin's frog *Rhinoderma darwinii*) with extinction, it is crucial to provide results that can be reliably used for mitigation actions. Never before have the combined effects of individual pseudoreplication and imperfect pathogen detection resulting from both sampling and diagnostic errors been accounted for in a single survey. Our study will contribute to improving inferences from field data in wildlife disease epidemiology.



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312 DETECTION OF MYCOBACTERIUM TUBERCULOSIS ANTIBODIES IN ASIAN ELEPHANTS IN SRI LANKA

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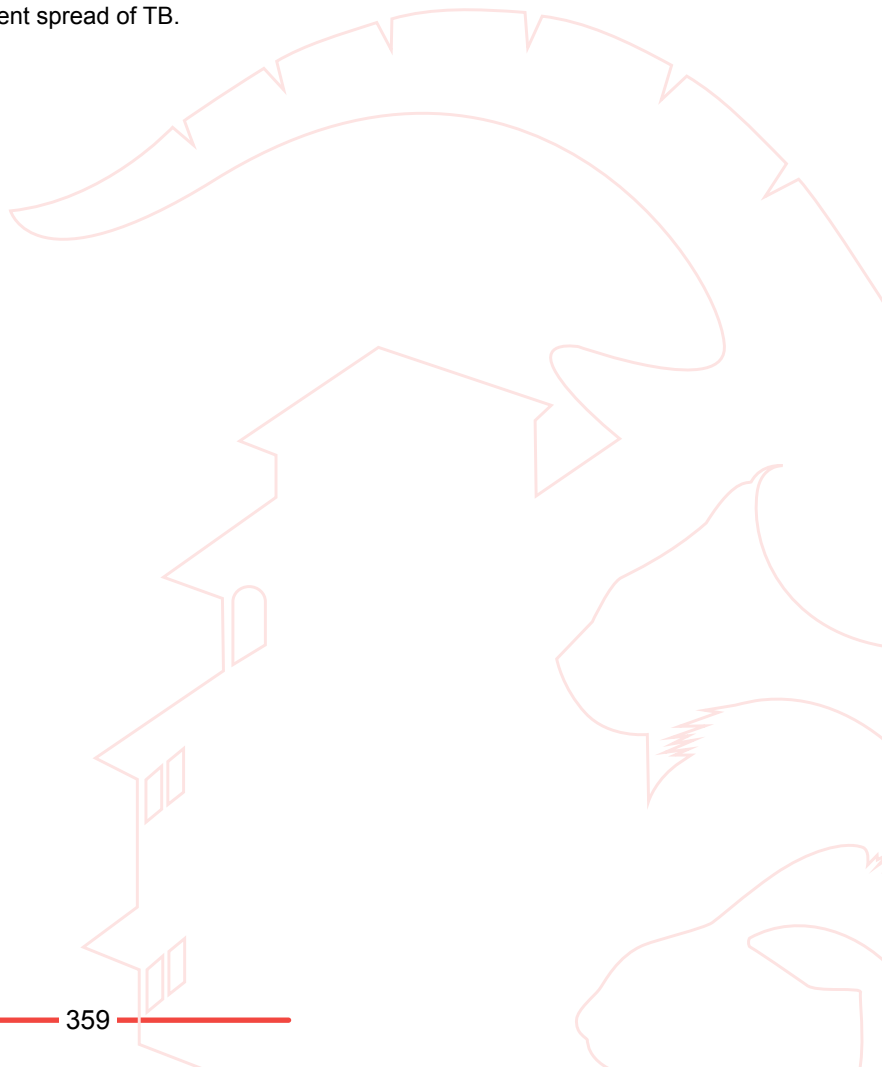
Keywords: DPP, Elephas Maximus Maximus, Mycobacterium Tuberculosis, Sri Lanka

Abstract Text

Tuberculosis is a re-emerging disease in man and elephants. Early detection of this chronic disease is still challenging. The zoonotic and reverse zoonotic nature of Mycobacterium tuberculosis is a threat to humans and elephants as well as to other wildlife species. Sri Lanka has the highest density of elephant population in Asia and was the first country to report TB in a wild Asian elephant. In this study, TB screening of captive Asian elephants in three different locations (Pinnawala Elephant Orphanage-PEO, Dehiwala Zoo and Ridiyagama Safari Park) in Sri Lanka was initiated in 2019 and still in progress.

So far blood samples have been collected from 150 elephants. A rapid immune-chromatographic test that can detect TB antibodies against ESAT-6, CFP-10 and MPB83 antigens (DPP Vet-TB assay for elephants Chembio-Diagnostics INC.) has been used for screening of 68 collected blood samples. At the time of sampling none of the elephants showed clinical signs of TB, while 7 elephants at PEO were under anti-TB treatment due to reactive DPP test prior to this study. The results from the present study showed that two elephants at Dehiwala zoo were reactive in 2019 and they were treated for TB thereafter. No elephant at Ridiyagama or PEO including 7 elephants under anti-TB treatment were reactive. The study also includes screening of elephant handlers which will be done in due course.

In conclusion, all elephants should be tested annually for TB along with their handlers especially before any transfer between locations to detect reactive animals to prevent spread of TB.





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136 MOLECULAR IDENTIFICATION OF SARCOCYSTIS WOBESERI-LIKE PARASITES IN A NEW INTERMEDIATE HOST SPECIES, THE WHITE-TAILED SEA EAGLE (*HALIAEETUS ALBICILLA*)

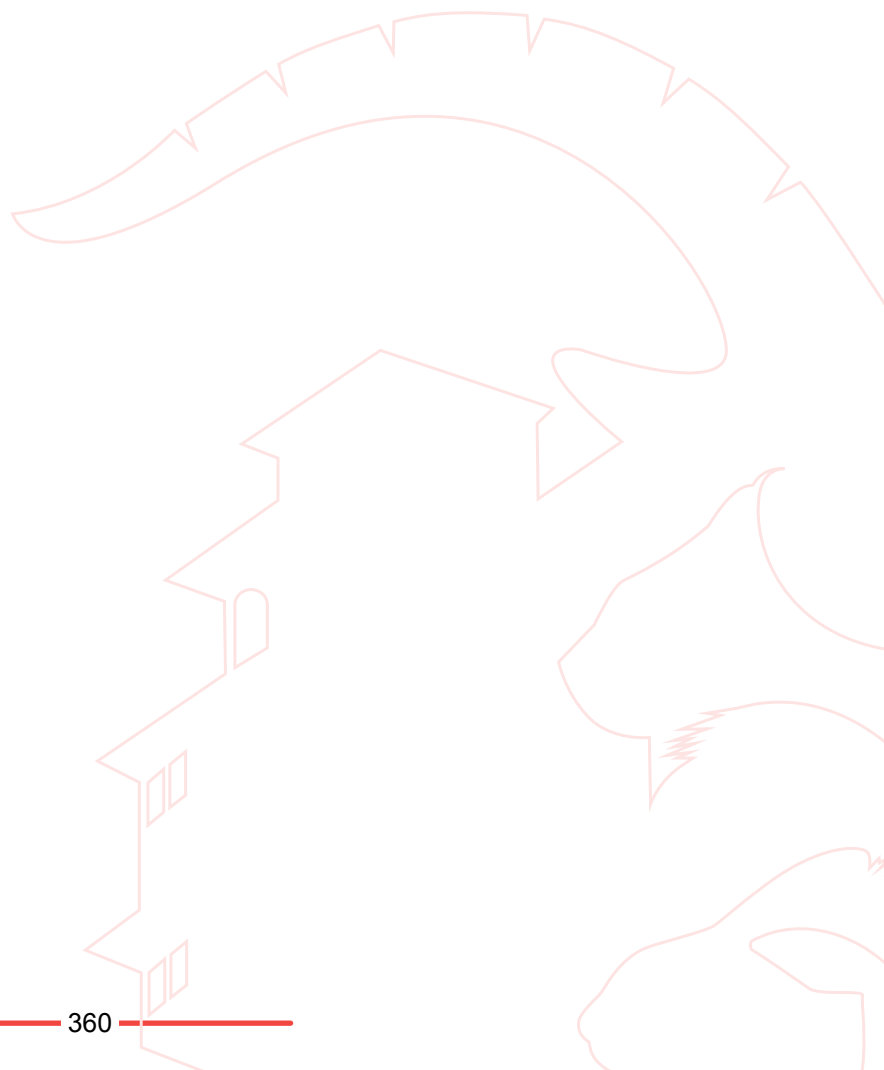
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Keywords: *Haliaeetus Albicilla*, *Sarcocystis*, *Sarcocystis Wobeseri*, White-Tailed Sea Eagle

Abstract Text

A reintroduced white-tailed sea eagle (*Haliaeetus albicilla*) in moderate body condition was found dead and submitted for post-mortem examination to the Institute of Zoology, Zoological Society of London. There were no signs of disease on gross pathological examination; however, histopathological examination of pectoral and cardiac muscle sections revealed the presence of encysted protozoan parasites. Polymerase chain reaction (PCR) amplification of extracted genomic DNA and sequencing of four regions: the 18S rDNA, 28S rDNA, internal transcribed spacer (ITS) 1 and RNA polymerase B (rpoB) loci, was carried out. Results confirmed the presence of a *Sarcocystis* species in pectoral and cardiac muscle which appeared phylogenetically similar to *Sarcocystis wobeseri*. This was the first report of *Sarcocystis wobeseri*-like infection in a white-tailed sea eagle, revealing a new intermediate host species for this parasite. Although there was no evidence of disease associated with this infection, findings were considered of interest in understanding the host range of the parasite.





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176 ANALYSIS AND SELECTION OF GENES ENCODING THE EXPRESSION OF PROTECTIVE ANTIGENS OF THE AFRICAN SWINE FEVER VIRUS FOR FURTHER DEVELOPMENT OF A VACCINE BASED ON ADENO-ASSOCIATED VIRUS VECTOR

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Keywords: African Swine Fever, Wildlife, Natural Focus Of Infection, Vaccine, Phylogenetic Analysis

1

Abstract Text

African swine fever (ASF) is a hazardous, highly contagious disease of domestic and wild Suidae, characterized by rapid spread, high mortality level of infected animals and threat to global food security. The natural focal potential of ASF is due to the spontaneous susceptibility of wild boars (*Sus scrofa*) and transmission of infection by argasid ticks that act as vectors and reservoirs of infection. The development of vaccines is considered to be the most effective measure to prevent and control the spread of ASF virus in the wildlife. Current approaches to the development of an ASF vaccine are focused on vaccines based on viral vectors, in particular, an adeno-associated viral vector. However, the key to the efficacy of such vaccines is the choice of the protective antigens.

The aim of the research was to select the genes encoding the expression of ASF virus protective antigens.

The data was retrieved using a systematic review. According to that, the largest number of studies in the world is aimed at developing vaccines based on such antigens as viral proteins P72, p54 and P30, encoded by the genes B646L, E183L and CP204L, respectively. The viral proteins pp60, EP402R, and p10, encoded by the CP530R, EP402R, and K78R genes, respectively, are also promising antigens for vaccine development.

Phylogenetic analysis of the nucleotide sequences of 6 genes and the amino acid sequences of the proteins encoded by them revealed that all ASF virus strains identified in Russia and a number of Eastern European countries belong to genotype II, and the sequence identity values are equal or close to 100%. Summarized data leads to that the multi-antigen vaccine against ASF can become an effective means of anti-epidemic measures to eliminate natural focus of infection in wildlife both in Russia and neighboring countries.



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178 WILDLIFE RABIES CONTROL AND MANAGEMENT IN TATARSTAN (RUSSIAN FEDERATION)

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Keywords: Rabies, *Vulpes Vulpes*, Vaccination, Wildlife, Eradication Program

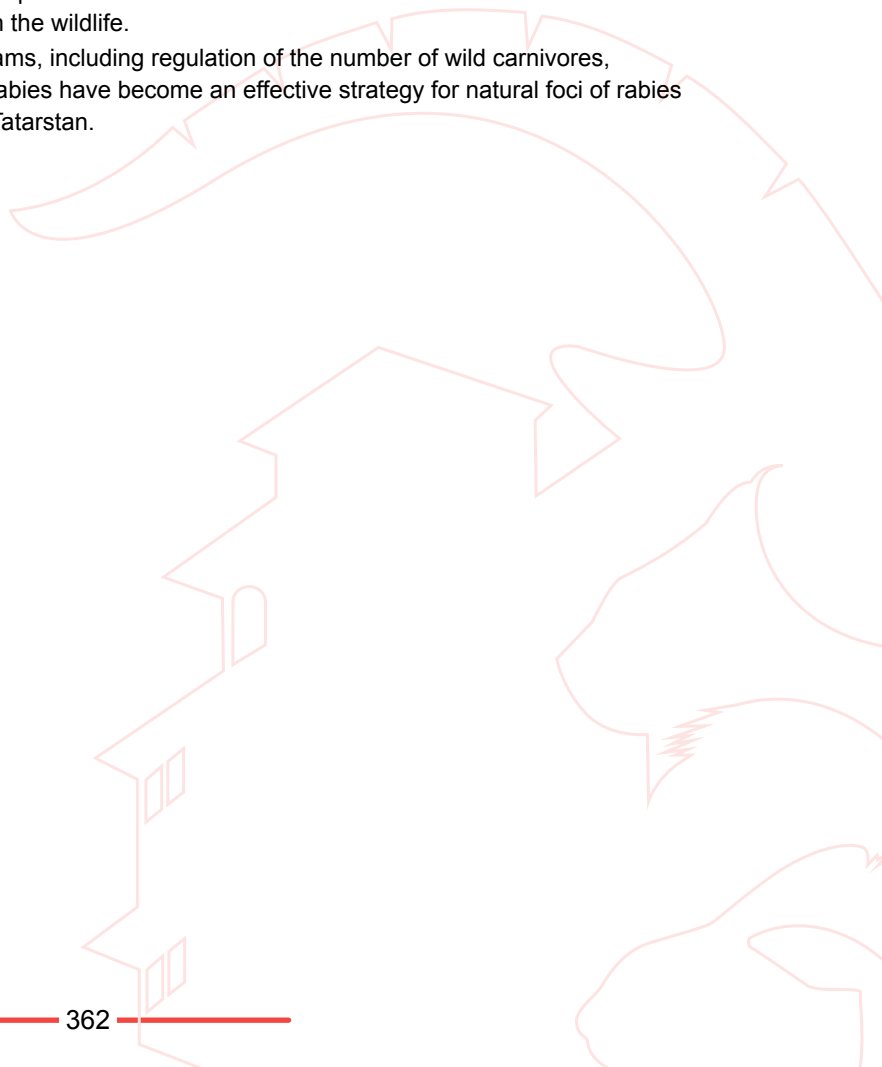
Abstract Text

Over the years, in Tatarstan, the activation of natural focus of rabies has been periodically noted, and the risk of introducing infection from adjacent regions remains. Sporadic outbreaks of rabies in animal populations are largely unpredictable, highlighting our lack of knowledge about how the virus is transmitted and spread in the wildlife. In this regard, comprehensive analysis of the geographical distribution of rabies, study the structure of animal species involved in the epidemic process, cyclic recurrence identification, seasonality, risk factors, along with effectiveness of preventive measures assessment remain as actual challenge.

Wild animals are involved in the epidemic spread of rabies infection in Tatarstan. Periodic rises in the incidence of rabies are observed every 2-3 years. In the species structure of the disease, foxes (*Vulpes vulpes*) account for the main share (96.9%) among wild carnivores. Rare cases of rabies have been observed also in other species. However, the level of their involvement in the epidemic process and the role in the infection transmission to wild herbivores, domestic animals and humans, has not been fully established.

Since 2016, there is the attenuation of the activity of natural infection cycles. The 15-fold decrease in wild rabies likelihood is primarily due to the large-scale oral vaccination campaigns. Annually, two campaigns for oral immunization of wild carnivores and official control of them in accordance with approved Rabies eradication programs are carried out. In addition to the above, the program to reduce the population of foxes also contributed to the stabilization of the rabies epidemic situation at a minimum level of incidence in the wildlife.

Thus, wildlife rabies control and management programs, including regulation of the number of wild carnivores, assessment of oral vaccination campaigns against rabies have become an effective strategy for natural foci of rabies eliminating and stabilizing the epidemic situation in Tatarstan.





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151 INSIGHTS ON THE DIET OF URBAN AMERICAN WHITE IBIS (*EUDOCIMUS ALBUS*) NESTLINGS

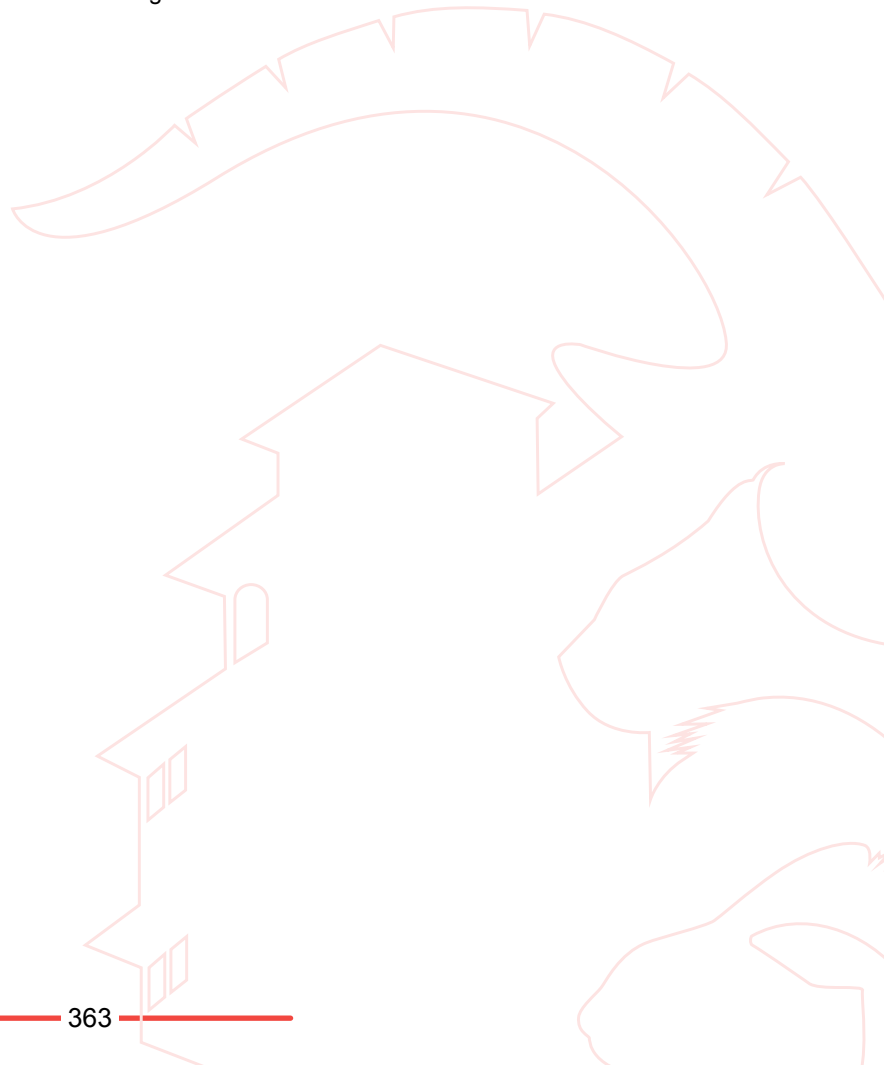
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Keywords: White Ibis, Urbanization, Diet, Stable Isotopes, Growth Rates

Abstract Text

Urban adapted species become abundant and likely to experience human-wildlife conflicts when they reproduce in urban environments. The American white ibis (*Eudocimus albus*), an urbanized wading bird in Florida, still largely returns to natural habitats to breed, but recently has established urban colonies. This project is part of a larger investigation to determine the productivity (hatch/fledging success) of these rookeries. Preliminary data suggests that ibises are as successful in urban habitats as in natural environments, likely because of reliable, continuous food availability provided at urban parks, zoos and landfills. This resource may allow ibises to produce higher fledging rates, but may also compromise nestling health. To better understand the diet fed to urban-raised nestlings, blood was collected from 25 nestlings (>7 days-old) at an urban colony in south Florida between April-July 2020 for stable isotope analyses. Results were compared with the isotopic signatures of captive-reared ibis (fed a known commercial diet), urban-ranging and natural-ranging adults, and reference food sources consumed by ibis (fish, invertebrates, and provisioned food). Additionally, body condition scores, body mass, and standard measurements were recorded once/weekly for every chick from hatch-fledging to address the impacts of diet on nestling growth rates. Stable isotope signatures from urban nestlings were most similar to urban-foraging adults and differed significantly from captive-reared ibis, and both adult and nestlings raised in the Everglades. Preliminary data indicates that both growth rates and body condition scores are lower in urban nestlings than natural chicks. These results suggest that anthropogenic food is an important resource for urban-breeding ibises, allowing this species to continuously exploit urban environments throughout its annual cycle, but it may also be impairing nestling growth. As with other similar species, this dependence on anthropogenic food may also be an important predictor for eventual conflicts and future need for management.





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192 ASSESSING DEER CARCASS TRANSPORTATION, PROCESSING, AND DISPOSAL HABITS AMONG MINNESOTA HUNTERS STATEWIDE AND WITHIN DISEASE MANAGEMENT AREAS

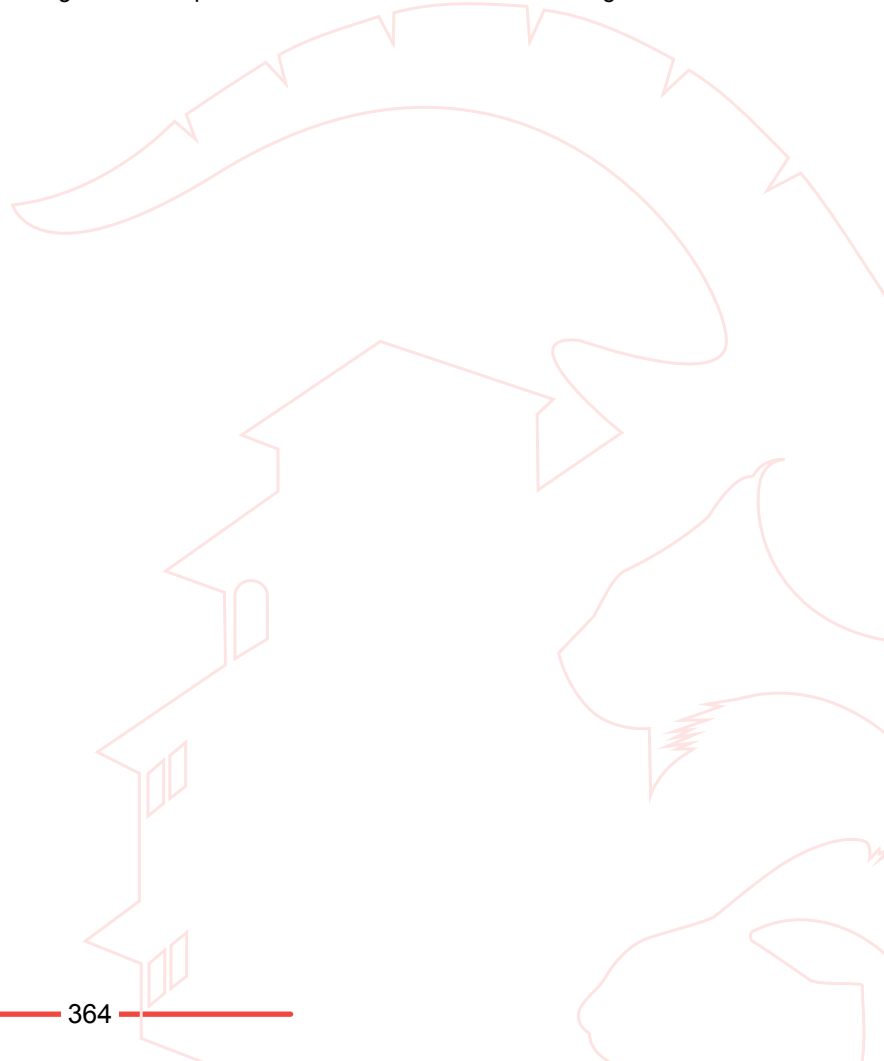
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Keywords: Chronic Wasting Disease, White-Tailed Deer, Cervid, Human Dimensions Of Wildlife

Abstract Text

Chronic wasting disease (CWD) has been identified as a high-priority wildlife disease due to the threat it presents to cervid populations and the sustainability of recreational hunting. Previous research has highlighted the movement, processing, and disposal of carcasses by hunters as a potential vector for CWD spread to novel areas. In Minnesota, hunters harvest, process and dispose of approximately 190,000 deer annually, making recreational hunting a potential vector for CWD spread to novel areas. In order to combat the spread of the disease, many managing agencies have implemented strict regulations pertaining to the movement and processing of deer carcasses harvested in CWD management areas. The temporal lag associated with the introduction of CWD within cervid populations and the onset of clinical symptoms could lead to spread of the disease in areas where disease management has not been implemented. In this study we described the processing, transportation, and carcass disposal habits of hunters both statewide and within a current disease management zone (DPA 604). Data were drawn from a survey of Minnesota hunters conducted during the winter and spring of 2020. A random sample was collected of individuals that hunt the CWD management zone (N=1,500) and statewide (N=3,500). Surveys were sent to these samples through two postal mail solicitations and an online solicitation through Qualtrics, which was substituted for the planned 3rd mail solicitation due to the complications related to the COVID-19 pandemic. Response rates for the statewide sample and the CWD management area were 32% and 33% respectively. Results revealed high variation in the transportation, processing, and carcass disposal habits both statewide and in the CWD management area. These findings have implications for vector tracing for future outbreaks and highlight the need to understand constituent habits and regulation compliance in the context of disease management.





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166 ANTIMICROBIAL RESISTANCE PROFILES IN WILD AND DOMESTIC RUMINANTS: AN ONE HEALTH APPROACH

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Keywords: Antimicrobial Resistance, Wildlife, Livestock, E. Coli, Enterococcus Spp.

Abstract Text

The Antimicrobial Resistance (AMR) is one the most important challenge for human and veterinary medicine in a sustainable ecosystem. The overuse or misuse of antibiotics has led to a wide spread of multi-resistant bacteria in the environment. The AMR patterns are related to mobile genetic elements frequently shared among the microbial communities. In this respect the wildlife can be considered as sentinel of emerging resistant bacteria, including pathogens hardly to treat with available antibiotics in both human and veterinary medicine. In this study, the AMR profiles of several *Enterococcus* spp. and *E. coli* isolates from wild and domestic ruminants were investigated in order to evaluate the role of the environment in the wildlife-livestock-human interface as source of resistant bacteria. The study was carried out in the Majella National Park (Italy) protected area and fecal samples from Apennine chamois, red deer, goats, sheep and cattle were collected. The populations under investigation were resident at different areas of the Park and their relative home ranges were defined by georeferencing data. Eighty-eight bacterial isolates were identified and tested for antimicrobial susceptibility by means of the microbiological investigations and Vitek® 2 System. In addition, PCR and qPCR assays were carried out in order to detect the resistance genes and the virulence factors, describing, for the first time in Italy, specific phenotypic and genetic patterns in bacterial strains from chamois and red deer.

The occurrence of resistant bacteria against critically important antibiotic (carbapenems, colistin, linezolid and vancomycin) carrying some virulence genes, resulted more frequent in wild and domestic ungulates sharing the grazing land. This evidence highlights the effect of food-producing animals and human activities on the environmental pollution or the potential role of wildlife as sentinel of emerging antibiotic resistance in different ecosystems.



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82 GASTROINTESTINAL PARASITES PREVALENCE AND SEASON DYNAMICS IN AN ENDANGERED BROWN BEAR (*URSUS ARCTOS*) POPULATION IN GREECE: PRELIMINARY RESULTS

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Keywords: : Brown Bear, Gastrointestinal, Parasites, Greece

Abstract Text

Brown bear (*Ursus arctos*) population has rebounded in Greece over the last 30 years. However, the species still faces several anthropogenic threats including habitat fragmentation and human caused mortality while its conservation status (CS) is at (U1). Parasites and parasitic diseases may present an additional threat to an endangered population. Furthermore, sympatric domestic animals and humans may be affected too. The purpose of this, ongoing, study is to investigate the occurrence of gastrointestinal parasites of brown bears for the first time in Greece, with special focus on testing the hypothesis that bears lower their parasitic load during hibernation and get reinfected gradually after den emergence.

Throughout the year 2020, 186 faecal samples were collected from various areas of bear's range of permanent presence. The samples were examined by two classical parasitological methods, i.e., ZnSO₄ flotation and formalin sedimentation. Positive samples were additionally examined by the modified McMaster method for the quantification of the result (eggs per gram, EPG).

Overall, 103 (55.38%) faecal samples were positive for parasites. More precisely, *Baylisascaris* spp. was found in 74 (71.84%) *Uncinaria* spp. in 39 (37.86%), *Dicrocoelium dentriticum* in 19 (18.44%), *Toxascaris* spp. in 1 (0.97%) *Capillaria aerophila*, in 5 (4.85%), *Sarcocystis* spp. and *Crenosoma* spp. in 3 (2.91%), *Eimeria* spp. in 2 (1.94%) and *Taenia* spp., *Linguatula serrata* and *Toxascaris* spp. in 1 (0.97%). Mixed infections by two or more parasite species were detected in 32 (31.06 %) samples. Less than 50 EPG were found in 67.57% and 90.91% of the positive samples for *Baylisascaris* spp. and *Uncinaria* spp., respectively. Finally, a seasonal variation was observed with the highest prevalence of positive samples during autumn and winter.



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108 UNRAVELLING ELEPHANT HERPESVIRUS PATHOGENICITY WITH TRANSCRIPTOMICS

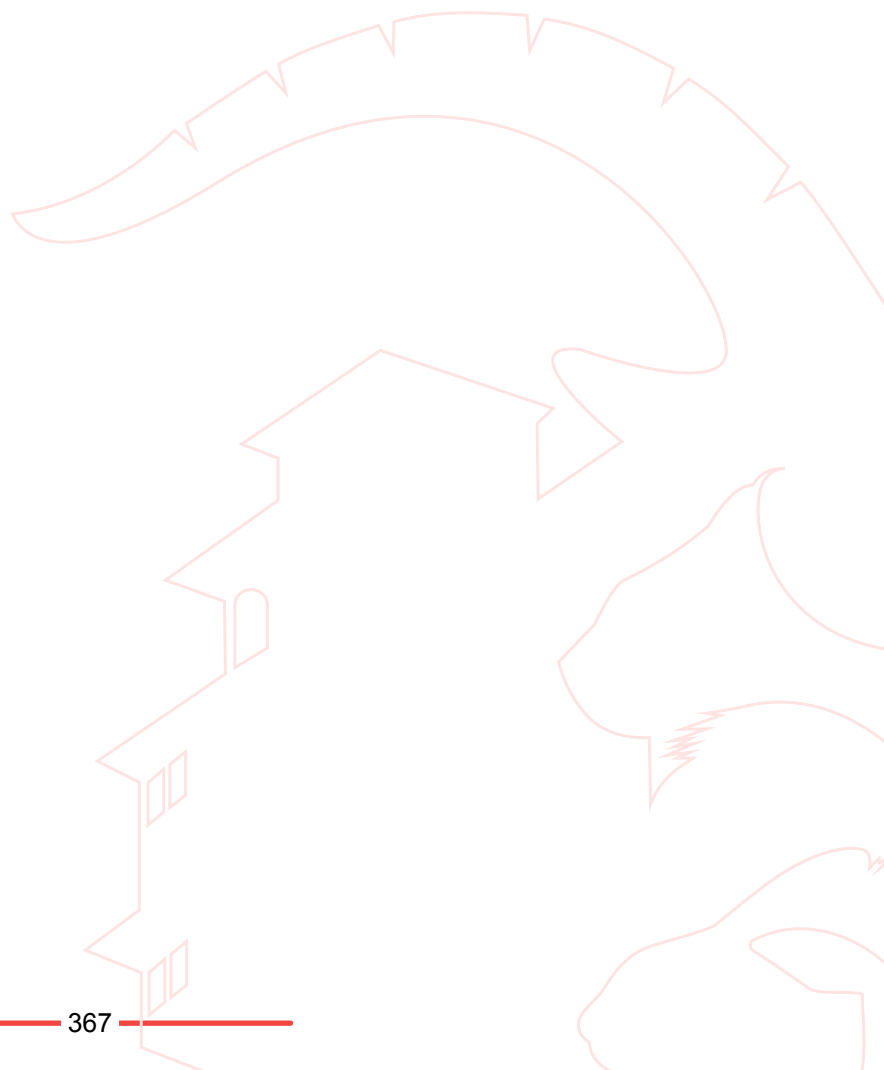
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Keywords: Elephant Endotheliotropic Herpesvirus, Asian Elephant, EEHV

Abstract Text

Elephant Endotheliotropic Herpesviruses are linked to deaths of juvenile Asian elephants with an acute haemorrhagic fever syndrome. The disease syndrome has a serious impact on breeding programmes of this endangered species with up to 25% of deaths of juveniles in captivity due to the disease syndrome. However most adult animals either in captivity or in the wild appear to have latent infections with one or more genotypes of the virus and to excrete it intermittently throughout life. What makes the difference between a life-long subclinical or latent infection and an acutely fatal disease in some animals is still not well understood. Current theories include the age of first infection compared with waning maternal antibody titre and the background genetics of the affected animals. This study examined Illumina RNAseq data from heart tissue from 4 EEHV and 5 control cases from Kerala India for both EEHV reads and differential host gene expression, providing insight into the gene regulatory networks differentially regulated in EEHV cases and the gene expression of the virus in these cases. Two viral genes were identified with a high proportion of reads mapping to them, EE1 (unknown function) and U11 (a tegument protein of unknown function) indicating that these genes may be important markers of the stage of the viral lifecycle (latent or lytic) and may be useful to develop as RT-qPCR based diagnostic tests for active viral infection.





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293 *EMYDOMYCES TESTAVORANS* ASSOCIATED SHELL DISEASE IN AN ENDANGERED POPULATION OF NORTHWESTERN POND TURTLES IN WASHINGTON, USA

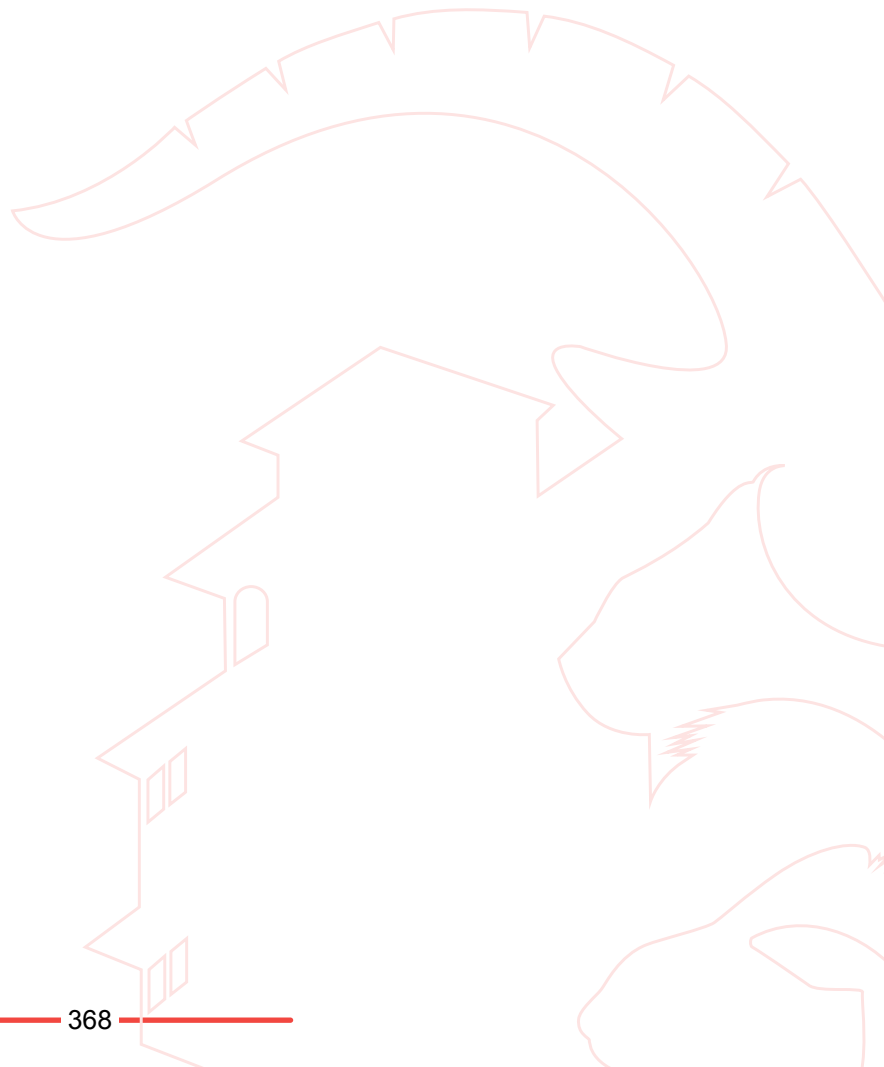
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Keywords: *Actinemys marmorata*, *Emydomyces testavorans*, Northwestern Pond Turtle, Shell Fungus

Abstract Text

Recovery efforts for the Washington state endangered Northwestern pond turtle (WPT; *Actinemys marmorata*) are threatened by shell disease. Affected turtles are infected with a newly described fungus, *Emydomyces testavorans*, that is closely related to other reptilian onygenalean fungi. During annual field assessments since 2015, WPT from 5 sites have been evaluated for characteristic lytic lesions within both the carapace and plastron through CT scans and biopsy to detect presence of the fungus. Over 450 scans have been completed on 228 individual free-living turtles. Based on CT scans, 199/228 (87%) of turtles were found to have at least a single lytic lesion. Disease progression is evident in repeat CT scans (n=212) conducted on the same individuals (n=78) over this five year period. While some affected turtles were wild (n=11), the vast majority of affected turtles had spent some time in managed care (head-start program; n=188). A subset of lesions (n=48) have been biopsied or swabbed for *E. testavorans* qPCR and infection was confirmed in all cases. On histopathology (n=12), affected turtles had evidence of osteonecrosis and epithelial lined inclusion cysts that extend into the shell bone and are filled with keratin and fungal hyphae. Systemic spread, to date, has not been documented. *E. testavorans* has also been identified in environmental samples from nests and other habitats in Washington. Ongoing research is aimed at assessing the microbiome among habitats, the impact of disease on individual and population level reproductive success, treatment and disease management strategies for turtles in head-start environments.





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76 TRACKING AN INVADER: WILDLIFE SURVEILLANCE FOR HAEMAPHYSALIS LONGICORNIS IN THE EASTERN U.S.

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Keywords: Haemaphysalis Longicornis, Ticks, Wildlife, Active Surveillance, Passive Surveillance

Abstract Text

Ticks often are best framed in a One Health context, as many utilize multiple hosts, and the pathogens they transmit can be of both veterinary and medical importance. One vector of recent significance in the U.S. is *Haemaphysalis longicornis*, the Asian longhorned tick (ALT). This tick is native to eastern Asia but has become invasive in several countries where it is a pest to a large range of hosts including livestock, companion animals, wildlife, and humans. To better assess the current distribution of ALT and to identify potential wildlife host species that are important for maintaining and possibly spreading it, we collected ticks from wildlife using active and passive surveillance techniques. Active surveys were conducted by collecting ticks from free-ranging animals at sites in NJ, VA, and TN with known ALT infestations. Passive, region-wide surveillance was conducted in collaboration with rehabilitation centers and state wildlife agencies. Rehabilitation centers were asked to collect ticks from all wildlife species, whereas agencies targeted cervids and bears for collections. Since 2017, we have collected ticks from 2,252 hosts from 22 states in the Southeast and Midwest U.S. Our surveillance detected ALT infestations in 8 states (KY, MD, NJ, NC, TN, PA, VA, WV) on 116 mammalian hosts, representing 12 species: whitetailed deer, elk, raccoon, Virginia opossum, striped skunk, coyote, red fox, gray fox, black bear, eastern cottontail, woodchuck, and *Peromyscus* sp. In addition, ALT was collected from four avian hosts, representing three species (red-tailed hawk, great-horned owl, and brown booby). These efforts resulted in numerous new host and geographic (state and county) records for ALT and offer insight into the distribution of this exotic tick. In addition, our large-scale passive surveillance network offers valuable information regarding the distribution and host associations for many native tick species of both public health and veterinary importance.



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163 TICK-BORNE ENCEPHALITIS IN THE SWEDISH MOOSE (*ALCES ALCES*)

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Keywords: Moose (*Alces Alces*), Histopathology, Meningoencephalomyelitis, Wildlife,

Abstract Text

Tick-borne encephalitis (TBE) is a zoonotic neurological disease caused by tick-borne encephalitis virus (TBEV), a flavivirus endemic in parts of Europe and Asia. Many animal species, including hoofed wildlife, have been suggested to play a role in the circulation of TBE viruses in nature. Seroconversion in moose (*Alces alces*), without apparent clinical disease, has repeatedly been reported in areas where TBEV-positive ticks are endemic. Prior to this study, the first and only published case of clinical neurological disease and concurrent infection of TBEV in a Swedish moose calf was reported in 1965. Here, the first two RT-qPCR-confirmed clinical cases of TBE in Swedish moose are presented.

Two female moose calves (found in Västra Götalands county and Södermanlands county) presented with compulsive walking in small circles, suggesting neurological disease. Both calves were humanely euthanised and samples were submitted to the National Veterinary Institute (SVA) for examination. Histopathological changes in the brains were consistent with non-purulent meningoencephalomyelitis. RT-qPCR examination (preceded by pan-virus array) of brain tissue was positive for TBEV, confirming infection. The entire genome of the two virus strains was sequenced and aligned with sequences from other TBE viruses collected in Sweden, from other parts of Europe, and the world. The algorithm used was kalign. Phylogenetic analyses classified the strains as TBEV-Eu. As recombination previously has been described for TBEV, the two moose strains were compared with other Swedish strains. No obvious signs of recombination were detected.

Meningoencephalomyelitis caused by TBEV should be a diagnostic consideration in moose calves presented with clinical signs of the central nervous system in areas where TBEV-positive ticks are endemic. At this time, the role of moose in the circulation of TBE viruses in nature is not well understood.



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62 PREVALENCE OF RESPIRATORY DISEASE IN EASTERN GREY SQUIRRELS (*SCIURUS CAROLINENSIS*) IN RELATION TO LEVELS OF AIR POLLUTION FOUND IN LONDON (UK)

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Keywords: Air Pollution, Eastern Grey Squirrel, Global Change, Urban Wildlife, Wildlife Health

Abstract Text

The increased rate of global urbanisation has recently exacerbated the significant public health problem of air pollution. Despite the known significant impact on human health, little is known about the effects of urban air pollution on wildlife health. In this study, we aimed to assess lung health in Eastern grey squirrel (*Sciurus carolinensis*) populations across an urban air pollution gradient mainly composed of particulate matter and nitrogen oxide. A total of 61 squirrels, from four different parks in London, were sampled to assess levels of pulmonary anthracosis, number of alveolar macrophages and presence of tracheal and lung diseases and inflammation. Sampled areas were classified as having high, medium or low pollution levels according to their mean annual values of particulate matter and nitrogen oxide. Overall, 15% percent of squirrels showed signs of pulmonary anthracosis and 20% had focal lung disease, including focal inflammation, presence of macrophages with vacuolated cytoplasm and endogenous lipid pneumonia. No significant differences regarding levels of pulmonary anthracosis and presence of lung disease were found between sampled areas. However, squirrels from the high pollution sites had a statistically significant higher number of alveolar macrophages compared to squirrels obtained from less polluted sampling sites. This study shows preliminary evidence for the impact of urban air pollution on wildlife health, but further studies are needed to confirm these findings and successfully control for potentially confounding variables.



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343 USE OF DYNAMIC NETWORK IN THE WILDLIFE-LIVESTOCK INTERFACE TO STUDY ENDEMIC AND EMERGING DISEASES

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Keywords: African Swine Fever, Animal Tuberculosis, Dynamic Network, Extensive Systems, Wildlife-Livestock Interface

Abstract Text

Dynamic networks are an analytical tool highly valued in epidemiology due to their potential to identify individuals or communities with a key role in the transmission of pathogens. By including the temporal dimension in the analysis is possible to consider the potential process of pathogen transmission along the time. This approach becomes more necessary in those interfaces where emerging diseases mean a challenge. The objective of this work was to characterise the network of interactions in a multi-host extensive system where wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) cohabit with livestock, and to simulate the potential transmission of *Mycobacterium tuberculosis* complex (MTB) and African swine fever virus (ASFV) within a dynamic network. To this end 6 red deer, 6 wild boar, 3 cattle and 10 domestic pigs were collared during autumn 2017–winter 2018 using GPS and proximity devices; besides, indirect interactions between animals through water points (as a potential source of pathogens) were considered. Close interspecific interactions were found to be scarce, but water points acted as an attractant for both wildlife and livestock, resulting in a high number of interspecific indirect interactions. The simulation showed that transmission of MTB may occur preferably from red deer to cattle in our studied system; in the case of ASFV, our simulation suggests that transmission from wild boar to pigs occurs more probably through water points. The results of this preliminary work highlight the relevant role that certain wild species could play in the transmission of pathogens in multihost systems. More in deep studies are necessary to understand the real role of water points for the transmission of the two diseases considered, both for pathogen maintenance or carcasses presence. Also, more empirical data (e.g. more collared individuals) is needed to estimate more reliable rates of interactions, specifically for direct interactions.



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180 DETECTION OF ATYPICAL PORCINE PESTIVIRUS (APPV) IN WILD BOARS IN NORTHERN ITALY

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Keywords: Atypical Porcine Pestivirus, Italy, Wild Boar

Abstract Text

Atypical porcine pestivirus (APPV), currently classified as pestivirus K, causes congenital tremor (CT) type A-II in piglets. After the first identification in the USA in 2015, the presence of APPV in domestic pigs was confirmed repeatedly in several countries in Europe, North and South America and Asia, and in wild boars in Europe and South Korea. By testing apparently healthy pigs we recently detected APPV in 1.84% of the samples. Healthy pigs and wild boars may have an epidemiological role as vehicles for APPV. Here, we report the APPV detection and genetic characterization in wild boars found dead or hunted from Lombardy and Emilia-Romagna regions (North Italy). We screened by real-time RT-PCR, targeting the NS5B gene, 911 samples (586 pool of viscera and 325 sera) collected both during the hunting season 2019-2020 and in the framework of the passive surveillance program for ASF in 2020. Phylogenetic analysis of NS3 region of positive samples was performed. Six APPV strains were identified out of 911 samples collected from wild boars, indicating an APPV prevalence of 0.65%. Two of the APPV-positive wild boars were detected in sera (0.61%) from Emilia-Romagna and four in pool of viscera (0.68%), collected respectively two from Lombardy and two from Emilia-Romagna. Sequences of NS3 fragments clustered with APPV sequences previously identified in Spain, Germany and Italy.

Wild boars are susceptible to APPV infection, although their role in the epidemiology of the virus is unknown. The prevalence of APPV among North Italy wild boars is low, as in Spain (0.23%) and South Korea (0.78%), but it is in contrast to the higher prevalence detected in northern Germany (19%).

In conclusion, the availability of molecular assays could contribute to better understand the epidemiology and pathogenesis of this novel pathogen and to implement tailored plans for detecting and control APPV infections.



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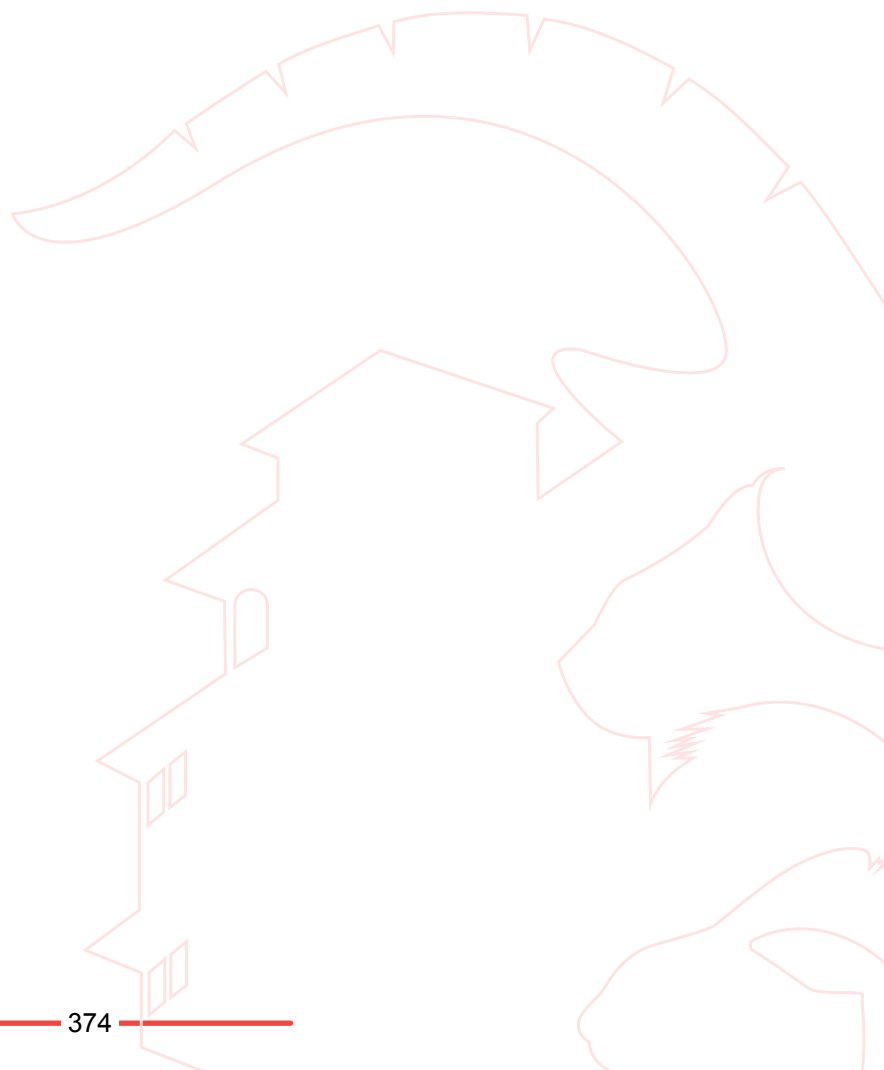
7 LOCOMOTOR BIOMECHANICS OF CHINESE PANGOLINS (*MANIS PENTADACTYLA*) WITH NORMAL AND AMPUTATED LIMBS/TAILS

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Abstract Text

Chinese pangolins (*Manis pentadactyla*) are on the edge of extinction due to the heavy demands of their scales. In Taiwan, however, the key threat they encounter is trauma, caused by illegal traps and dog attacks. The difficult decision of amputation is often made by rescue centres to save their lives. However, whether to release the amputees back to the wild is purely based on subjective criteria. Therefore, there is a need for a better understanding of pangolin locomotion as part of the evaluation of their welfare and suitability for release. The aims of this study were to 1) quantify locomotor parameters of normal Chinese pangolins and 2) to investigate whether there are differences in gait parameters between normal and amputated pangolins. Velocity and ground reaction forces were collected from ten Chinese pangolins from Taipei zoo, Taiwan. The mean velocity of the five normal pangolins was 0.220, ranging from 0.092 to 0.326 (metre/second). The peak vertical forces exerted by the hindlimbs of the pangolins were 1.7 times greater than the forelimbs, which is uncommon in mammalian species. The mediolateral forces indicated that the pangolins were pushing outwards during walking. The horizontal forces (acceleration/deceleration) was consistent with most other mammals. No significant differences in any locomotor parameters were found between normal and amputated pangolins. However, due to the small sample size in each subgroup and the limitation of time and equipment, the results of this study were not conclusive to create the criteria for releasing the amputees back to the wild; further research, biological, ecological and behavioural considerations are needed.





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342 METHOD COMPARISON OF GLUCOSE CONCENTRATIONS OBTAINED VIA GLUCOMETER, NOVA ANALYZER, AND PLASMA CHEMISTRY ANALYZER AND PERFORMANCE OF THREE GLUCOMETERS IN COLD-STUNNED KEMP'S RIDLEY TURTLES (*LEPIDOCHELYS KEMPII*)

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Keywords: Cold-Stun, Glucometer, Glucose, Kemp's Ridley Turtle, *Lepidochelys Kempii*

Abstract Text

Glucose is a vital diagnostic analyte in cold-stunned sea turtles. Identifying glucose derangements in ill sea turtles is critical for guiding treatment plans and subsequent diagnostic test decisions. Handheld glucometers have several advantages to benchtop analyzers as they require small blood sample, are inexpensive, and provide rapid results. Glucometers have been used in sea turtles though the methodology has not been validated until recently. The objective of this study was to compare whole blood glucose measurements obtained via EasyTouch glucometer to whole blood Nova analyzer and plasma chemistry analyzer in cold-stunned Kemp's ridley turtles (*Lepidochelys kempii*) to determine the validity of glucometer data. Glucose measurements were obtained from whole blood samples collected for routine diagnostics (Nova, complete blood count/chemistry, and/or packed cell volume [PCV]/total solids) over a range of turtle body temperatures and PCV values. EasyTouch glucometer and Nova analyzer data had significant positive agreement and the best level of agreement for all method comparisons. The most accurate EasyTouch glucometer results were obtained with PCV values $\geq 25\%$ and body temperature $> 21.1^\circ\text{C}$.

The following cold-stun season, we compared the performance of three different glucometer brands that utilize different electrochemical technologies: EasyTouch, Contour Next, and AlphaTrak2. AlphaTrak2 glucometer yielded higher glucose data than EasyTouch and Contour Next across all temperatures and PCV values while Contour Next glucose values were lower than EasyTouch and AlphaTrak2 across all temperatures and PCV values. Glucometer performance varied with PCV and should be considered when analyzing glucose via glucometer in Kemp's ridley sea turtles.



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324 ACTUALIZATION OF THE FERAL AMERICAN MINK (*NEOVISON VISON*) DISTRIBUTION IN EUROPE: A POTENTIAL RISK SPECIES FOR SARS-COV2

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Keywords: Distribution, Europe, Neovison Vison, Risk Assessment, SARS-CoV-2

Abstract Text

Besides being a threat to conservation, the American mink (*Neovison vison*) also has the potential to play a crucial role in the ongoing pandemic, as it was demonstrated to be a susceptible host for a mutant version of the SARS-CoV-2 and capable of transmitting it back to humans. This virus can potentially be present also in feral specimens.

Despite control and eradication plans, the American mink is still quite widespread in the continent and there is lack of information about its distribution, with the last mapping in Europe dated 2006. The aim of the project was to gather information about the presence and distribution of this species, creating a harmonized map of Europe, pointing out the trends over the years and the issues concerning harmonization of population data.

In the frame of the ENETWILD project, we managed to collect information about the presence of American mink in all the western European countries and most of the eastern ones. Data were harmonized from different sources and spatial resolutions, grouped by year and transformed in 10x10km grid of presence and absence. Maps were compared to outline changes over time. We took Spain as a model for a more detailed work, where data of captures were related to capture effort: allowing a density index to be created that gave a better picture of the situation. We also reviewed the European current mink farming situation and the existence of control schemes for feral populations.

This information will be extremely useful for risk assessment at a European level: it could represent the basis for coordinating the efforts to control a still spreading species with a relevant health interest. Moreover, the issue of a harmonized data collection for wildlife species clearly emerges as key element to implement to obtain better quality and more useful data.



248 INVESTIGATING THE SARCOPTIC MANGE OUTBREAK IN THE IBERIAN IBEX POPULATION FROM PORTS DE TORTOSA I BESEIT, SPAIN

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Keywords: Epidemiology, Iberian Ibex, Outbreak, Sarcoptes Scabiei, Sarcoptic Mange

Abstract Text

Since the first description of sarcoptic mange in Iberian ibex (*Capra pyrenaica*) in 1987, this disease has affected most of the Mediterranean populations of the species, with variable incidence, severity, and demographic outcomes. In December 2014, the last outbreak of sarcoptic mange in Iberian ibex was detected in Ports de Tortosa i Beseit (PTB) in Catalonia (northeastern Spain).

Since 2015, the epidemic has been monitored in PTB by visual diagnosis of free-ranging ibexes (n=3145) and sampling (muscle, sera, kidney, feces, and skin) of the hunted-harvested individuals (n=459). Date, location, age, sex, and visual mange status were recorded. The presence of *Sarcoptes scabiei* was assessed through skin scrapings and hydroxide potassium digestions, and the sera were tested for sarcoptic mange antibodies. All the information, including environmental variables (vegetation, orography, and meteorological variables), was analyzed with R version 4.0.2. through Generalized Additive Models (GAMs) and Factor Analyses Mixed Data.

This outbreak started northwards from PTB and spread through the whole area in five years, with the greatest expansion during 2018. Generally, juveniles and kids had less severe forms of mange than adults, and females than males. In addition, herds containing many Iberian ibexes were more often spotted during fall and winter.

Our GAMs showed a significant relationship between age class, altitude, slope, Enhanced Vegetation Index, humidity, temperature, size of the herd, and sarcoptic mange clinical status. Males were detected at decreasing altitudes when mange severity increased, with severely affected males lowest and the healthy ones highest. Furthermore, many females (mostly mildly affected) were found at lower altitudes than many males (severely and mildly affected).

This study provides insights on the factors determining the evolution of sarcoptic mange in a naïve Iberian ibex population and may help to understand mange dynamics and to design appropriate surveillance, monitoring, and management strategies.



243 GENERALIZED TUBERCULOSIS DUE TO MYCOBACTERIUM CAPRAE IN A BLIND RED FOX (*VULPES VULPES*) AND ITS EPIDEMIOLOGICAL CONTEXT

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Keywords: Fox, *Vulpes Vulpes*, *Mycobacterium Caprae*, Tuberculosis, Wildlife-Livestock Interface

Abstract Text

Animal tuberculosis (TB), caused by *Mycobacterium tuberculosis* complex (MTBC) is a multi-host disease in the Iberian Peninsula. Even though red foxes are susceptible to MTBC, their involvement in the epidemiology of TB is largely unknown.

In February 2021, an adult female fox was admitted to Vallcalent Wildlife Rehabilitation Centre (Lleida, Catalonia). The animal was blind, depressed and emaciated (2.94 kg). After clinical examination, it was humanely euthanized. On postmortem examination, it had a disseminated TB infection including a diffuse granulomatous pericarditis with abundant caseous exudate filling the pericardial sac. Histologically, lesions consisted of diffuse granulomatous infiltration or multifocal granulomas with caseous necrosis in multiple tissues, including the brain. Interestingly, bilateral granulomatous choroiditis and vitritis were established as the cause of the blindness. Ziehl-Neelsen stain revealed a high number of acid-fast bacteria in all tissues, especially in the kidneys, suggesting an intense dissemination of mycobacteria through urine.

DNA of MTBC was detected by direct PCR from tissue homogenates (kidney and mediastinal lymph node). Characterization of DNA by DVR-spoligotyping identified *Mycobacterium caprae* with the spoligotype pattern SB0415. Mycobacterial culture confirmed this result.

Interestingly, the same spoligotype was isolated in a bovine TB outbreak in a cattle herd of the same municipality in 2019. In addition, this spoligotype is often isolated in a regional breed of goats (Blanca de Rasquera), although their role in this focus was not confirmed since goats are not submitted to mandatory TB surveillance in Catalonia.

This case showed an unusual clinico-pathological presentation of tuberculosis in wild or domestic animals, with blindness as one of the major clinical signs and a diffuse tuberculous pericarditis. The results strongly suggest a local circulation of *M. caprae* between livestock and wildlife. Further studies are required to assess the TB outbreak extension and the epidemiological role played by different animal hosts.



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184 EXPERIMENTAL MYCOBACTERIUM MICROTI INFECTION IN BANK VOLES (*MYODES GLAREOLUS*)

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Keywords: Experimental Infection, Mycobacterium Microti, Tuberculosis, Voles, Wild Rodents

Abstract Text

Wild rodents, particularly voles, are described as the maintenance hosts of *Mycobacterium microti*, a member of the *Mycobacterium tuberculosis* complex. Within this group of pathogens, *M. bovis* and *M. caprae* are the main causative agents of animal tuberculosis (TB), posing a risk of infection for humans. *M. microti* is difficult to be detected in TB surveillance plans in livestock and wildlife. However, its role needs to be assessed since it might interfere with current diagnostic tools of *M. bovis* / *M. caprae* infections, affecting the efficacy of eradication campaigns, particularly in low TB prevalence scenarios.

To better understand the pathogenesis and ecology of TB in voles, an experimental model was set up to characterize *M. microti* infection in laboratory Bank voles (*Myodes glareolus*). Both intragastric and intraperitoneal inoculation routes were assessed as well as two different doses (104 and 106 CFU/0.1mL). Voles were culled and necropsied at different post-inoculation time points to assess disease progression. Histopathology, Ziehl Neelsen staining, serology, tissue, faeces and oral swab PCR and mycobacterial culture results are reported.

The model allowed us to faithfully reproduce the disease phenotype described in free ranging voles. Multifocal granulomatous lesions were observed in the liver consistent with a hematogenous spread of mycobacteria. Diffuse granulomatous infiltrate was observed in the spleen and lymph nodes. Seldom focal granulomas were observed in the lungs. Less frequently, muscular granulomas were observed. Unchallenged animals were housed with the inoculated ones to assess horizontal transmission and, despite mycobacteria excretion could not be demonstrated in faeces nor oral swabs, one contact vole seroconverted and showed incipient disease lesions, suggesting in vivo horizontal transmission between voles.

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350 GLOBAL GEOGRAPHIC PATTERN OF STUDIES ON ZOOBOTIC DISEASES IN WILD BOAR (*SUS SCROFA*) AND RED DEER (*CERVUS ELAPHUS*)

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Keywords: Biogeography, Large Game, Zoonosis, Zoonotic Pathogen

Abstract Text

Wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) are the main large game species distributed worldwide. They are also two of the most important hosts of zoonotic pathogens and have an important role in the zoonotic diseases cycle in the wildlife-human interface. The aim of this systematic review was compiling the geo-information of the studies that include both zoonotic pathogens and at least one of the 2 species of interest (wild boar and/or red deer), published in the last 20 years.

The search was conducted in PubMed and ScienceDirect databases using the search strategy “((*sus scrofa* OR wild boar OR *cervus elaphus* OR red deer) AND (zoonosis OR zoonot* OR infectious disease))” in February 2021. The systematic review has the following inclusion criteria: species of interest, confirmed zoonosis and presence of natural infection, and exclusion filters: articles in english, stipulated timeline (2001-2020) and access to full article. We assessed 1419 articles and revised all abstracts, then full-reviewed 323 unrepeated articles and included 271 studies fulfilling selection criteria.

In the last 20 years, geographically, we observe an inequality in the pattern of distribution of studies. Focusing mainly on European continent (202 of 271 included studies), followed by the Asian (n=31) and American continent (n=32). Remaining over the past 20 years, there are few african studies (n=1) and originating in Oceania (n=5). With this systematic review a European centralized pattern of studies on zoonosis in wild boar and red deer in last 20 years was illustrated.

Based on One Health concept and prioritizing the issue of occurrence of zoonotic diseases in large game species as a matter of public health, there must be increasing concern about that. The need for more research at the global level is evident to improve the knowledge and the potential risk in wild-life-livestock-human interface.



380 FIRST DESCRIPTION OF METACUTEREBRA BAERI INFESTING A CRITICALLY ENDANGERED ECUADORIAN WHITE-FRONTED CAPUCHIN MONKEY (CEBUS ALBIFRONS AEQUATORIALIS) IN TUMBES, PERU

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Keywords: Myiasis, Metacuterebra, Cebus Aequatorialis, Botfly, COI

Abstract Text

Botflies (Diptera: Oestridae) is one of the most diverse and relevant groups of domestic and wild mammal insect parasites. *Metacuterebra* (*Cuterebra*) *baeri* is the only known botfly species that targets neotropical primates, and precisely, howler monkey (*Alouatta* spp.) is the specific host. Moreover, larval parasitic prevalence has been correlated with primate mortality in field studies and little is known about the presence of this parasite in other primate species. We analysed samples of larvae obtained from a fresh carcass of an adult female Ecuadorian White-fronted Capuchin Monkey (*Cebus albifrons aequatorialis*) found in Parque Nacional Cerros de Amotape, Tumbes, Peru. Morphological and molecular larvae analyses were performed using stereoscopic microscope and mitochondrial gene (Cytochrome Oxidase I - COI). Phylogenetic trees were constructed by Maximum Likelihood (ML) and Bayesian Inference methods.

The larvae were preliminarily identified as specimens of the second instar (L2) of *M. baeri*. These had pale pink in color, with robust cuticular spines, serrated edges, smooth and densely packed on the entire surface of the body. Posterior spiracles with an inconspicuous peritreme and two slightly curved slits, which are surrounded by a chitinous rima. The COI isolated sequence (~572 bp) presented 95% of identity compared with a GenBank sequence of *M. baeri* (Accession Number) obtained in Costa Rica (1957). The larvae phylogenetic trees showed a monophyletic group with *M. baeri* with high posterior probability (>0.98) and bootstrap values (99). Morphological description and genetic evaluation suggest that larvae studied are *M. baeri*.

We cannot asseverate that larval parasitism influenced the primate death. Effect of larval parasitism on primate population mortality requires large field studies and we highlight the importance of these efforts oriented to the evaluation of the critically endangered *C. aequatorialis*. This report constitutes the first description of *M. baeri* infesting an Ecuadorian White-fronted Capuchin monkey in northern Peru.



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286 OCCURRENCE OF CHLAMYDIACEA IN WILD BIRDS

Sandro Stalder¹, Nicole Borel², Sarah Albini³, Hanna Marti⁴, Barbara Renate Vogler⁵

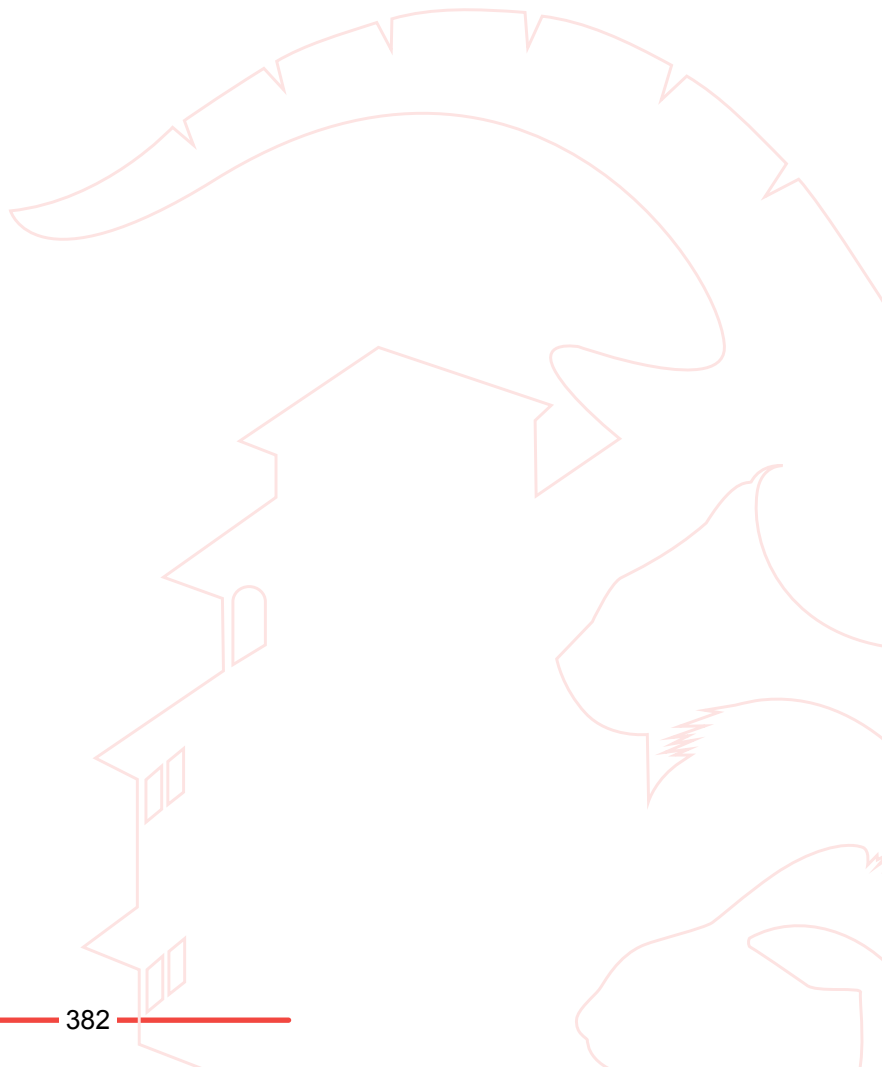
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Keywords: *C. Buteonis*, Chlamydiaceae, *C. Psittaci*/*C. Abortus* Intermediates, Wild Birds

Abstract Text

Wild birds are a known reservoir for several *Chlamydia* species, e.g. *Chlamydia* (*C.*) *psittaci*, *C. abortus*, *C. avium*. Taking into consideration that *C. psittaci* and *C. abortus* are zoonotic pathogens and the zoonotic potential of other *Chlamydia* species is unknown, wild birds shedding these bacteria pose a risk for the health of humans with close contact to these birds. Several studies found genetically intermediate species between *C. psittaci* and *C. abortus* in birds. One of these intermediates, found in a red-shouldered hawk, was recently classified as the new species *C. buteonis*.

This poster presents three studies on the occurrence of Chlamydiaceae in wild birds from Switzerland and from falcons from the United Arab Emirates (UAE), with a special focus on intermediate species. In the first study, 483 samples from 253 corvids and 645 samples from 341 raptors from Switzerland were investigated. Chlamydiaceae were detected in 23.7% of the corvids and 5.9% of the raptors. The most frequently detected chlamydial species were *C. psittaci* 1V in corvids and *C. psittaci* M56 in raptors. In the second study, 449 samples of 339 Swiss wild birds representing 42 species (songbirds, waterfowl and others) were included. Three birds (15%) from the family Columbidae harbored Chlamydiaceae which were identified as *C. psittaci* in two cases. The chlamydial species from the third pigeon could not be further classified. The third study describes the occurrence of *C. buteonis* in gyrfalcons and gyr/peregrine hybrids from the UAE. It is the first report of *C. buteonis* in falcons and on the Arabian Peninsula. Clinical signs in six out of seven falcons such as weakness, vomiting and diarrhea suggest that *C. buteonis* might be pathogenic.





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359 NON-LETHAL SAMPLING TECHNIQUES IN INVERTEBRATES: PRACTICAL REPLACEMENTS AND REFINEMENTS TO IMPROVE INVERTEBRATE WELFARE

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Keywords: Animal Welfare, Coelomic Fluid, Hemolymph, 3Rs

Abstract Text

Wildlife disease monitoring, health surveillance, and research efforts often involve terminally collected samples in invertebrate species. However, lethal sampling may not be sustainable with an increasing number of invertebrate species changing conservation status. It may also become unacceptable due to changing public attitudes and increasing concerns for animal welfare by the scientific and wildlife communities surrounding the limited reported euthanasia methods for invertebrates.

The 3Rs (replacement, reduction, and refinement) were originally developed in 1959 by Russell and Burch to improve laboratory animal welfare but are generally applicable to any situation where animals are under human care or use. In invertebrate research, lethal sampling techniques can be replaced with non-lethal procedures, including collection of hemolymph, coelomic fluid, and tissue biopsies. These sample types provide a non-lethal modality to evaluate invertebrate health and monitor for diseases. Current guidelines for blood draws in mammals limit blood removal to 10% of the total circulating blood volume, but no analogous recommendations exist for invertebrates.

Hemolymph, coelomic fluid, and tissue biopsies are suitable for readily available diagnostics, as well as advanced molecular analyses. In addition to preserving the life of the animal being sampled, these techniques can be further refined to reduce animal stress by minimizing the amount of body fluid or tissue removed, using anaesthetics and analgesics, and improved, non-aversive handling techniques. With best practice methodologies for replacements and refinements, the welfare of invertebrates can be improved while achieving objectives via non-lethal sampling in any diagnostic or research setting.



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210 SPATIAL ANALYSIS OF HEMATOLOGIC VARIABLES AND PATHOGEN DETECTION IN BLANDING'S (*EMYDOIDEA BLANDINGII*) AND PAINTED (*CHRYSEMYS PICTA*) TURTLES IN KANE COUNTY, ILLINOIS

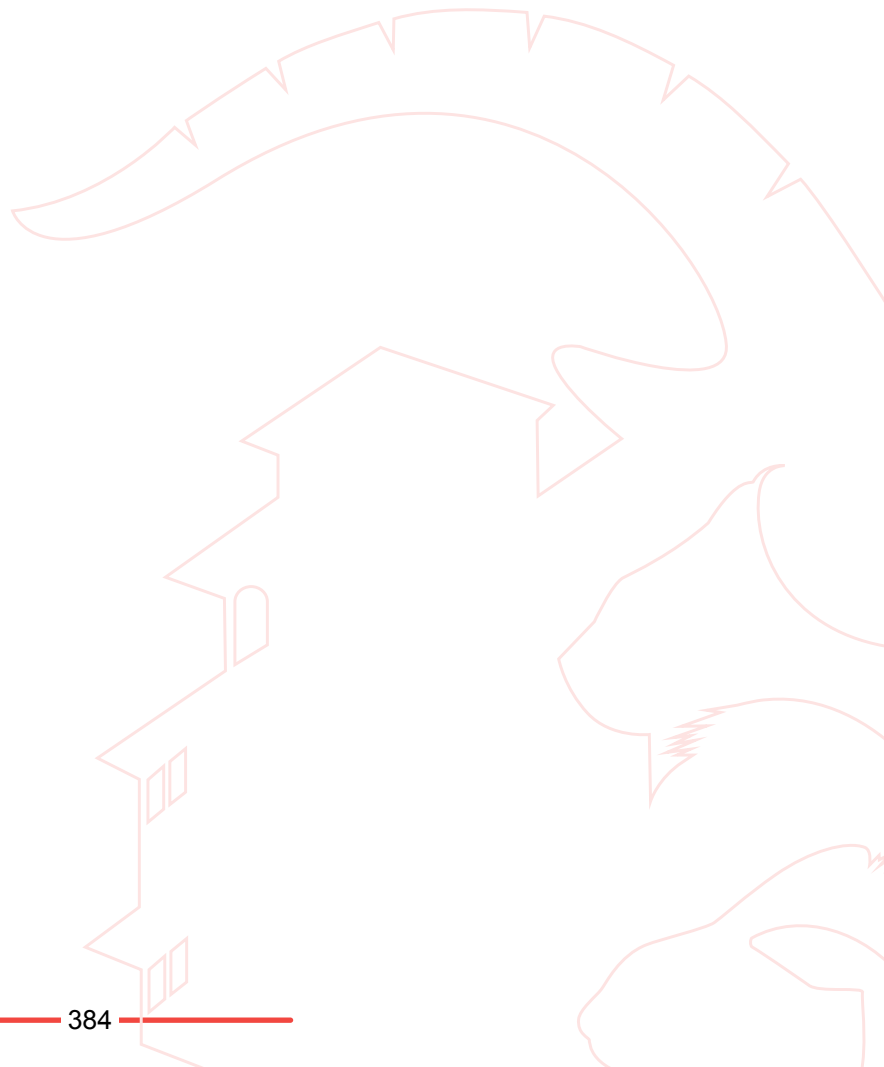
Michelle Waligora¹, Alexis Davidson¹, William Graser², Laura Adamovicz^{1,3}, Emilie Ospina^{1,3}, Matthew Allender^{1,3,4}

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Keywords: Blanding's Turtle, *Chrysemys Picta*, *Emydoidea Blandingii*, Geographical Information Systems, Painted Turtle

Abstract Text

The Blanding's turtle (*Emydoidea blandingii*) is a state endangered chelonian in Illinois. The Kane County Forest Preserve uses mark-recapture and radiotelemetry to monitor their Blanding's and painted turtle (*Chrysemys picta*) populations. Health assessments of both species have been conducted to establish reference intervals for hematology and plasma biochemistries. Blanding's turtles have been utilized as a sentinel species for ecological health. Since 2019, painted turtles have been studied concurrently with Blanding's turtles to determine if they are a suitable surrogate species for determining health and disease prevalence within the local environment. Health parameters and pathogen prevalence data from 48 Blanding's turtles and 73 painted turtles were collected at four sites over a nine-week period, then mapped using geographical information systems (GIS). Hotspot analysis was performed for packed cell volume (PCV), white blood count (WBC), total solids (TS), erythrocyte sedimentation rate (ESR), hemoparasite and ectoparasite presence, and occurrence of positive disease cases. Clusters of values associated with poor health were observed in both species and associated with discreet locations. In painted turtles, a site was identified with a hotspot of disease prevalence and coldspot of PCV. A different site in Blanding's turtles was also detected with a PCV coldspot. Using spatial analysis to identify such areas may help direct the focus for restoration efforts. Establishing a GIS model in Kane County may drive future decisions to release and trap at certain sites as well as detect shifts in ecosystem health across the study area.





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6 EFFECT OF URBAN HABITAT USE ON PARASITISM IN MAMMALS: A META-ANALYSIS

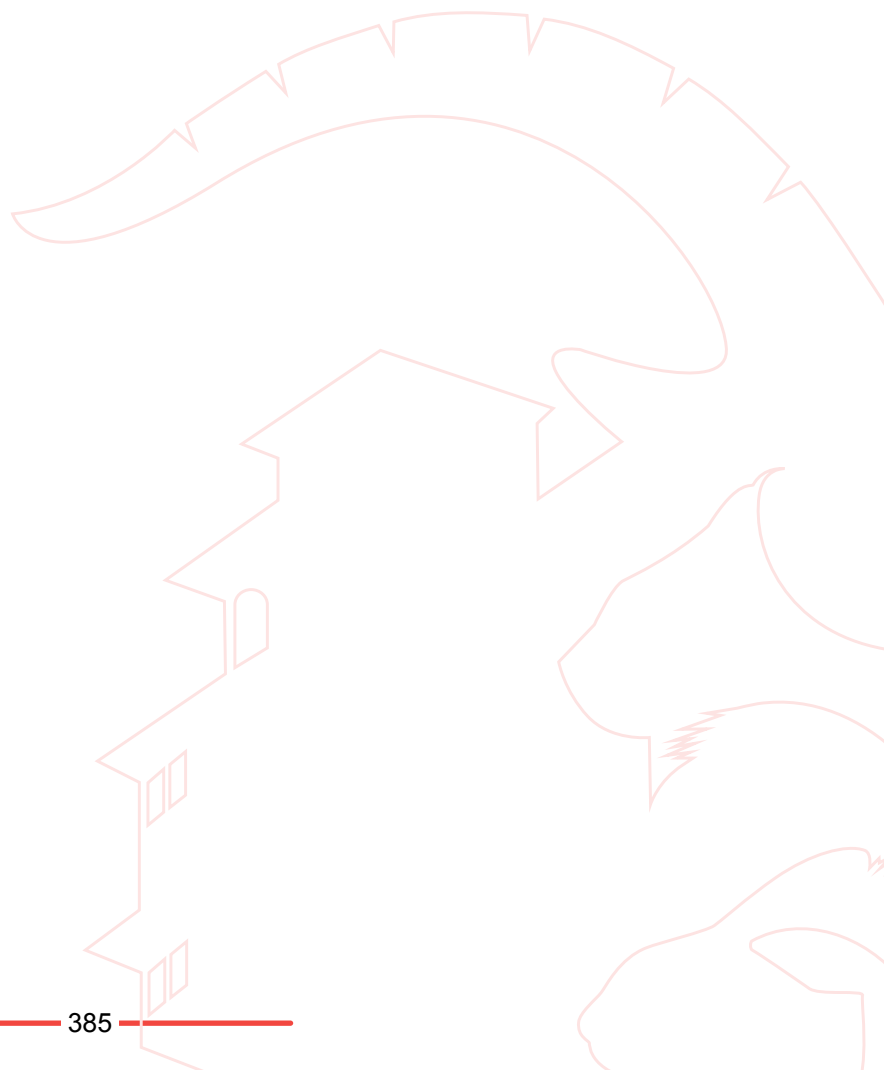
Courtney S. Werner, Charles L. Nunn

Duke University, Durham, United States

Keywords: Meta-Analysis, Parasite, Prevalence, Transmission, Urbanization

Abstract Text

Rates of urbanization are increasing globally, with consequences for the dynamics of parasites and their wildlife hosts. A small subset of mammal species have the dietary and behavioural flexibility to survive in urban settings. The changes that characterize urban ecology—including landscape transformation, modified diets and shifts in community composition—can either increase or decrease susceptibility and exposure to parasites. We used a meta-analytic approach to systematically assess differences in endoparasitism between mammals in urban and non-urban habitats. Parasite prevalence estimates in matched urban and non-urban mammal populations from 33 species were compiled from 46 published studies, and an overall effect of urban habitation on parasitism was derived after controlling for study and parasite genus. Parasite life cycle type and host order were investigated as moderators of the effect sizes. We found that parasites with complex life cycles were less prevalent in urban carnivore and primate populations than in non-urban populations. However, we found no difference in urban and non-urban prevalence for parasites in rodent and marsupial hosts, or differences in prevalence for parasites with simple life cycles in any host taxa. Our findings therefore suggest the disruption of some parasite transmission cycles in the urban ecological community.





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195 EFFECT ON PULMONARY HEALTH OF WHITE-TAILED DEER UNDER PRESENCE OF LUNGWORM

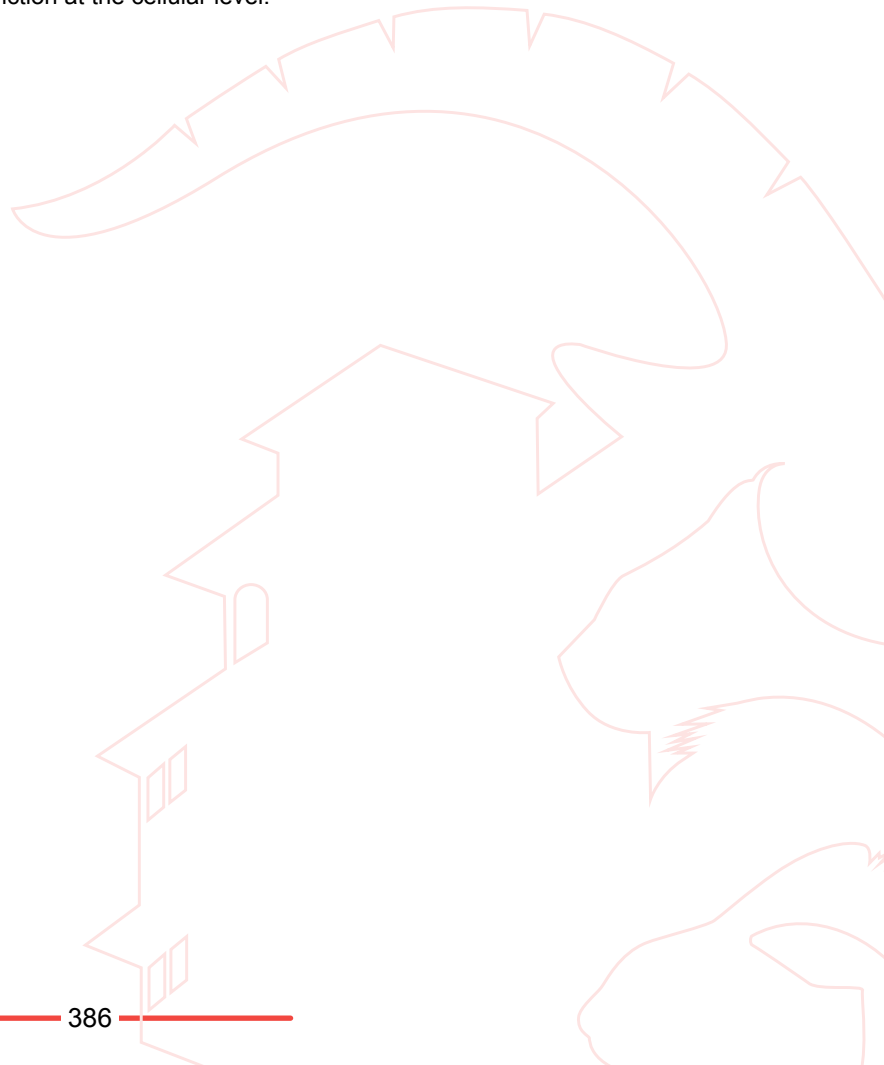
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Keywords: Dictyocaulus Viviparous, Histological Technique, Lungworm, Odocoileus Virginianus, White-Tailed Deer

Abstract Text

Parasite burdens among wildlife populations create sublethal impacts that affect morphological and physiological systems at multiple scales. Dictyocaulid lungworms (*Dictyocaulus viviparous*) is one example of a parasite with the capability to alter the cellular composition within the pulmonary structures of its host. Animals infected may develop pulmonary nematodiasis (lungworm disease), and in advanced stages they may display pneumonia-like symptoms, creating physiological distress and an increasing in the host's vulnerability to subsequent ecological stressors. Our objective was to assess the prevalence of lungworm in white-tailed deer (*Odocoileus virginianus*) in Cobleskill, New York, and to compare cellular structure of lung tissue between healthy and lungworm-infected white-tailed deer. We hypothesized a more pronounced disturbance in cellular components of pulmonary tissue where lungworm was detected. Seven white-tailed deer of different sex-age classes were necropsied following wildlife-vehicle collisions in Schoharie County, New York between March-April, 2021 and sections of lung tissue were extracted, processed, and evaluated using histological technique. We found that lungworm was detected in all specimens. Every subject also indicated a triggered immune response and varied from an acute to chronic inflammatory counterreaction. Some slides indicated other health conditions such as desmoplasia and severe pleuritis. Despite our small sample size, these results suggest that lungworm prevalence is high in white-tailed deer populations in central New York, a largely agricultural area where other lungworm hosts frequently interact with deer. Further, we were able to document that, under the presence of a lungworm infection, pulmonary tissue is altered from its natural composition. These alterations can pose several health concerns that may impact an animal's pulmonary function at the cellular level.





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281 WILDLIFE POISONING IN SWITZERLAND

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Keywords: Barbiturates, Poisoning, Scavenging, Toxicology, Wildlife Mortality

Abstract Text

During the last decades Switzerland experienced population recoveries and successful reintroductions of a large variety of wildlife species. This development was facilitated through an increasing environmental awareness of the general public and governmental conservation actions. However illegal killings of wildlife are still an issue. Poisoning is known as a silent, cheap and easy method to kill and its high risk to harm non-target species including humans makes it especially dangerous. The aim of this study was to get an overview of wildlife poisoning in Switzerland regarding affected species, applied poisons, observed pathologies and spatio-temporal distribution. Our data based on necropsy reports from 20 years (2000-2019) of wildlife diagnostic service performed at the Centre for Fish- and Wildlife Health, Switzerland. Out of 188 suspected cases, suspicion was confirmed through toxicological analyses and circumstantial evidence in 90 cases. Of these, mammals and birds accounted for 35% and 65%, respectively. Red fox (*Vulpes vulpes*), Eurasian lynx (*Lynx lynx*), common buzzard (*Buteo buteo*), pigeon (*Columba sp.*), red kite (*Milvus milvus*) and golden eagle (*Aquila chrysaetos*) were the most frequent victims. Overall 17 different toxic agents were detected, including carbamates (37%), chloralose (16%) and barbiturates (15%). Both case numbers and intoxication incidents increased throughout the study period. The majority of intoxication events (81%) affected more than one animal. Macro- and histopathological findings were typically unspecific. The high proportion of carnivorous species among poisoned wildlife might result from an increased risk of intentional poisonings in humancarnivore conflicts and unintentional poisonings through scavenging. The detection of barbiturates among the three most commonly detected poisons is both surprising and alarming as they are only accessible to medical professionals. These findings suggest that most barbiturate poisonings may have resulted through scavenging on euthanised domestic animals, which highlights the need to increase risk awareness among veterinarians.



285 PREVALENCE, MOLECULAR DIVERSITY, AND EVIDENCE OF ZONOTIC TRANSMISSION OF ENTERIC PROTISTS BETWEEN CAPTIVE NON-HUMAN PRIMATES AND THEIR CARETAKERS IN FOUR SPANISH ZOOS

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Keywords: Captive Primates, Enteric Parasites, Zoo, Epidemiology, Zoonotic Transmission

Abstract Text

The protozoa *Giardia duodenalis* and *Cryptosporidium* spp., the stramenopile *Blastocystis* sp., and the microsporidia *Enterocytozoon bienersi* are among the pathogens able to infect and cause gastrointestinal manifestations both in human and non-human primates (NHP). This study investigated the occurrence, molecular diversity, and zoonotic potential of pathogenic and commensal protist species in captive NHP species.

A molecular-based epidemiological survey was carried out in captive NHP and their caretakers in four Spanish zoological gardens in Madrid (Madrid Zoo Aquarium and Faunia), Cantabria (Santillana del Mar Zoo) and Barcelona (Zoo de Barcelona). Faecal samples (n=326) belonging to 41 NHP species (27 genera) and caretakers (n=62) were collected between October 2018–January 2021. The detection of pathogenic/non-pathogenic protist species was carried out by PCR and Sanger sequencing.

In NHP, *Blastocystis* sp. was the most prevalent species found (27%, range: 14–41%), followed by *G. duodenalis* (19%, range: 14–29%), *Cryptosporidium* spp. (1%, range: 0–3%), and *E. bienersi* (1%, range: 0–1%). Sequence analyses revealed the presence of six subtypes including ST1 (38%), ST5 (21%), ST3 (17%), ST2 (12%), ST4 (5%), and ST8 (2%) within *Blastocystis* sp. (n=89), assemblages A (19%) and B (81%) within *G. duodenalis* (n=16), *C. hominis* (50%) and *C. parvum* (50%) within *Cryptosporidium* spp. (n=4), and genotypes Type IV (50%) and CM18 (50%) within *E. bienersi* (n=2). Non-pathogenic *Entamoeba dispar* (10%) and *Balantioides coli* (2%) were also detected. In caretakers, *Blastocystis* sp. (29%, range: 27–33%), *G. duodenalis* (2%, range: 0–3%), and *Cryptosporidium* spp. (3%, range: 0–7%) were the only pathogenic protist species detected. Evidence of zoonotic transmission involving *Blastocystis* ST1 allele 2, ST2 alleles 11 and 12, and ST4 allele 42 were found.

Asymptomatic infection/carriage of enteric protists is common among NHP and their caretakers. Evidence of zoonotic transmission might be indicative of insufficient personal hygienic practices during animal management and care



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PLEURODELES WALTL
Iberian ribbed newt



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